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How much are isolated relict forest reserves influenced by local and external factors? A case study on vegetation and moths in Northern Italy

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How much are isolated relict forest reserves influenced by local and external factors?

A case study on vegetation and moths in Northern Italy

Titlepage: *Acontia lucida* in Pineta san Vitale. The picture exemplarily stands for the dependence of moths on both: local factors (like the flower serving as nectar resource) and regional characteristics (represented by the landscape in the background). © Britta Uhl.

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1. Abstract

Insect decline has become a widely discussed topic in science and mainstream media in recent years. But besides the general conclusion that insects are disappearing, we often still lack in information what drivers are causing this phenomenon. Multiple predictors are in discussion to negatively affect insect biodiversity. But are some factors more important than others? And how do these multiple predictors influence the different aspects of biodiversity? These are the questions I want to address in my thesis.

I chose 60 study sites situated within two Mediterranean coastal forest reserves in North-eastern Italy – Pineta san Vitale (PsV) and Pineta di Classe (PdC) – that once formed one contiguous coastal forest but are today isolated from each other and surrounded by anthropogenically modified landscapes. By analyzing multiple possible drivers, my aim was to achieve a deeper understanding of how biotic communities in isolated conservation areas are influenced by multiple environmental gradients and how biodiversity in such reserves could be better preserved in future.

First, I analyzed how vegetation is influenced by environmental predictors. Plants, building the first trophic level, are the basis of every terrestrial food-web and therefore are essentially determining, how a habitat looks like and which species of other groups of organisms may colonize it. This is even more important for phytophagous organisms that have direct trophic links with often rather specific host plants. The composition and species diversity of plants can be driven by local circumstances, such as abiotic soil conditions, and landscape-scale attributes, such as land use in the surroundings of a reserve. In the case of my 60 study sites, which all were located within mixed oak and pine forest, plant species richness and functional dispersion at the local site level were positively affected by the proximity to water canals. However, near these canals, there were also more salt tolerating plants and the vegetation was characterized by higher mean nutrient indicator values. Furthermore, mean nutrient indicator values inside the reserves were increasing with higher proportions of agricultural land around the conservation areas. These findings indicate nutrient spill-over as well as salt water intrusion, which both are mainly caused by human actions outside the proper reserves. The amount of anthropogenically modified areas in the surroundings also led to the disappearance of plants with more restricted distributional ranges, being replaced by widely distributed ones. So, landscape-scale human actions might indirectly drive biotic homogenization of plant communities inside conservation areas.

Based on these results, the next question was: Do these findings translate to the next trophic level? How are moths – as an example for a species-rich, mobile, predominately phytophagous insect group – influenced by local and landscape-scale predictors? From 2015 to 2017, I sampled moths at all the 60 locations, using automated light traps. Every site was sampled twice, one time in early summer (June) and one time in late summer (August). In total, 23870 individuals of 392 species (comprising 32 families) were available for analysis.

The first aspect of moth diversity I examined was small-scaled α-diversity and the number of caught individuals per site. To describe the environmental conditions that possibly might affect moth diversity I used 14 local site descriptors, like plant diversity and forest structure, and another 14 landscape-scale factors, like landscape diversity and the proportion of modified areas around light-trapping sites. These 28 factors were condensed through a Principal Component Analysis, resulting in five local and five landscape-scale PC-axes being used as predictors in linear mixed effects models. Small-scaled α-diversity patterns of moths were mainly influenced by local site characteristics. Especially the number of plant species and a near-natural forest structure turned out to positively affect moth diversity. The diversity of nearby natural habitat structures also promoted higher local moth diversity, while landscape character-

istics were less relevant. However, the diversity of near natural landscape elements within a 500-1000m radius positively affected the number of moth individuals. So, while favorable local conditions might be able to preserve the local α-diversity of moths, the landscape context plays a major role for individual numbers and regional γ-diversity. Integrating landscape-scale actions in conservation management therefore might be crucial not only for preserving the regional diversity, but also for maintaining a high number of insects, being important as food resource for higher trophic levels like birds and bats, but also likely relevant as pollinators of many flowering plants.

By zooming into moth species composition (differentiation diversity), I found local and landscape-scale predictors to play equally important roles in shaping moth assemblages. Proportional β-diversity additionally was used to get an insight in how the different predictors affect moth communities. On the local scale, differentiation diversity was correlated to forest age and density. Additionally, mean soil humidity and nutrient content (described via plant indicator values) affected species composition. With the lack of typical forest species at dry, dense and young forest sites, it seems that subtractive heterogenization was the process underlying the observed β-diversity patterns. Looking at the landscape context, moth community composition changes were idiosyncratic relative to the landscape context. For PdC, the proportion of human-modified areas within 500m radius played an important role in shaping moth communities. In PsV, where less agricultural fields occur in the surroundings, the proximity to the industrial harbor of Ravenna significantly affected moth community composition. Here the loss of rare species near urban areas is believed to cause the observed patterns in β-diversity. In conclusion, anthropogenic actions seem to act very specifically on local communities. These findings emphasize that instead of perpetuating generalizations based on large-scale meta-analyses, it is always important to investigate focal areas of interest individually.

In an attempt to link moth community composition with ecosystem functions, I finally analyzed functional richness, redundancy and niche occupation of these insects. Biodiversity erosion can directly affect ecosystem resilience, because species richness itself can be described as the natural insurance capital of an ecosystem. With more species around, there is a higher chance to compensate disturbance, because even if some species disappear, others might take their place and guarantee that the functional niche keeps being occupied. To investigate the functional diversity of moths in PsV and PdC, I collated information on 387 species and 14 ecological traits. The analysis of the functional dendrogram led me to define 25 different functional groups, which were used to score niche occupation and functional redundancy. Similar to my findings on species composition both, local and regional environmental predictors played a significant role for shaping functional diversity. The humidity-nutrient gradient again was the strongest local predictor, but also plant diversity positively affected functional moth richness, redundancy and niche occupation at the site scale. On the landscape scale, landscape diversity around the light-trapping sites was most important. With diverse near-natural landscapes around, functional richness and redundancy was increasing, as well as niche occupancy. Landscape fragmentation, in contrast, had negative effects on the investigated functional components.

Collectively, these findings underline 1) the importance of a near-natural, old grown open forest structure with a well developed understory and a diverse, species rich vegetation on the local scale. Such forests cannot only preserve the local α-diversity, but also might show better ecosystem function and resilience, as they maintain higher functional richness and redundancy. 2) The indispensability of landscape-scale actions for successful conservation management can be concluded throughout all studied aspects of diversity. Landscape diversity does not only play a major role for preserving insect numbers, but also for γ-diversity, functional richness and redundancy. Finally, the analysis of species composition confirmed that landscape-scale anthropogenic impacts do not end at the reserve borders – they also affect biota inside conservation areas. If we want to counteract insect decline, we cannot only rely on isolated conservation area patches. We also have to think about ameliorating management methods towards a more sustainable land use in order to preserve the multifunctionality of ecosystems.

2. Zusammenfassung

Das Insektensterben ist in den letzten Jahren zu einem viel diskutierten Thema in der Wissenschaft und in den Mainstream-Medien geworden. Abgesehen von der allgemeinen Schlussfolgerung, dass Insekten verschwinden, fehlen uns jedoch häufig Informationen darüber, welche Treiber dieses Phänomen verursachen. Zwar werden mehrere Prädiktoren diskutiert welche die Artenvielfalt von Insekten negativ beeinflussen könnten. Aber sind einige dieser Faktoren wichtiger als andere? Und wie beeinflussen diese multiplen Prädiktoren die verschiedenen Aspekte der Biodiversität? Dies sind die Fragen, mit denen ich mich in meiner Arbeit beschäftige.

Ich habe 60 Untersuchungspunkte ausgewählt, die sich in zwei mediterranen Küstenwaldreservaten (Pineta san Vitale (PsV) und Pineta di Classe (PdC)) im Nordosten Italiens befinden. Die beiden Gebiete, die einst Teil eines zusammenhängenden Küstenwaldes waren, sind heute voneinander isoliert und umgeben von anthropogen modifizierten Landschaften. Durch die Analyse mehrerer möglicher Treiber wollte ich ein tieferes Verständnis darüber erlangen, wie biotische Gemeinschaften in isolierten Schutzgebieten durch verschiedene Umweltgradienten beeinflusst werden und wie die biologische Vielfalt in solchen Reservaten in Zukunft besser erhalten werden kann.

Zunächst analysierte ich wie die Vegetation durch Umweltprädiktoren beeinflusst wird. Da Pflanzen die erste trophische Ebene bilden sind sie die Grundlage jedes terrestrischen Nahrungsnetzes, bestimmen im Wesentlichen das Aussehen eines Lebensraumes und welche Arten anderer Organismengruppen diesen besiedeln können. Dies trifft vor allem für phytophage Organismen zu, die direkte trophische Verbindungen zu oft spezifischen Wirtspflanzen haben. Die Zusammensetzung und Artenvielfalt von Pflanzen kann durch lokale Umstände wie abiotische Bodenbedingungen und landschaftliche Merkmale wie Landnutzung in der Umgebung eines Schutzgebiets bestimmt werden. Bei meinen 60 Untersuchungsstellen, die sich alle in Eichen- und Pinienmischwaldhabitaten befanden, wurden der Pflanzenartenreichtum und die funktionelle Streuung auf lokaler Standortebene durch die Nähe zu Wasserkanälen positiv beeinflusst. In der Nähe dieser Kanäle gab es jedoch auch mehr salztolerantere Pflanzen und die Vegetation war durch höhere mittlere Nährstoffindikatorwerte gekennzeichnet. Darüber hinaus stiegen die mittleren Nährstoffindikatorwerte innerhalb der Reservate, wenn ein höherer Anteil landwirtschaftlicher Flächen in der Umgebung zu finden war. Diese Ergebnisse deuten auf einen Eintrag von Nährstoffen sowie auf das Eindringen von Salzwasser hin, wobei beides hauptsächlich durch menschliche Handlungen außerhalb der entsprechenden Reservate verursacht wird. Die Menge der anthropogen veränderten Gebiete in der Umgebung führte auch zum Verschwinden von Pflanzen mit eingeschränkten Verbreitungsarealen, welche durch weit verbreitete Arten ersetzt wurden. Menschliche Handlungen im Landschaftsmaßstab könnten also indirekt die biotische Homogenisierung von Pflanzengemeinschaften in Naturschutzgebieten fördern.

Basierend auf diesen Ergebnissen war die nächste Frage: Lassen sich diese Ergebnisse auf die nächste trophische Ebene übertragen? Wie werden Nachtfalter - als Beispiel für eine artenreiche, mobile, überwiegend phytophage Insektengruppe - von lokalen und landschaftlichen Prädiktoren beeinflusst? Von 2015 bis 2017 habe ich an allen 60 Standorten Nachtfalter mit automatischen Lichtfallen untersucht. Jeder Standort wurde zweimal beprobt, einmal im Frühsommer (Juni) und einmal im Spätsommer (August). Insgesamt standen 23870 Individuen von 392 Arten (bestehend aus 32 Familien) zur Analyse zur Verfügung.

Der erste Aspekt der Nachtfaltervielfalt, den ich untersuchte, waren kleinräumige α-Diversitätsmuster und die Anzahl der gefangenen Individuen pro Standort. Um die Umweltbedingungen zu beschreiben,

die möglicherweise die Nachtfalterdiversität beeinflussen könnten, verwendete ich 14 lokale Standortdeskriptoren wie Pflanzenvielfalt und Waldstruktur sowie weitere 14 Faktoren im Landschaftsmaßstab wie Landschaftsvielfalt und den Anteil von durch den Menschen genutzten Flächen um die Leuchtstandorte. Die 28 Faktoren wurden durch eine Hauptkomponentenanalyse kondensiert, was dazu führte, dass fünf lokale PC-Achsen und fünf PC-Achsen im Landschaftsmaßstab als Prädiktoren in linearen, gemischten Modellen verwendet wurden. Kleinräumige α-Diversitätsmuster von Nachtfaltern wurden hauptsächlich durch lokale Standortmerkmale beeinflusst. Insbesondere die Anzahl der Pflanzenarten und eine naturnahe Waldstruktur wirkten sich positiv auf die Nachtfalterdiversität aus. Die Vielfalt der nahe gelegenen natürlichen Lebensraumstrukturen förderte ebenfalls eine höhere lokale Diversität, während weiterräumige Landschaftsmerkmale weniger relevant waren. Die Vielfalt naturnaher Landschaftselemente in einem Umkreis von 500 bis 1000 m wirkte sich hingegen positiv auf die Anzahl der gefangenen Falter aus. Daraus folgt, dass günstige lokale Bedingungen möglicherweise die lokale α-Diversität von Nachtfaltern bewahren können, während der Landschaftskontext eine wichtige Rolle für die Individuenzahl und die regionale γ-Diversität spielt. Die Integration von Maßnahmen auf Landschaftsebene in das Naturschutzmanagement könnte daher nicht nur für die Erhaltung der regionalen Diversität von entscheidender Bedeutung sein. Landschaftsdiversität gewährleistet auch eine hohe Insektenanzahl, welche als Nahrungsquelle für höhere trophische Ebenen (beispielsweise Vögel und Fledermäuse) wichtig ist, und darüber hinaus durch die Bestäubungsleistung Relevanz für viele Blütenpflanzen hat.

Durch die nähere Betrachtung der Zusammensetzung der Nachtfaltergemeinschaften (Differenzierungsdiversität) fand ich heraus, dass Prädiktoren auf lokaler und landschaftlicher Ebene eine gleich wichtige Rolle für die Artenzusammensetzung zu spielen scheinen. Die proportionale β-Diversität wurde zusätzlich verwendet, um einen Einblick zu erhalten, wie sich die verschiedenen Prädiktoren auf Nachtfaltergemeinschaften auswirken. Auf lokaler Ebene war die Differenzierungsdiversität vor allem mit dem Alter und der Dichte der Wälder korreliert. Zusätzlich beeinflussten die durchschnittliche Bodenfeuchtigkeit und der Nährstoffgehalt (beschrieben über Pflanzenindikatorwerte) die Artenzusammensetzung. Angesichts des Fehlens typischer Waldarten an trockenen, dichten und jungen Waldstandorten scheint die subtraktive Heterogenisierung der Prozess zu sein, der den beobachteten β-Diversitätsmustern zugrunde liegt. Mit Blick auf den Landschaftskontext waren die beobachteten Unterschiede in der Zusammensetzung der Nachtfaltergemeinschaft sehr eigenwillig. Für PdC spielte der Anteil der vom Menschen veränderten Gebiete im Umkreis von 500 m eine wichtige Rolle bei der Zusammensetzung der Nachtfaltergemeinschaften. In PsV, wo weniger landwirtschaftliche Felder in der Umgebung vorkommen, wirkte sich die Nähe zum Industriehafen von Ravenna erheblich auf die Zusammensetzung der Nachtfaltergemeinschaft aus. Hier wird angenommen, dass der Verlust von Arten in der Nähe von anthropogen geprägten Gebieten die beobachteten Muster in der β-Diversität verursacht. Zusammenfassend scheinen anthropogene Einflüsse sehr spezifisch auf lokale Gemeinschaften zu wirken. Diese Ergebnisse unterstreichen die Wichtigkeit, Flächen individuell zu untersuchen, anstatt fortlaufend Verallgemeinerungen auf der Grundlage umfangreicher Metaanalysen zu suchen.

Um die Zusammensetzung der Nachtfaltergemeinschaft mit der Ökosystemfunktion zu verknüpfen, analysierte ich schließlich die funktionelle Diversität, Redundanz und Nischenbesetzung dieser Insekten. Die Erosion der biologischen Vielfalt kann sich direkt auf die Widerstandsfähigkeit des Ökosystems auswirken, da der Artenreichtum selbst als „natural insurance capital“ eines Ökosystems bezeichnet werden kann. Wenn mehr Arten vorhanden sind, besteht eine höhere Wahrscheinlichkeit, Störungen zu kompensieren, denn selbst wenn einige Arten verschwinden können andere ihren Platz einnehmen und sicherstellen, dass die funktionelle Nische weiterhin besetzt ist. Um die funktionelle Diversität von Nachtfaltern in PsV und PdC zu untersuchen, habe ich Informationen zu 387 Arten und 14 ökologischen Merkmalen zusammengestellt. Durch die Analyse des funktionellen Dendrogramms konnte ich 25 verschiedene funktionelle Gruppen definieren, die zur Bewertung der Nischenbesetzung und der funktionellen Redundanz verwendet wurden. Ähnlich den Ergebnissen zur Artenzusammensetzung spielten sowohl lokale als auch regionale Umweltprädiktoren eine wichtige Rolle für die funktionelle Diversität. Der Feuchtigkeits-Nährstoff-Gradient war erneut der stärkste lokale Prädiktor, aber auch die Pflanzenvielfalt wirkte sich positiv auf den funktionellen Reichtum der Nachtfalter, die Redundanz und die Nischenbesetzung aus. Im Landschaftsmaßstab war die Landschaftsdiversität um die Leuchtstandorte am wichtigsten. Mit verschiedenen naturnahen Landschaften nahmen funktioneller Reichtum und Redundanz sowie die Nischenbesetzung zu. Die Landschaftsfragmentierung hatte dagegen negative Auswirkungen auf die untersuchten Komponenten funktioneller Diversität.

Zusammenfassend unterstreichen diese Ergebnisse 1) die Bedeutung einer alten, naturnahen und lichten Waldstruktur mit gut entwickelten Unterholz und einer vielfältigen, artenreichen Vegetation. Solche Wälder können nicht nur die lokale α-Diversität bewahren, sondern zeigen auch verbesserte Widerstandsfähigkeit und Ökosystemfunktion, da sie höheren funktionellen Reichtum und höhere funktionelle Redundanz aufweisen. 2) kann die Unentbehrlichkeit von Maßnahmen im Landschaftsmaßstab für ein erfolgreiches Naturschutzmanagement in allen untersuchten Aspekten der Diversität festgestellt werden. Die Landschaftsvielfalt spielt nicht nur eine wichtige Rolle für die Erhaltung der Insektenzahlen, sondern auch für die γ-Diversität, den funktionellen Reichtum und die funktionelle Redundanz. Schließlich bestätigte die Analyse der Artenzusammensetzung, dass anthropogene Auswirkungen im Landschaftsmaßstab nicht an den Schutzgebietsgrenzen enden, sondern auch die Lebewesen in Schutzgebieten beeinflussen. Wenn wir dem Rückgang von Insekten entgegenwirken wollen, können wir uns nicht nur auf isolierte Schutzgebiete verlassen. Wir müssen auch darüber nachdenken, die Bewirtschaftungsmethoden für eine nachhaltigere Landnutzung zu verbessern, um die Multifunktionalität von Ökosystemen zu erhalten.

3. List of manuscripts included in this thesis with statement on personal contribution

Chapter 6: Local, forest stand and landscape-scale correlates of plant communities in isolated coastal forest reserves (2020) Plant Biosystems: 1-13.
DOI: https://doi.org/10.1080/11263504.2020.1762776
Britta Uhl, Mirko Wölfling, Konrad Fiedler

Personal contribution:

- Field work and identification of plants
- Sampling of local environmental variables and analysis landscape composition
- Statistical analysis under supervision of Konrad Fiedler
- Literature survey, figure preparation, drafting and co-writing of the manuscript

Chapter 7: Understanding small-scale insect diversity patterns inside two nature reserves - the role of local and landscape factors (2020) Biodiversity and Conservation 29 (7): 2399-2418.
DOI: https://doi.org/10.1007/s10531-020-01981-z
Britta Uhl, Mirko Wölfling, Konrad Fiedler

Personal contribution:

- Field work and identification of moths
- Sampling of local environmental variables and analysis landscape composition
- Statistical analysis under supervision of Konrad Fiedler
- Literature survey, figure preparation, drafting and co-writing of the manuscript

Chapter 8: From forest to fragment: Compositional differences in coastal forest moth assemblages and their environmental correlates (submitted)
Britta Uhl, Mirko Wölfling, Konrad Fiedler

Personal contribution:

- Field work and identification of moths
- Sampling of local environmental variables and analysis landscape composition
- Statistical analysis under supervision of Konrad Fiedler
- Literature survey, figure preparation, drafting and co-writing of the manuscript

Chapter 9: Qualitative and quantitative loss of habitat at different scales affects functional moth diversity within two Mediterranean conservation areas (submitted)
Britta Uhl, Mirko Wölfling, Konrad Fiedler

Personal contribution:

- Field work and identification of moths
- Sampling of local environmental variables and analysis landscape composition
- Statistical analysis under supervision of Konrad Fiedler
- Literature survey, figure preparation, drafting and co-writing of the manuscript

4. Selection of already published contributions

- Uhl, B. and Wölfling, M. (2015). Anthropogenic influences on the condition of Pinus pinea L. and Quercus robur L. in Pineta san Vitale (Ravenna, Italy). *Journal of Mediterranean Ecology 13*: 5-12.

- Uhl, B., Wölfling, M., Fiala, B., Fiedler, K. (2016). Micro-moth communities mirror environmental stress gradients within a Mediterranean nature reserve. *Basic and Applied Ecology 17*: 273-281. https://doi.org/10.1016/j.baae.2015.10.002

- Wölfling, M., Becker, M. C., Uhl, B., Traub, A., Fiedler, K. (2016). How differences in the settling behaviour of moths (Lepidoptera) may contribute to sampling bias when using automated light traps. *European Journal of Entomology 113*: 502-506. https://doi.org/10.14411/eje.2016.066

- Wölfling, M., Uhl, B., Fiedler, K. (2019). Multi-decadal surveys in a Mediterranean forest reserve–do succession and isolation drive moth species richness? *Nature Conservation 35*: 25-40. https://doi.org/10.3897/natureconservation.35.32934

- Uhl, B., Wölfling, M., Fiedler, K. (2020). Understanding small-scale insect diversity patterns inside two nature reserves: the role of local and landscape factors. *Biodiversity and Conservation 29*: 2399-2418. https://doi.org/10.1007/s10531-020-01981-z

- Uhl, B., Wölfling, M., Fiedler, K. (2020). Local, forest stand and landscape-scale correlates of plant communities in isolated coastal forest reserves. *Plant Biosystems (in press)*: 1-13. https://doi.org/10.1080/11263504.2020.1762776

- Wölfling, M., Uhl, B., Fiedler, K. (2020). Ecological drift and directional community change in an isolated Mediterranean forest reserve – larger moth species under higher threat. *Journal of insect science* (in press). doi: 10.1093/jisesa/ieaa097

5. Introduction

5.1 Global biodiversity loss in the Anthropocene

As long as our planet exists, humans are the only species changing the Earth's ecosystems and climate so fast that a new earth age is supposed to be named after one single species: The Anthropocene. Although it is not easy to define when exactly we started to take that influential role in the global biome (Lewis & Maslin 2015), it is undisputed that human actions altered global water and nutrient cycles, carbon storage and climate (Kroeze et al. 2013; Ripple et al. 2019; Sanderman et al. 2017). By doing so, we exploited Earth's resources, pushing terrestrial biodiversity beyond its planetary boundary (Newbold et al. 2016) and inducing the sixth mass extinction in Earth's history (Ceballos et al. 2015).

Biodiversity loss can be detected in many taxa, e.g. in plants (Pimm & Raven 2017), insects (Bell et al. 2020; Habel et al. 2019a; Leather 2018), fish (Hutchings & Reynolds 2004), and terrestrial vertebrates such as amphibians, reptiles, birds and mammals (Ceballos et al. 2017). Being one of the most severe problems of our times, the loss of diversity itself can affect ecosystem function and resilience and will also loop back on human health and well-being, as important ecosystem services get lost along with species that go extinct (Oliver et al. 2015).

The easiest example of human dependence on biodiversity can be seen by looking at insects: This species rich group interacts with humans in many ways, offering one of the most important ecosystem services: Pollination of angiosperm plants. 35% of our food resources are directly depending on insect pollination (Klein et al. 2007), and most of the nutrients being important for an adequate human diet, like vitamin C and A, calcium and folic acid, are supplied by animal pollinated plants (Eilers et al. 2011). The economic value of this ecosystem service therefore is estimated at 153 billion € (172 billion $) worldwide (Gallai et al. 2009). Besides pollination, insects are very important for pest control (Kremen & Chaplin-Kramer 2007), as the occurrence of insect herbivores is often balanced by predatory and parasitoid pressure (Gould et al. 1990; Maron & Harrison 1997; Thies et al. 2011). Disturbing the complex interplay between herbivores and predators can lead to herbivore mass reproductions, affecting agricultural and forest management (Myers et al. 1989; Rusch et al. 2016). Hence, the valuation of natural pest control potential, e.g. in agricultural systems, is estimated between 48 – 888.9 billion € (54 billion – 1 trillion $) worldwide (Naylor & Ehrlich 2012).

However, insects recently have become ever less in their biomass, abundance and diversity (Hallmann et al. 2017; Seibold et al. 2019). Although there are many drivers in discussion for causing these dramatic insect declines (Habel et al. 2019a), our current knowledge about the multiple factors causing insect loss is still limited (Saunders 2019). How do different environmental variables and scales of effect contribute to diversity loss? And are different aspects of diversity also differentially affected? These and other questions need to be considered closely, to ameliorate our understanding of insect diversity loss in the Anthropocene.

5.2 Understanding ecosystem complexity

An "ecosystem" is defined by the UN Convention on Biological Diversity as a dynamic complex of plant, animal and micro-organism communities and their non-living environment interacting as a functional unit (CBD 1992). Besides basic aspects like the position of any system with respect to climate zones and geological properties, a great number of local and regional factors determine natural areas and the organisms living there. Local abiotic conditions fundamentally determine which biota from a regional species pool may colonize a given location. In terrestrial ecosystems, light availability is as important as water supply, nutrient availability or microclimatic conditions. All the protagonists of the biocenosis, namely the microbiome, fungi, plant communities and animals, interact with the abiotic compounds but also with each other at different levels. On the regional scale, landscape composition and configuration plays an important role for distributional patterns of organisms. For example, the amount and connectivity of habitats are key factors determining species distribution in metapopulation theory (Legrand et al. 2017). Hence, due to this complexity ecosystems until today pose a challenge to scientific investigation.

Furthermore, biodiversity itself is an important attribute of all ecosystems. The regional species pool, viz. γ diversity, can be seen as “natural insurance capital” (Yachi & Loreau 1999), which means that with an increasing biodiversity, there is an increasing pool of species that makes an ecosystem more capable to react on environmental change. The regional γ-diversity therefore plays a key role for ecosystem functioning and resilience (Oliver et al. 2015), what underlines the importance of landscape-scale actions to counteract regional-scale diversity loss (Landis 2017). Besides, the number of species and their abundance distribution on the local scale, which is commonly known as α-diversity, also plays an important role for conservation ecology and management. Studies of α-diversity can reveal both, locally important and species-rich habitats and small-scale species losses due to environmental constraints.

Both, α- and γ-diversity can be summed up as inventory diversity measures, giving information on how many species can be found at the local and regional scale (Jurasinski et al. 2009). In contrast, β-diversity measures can give insight into species turnover. However, β-diversity always has been used as term for many different aspects of species composition and turnover and was ever since the introduction of the term by Whittaker (1960) lacking in a clear definition (Tuomisto 2010). Relating α-diversity to the larger scale γ-diversity, β-diversity originally describes a multiplicative or additive partitioning value (Anderson et al. 2011). Nowadays, this concept is more clearly defined as “proportional” (Jurasinski et al. 2009) or - in the case of multiplicative partitioning - “true” β-diversity (Tuomisto 2010). Investigations on the change in species composition are throwing a light on another aspect of β-diversity, which is called differentiation- or variation diversity (Anderson et al. 2011; Jurasinski et al. 2009). This aspect can be used to assign the variation in community structure to different environmental factors and is recently the most often studied aspect of β-diversity (Jurasinski et al. 2009).

Nevertheless, inventory diversity measures such as α- and γ-diversity, as well as proportional and differentiation β-diversity measures do not give any information about a species’ role in an ecosystem. In species richness and alpha diversity measurements, all species are treated as being equal and their function remains beyond consideration (Bengtsson 1998). The resilience of an ecosystem in relation to external disturbances and stress factors can be defined more precisely by zooming into species functions. Functional diversity takes into account which ecological niche is occupied by the different species. So, species are viewed through their functional traits, viz. their physiological and ecological characteristics. With more functional redundancy, which means more species occupying the same or very similar ecological niches, the resilience of an ecosystem increases, as species with similar ecological functions might react differently to environmental perturbations and some representatives might survive ecosystem changes (Oliver et al. 2015).

5.3 Effects of human actions on biodiversity

So, how do anthropogenic actions affect biodiversity? Human kind nowadays has altered most of the terrestrial areas. About 75% of the Earth's land surface is believed to face direct or indirect anthropogenic influences that more or less affect local ecosystems and biodiversity (Venter et al. 2016). Land use change therefore is recognized as the biggest threat to biodiversity (Newbold et al. 2015), because local communities cannot react properly on the fast and severe alterations in ecosystem structure. The different facets of land use change comprise multiple aspects of human interventions directly threatening biotic communities on site (α-diversity), such as increased pesticide use (Hahn et al. 2015), intensified management (Allan et al. 2015; Habel et al. 2019b) or urbanization (van Klink et al. 2020). But also nearby semi-natural habitats can be affected indirectly by land use, due to pollutant (Zvereva & Kozlov 2010) and pesticide drift (Botías et al. 2019; Botías et al. 2016; Zivan et al. 2016) or eutrophication after nutrient influx (Carvalheiro et al. 2020; Haddad et al. 2000). Finally, also light pollution plays a role for diversity loss, even though mainly affecting nocturnal animals (Owens et al. 2020; Owens and Lewis 2018).

On the landscape level, land use change often results in landscape simplification which leads to a regional scale biotic and functional homogenization (Gámez-Virués et al. 2015). Reduced regional γ-diversity furthermore can affect local communities, as with a diminished landscape-wide species pool, fewer species are available for inhabiting a biotope or re-occupy a habitat after environmental change (Tscharntke et al. 2012). Biotic homogenization therefore can have severe effects on ecosystem resilience and might reduce ecosystem function (Van Der Plas et al. 2016; Fig. 5.1).

As a side effect of landscape simplification, remaining near-natural habitats become ever more fragmented, by losing area and having reduced connectivity between habitat patches. Smaller and isolated habitat patches often fail in being able to preserve particularly the more specialized species (Keinath et al. 2017; Slade et al. 2013) and face further threats such as edge effects (Haddad et al. 2015), and reduced genetic diversity due to disrupted gene flow between populations (Habel & Schmitt 2018).

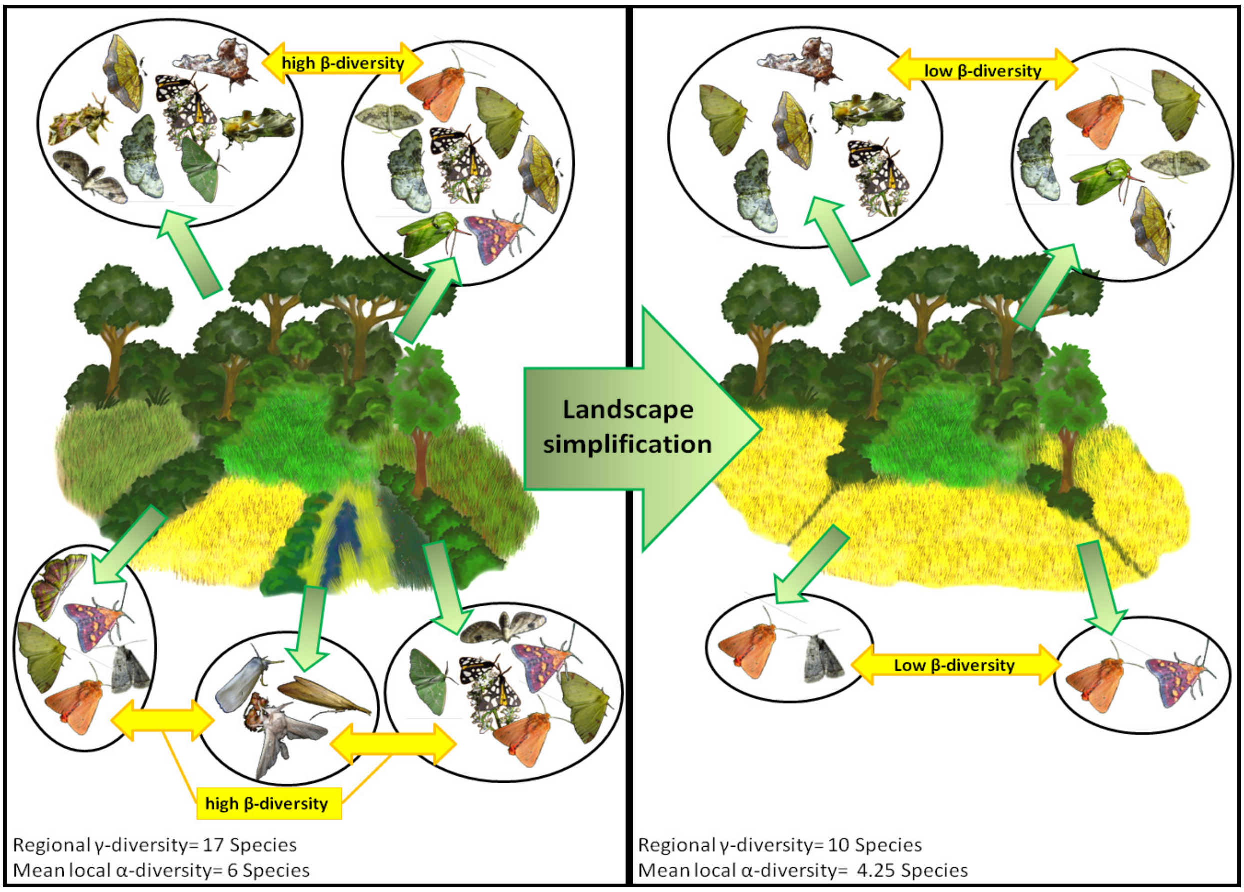

Figure 5.1: Schematic overview of the effects of landscape simplification on different aspects of insect biodiversity. With fewer habitats available in the surroundings, there is a reduced regional species pool (visualized above by the disappearance of open grassland and reed habitat species) resulting in lower γ-diversity. Additionally, regional-scale species turnover (β-diversity) decreases as there are fewer different habitats. With the local species assemblage being dependent on the available regional species pool, also α-diversity decreases. Additionally, increased edge effects due to fragmentation might drive species extinctions on the small-scale.

5.4 Study area

The Mediterranean Basin as one of the global biodiversity hotspots is supposed to receive special appreciation in conservation activities (Myers et al. 2000), but faces manifold threats on natural areas, such as climate change (Appiotti et al. 2014) and increased human activities (Venter et al. 2016), leading to habitat loss (Barredo et al. 2016) and land use change (Falcucci et al. 2006).

Climate change has particularly severe effects on the Mediterranean region, such as increasing air temperatures in all seasons and decreasing rainfall in winter, spring and summer (Appiotti et al. 2014). This leads to ever longer drought periods in spring and summer and more extreme storm events in autumn and winter (Giambastiani et al. 2017). The increasing drought affects hydrology and consequently leads to land degradation, weakens vegetation regeneration ability, is correlated to microbial carbon loss and also affects heavy metal contamination in surface waters through altered biochemistry processes between water sediments and water (Colombani et al. 2016; Doblas-Miranda et al. 2017; Tsiafouli et al. 2018). Moreover, increased summer drought fosters the risk of recurrent forest fires (Moriondo et al. 2006).

Land use change is another constraint affecting biodiversity in the Mediterranean region. However, it is not human land use per se that threatens local ecosystems. In fact, human activities have shaped landscapes and ecosystems of the Mediterranean basin for millennia (Brooks et al. 2002). Although today only 4.6 % of primary vegetation is remaining, the long time of different traditional land use practices also is one reason for the great environmental diversity (Blondel 2006). The loss of these particular traditional farming practices, both through land use intensification or abandonment, affects Mediterranean landscapes and alters habitat structures within this biodiversity hotspot (Falcucci et al. 2006).

Taking a look at my study region of interest, the plain of river Po, located in northern Italy with its delta at the Adriatic coast side, is a good example for an intensively used and densely populated Mediterranean region. With 30 000 km² of land area (36% of Italy's agricultural production) being used for agriculture (Manieri 2009) on the one hand, and the big national park of the Po Delta with 536.53 km² of conservation area (Ente di gestione per i Parchi e la Biodiversità 2020) on the other hand, the region is characterized by strong contrasts. Especially near the coast, high human population densities, more urban areas and an ever growing tourism industry impacts remaining near natural areas and threatens biodiversity (Falcucci et al. 2006).

Additionally, the whole region is affected by land subsidence, as an effect of groundwater pumping and off-shore gas production. In recent times, average subsidence rates have decreased, but still the land drops by about 2.7 mm/year (Teatini et al. 2005). As a consequence the region has also to deal with soil salinization because hydraulic gradients between freshwater reservoirs and seawater are changing. Heavy drainage systems, the limited precipitation rates in summer and increasing surface water evaporation even enhance this effect (Giambastiani et al. 2007; Mollema et al. 2010). Increasing soil salinity prompts changes in plant species richness and diversity (Antonellini & Mollema 2010), alters plant community composition (Gerdol & Viciani 2018), is correlated with lower crown density of oak and pine trees (Uhl & Wölfling 2015) and leads to differences in ectomycorrhizal communities of declining oak trees (Montecchio et al. 2004).

My own thesis research focused on two coastal pine forest reserves, namely Pineta san Vitale (PsV) and Pineta di Classe (PdC) (Fig. 5.2). These two reserves, which cover an area of about 9 km² each, form two isolated southern parts of the biosphere reserve and national park "Parco regionale del Delta del Po" and they have attained high legal conservation status, protected as important Bird and Natura 2000 area (Po Delta, United Nations Educational Scientific and Cultural Organisation 2015; BirdLife International 2018; Joint Nature Conservation Committee 2017a, 2017b).

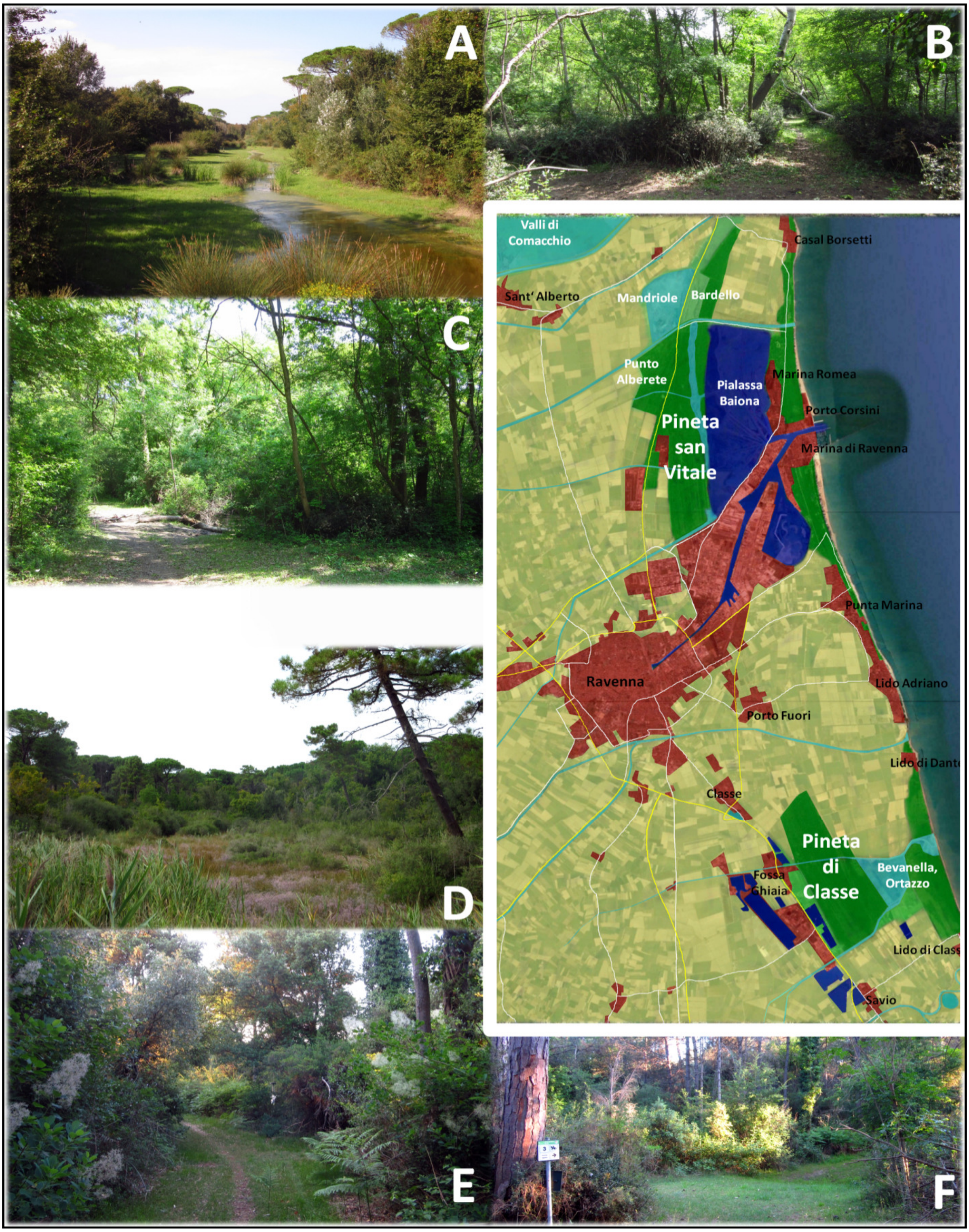

Figure 5.2: Map of the study region (right) and the two reserves Pineta san Vitale and Pineta di Classe. Urban areas are red (and named in black), agricultural fields are yellow. Natural areas (named in white) are dark green (forest), light green (open grassland) and turquoise (reed and shallow waters). Open water bodies are dark blue. The pictures exemplarily show habitats in Pineta san Vitale (A: general overview, B: the light trap site V6 with dense *Ruscus aculeatus* understory, C: site V10) and Pineta di Classe (D: general overview, E: site C23 with a mixed understory consisting of *Cotinus coggygria* and *Pteridium aquilinum*, F: site C27, with evergreen understory built up by *Phillyrea angustifolia* and *Quercus ilex*).

As both areas are believed to have been inter-connected in the 18th century, they represent two remaining fragments of an initially large-scaled, 36 km long, contiguous, near-natural coastal forest, with similar bedrock (mostly sandy ground) and similar historical development in terms of human utilization. The geological development of the area took a new trajectory from the 5th century onwards, when the coastline changed. Both forest sites have grown on paleodunes, which is also decisive for the potential natural vegetation of the two reserves (Lazzari et al. 2010). On top of each paleodune, dry soil conditions lead to the establishment of a mix of downy oak and pine forest as potential climax vegetation, being also the dominant habitat structure today inside the two reserves. Where the forest is not so dense or at forest clearings, open grass vegetation occurs in patches. In the shallow valleys more humid areas can be found, with hygrophilous forest sites and open reed vegetation. Along the human-made canal systems and at flooded sites, also reed vegetation can be found.

Even though the pine forests where once man made to produce wood and pine seeds, long times of succession after abandoning traditional land use forms and subsequent protection of the pine woods rendered both sites into typical Mediterranean, near-naturally structured forests, providing habitat for many plant and animal species. The two forest relicts are nowadays divided by the harbor and industry zone of Ravenna and are surrounded by agricultural land and open habitats. The degree of isolation has increased over the past centuries, as for the end of the nineteenth century, larger forest areas with small forest patches between PsV and PdC were still documented. The last records of habitat loss can be traced back to the 1930ies, when the industrial area of Ravenna was developed and the southern parts of ancient PsV were therefore logged (Malfitano 2002).

Also land subsidence and subsequent soil salinization (see above) have today severe impacts on the reserves. Chemical analyses of the groundwater reservoirs in PsV have indicated influx of hypersaline water from the neighboring lagoon “Pialassa Baiona”, as a result of changed hydraulic gradients caused by freshwater pumping (Mollema et al. 2013). This leads to water salinity values of up to 22 g/l, especially near the lagoon and in vicinity to the Lamone river (Antonellini et al. 2008). In PdC, with its low hydraulic conductivity and a freshwater table 2m above sea level, salinity values are much lower, with about 0.4 to 6 g/l in the surface waters of the reserve (Antonellini et al. 2008). Seawater intrusion is further weakened here by a natural dune system along the coast side neighboring PdC, but nevertheless the ground water bodies, which have distinct fresh water imprint, are saline or brackish (Mollema et al. 2013).

The isolated location with the surrounding landscape being anthropogenically over-used and distorted at large scales might affect the areas negatively. This entire situation likely threatens the sensitive forest ecosystem. Nutrient influx in terrestrial systems of the Po delta region is to date not well studied. Pollution and pesticide emissions have been partly investigated, but also remain incompletely understood (Antisari et al. 2009; Lucialli et al. 2007).

Collectively, all these influences from the surrounding landscape, as well as the isolated and fragmented nature of the two pine forest remnants, stimulate to ask whether under current circumstances these areas still may effectively serve their function as a refuge for threatened Mediterranean biodiversity. This also leads to address the question to what extent local factors (that might be amenable to conservation management on site) or rather regional to landscape-level processes (that cannot be solved through conservation planning) are the essential drivers of biota in the two study areas.

5.5 Main hypotheses of this work

In my thesis, I address multiple aspects affecting isolated nature reserves. The main focus will deal with nocturnal Lepidoptera (moths, viz. Macroheterocera and the so-called "micro-moths"), as representatives for species rich, relatively mobile and predominately phytophagous insect groups. Moths are an important part of an ecosystem as pollinators, herbivores and as prey for insectivorous animals. This large insect group can easily be surveyed by light traps, can be sampled in great numbers to achieve a solid database for later statistical analysis, and offer a wide variety of specialist and generalist herbivore or, more rarely, detritivore species. Furthermore, moths have often been successfully used in earlier studies investigating biotic responses to environmental gradients at various spatial scales (Luque et al. 2011; Mangels et al. 2017). Vegetation, as an important local factor for moth communities, will also be analyzed. Specifically, in my thesis I addressed the following hypotheses:

I expected plant communities to be mainly determined by local factors like soil conditions or microclimate, but local plant richness or species composition can be further modulated by land use in the surrounding landscape matrix.

- Vegetation inside the reserves is not primarily determined by the surrounding landscape (viz. there is no landscape modulated plant species pool affecting variation of vegetation inside the forests). Instead, most plants within the relict forests are remains of the previously contiguous, coastal forest with only few species originating from outside the reserves.
- However, land use in adjacent areas has effects on vegetation, because of nutrient influx and altered soil conditions. Hence variation in mean Ellenberg indicator values as well as in plant species composition is expected when the proportion of human-modified areas within the surroundings of the sampling sites increases.

In contrast, I expected communities of moths, which are more mobile than plants, to be roughly equally shaped by local and landscape-scale characters. Specifically I test the following predictions:

- PsV has higher moth α-diversity and subsequently also higher γ-diversity than PdC, even though it is more affected by pollution and soil salinity. Surrounding landscapes and the habitats inside the park are more heterogeneous and so “dissimilarity of local communities determines biodiversity and overrides negative local effects” (following Tscharntke et al. (2012)).
- In general, moth α-diversity across all 60 sites is positively influenced by plant diversity, a near-natural forest structure and the diversity of near-natural areas on the landscape scale.
- Moth species turnover (proportional/true β-diversity) is mostly determined by local vegetation structure, while moth community composition (differentiation/variation β-diversity) is influenced by local and landscape-scale variables alike.
- Functional composition of Lepidoptera is changing along the different gradients, depending on the local vegetation and the landscape-scale habitat availability.
- Strongly disturbed sites show higher species turnover (subtractive heterogenization sensu Socolar et al. (2016)) and reduced functional niche occupation.

5.6 Study design

To be able to determine small-scale changes across communities, each reserve was divided into thirty 600x600m² quadratic cells. Inside each of these quarters, a location suitable for light-trapping of moths was selected as study site. For selection, the sites had to be located at habitats with downy oak and pine forest mix with at best 100m distance to other habitats, they had to be fairly accessible from one of the numerous forest pathways, and they should be located at small forest clearings or pathway crosses, to enhance light trap efficiency by avoiding flight barriers like dense bushes or trees.

At each location, I tried to collate a multitude of environmental information, to characterize the pertinent habitat. Abiotic factors were considered by taking five surface soil samples four times a year (April, June, August and September) around the light trap location at each of the 60 sites. Average values of the soil pH-value and of electric conductivity (EC) were then obtained from twenty replicate measurements per site. Through EC values, mean surface soil salinity could be calculated. Compared to the surface water salinity maps provided by Antonellini et al. (2008), my measured surface soil salinity values mainly agreed with the suggested surface water values of the maps, indicating that not only water inside the reserves is salinated, but also the surface soil.

Tree crown density was determined using a densitometer. For this purpose, four densiometer reads (one in each cardinal direction) were made in spring, early summer, high summer and late summer at every site (Fig. 5.3). Temperature was measured during the moth sampling nights using data loggers.

Figure 5.3: Left: Densiometer analysis in Pineta san Vitale; right: herb layer analysis in Pineta san Vitale.
Photos: Britta Uhl and Mirko Wölfling

For vegetation analysis, three vegetation layers were investigated. The herb and shrub layer was characterized using the Braun-Blanquet method (Braun-Blanquet 1951). At each of the 60 locations, five 1x1m² herb layer plots and five 5x5 m² shrub plots in the direct surroundings of the light trap were conducted to map the species composition and distribution patterns of shrubs and of herbs (Fig. 5.3). All plant species were identified to species level using Aichele et al. (1998), Bassi (2004) and Senghas & Seybold (2003). As all vascular plant species of both reserves have previously been listed by the local conservation organization L'ARCA, it was possible to ascertain their correct identification using Lazzari et al. (2010). From the 844 vascular plant species that are known from the forests Pineta san Vitale, Pineta di Classe and Pineta di Cervia, 216 species were found at the 60 downy oak forest locations (Fig. 5.4). For all plant species recorded during surveys, indicator values were extracted from Ellenberg et al. (2001) and Pignatti et al. (2005).

Figure 5.4: Some of the plant species of the study areas. Beginning from the upper left: *Ajuga reptans*, *Lonicera caprifolium, Buglossoides purpurocaerulea, Berberis vulgaris*, *Neotinea tridentata*, *Euphorbia cyparissias*, *Gladiolus italicus*, *Ranunculus bulbosus*, *Crataegus monogyna*, *Campanula rapunculus*, *Centaurium erythraea*, *Ornithogalum orthophyllum*, *Asparagus acutifolius*. Photos: Britta Uhl

The tree layer was analyzed using the point-centered-quarter method (PCQ), with ten PCQ measurements at each location. For PCQ, the vicinity of a randomly chosen stand is separated into four quarters by using a compass. Then, the distances to the four nearest trees (one in each quarter) are measured (Cottam & Curtis 1956). These four trees were identified on species level and measured for their height and diameter at breast height. From these data, forest density, absolute and relative density of tree species, and dominance and frequency of individual tree species were calculated following the protocol of Mitchell (2010). The proportion of deadwood around the sampling location was estimated by sight.

For all the sampled plant species, information about their functional characteristics was collected from published literature. 46 functional traits like pollination method, fruit-type, flowering period or leaf structure were entered into a trait matrix that was later used to analyze the functional diversity of plant communities.

Moth communities were characterized using samples taken with automated light traps, equipped with two 60 cm light tubes and powered by a 12V dry battery pack. At every location, one sample in early summer and one sample in the high summer period were taken. Sites were sampled in randomized order during the three years of field work, to avoid sampling bias based on annual variation in moth phenology. Sampling was normally done at best weather conditions, i.e. in warm nights without rain, mostly trying to avoid full moon periods. When an insufficient number of moth individuals was collected (because of changing weather like sudden rain or because of technical problems), a second sample was made. All specimens were identified using faunal monographs (e.g. Segerer & Hausmann 2011; Slamka 2006, 2008, 2013) or web pages (www.lepiforum.de, www.ukmoths.org.uk). These references were also used to extract life-history traits, distributional limits and other ecological characters for subsequent functional analysis. In total, 23870 moth individuals of 392 species (comprising 32 families) were collected, identified and used for the later analyses (Fig. 5.5).

Figure 5.5: Some of the moth species, found at the two reserves. Beginning from the upper left: *Callopistria juventina*, *Alabonia geoffrella*, *Thetidia smaragdaria*, *Euchromius superbellus*, *Araeopteron ecphaea*, *Eupithecia centaureata*, *Idaea muricata*, *Idaea filicata*, *Arctia villica*, *Pseudoips prasinana*, *Cyclophora annularia*, *Palpita vitrealis*, *Apeira syringaria*, *Cnaedimophorus rhododactyla*, *Homoeosoma sinuella*, *Idaea politaria*, *Acontia lucida*, *Aedia leucomelas*. Photos: Britta Uhl

Investigations on the landscape level included measurements of the distance of light-trapping sites to potential effect sources and by analyzing the composition of the landscape relative to land use types. Distance measurements related to the nearest industrial plants, forest edges, and water canals. Proportions of open water, reed, open habitats, agricultural land and human buildings were measured within a radius of 200 m (direct surroundings), 500 m (medium-scaled landscape patterns, comprising surrounding habitat structures) and 1000m (large-scaled landscape patterns, comprising neighboring agricultural land, canals or the lagoon) around the trap sites.

In total, I collected information on 28 variables (fourteen local and fourteen landscape-scale factors) possibly affecting moth communities. I then used this data to link, in a correlative approach, various aspects of insect community patterns with both, local and landscape-level attributes of the sampling sites to assess which of these two spatial scales are more important in shaping variation of insect biodiversity inside conservation areas. First, within the following chapter, the interactions between abiotic local, forest stand and landscape compositional factors and local vegetation will be analyzed (Chapter 5). Subsequently, possible influences of these multiple variables on moth species numbers and diversity (Chapter 6), species composition (Chapter 7) and functional diversity (Chapter 8) will be investigated.

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6. Local, forest stand and landscape-scale correlates of plant communities in isolated coastal forest reserves

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Abstract

In mixed oak stands situated within two isolated forest reserves in NE Italy, we investigated how plant communities are modulated by local conditions, forest structure, and landscape attributes. Species richness and functional dispersion increased towards canals, whereas soil salinity, canopy density or landscape heterogeneity were less relevant. Mean nutrient indicator values increased near canals and with higher proportions of agriculture around. Functional dispersion decreased at wet, nutrient rich sites. Also the proportion of salt tolerant species increased towards canals, but was unrelated to measures of soil salinity. At sites with more modified landscapes around, widely distributed species were more prevalent, at cost of plants with restricted distributional ranges. Hence, biotic homogenization is fostered inside the reserves through landscape modification in their surroundings. In contrast to species richness, composition turned out to be markedly modulated by environmental variation, with local site factors, forest stand structure and landscape attributes contributing to roughly the same extent. Conservation practices should therefore not only focus on managing local conditions, but also take landscape structure into account. For coastal forests, dry and open, nutrient poor sites are of special conservation concern, which are believed to most closely resemble the original diverse vegetation of these Mediterranean habitats.

Keywords

Mediterranean forests, species composition, vegetation change, biotic homogenization, landscape-scale influence, plant diversity, conservation management, nutrient spill-over

Introduction

The Mediterranean basin is one of the Earth’s biodiversity hotspots and – as such – home of about 25000 native plant species (Cuttelod et al. 2009; Myers et al. 2000). Of these, about 50% are endemic to the region (Cowling et al. 1996). The evolution of today’s Mediterranean landscapes is strongly linked to millennia of human land use, which historically contributed to the diverse and heterogeneous habitats (Blondel 2006). However, over the past decades accelerated land use change, either through abandonment or through intensification, render Mediterranean habitats one of the globally most endangered areas facing biodiversity loss (Lavergne et al. 2005) and landscape homogenization (Geri et al. 2010). While inland, forest areas are increasing at the cost of open landscapes, coastal transformation led to the disappearance of most forest sites because of human population growth and urbanization, mass tourism and agricultural intensification (Falcucci et al. 2006). Remnant forest patches are often small sized, fragmented habitats which are highly isolated from another as they are surrounded by anthropogenically modified land (Teixido et al. 2010). Setting aside these areas from land use as nature reserves forms an important part of conservation strategies to mitigate biodiversity loss (Araújo et al. 2007; Doxa et al. 2017). However, there are still environmental variables influencing the plant communities in isolated reserves. These factors can principally be distinguished into three groups:

- Primarily, natural variation in topography, local edaphic and hydrological conditions determines which plants from the regional species pool can populate an area, thereby forming the ‘potential natural vegetation’ (Molina-Venegas et al. 2016).
- Second, factors associated with land use history usually have left their imprint, for example with regard to tree species composition, tree density and age structure of stands in case of forested sites (Burrascano et al. 2017; Sabatini et al. 2014).
- Finally, local ecological conditions may be altered by pressures that arise from the landscape around the reserve, for example soil salinization (Mollema et al. 2013), spill-over of pollutants and fertilizers (Bussotti & Gerosa 2002; van Dobben & de Vries 2017), or increasing drought stress in the course of climate change (Liu et al. 2018; Peñuelas et al. 2017; Tsiafouli et al. 2018). Landscape-scale drivers of biota inside reserves also include edge effects (Wuyts et al. 2013), reduced habitat size, or the extent of fragmentation and isolation of reserves (Luzuriaga et al. 2018; Rosati et al. 2010; Malavasi et al. 2016).

So, human activities can alter plant communities through past and present land use intensity and management within reserves as well as through landscape-scale effects acting from the outside. As a consequence, functional homogenization, declining species diversity or the invasion of alien species can be observed in many conservation areas (Bazzichetto et al. 2017; Clavel et al. 2011; Malavasi et al. 2016).

In this study, using two protected coastal forest remnants in north-eastern Italy as an example, we address different aspects of local, (land use history driven) forest and landscape characteristics in relation to their vegetation. By doing so, we aim to uncover the hierarchy of influences these factors have in shaping coastal forest plant communities. Especially, we focus on subtle differences in plant diversity, functional diversity and species composition within contiguous forest stands of broadly similar type. Two suites of anthropogenic factors are of special concern here. (1) The entire region is subject to increase in soil salinization, as a consequence of land subsidence (Mollema et al. 2013) (2) Directly adjacent to the two reserves there are large areas under intense agricultural use (Musolino et al. 2018) and highly urbanized areas (Lucialli et al. 2007). It is therefore likely that the surroundings of the two forest reserves have substantial influence on the local vegetation inside. In particular, we address the following questions:

- Can attributes of the local plant communities such as species richness, functional diversity or mean indicator values be related to any of the observed factors?
- Are landscape factors (e.g. the extent of modified land surrounding focal plots) driving plant communities from typical Mediterranean composition towards dominance by cosmopolitan species?
- Are local plant communities changing with the degree of soil salinization or is there a more general shift to salt tolerant plants all over the reserve areas?
- How much variation in plant community composition can be described at each of the three spatial scales (i.e. local, forest stand, and landscape level)?

Methods

Study area

The coastline around Ravenna, NE Italy, has developed over centuries through sedimentation by the river Po and therefore is until today characterized by sandy soils and paleodunes (Antonellini et al. 2008). Our study sites were located inside two isolated relict forest reserves, Pineta san Vitale (hereafter PsV) and Pineta di Classe (hereafter PdC). Both reserves comprise an area of approximately 10 km², with PsV being elongated with 7x1.5 km² in shape and PdC having a more compact shape of about 5x2 km². Both forests have a long history of human land use and management. Around 500 BC, when the first settlements of what today constitutes the city of Ravenna were built, large areas of mixed oak forests (mainly *Quercus robur* L. and *Quercus pubescens* WILLD.) are believed to have covered the coastal areas (Andreatta 2010). About 400-500 AC historical notes for the first time mention “pine woods” in the area, which are believed to indicate the presence of *Pinus sylvestris* L. and *Pinus nigra* J.F. ARNOLD.

The area where PsV and PdC today are located is believed to have been developing in the 10th - 15th century through sedimentation (Buscaroli et al. 2011). Only during the 10th and 11th century, when the forests were property of different abbeys (on which the recent names “san Vitale” and “Classe” are still based), stone pine trees (*Pinus pinea* L.) were introduced to the region. Stone pines were mainly planted on top of the paleodunes. In between, where soil conditions did not match the needs of pine trees, other forest types like mixed deciduous forest and riparian forest remained (Andreatta 2010). From the 12th century onwards, Ravenna’s pine forests were used for pine nut harvest and wood production as well as for cattle grazing (Andreatta 2010). Until the end of the 18th century, these forests had reached their maximum expansion of about 6000ha (Malfitano 2002). From 1796 onwards, many trees were cut down for ship building and for the sake of urban development. The forest areas got increasingly fragmented until only about 2000ha, split up between the two areas PsV and PdC, were left (Andreatta 2010; Malfitano 2002). Pine nut production and other management practices were finally abandoned in 1988, when the “Parco regionale del Delta del Po” was established, protecting the two forests from further degradation (Enrica Burioli, pers. communication, Consorzio Del Parco Regionale Del Delta Del Po 2004). Being a part of the Parco regionale del Delta del Po, listed as UNESCO biosphere reserve (Po Delta, United Nations Educational Scientific and Cultural Organisation 2015) and Natura 2000 sites and also partly flagged as important bird area (Bird Life International 2019), Ravenna’s coastal forests are today of high legal conservation status. After their planting during the Middle Ages, the ancient open pine woods developed due to natural succession and are today dominated by a mix of oak and pine forest (Wölfling et al. 2019), but also other vegetation types like grassland on sandy soils, reed vegetation and riparian forest sites can be found (Merloni & Piccoli 1999; Piccoli & Merloni 1999).

As the entire Po plain is today one of the most important areas for agricultural use in Italy (Musolino et al. 2018), conservation interests and intensive land use often collide here. Also around PsV and PdC, highly modified landscapes including arable land, the industrial harbor of Ravenna and urban areas are a source of pressures on the nature reserves that are designated for conserving Mediterranean biodiversity.

Data collection

We partitioned each reserve into 30 grid cells (600 x 600m²). In each grid cell, one sampling location was chosen by considering three criteria (Fig. 6.1). (1) All sites should be situated inside the same vegetation type, viz. a mixture of oak and pine forest. This tree composition is closest to the former natural vegetation of the paleodunes. (2) Other habitat types like reed vegetation or open grassland should be at least 100m away from the sampling location. (3) The sites had to be accessible from one of the numerous small pathways through the forests.

Data collection took place from 2015 to 2017. Each year, 20 of the 60 locations were chosen randomly (ten in each reserve) and then sampled once between April and September. At each location soil samples, tree crown density and all plant species forming the herb, shrub and tree layer were analyzed.

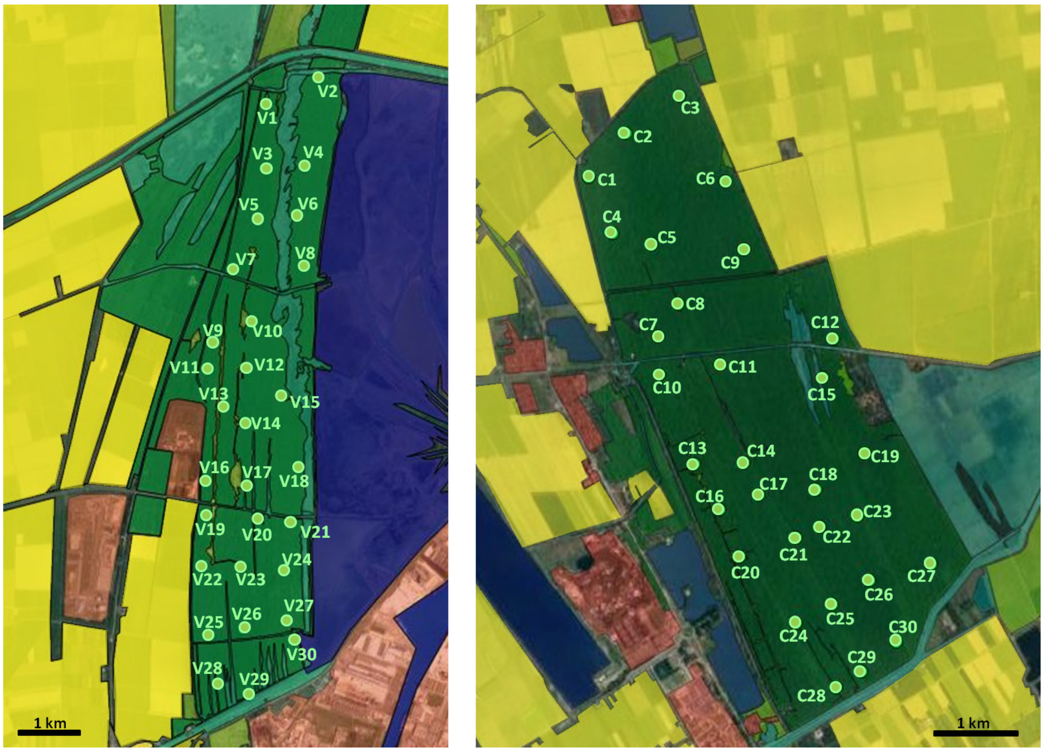

Figure 6.1: Schematic maps of the two study coastal pine forest reserves near Ravenna, NE Italy (left: PsV, right: PdC) and locations of the sampling sites (green dots, V1-30 in PsV, C1-30 in PdC). Landscape indicated by colors: forest (dark green), open habitats (light green), arable land (yellow), buildings (red), reed (light blue) and open water (dark blue). Modified using QGIS based on satellite images extracted from Google Maps^{TM}.

The herb layer was sampled in April within five randomly chosen 1x1m² plots per site. Each plot took approximately 0.5-1h of time to register, resulting in about 2.5-5h herb layer sampling per location. If necessary, flowering characteristics required for the identification of species were additionally checked in June. For the shrub layer five 5x5m² plots per location were analyzed in September. All plants were identified to species level using different monographs (Aichele et al. 1998; Bassi 2004, Senghas & Seybold 2003) as well as the internet page www.actaplantarum.org. For further analyses, only plant species incidences per site were considered (Appendix 6.1).

For measurements of soil factors, 20 soil samples per location (five samples each in April, June, August and September) were taken. pH value and electric conductivity (EC) were measured using a Multiparameter Meter HI 9813 (Hanna Instruments). Out of these 20 measurements, a mean pH and a mean EC value (as proxy for soil salinity: Malicki & Walczak 1999) were calculated for each site. Further abiotic characteristics like humidity, local temperature, soil nutrients and light availability were inferred from Ellenberg's indicator values of all plant species observed per site. Ellenberg indicator values have often proven as suitable proxies for the microclimatic and edaphic conditions they represent (Schaffers & Sýkora 2000). To this end, indicator values for all recorded plant species were extracted from Pignatti et al. (2005) and a non-weighted mean Ellenberg indicator value was calculated.

Composition and structure of the tree layer was recorded by doing ten point-centered-quarter (PCQ) analyses per site in August following Mitchell (2010). PCQ as a distance-based method has some disadvantages compared to plot-based methods, like a larger sampling bias leading to over- or underestimations of the real community level forest density (Bryant et al. 2004). But as forest understory vegetation – especially shrub vegetation – in PsV and PdC is quite dense, no plot-based analyses were physically feasible. For the PCQ analyses, species identity and diameter at breast height (by only taking into account stems with a circumference bigger than 10 cm) of 40 trees (four trees per PCQ) were noted. Furthermore the height of these trees was estimated by taking pictures of the whole tree together with a 1m ruler as scale. The trees on the pictures were then measured using the program ImageJ 1.45s (Schneider et al. 2012). Out of these records, mean basal area and its standard deviation (as proxies for forest age and stand heterogeneity), mean tree height, forest density (as number of stems/ha) and forest cover (defined after Mitchell (2010) as stem density × mean basal area, in m^2/ha) of conifer and deciduous trees were calculated. Tree crown density was measured at four random points using a manual densiometer (Forest densiometers, Robert E. Lemmon, Rapid City) four times each in April, June, August, September, resulting in 16 crown density measurements per location. Again, the mean value of these entered into subsequent statistical analyses.

Landscape composition and structure was analyzed using the software QGIS (QGIS Development Team 2018), based on satellite images from 2017 provided in Google Maps^{TM}. All calculations were done for a 1000m buffer around each location, as larger landscape scales are believed to be more important for plant species composition than smaller ones (Amici et al. 2015). Specifically, from the satellite images the proportions (area) of forest, open grassland, reed vegetation, open water bodies, buildings, agricultural land and other structures (including roads and gardens) were recorded. Subsequently, forest, open grassland and reed vegetation were summarized as "near-natural areas". As a corollary, buildings, agricultural land and other habitat structures were summarized as "modified land". Furthermore, edge density in the landscape (expressed as length of all habitat edges per ha) and landscape diversity (expressed as Shannon diversity of fractions of area of the aforementioned elements, in its exponential version) were calculated (Clément et al. 2016; Schindler et al. 2015). Finally, the nearest distance from each site to structural components of the landscape such as water canals and forest edges was measured using QGIS. All measured local, forest stand and landscape factors are shown in Table 6.1.

Data analysis

For the calculation of distance based plant functional diversity, a matrix consisting of 46 traits was compiled. This matrix contained plant characteristics such as the life-form, presence of spines, resin or latex secretion, maximum plant height, root type, various flower and leaf attributes (like flowering time, leaf structure, phyllotaxy, pubescence, pollination syndrome, seed dispersion type and leaf phenology) as well as habitat and distribution characteristics (including Ellenberg indicator values, distributional range, or salt tolerance) (Appendix 6.2). Information about plant traits was collated from monographs (Aichele et al. 1998, Bassi 2004, Burnie 2007, Schönfelder & Schönfelder 2011, Senghas & Seybold 2003) as well as from the internet page www.actaplantarum.org. Information about salt tolerance was gathered from

Böhling (1995), Flückiger (2007), Ellenberg & Leuschner (2010) and the internet page https://www.infoflora.ch. For analysis, we scored all plant species known to grow naturally on salt-influenced soils or to tolerate salt under urban conditions as 'salt-tolerant'. We further scored plant species according to their natural distributions into Mediterranean and widely distributed species. Functional diversity calculations were done in the R environment (R Core Team 2018) using the packages 'vegan' (Oksanen et al. 2018) and 'FD' (Laliberté et al. 2014; Laliberté & Legendre 2010). We used functional dispersion (FDis) as suggested by Laliberté & Legendre (2010) as this functional diversity index is not dependent on species richness per se (like e.g. functional richness) and can also deal with incidence based species data, where it represents the unweighted mean distance to the centroid (viz. the dispersion of species in trait space) (Laliberté & Legendre 2010). For the hierarchical clustering tree of functional traits, the "hclust" function based on Gower dissimilarity and the Ward.D2 method was used. Functional dispersion analysis was done with the "dbFD" function, using the trait matrix and the incidence table of all observed vascular plants (herbs, shrubs and trees together).

Table 6.1: List of all measured local, forest stand, and landscape-level factors.

Local factors	Forest stand factors	Landscape factors
Soil pH	Mean tree basal area (cm²)	Distance to nearest forest edge (m)
Soil salinity (mg/l)	Standard deviation of tree basal area (cm²)	Distance to nearest canal (m)
Ellenberg indicator for light	Mean tree height (m)	Edge density (m/ha)
Ellenberg indicator for temperature	Forest density (number of stems/ha)	Landscape diversity (exponential Shannon)
Ellenberg indicator for humidity	Proportion of deciduous tree biomass (= deciduous biomass/complete biomass)	Natural areas (proportion)
Ellenberg indicator for nutrients	Crown density (proportion of visible sky)	Agricultural land (proportion)

To compare plant gamma diversity between the two study areas, total plant species richness for each reserve was estimated by doing a sample based extrapolation after Chao et al. (2016) using the program iNEXT. Indicator plant species for each of the two reserves were extracted using the "indval" function with the "labdsv" package (Roberts 2016). Differences between local species richness and local FDis of the PsV and PdC locations were tested using student's t-test with the basic "stats" package in R.

All environmental factors available for each site (Tab. 6.1) were checked for normality and transformed if necessary. Proportions were logit transformed (Warton & Hui 2011). To assess how averaged local plant indicator values for humidity, temperature, light and nutrients are related to local, forest stand and landscape factors, linear mixed effects models were constructed, using the package "nlme" (Pinheiro et al. 2018). Reserve identity (PsV or PdC) was included as random factor.

Subsequently for further multivariate analysis, all environmental factors were z-transformed to a mean of 0 and a standard deviation of 1, to alleviate differences in their scaling. In order to reduce the number of possible predictor variables to be included in regression models, and to alleviate problems with multicollinearity of the various raw variables, a PCA (with varimax rotation) was performed separately for each group of variables (local, forest stand, and landscape level). PCAs were calculated by using the package "psych" (Revelle 2017). From each PCA, the first three factors were retained. PC-axes were interpreted and named by taking a look at their factor loadings with regard to the raw variables.

These PCs then served as predictors in linear mixed effects models. Local species richness (i.e. the number of plant species sampled at each location) and local FDis were used as response variables, respectively. Furthermore, logit transformed proportions of mediterranean and widely distributed species as well as logit transformed proportions of salt tolerant species per location were used as response variables. Reserve identity (PsV or PdC) was modeled as random factor which also controls for possible spatial autocorrelation in the data. For calculation and visualization of linear mixed effects models, the packages “nlme” (Pinheiro et al. 2018) and “ggplot2” (Wickham 2016) were used.

Table 6.2: General information on plant species richness, FDis and Mean Ellenberg indicator values in PsV and PdC. Significant differences between both reserves are marked in bold.

	PsV	PdC	t-value	p-value
Recorded richness	162	161	-	-
Estimated total plant richness	194.2±15.6	194.5±16.9	-	-
Mean Plant richness (per location)	36.6±5.7	33.0±5.3	2.57	0.01*
Mean Plant FDis (per location)	0.18±0.01	0.18±0.01	-1.04	0.30
Mean indicator value: Humidity	4.19±0.1	4.09±0.1	1.18	0.25
Mean indicator value: Temerature	6.48±0.07	6.51±0.07	-0.61	0.54
Mean indicator value: Nutrients	4.41±0.2	4.22±0.2	1.60	0.11
Mean indicator value: Light	6.66±0.1	6.54±0.1	1.74	0.09

For analysis of plant species composition we entered two of the three PC-axes of each PCA (local, forest stand, and landscape) as factors in a canonical analysis of principal coordinates (CAP) using the “capscale” function in the “vegan” package (Oksanen et al. 2018). Here, reserve identity was also included as a predictor. CAP was done based on a Sørensen-distance matrix of plant species lists of all sites. For significance testing, a permutation test with 1000 randomizations was applied.

Table 6.3: Plant species emerging as indicator species for PsV and PdC and their indicator values, as obtained from the „indval“ function

PdC indicator species	**Indicator value**
Buglossoides purpurocaerulea (L.) HOLUB	0.59
Phillyrea angustifolia L.	0.50
Quercus ilex L.	0.45
Cotinus coggygria SCOP.	0.43
Pyracantha coccinea M. ROEM.	0.39
Brachypodium phoenicoides (L.) ROEM. & SCHULT.	0.38
Carex liparocarpos GAUDIN	0.37
Silene vulgaris (MOENCH) GARCKE	0.28
Cornus sanguinea L.	0.24
Pinus sylvestris L.	0.20

Results

In total, we recorded 213 plant species, with 110 species shared between both reserves, 52 species only found in PsV, and 51 species restricted to PdC. Observed as well as estimated gamma diversity was almost identical between the two forests, while mean observed plant species richness per site was significantly higher in PsV than in PdC. FDis per site did not differ significantly between the two reserves (Tab. 6.2).Typical indicator species for PsV were e.g. *Ranunculus bulbosus* L., *Prunus spinosa* L. and *Populus alba* L., while in PdC species like *Buglossoides*

Table 6.3 (continued): Plant species emerging as indicator species for PsV and PdC and their indicator values, as obtained from the „indval“ function

PsV indicator species	Indicator value
Ranunculus bulbosus L.	0.52
Populus alba L.	0.51
Luzula campestris (L.) DC.	0.50
Euonymus europaeus L.	0.49
Anthoxanthum odoratum L.	0.47
Prunus spinosa L.	0.45
Fraxinus ornus L.	0.39
Cerastium semidecandrum L.	0.35
Hypochaeris radicata L.	0.31
Potentilla reptans L.	0.29
Prunella vulgaris L.	0.29
Pyrus communis L.	0.27
Geranium robertianum L.	0.24
Vincetoxicum hirundinaria MEDIK.	0.24
Arum italicum MILL.	0.20
Campanula rapunculus L.	0.20
Galium mollugo L.	0.20

purpurocaeruleum (L.) HOLUB, *Cotinus coggygria* SCOP. and *Quercus ilex* L. more commonly occurred. All recognized indicator species are listed in Table 6.3.

We found strong positive relationships between mean Ellenberg values of the vegetation with the proximity to water canals (Tab. 6.4, Fig. 6.2 A-B). The average nutrient indicator value increased with the proportion of agricultural areas in the surroundings (Tab. 6.4, Fig. 6.2C). Furthermore, the indicator value for temperature decreased with the mean basal area of trees (Tab. 6.4, Fig. 6.2D).

The PCA of the six local factors resulted in three axes, which collectively captured 78% of total variance. The PCLoc1 axis can be interpreted as a gradient from dry and nutrient poor locations with open canopy to shady, humid and nutrient rich sites. The PCLoc2 axis mainly represents a gradient in temperature, while the PCLoc3 reflects the gradient in soil pH and salinity.

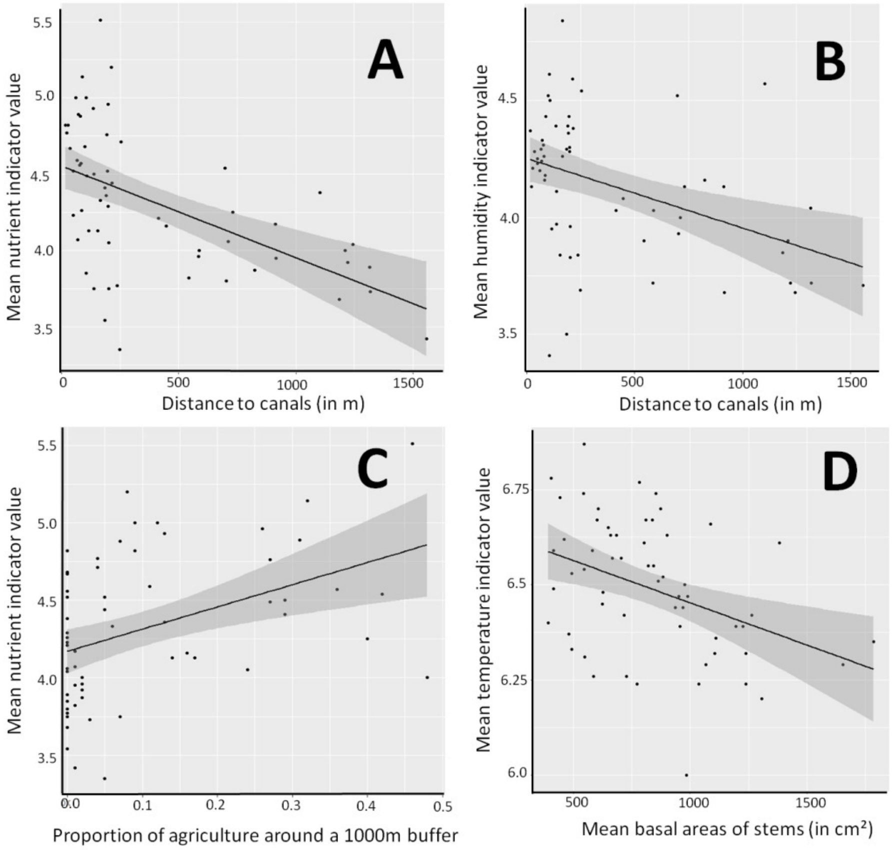

Figure 6.2: Factors influencing mean Ellenberg indicator values for nutrient availability (A and C), humidity (B), and temperature (D) in 60 local species lists collated in the two reserves PsV and PdC. Dark grey shaded areas mark the 95% confidence bands of the linear regression (black line).

Table 6.4: Results of linear mixed effects models. Random factor was always the reserve identity (PsV or PdC). Each row represents a separate statistical model. Plant species richness, plant FDdis, widely distributed species, Mediterranean species and salt tolerant species are only named once as response, but refer to all the predictors within the same box. Statistically significant relationships printed in bold face.

Response variable	Predictors (increasing values)	t-value	Standard error	p-value	Residual variation
Mean indicator value: Humidity	**Distance to canals**	**-3.21**	**0.07**	**0.002**	**0.28**
Mean indicator value: Nutrients	**Distance to canals**	**-5.19**	**0.1**	**<0.001**	**0.39**
Mean indicator value: Nutrients	**Proportion of agricultural areas**	**3.38**	**0.07**	**<0.001**	**0.42**
Mean indicator value: Temperature	**Mean basal area of trees**	**-3.23**	**<0.001**	**0.002**	**0.16**
Plant species richness	Wet, nutrient rich sites	-0.62	0.72	0.54	5.51
	Cooler sites	0.88	0.75	0.38	5.50
	High pH and soil salinity	-0.93	0.78	0.36	5.50
	Old, open forest	0.80	0.73	0.43	5.50
	Heterogeneous forest	0.86	0.72	0.39	5.49
	Crown density	-0.24	0.72	0.81	5.52
	Forest center sites	-0.76	0.72	0.45	5.49
	Landscape heterogeneity	-0.20	0.76	0.84	5.52
	Distance to canals	**-3.60**	**0.69**	**<0.001**	**5.16**
Plant FDis	**Wet, nutrient rich sites**	**-3.21**	**0.0008**	**0.002**	**0.006**
	Cooler sites	-0.92	0.0009	0.36	0.007
	High pH and soil salinity	-1.87	0.0009	0.07	0.007
	Old, open forest	-1.39	0.0009	0.17	0.007
	Heterogeneous forest	**3.65**	**0.0008**	**<0.001**	**0.006**
	Crown density	-1.53	0.0009	0.13	0.007
	Forest center sites	-0.18	0.0009	0.86	0.007
	Landscape heterogeneity	-0.08	0.0009	0.94	0.007
	Distance to canals	**-2.24**	**0.0008**	**0.003**	**0.006**
Widely distributed species	**Landscape heterogeneity**	**2.3**	**0.04**	**0.03**	**0.29**
	Forest center sites	-0.73	0.04	0.47	0.30
	Distance to canals	-0.45	0.04	0.65	0.30
Mediterranean species	**Landscape heterogeneity**	**-2.23**	**0.06**	**0.03**	**0.40**
	Forest center sites	1.34	0.05	0.19	0.42
	Distance to canals	0.61	0.06	0.54	0.42
Salt tolerant plants	Soil pH and salinity	-0.76	0.07	0.45	0.50
	Distance to canals	**-3.70**	**0.06**	**<0.001**	**0.46**

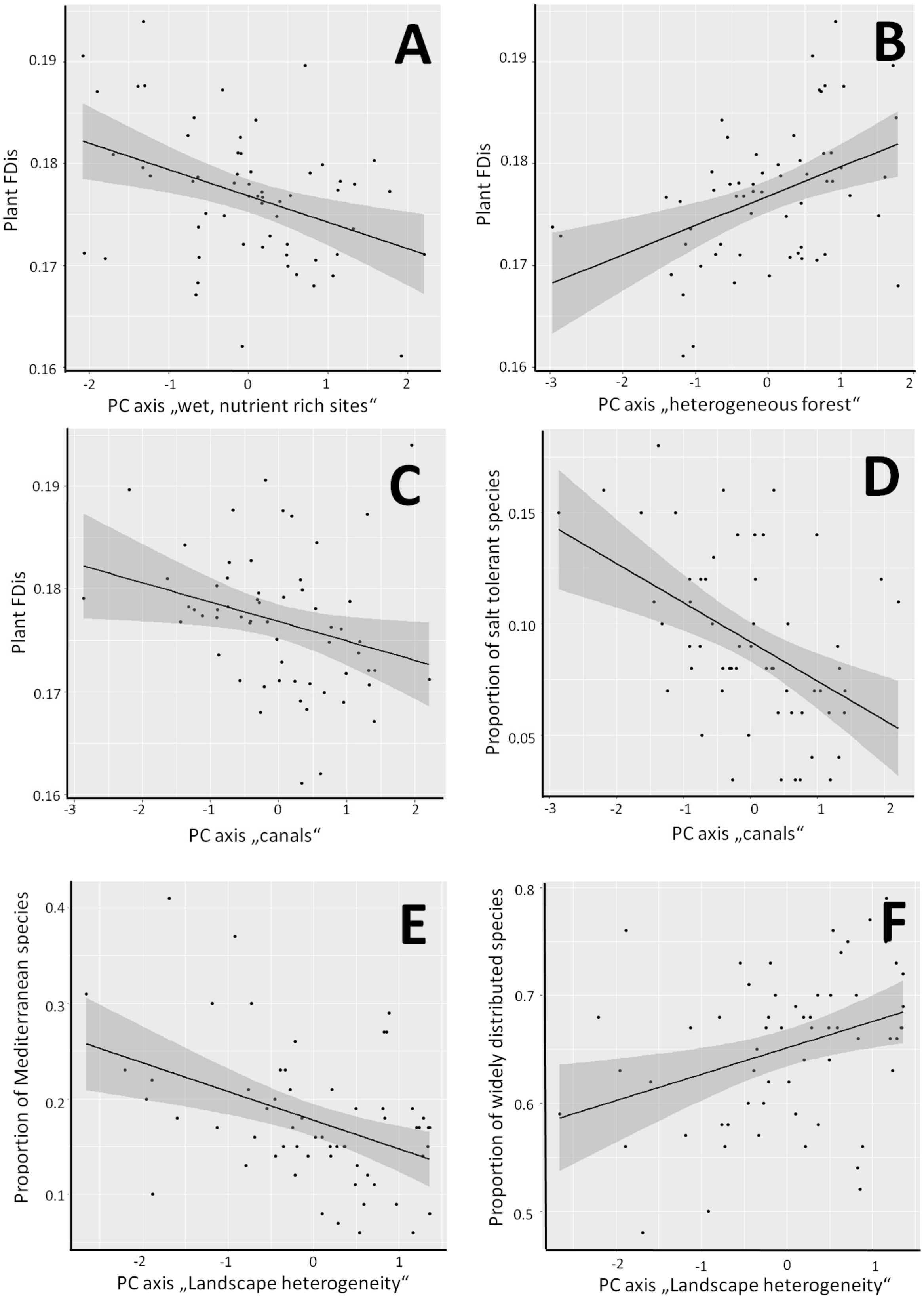

Figure 6.3: Factors influencing (A-C) plant functional dispersion (FDis), (D) proportion of salt tolerant species, (E) proportion of Mediterranean species, (F) proportion of widely distributed species in 60 local species lists collated in the two reserves PsV and PdC. Dark grey shaded areas mark the 95% confidence bands of the linear regression (black line).

Among the six descriptors of forest stand structure, the three first PCs accounted for 79% of total variation. Here, PCFor1 depicts the gradient from dense forest stands with many small and young trees to more open and old grown forest locations with fewer, but taller stems. PCFor2 represents forest heterogeneity and PCFor3 tree crown density.

Finally, at the landscape level the first 3 PC axes summarized 89% of variation. PCLand1 mirrors the gradient from sites situated at the reserve edges (surrounded by high proportions of agricultural land and high landscape diversity) into the centers of the forest with high proportions of natural areas and lower habitat diversity around (because of the lack of modified landscape elements). PCLand2 represents landscape heterogeneity and diversity around the sites. PCLand3 can be interpreted as distance to canals. The main outcome of all three PCAs is summarized in Table 6.5.

Table 6.5: Factor loadings of the PC axes obtained from three separate PCAs for local, forest stand, and landscape variables, respectively. PC axes are named after the raw variables with the highest factor loadings and subsequent ecological interpretation. Factor loadings >0.6 are marked in bold. Ellenberg indicator values are abbreviated with IV.

Local	PCLoc1 =Wet, nutrient rich sites	PCLoc2 =Cooler sites	PCLoc3 =High pH and soil salinity
pH	-0.06	-0.13	**0.85**
Salt	0.01	0.27	**0.75**
IV_Light	**-0.89**	0.13	0.00
IV_Temp	-0.09	**-0.87**	-0.09
IV_Humidity	**0.71**	0.59	0.06
IV_Nutrients	**0.82**	0.40	-0.11
Forest	PCFor1 =Old, open forest	PCFor2 =Heterogeneous forest	PCFor3 =High crown density
Tree height	**0.85**	-0.11	0.09
Standard deviation basal area	0.36	**0.68**	0.30
Crown density	-0.04	-0.02	**0.94**
Mean basal area	**0.81**	0.48	0.14
Forest density	**-0.80**	-0.13	0.34
Proportion of deciduous trees	0.08	**-0.83**	0.20
Landscape	PCLand1 =Site in center of forest	PCLand2 =Landscape heterogeneity	PCLand3 =Distance to canals
Distance to edges	**0.89**	-0.09	0.10
Distance to canals	0.12	-0.29	**0.95**
Edge density	0.04	**0.90**	-0.29
Landscape diversity	**-0.65**	**0.65**	-0.26
Natural areas	**0.87**	-0.39	0.12
Agricultural land	**-0.81**	-0.36	0.01

GLMM results indicated that FDis decreased at more wet and nutrient rich sites and with lower forest heterogeneity (Tab. 6.4, Fig. 6.3A-B). Furthermore, plant species richness and plant FDis per site were significantly related to the distance of sites to the nearest canal (Tab. 6.4, Fig. 6.3C). All other tested site descriptors had no detectable influence on vascular plant richness or FDis.

The proportion of salt tolerant species was not influenced by local salinity values taken from own soil measurements, but increased towards the canals (Tab. 6.4, Fig. 6.3D). The proportion of Mediterranean plant species declined with increasing landscape heterogeneity in the surroundings (Tab. 6.4, Fig. 6.3E), while widely distributed species increased (Tab. 6.4, Fig. 6.3F).

In contrast to the analyses of species richness or functional dispersion, all tested PC axes were significantly related to variation in local plant community composition. The position of sites along the humidity and nutrient gradient (p=0.001) and its temperature conditions (p=0.001) accounted for 8% of the observed variation. Forest age and density (p=0.002) and crown density (p=0.001) explained another 7.7%, while landscape heterogeneity (p=0.001) and the distance to canals (p=0.001) explained 7.8% of variation. Differences between the two reserves (p=0.001) accounted for a further 4.6% of variation.

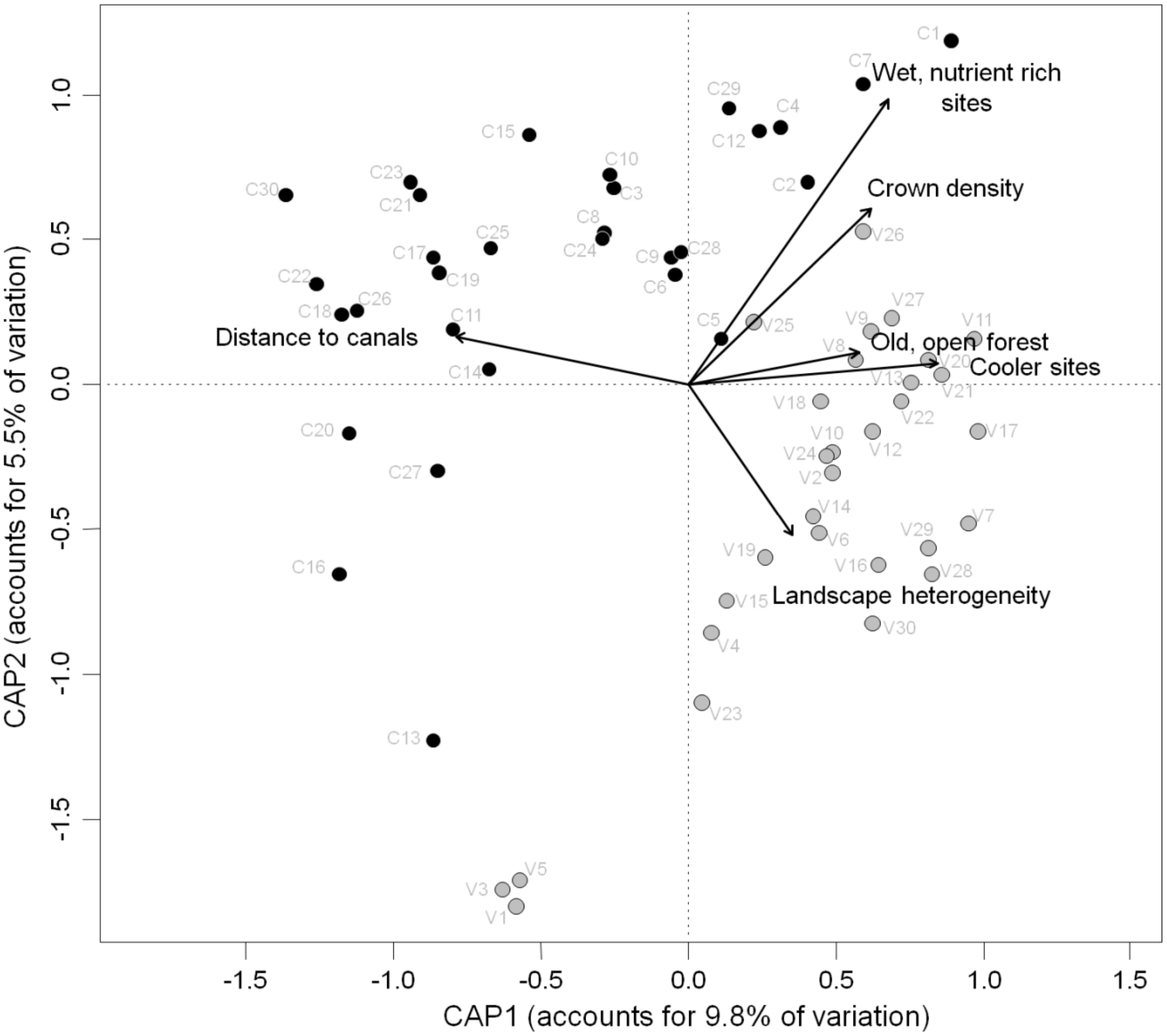

Figure 6.4: Constrained ordination plot (canonical analysis of principal coordinates) of the plant community composition at 60 sites in the two pine forest reserves PsV and PdC. Included environmental variables are six (two each from local, forest stand, and landscape aspects) of the nine PC axes representing the factors listed in Table 6.1. Locations in PsV colored in grey, locations in PdC in black.

So, altogether 28.2% of variation in local vascular plant species composition could be attributed to the 7 factors chosen for matrix regression analysis, with local, forest stand, and landscape factors all contributing in roughly equal manner (Fig. 6.4). The CAP ordination further revealed two clusters clearly separating sites situated in PsV from those in PdC, what again underlines the difference in plant species composition between the two reserves. PdC sites were more scattered than PsV sites. Moreover, three PsV sites, viz. V1, V3 and V5, were clearly distinct from all other study sites in reduced ordination space. In PdC four locations, C13, C16, C20 and C27, clustered separately from the rest of all PdC sites (Fig. 6.4). All these sites were characterized through very dry and nutrient poor conditions with low crown density.

Discussion

Even though our study sites were all located in stands of the same forest type on paleodunes, dominated by oak trees, our results showed substantial variation in the diversity and species composition of plant communities. We observed significant differences in mean plant species richness between PsV and PdC, with sites in PsV on average having more species. In contrast, estimated gamma diversity showed no such difference between the two reserves. Alien invasive species seem to date not problematic in the two reserves, as only 7 alien species (e.g. *Ailanthus altissima* (MILL.) SWINGLE, *Erigeron sumatrensis* RETZ., *Robinia pseudoacacia* L.) were found sporadically and never occurred in large numbers.

Species composition varied between PsV and PdC, although there was a large basic species pool which both reserves had in common. Overall, the species lists were dominated by plants widespread in Mediterranean ecosystems, but also a few internationally protected species (e.g. the orchids *Anacamptis pyramidalis* (L.) RICH., *Anacamptis coriophora* (L.) R.M.BATEMAN, PRIDGEON & M.W.CHASE, *Anacamptis morio* (L.) R.M.BATEMAN, PRIDGEON & M.W.CHASE, *Neotinea tridentata* (SCOP.) R.M. BATEMAN, PRIDGEON & M.W. CHASE, *Platanthera chlorantha* (CUSTER) RCHB. and *Serapias vomeracea* BRIQ.) occurred in the reserves. Besides some xerophilous plant species like *Hypochaeris radicata* L., many of the PsV indicator species were hygrophilous like *Populus alba* L., *Potentilla reptans* L. and *Prunella vulgaris* L., while PdC indicator species often are bound to dry habitats like *Phillyrea angustifolia* L., *Carex liparocarpos* GAUDIN and *Quercus ilex* L.. So, local conditions in PsV may be characterized by higher humidity in comparison to PdC. However, there was no general difference in mean Ellenberg humidity values between PsV and PdC (Tab. 6.2).

Humidity and nutrient availability were significantly higher in proximity to the canals and indicates that they may contribute to eutrophication in these two Mediterranean coastal forests. Local nutrient availability inside the reserves increased with the proportion of agricultural areas around the study sites. Agricultural areas are known as major source of NOx pollution (Almaraz et al. 2018). The influence of fertilizers on plant communities has often been shown in agricultural environments (van den Berge et al. 2019) and computer models (Kros et al. 2014). Moreover, atmospheric nitrogen deposition can influence biodiversity and change vegetation (van Dobben & de Vries 2017; Tilman & Isbell 2015). For our study region Lucialli et al. (2007) demonstrated the contribution of the industrial harbor and its traffic to air pollution, which might also influence the nearby forest reserve PsV. So, besides aquatic nutrient transport through the canals, airborne deposition of NOx from the harbor of Ravenna must be taken into account. The observed increase of nutrient indicating plants at sites with more agricultural areas in their vicinity indicate a strong influence of intensive land use on protected areas, even with rather low proportions of agricultural areas (which never exceeded 48% of area in a 1000m buffer).

Higher forest age (inferred from larger mean basal area of stems) was associated with lower temperature scores of the vegetation. This highlights the potential of old-growth forests to moderate microclimatic conditions and thereby even counteract adverse effects of climate change (Frey et al. 2016). Older forest stands also had higher structural heterogeneity. The biggest and probably oldest trees in the study area are stone pine trees (*Pinus pinea* L.), which build up an upper canopy layer above the tree crowns of oaks (*Quercus* sp. L.), ash trees (*Fraxinus* sp. L.) and poplars (mainly *Populus alba* L.). Ehbrecht et al. (2019) found that structural heterogeneity buffers the diurnal temperature variation in central European forests, and supposed that this effect might be even more pronounced in regions with low summer precipitation like the Mediterranean area. So the observed lower temperature scores as inferred from plant indicator values might also be modulated by forest structural heterogeneity.

Plant species richness and FDis decreased with the distance of sites to canals. The canals as structural element break up the forest structure, enabling plant species dispersal and establishment of more light-demanding species. Furthermore, water is one of the limiting factors in dry Mediterranean ecosystems. Aridity is known to decrease plant richness and functional diversity at large scales and along with different management intensity (de la Riva et al. 2018; Rota et al. 2017). Close to the canals, constant water supply is ensured even in hot summer months like July and August. As a consequence, tree crown density increases as well as plant richness and functional diversity.

Otherwise, high humidity and especially nutrient availability can also decrease functional diversity and furthermore lead to functional homogenization (Helsen et al. 2013; Reinecke et al. 2014). Nitrogen deposition is a severe problem for terrestrial plant diversity, especially in the Mediterranean region (Bobbink et al. 2010). In line with this, also in our two forest reserves FDis decreased at humid and nutrient rich sites.

Another factor influencing plant FDis was forest heterogeneity. The more heterogeneous the forest stands around the location were, the more increased plant FDis. The “Forest heterogeneity” PC-axis mainly was determined by the standard deviation of stems and a decline in the proportion of deciduous trees. Some locations were characterized by very dense young tree stands with elms as dominating tree species. Here, forest stands often were very monotonous and showed low variety in available niches. In contrast, parts of the reserves where big and old pine trees could be found were often very heterogeneous in structure. Here, younger trees and bushes grow in between and also forest clearings exist on which sandy soils enable the establishment of diverse herbs. Therefore, structural heterogeneity seems to increase FDis, as with more structures more microhabitats are available.

Besides the positive aspects of water canals on plant richness and FDis, they also serve as source of soil salinity (Antonellini et al. 2008). Salt water intrusion and subsequent soil salinization is a severe environmental problem of the whole coastal region of the Emilia-Romagna, caused by land subsidence and ground water pumping which disturb the coastal hydraulic gradients and increase the influx of seawater (Mollema et al. 2013). In line with this, we detected a higher proportion of salt tolerant species near canals. In contrast, the PC-axis representing measured soil salinity did not correlate with the proportion of salt tolerant plants. Reasons for this might be the generally high soil salinity all over the reserves, with values between 1-25 g/l (Antonellini et al. 2008), leading to an all-over occurrence of salt tolerant plants inside the reserves. Indeed, we observed on average 9% salt tolerant species per location.

With regard to species distributional ranges, we found a significant decrease of Mediterranean species with higher landscape heterogeneity, whereas widely distributed species were concomitantly increasing. As landscape heterogeneity and diversity in our study were not only driven by the structure and number of natural habitats, but also strongly by the prevalence of modified landscape elements like buildings, gardens, agricultural areas, streets and hedges, we conclude that the disappearance of species with restricted distributional ranges is an effect of anthropogenic modification of the landscape. Land use change is known as a severe constraint on Mediterranean coastal regions and its plant diversity and leads to the disappearance of coastal forests (Falcucci et al. 2006; Hevia et al. 2016). Additionally, urban areas and other human modified landscapes are a source for alien and cosmopolitan plant species (Kühn et al. 2017). So, the landscape-scale effect on the prevalence of plants with restricted Mediterranean ranges is in line with previous findings and expectations.

Canonical analysis of principal coordinates confirmed the differences in species composition between PsV and PdC. Old grown, rather open forest sites with lower temperature scores were more often found in PsV, while PdC locations were characterized by lower heterogeneity of the surrounding landscape and a larger distance to canals. So, water availability might be reduced in PdC, what might explain some difference in species composition, resulting in xerophilous plants contributing more to indicator species in PdC. Nevertheless, wet and nutrient rich sites, being similar in their species composition and indicating a basic common species pool, were found in both reserves. Species turnover was higher in PdC than in PsV resulting in a more scattered cluster of sites in the ordination plot compared to the more compact one of PsV. A slightly higher beta diversity might compensate the lower mean species richness per site in PdC, resulting in the equal total plant richness found in both reserves. Some locations of PsV and PdC were clearly distant to the main cluster. In PsV, especially sites V1, V3 and V5 formed a separate group. These locations were all situated in the north-west of PsV, where the forest is characterized by very dry conditions. These sites were chosen at small forest clearings due to limited accessibility, resulting in a relatively low crown density. There, sandy underground and grass vegetation could be found. However, these aspects are not exclusive for V1, V3 and V5, but also occurred at other study sites. Within PdC, sites C13, C16, C20 and C27 showed - analogous to the situation in PsV - some distance in plant species composition to the other PdC locations. Again, these sites were mainly situated on dry and sandy habitats with low crown density. But here the forest structure often was not as semi-natural as at the aforementioned PsV sites. Rather, sites C13, C16 and C20 were characterized by monotonous pine plantations (mainly *Pinus sylvestris* L., *Pinus nigra* J.F. ARNOLD and *Pinus pinaster* AIT., but not *Pinus pinea* L.) also resulting in another classification of their main habitat structure at official vegetation maps (Piccoli & Merloni 1999). This area has been planted only about 30 years ago, without taking into account conservation and biodiversity management practices (Enrica Burioli, pers. communication). These plantations, however, are today left unmanaged, resulting in a successive change in vegetation structure, with young oak trees now growing in between, such that forest structure approaches that of semi-natural mixed forest sites. There are also no clearings, but broad paths breaking up the monotonous plantation structure and enabling light-demanding herb and shrub layer species to grow. Another characteristic that all of these outlying sites (whether in PsV or PdC) had in common, is a relatively low nutrient availability, resulting in low mean nutrient-Ellenberg indicator values. Under a conservation perspective, these sites (V1, V3, V5, C13, C16, C20 and C27) are of high interest, because here species of dry and open, nutrient poor habitats (like *Euphorbia cyparissias* L., *Helianthemum nummularium* (L.) MILL., *Sanguisorba minor* SCOP. and *Teucrium chamaedrys* L.) can be found. Furthermore, at all of these sites, protected orchid species can be found, underlining the importance of open forest structures.

Comparing the influence of local, forest stand, and landscape-scale attributes on plant community composition, each spatial aspect seemed to play an equally important role. In coastal dune habitats Sperandii et al. (2019) detected local factors to be the most important drivers of species richness and focal species cover, while human mediated disturbance and landscape structure were less relevant. Here, the selective conditions of dune ecosystems as clear examples of habitat filtering favor the establishment of plant species especially adapted to this environment. For coastal forest habitats, where local conditions are not this extreme, there appears to be no such weighting on one of the observed spatial aspects. Rather, all spatial scales are important for determining local community assembly. So, forest management and conservation practices alone cannot preserve plant communities without taking landscape structure into account (Vellend et al. 2017). In return, landscape structure is also not the dominant source of plant community variation inside these two forest reserves.

Conclusion

Local, land use history driven and landscape-scale effects equally shape local plant composition in the two forest reserves under study. Therefore, all spatial scales, as well as land use history should be taken into account for effective conservation practices. Forest clearings and other open forest structures were important habitats inside the coastal forest reserves, which most likely comprised fractions of the ancient plant communities. Such dry and open, sandy, nutrient poor habitats might once have been found throughout the paleodune habitats, but nowadays are endangered through nutrient spill-over and natural succession. Nutrient import seems to mainly occur through water canals and from the agricultural landscape around the reserves. So, the landscape scale here plays an important role driving eutrophication of terrestrial habitats, what finally leads to lower plant functional dispersion. The proportion of modified areas also leads to the replacement of genuinely Mediterranean species through more widely distributed ones. Here, land use and landscape-scale characteristics clearly seem to drive biotic homogenization also inside protected, but isolated coastal forest reserves.

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7. Understanding small-scale insect diversity patterns inside two nature reserves - the role of local and landscape factors

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Abstract

Insect decline has become a major topic in scientific research, yet the relative roles of multiple factors on insect communities are still incompletely known. Our aim was to elucidate the significance of variation in local habitat quality and landscape context on moth diversity in two nature reserves in North-eastern Italy. We evaluated 14 local descriptors like plant diversity or forest structure, and 14 landscape-scale components like habitat diversity and the distance to forest edges, condensed through a Principal Component Analysis. PC-axes served as predictors in linear mixed effects models, with moth diversity and catch size (corrected for the influence of temperature and humidity) as response variables. Furthermore, sites were sorted into four groups: 'high habitat quality', 'high landscape diversity', 'moderate quality' and 'low quality'. This was done to test whether local or landscape factors interact in modulating insect diversity. Our results indicate a strong influence of local factors, especially plant richness and biomass, on small-scale moth diversity. High diversity of nearby natural habitats also had a positive effect, while there was no correlation with landscape-scale attributes. Contrastingly, moth numbers were influenced by landscape diversity in 500-1000m radius. So, although high local habitat quality supports higher moth alpha diversity, it is also important to maintain the diversity of natural habitats on the landscape scale to preserve insect biomass and gamma diversity inside isolated reserves. Conservation efforts should be directed to preserve high vegetation and habitat diversity within reserves, while simultaneously keeping more varied landscapes around reserves might help stabilizing local insect assemblages.

Keywords

Biodiversity loss, moth communities, plant diversity, habitat diversity, Mediterranean coastal forests, conservation management

Introduction

Human-kind is drastically transforming the world's environment in the "anthropocene" (Zalasiewicz et al. 2010) leading to the overexploitation of natural resources and the loss of natural habitats (Lewis & Maslin 2015; Sanderman et al. 2017). Remaining natural areas are often highly fragmented and their quality as habitat for endangered biota may be further reduced due to spill-over effects from the surrounding landscape matrix (Habel et al. 2019a). Land use change is a prime reason why we are now facing the sixth global mass extinction (Ceballos et al. 2015). Insect decline has become a prevalent topic of mainstream media and scientific research in the last years (Hallmann et al. 2017; Leather 2018; Sánchez-Bayo & Wyckhuys 2019; Saunders 2019). But overshadowed by manifold dramatic statements, it has got lost how little we still know about insect populations and how they are regulated by environmental factors (Saunders 2019). Case studies as well as meta-analyses concerning insect decline might be biased due to researchers' expectations, an overly strong focus on single-factor-observations, an inappropriate mixing of correlation with causation (Altman & Krzywinski 2015) or by subjective research criteria

(Simmons et al. 2019). In fact, a multitude of drivers is in discussion to cause insect declines many of which are somehow attached to land use change (Habel et al. 2019a).

On the local scale, animal biodiversity is contingent upon the number of niches, and thus structural heterogeneity, provided by a site (Levine & HilleRisLambers 2009). In human-dominated landscapes, intensification of grassland and agricultural management reduces insect abundance and species richness (Chisté et al. 2016; Gámez-Virués et al. 2015; Habel et al. 2019c; Mangels et al. 2017). Similarly, forest management practices influence diversity (Thorn et al. 2015), functional composition (Gossner et al. 2013) and pest control potential of insect communities (Kärvemo et al. 2017). On the other hand, the loss of extensive land use practices is especially a problem for semi-natural grasslands (Uchida et al. 2016) and Mediterranean landscapes (Falcucci et al. 2006), where anciently open habitats disappear because of natural succession and subsequent forest regrowth. As natural succession changes profoundly the available habitats, also alterations in insect community composition can be observed (Habel et al. 2019b; Wölfling et al. 2019).

While the local quality of every site in terms of biodiversity is determined by the number of niches and the amount of resources it offers to biota, metapopulation and metacommunity theory predict that also the landscape context is important, since the processes of local extinction and recolonization strongly depend on landscape-scale aspects (Legrand et al. 2017). At this larger spatial scale, land use change often leads to the loss of natural areas and so reduces the amount of suitable habitats for many organisms. Landscape-scale effects comprise fragmentation and isolation of natural areas, reducing biodiversity and ecosystem functioning (Haddad et al. 2015) as well as disrupting gene flow between populations what can lead to local extinctions (Habel & Schmitt 2018). Furthermore, the dispersion behavior of species might be differentially affected favoring generalists to colonize secluded habitats (Habel & Schmitt 2018; Keinath et al. 2017), what can lead to functional homogenization and the loss of specialist species (Gámez-Virués et al. 2015).

Besides fragmentation and isolation, also landscape heterogeneity matters. This aspect can be dissected into two main components, compositional heterogeneity (e.g. landscape diversity) and configurational heterogeneity (e.g. edge density or habitat patch structure) (Perović et al. 2015). Reduced configurational heterogeneity is known to drive biotic homogenization and biodiversity loss (Gallé et al. 2019; Gámez-Virués et al. 2015; Hass et al. 2018; Perović et al. 2015), while high compositional heterogeneity, like a mix of different extensive grassland management methods, has been shown to enhance species diversity (Bonari et al. 2017; Fiedler et al. 2017). Most studies concerning landscape configuration and composition focus on open and agricultural landscapes. However, studies on poplar forest arthropods (Wang et al. 2019) and forest parasitoid metacommunities (Marrec et al. 2018) indicate that similar processes act in woodland habitats.

Talking about landscape-scale effects, ecological consequences of agricultural and forest management practices do not end at the field border. In fact, landscape-scale intensive land use is often discussed as key driver also reducing insect diversity and biomass within nature reserves (Seibold et al. 2019). Nutrients may drift from agricultural soils into water systems (Swaney et al. 2012) and also contribute to airborne NOx content (Almaraz et al. 2018). The eutrophication of ecosystems, arising from intensive agriculture, has been linked to changes in forest vegetation structure (van Dobben & de Vries 2017) and plant species loss (Simkin et al. 2016). Elevated nitrogen concentrations in plants can influence insect herbivores (Kurze et al. 2017, Kurze et al. 2018), but their effects on insect communities are still insufficiently investigated (Nijssen et al. 2017). However, plant-herbivore interactions seem to be altered by nitrogen input which also appears to favor pest outbreaks (Li et al. 2016). Besides nitrogen, pesticides are another major problem related to intensive agriculture. Not only can pesticides have adverse effects on non-target arthropods (Pisa et al. 2014), they may also drift into adjacent habitats (Botías et al. 2016; Zivan et al. 2016) where they affect pollinators and predacious insects (Krupke et al. 2017; Monteiro et al. 2013).

Finally, also light pollution impacts on nocturnal insects. Van Langevelde et al. (2018) found that moth species which are attracted to light have more strongly declined over the past decades than diurnal moths or species with no phototactic behavior. Light pollution may desynchronize internal clocks, disrupt behavioral synchronicity and reduce fitness through flight-to-light behavior (Owens & Lewis 2018). Furthermore, light exposure can alter important ecological interactions like pollination (Knop et al. 2017) and top-down control by parasitoids (Sanders et al. 2018). This has led to the assumption that light pollution is an important driver of insect decline (Owens et al. 2020).

While these multiple drivers of insect decline are often reviewed (Habel et al. 2019a; Sánchez-Bayo & Wyckhuys 2019), there is a lack in case studies investigating more than one or two factors simultaneously. We here tried to gather information on a wide range of factors which we suspected to modulate variation in moth diversity inside two isolated nature reserves. Our focus was on small-scaled changes in insect species diversity and individual numbers (as a proxy for nocturnal insect biomass), which we relate to local factors like plant richness or forest structure, and to landscape-scale parameters. Moths were chosen as target organisms, since this species-rich insect group is relatively easy to identify and sample in large numbers amenable to statistical analysis by automated light trapping (New 2004). Moth assemblages have often proven as suitable indicators mirroring environmental gradients (Uhl et al. 2016), and quickly responding to environmental change (Mangels et al. 2017; Rákosy & Schmitt 2011).

The main research question of our study was whether landscape-scale factors (‘context’) or local factors (‘quality’) are more important in shaping local variation in insect species diversity. Specifically, we tested the following hypotheses:

- Local plant species richness and forest heterogeneity increase moth diversity.
- Moth diversity and abundance are higher at sites with higher natural habitat diversity in the surroundings.
- The amount of, and vicinity to, modified landscapes negatively affects moth diversity.
- Even favorable local site conditions might fail in preserving insect diversity, when surrounding landscapes are simplified too much or altered.

Methods

Study areas

The study areas, Pineta san Vitale (hereafter PsV) and Pineta di Classe (hereafter PdC), are two isolated coastal relict forest reserves near Ravenna (NE Italy). Anciently, PsV and PdC were part of one big coastal forest area on sand dunes that developed between the 10th and 15th century through sedimentation (Buscaroli et al. 2011). The relatively open pine forests were used for cattle grazing, pine nut harvest and wood production (Andreatta 2010). At the end of the 18th century, about 6000ha of land were covered by these forests (Malfitano 2002). But then, abandonment of extensive land use practices, coastal urbanization and agricultural intensification lead to diminution and fragmentation. Today only the two forest patches PsV and PdC remain, with a total area of about 2000ha (Andreatta 2010; Malfitano 2002). Within these reserves, the former open pine woods subsequently changed due to succession into more natural forest (Wölfling et al. 2019). Today they are dominated by a mix of oak and pine forest sites, but also other habitats like reed vegetation, riparian forest and open sites can be found (Merloni & Piccoli 1999; Piccoli & Merloni 1999). Both reserves have high legal conservation status as part of the national park Po Delta (Consorzio del parco regionale del delta del Po 2004), UNESCO biosphere reserves (Po Delta, United Nations Educational Scientific and Cultural Organisation 2015), Natura 2000 sites (Joint Nature Conservation Committee 2017a, 2017b) and important bird area (BirdLife International 2019).

Surrounding landscapes are under intensive land use, as the Po plain is one of the most important agricultural areas in Italy (Musolino et al. 2018). Especially around PdC, large areas of agricultural land isolate the forest from any other patches of natural habitat. Furthermore, the industrial harbor of Ravenna directly neighbors the southern borders of PsV and is known to affect air and water quality of nearby habitats (Guerra et al. 2014; Lucialli, Ugolini & Pollini 2007; Uhl & Wölfling 2015).

Sampling sites

We chose 60 sites in mixed oak and pine forest areas (30 in each reserve), equally spread all over the reserve area (Fig. 7.1). With PsV having an area of about 950ha and PdC comprising an area of 900ha, each of the 30 sampling points per reserve had about 500m distance to its nearest neighbor. This was aimed to reduce spatial autocorrelation between data points. To ensure comparability, all light trapping sites were situated in mixed oak and pine forest, with - as far as possible - about 100m distance to other habitat structures. Sites furthermore had to be suitable for automated light trapping, which means that all of them were at small forest clearings to warrant sufficient light emission around the trap. Data were collected from April to September in the years 2015 to 2017. Each year 20 sites randomly chosen out of the 60 locations were sampled.

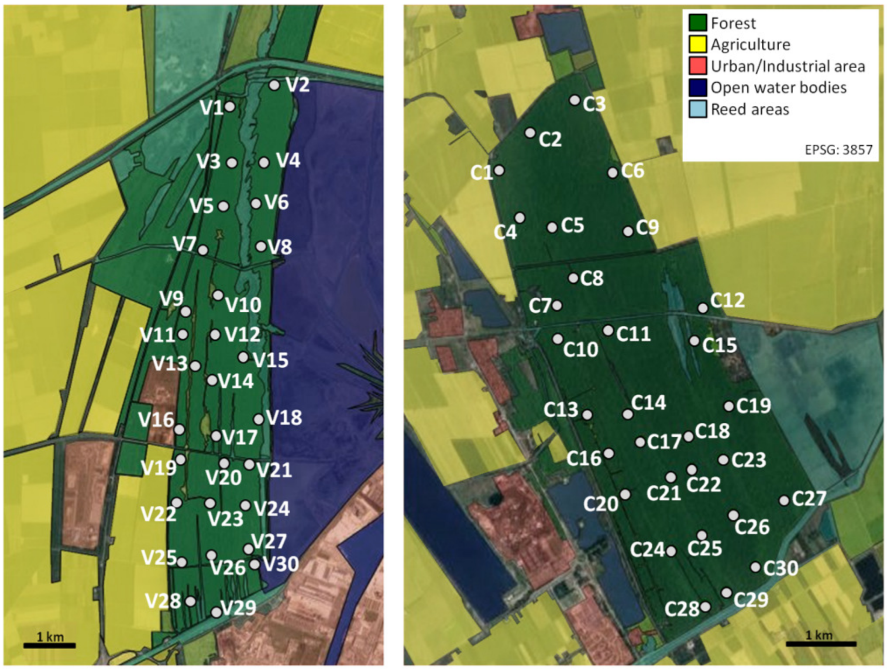

Figure 7.1: Images of the two study areas Pineta san Vitale (left) and Pineta di Classe (right) based on Google MapsTM satellite images and modified via QGIS. The 60 light-trap sites are shown in white. Colored areas indicate the landscape type like described in the legend. The coordinates of the study areas are: 44°27’48.09’’ - 44°31’39.15’’ N; 12°13’01.08’’- 12°14’16.97’’ O (PSV), 44°19’35.00’’ - 44°22’36.35’’ N; 12°15’35.51’’ – 12°18’04.46’’ O (PdC)

Data sampling

To analyze landscape patterns, we used the program QGIS (QGIS Development Team 2018), based on satellite images of the reserves taken in 2017, as provided in Google Maps^{TM}. Within 200, 500 and 1000m buffers around each of the 60 sites, proportions of the following habitats were measured: forest area, open sites, reed vegetation, arable land, open water bodies and urban/industrial areas (Tab. 7.1). Out of the first three habitats (forest, open sites, reed) we calculated natural habitat Shannon diversity, as these landscape elements are supposed to be suitable natural habitats for moths. Arable land and urban/industrial areas were summed up as “modified landscapes”. Edge density (in m/ha) served as a proxy for landscape heterogeneity. Furthermore, for each light-trap site the distance to the nearest water canal, the industrial harbor and the nearest forest edge were measured (Tab. 7.1).

Table 7.1: Environmental factors assessed for all 60 light-trap sites in the two forest reserves Pineta san Vitale und Pineta di Classe (NE Italy) as possibly influencing species diversity or abundance of moths. The background for each variable and its possible influence on moths is shortly sketched in the column “Rationale”

Landscape factors	
Factor	Rationale
Distance to forest edges (in m)	The distance to forest edges (edge effects) can influence the abundance of moth species with strong forest affinity (Slade et al. 2013)
Distance to canals (in m)	Canals ensure water supply inside the forest reserves and thereby alter plant community composition (Uhl et al submitted) and possibly herbivore communities
Distance to industry (in m)	The distance to industrial plants was correlated with micro-moth functional diversity in one of the study areas (Uhl et al. 2016)
Proportion of open habitats in 200m radius (logit transformed)	Factors characterizing the amount of nearby habitats, as habitat amount is an important factor for moth species richness (Merckx, Dantas de Miranda, and Pereira 2019)
Proportion of reed habitats in 200m radius (logit transformed)	
Proportion of open habitats in 1000m radius (logit trasformed)	Characterizes the landscape composition also at larger scales (see Merckx, Dantas de Miranda, and Pereira 2019) Forest habitat amount was only included here at larger scales, as by definition this was the main habitat type at small scales (mainly >90%) in the present study
Proportion of reed habitats in 1000m radius (logit transformed)	
Proportion of forest habitats in 1000m radius (logit transformed)	
Diversity of natural habitats in 200m radius	Diversity of natural habitat structures (viz. forest, open non arable areas and reed) is a measure of compositional heterogeneity, which is known to positively affect butterfly diversity in managed grasslands (Perović et al. 2015). Three different scales (200m, 500m and 1000m radius around the sampling location) were considered here.
Diversity of natural habitats in in 500m radius	
Diversity of natural habitats in 1000m radius (in m/ha)	
Edge density in 500m radius (in m/ha)	A measure for landscape configurational heterogeneity. In agricultural and grassland areas, configurational heterogeneity is known to affect pollinator abundance (Hass et al. 2018) and butterfly trait dominance (Perović et al. 2015). Two different scales (500 and 1000m radius around the sampling location) were considered.
Edge density in 1000m radius (in m/ha)	
Proportion of modified landscapes (logit transformed)	Modified landscapes are defined as sum of agricultural and urban areas (including streets and gardens). Used as a proxy for potential land use induced negative influences such as pesticide drift, light or air pollution (Lucialli, Ugolini, and Pollini 2007; Knop et al. 2017; Zivan, Segal-Rosenheimer, and Dubowski 2016)

Table 7.1 (continued): Environmental factors assessed for all 60 light-trap sites in the two forest reserves Pineta san Vitale und Pineta di Classe (NE Italy) as possibly influencing species diversity or abundance of moths. The background for each variable and its possible influence on moths is shortly sketched in the column "Rationale"

Local factors	
Factor	Rationale
Plant species richness	Plant species richness is known to positively affect moth species richness (Root et al. 2017); many moth species are host-specific herbivores during their larval stages
Functional dispersion of plants	Experimental studies indicate an influence of functional plant composition on arthropods (Symstad, Siemann, and Haarstad 2000)
Herb heterogeneity	Plant and animal beta diversity appear to be related (Zellweger et al. 2017)
Shrub heterogeneity	
Indicator value "nutrients"	Elevated nutrient contents of plants may shape the fitness of herbivorous insects (Kurze, Heinken, and Fartmann 2018) and therefore might also affect diversity
Indicator value "humidity"	Water availability shapes plant communities and reduces plant functional diversity in Mediterranean grasslands (Nogueira et al. 2018) and might therefore also influence moth diversity
Indicator value "temperature"	This indicator value is used as a proxy for the local microclimate, which can influence insect species richness and composition (Buse et al. 2015)
Forest density (in trees/ha)	Forest - especially host tree - density is known to affect moth pest outbreaks (Damien et al. 2016)
Crown density (logit transformed)	Canopy openness is linked to enhanced butterfly richness and abundance (Ohwaki et al. 2017) and also affects moth communities (Beck, Brehm, and Fiedler 2010)
Cover of deciduous trees (in m^3/ha)	A proxy for above ground biomass of deciduous trees. Forest community structure can alter herbivore communities (Jeffries, Marquis, and Forkner 2006)
Cover of conifer trees (in m^3/ha)	A proxy for above ground biomass of conifer trees. Forest community structure can alter herbivore communities (Jeffries, Marquis, and Forkner 2006)
Mean basal area	Used as proxy for forest age. Age and size class distribution (structural heterogeneity) can alter herbivore communities (Jeffries, Marquis, and Forkner 2006)
Standard deviation of basal areas	Used as proxy for forest structural heterogeneity. Age and size class distribution (structural heterogeneity) can alter herbivore communities (Jeffries, Marquis, and Forkner 2006)
Proportion of dead trees (logit transformed)	Estimation for tree mortality and forest health, which is known to affect ecological communities (Anderegg, Kane, and Anderegg 2012)

Vegetation was analyzed by doing five 1x1m^2 herb plots and five 5x5m^2 shrub plots per sampling site. Inside these plots, which were randomly chosen, all plant species were identified and recorded. Forest crown density was measured using a densiometer (Forest densiometers, Robert E. Lemmon, Rapid City). The proportion of dead standing trees around the light-trap location was estimated by sight. For analyzing forest structure, 10 point-centered quarter analyses as described by Mitchell (2010) were performed per light-trap site.

Tree species identity and height as well as their basal areas were also noted. From these measurements, forest density (in trees/ha), mean basal area per site (in m^2/ha) and the standard deviation of basal areas (as proxy for forest age heterogeneity) were calculated. Additionally, we estimated the cover of deciduous and conifer trees per site (in m^2/ha). From the plant lists (herb, shrub and tree species), plant species richness and the mean Ellenberg indicator values for soil nutrients, humidity and temperature per site were calculated. To take functional aspects of the vegetation into account, functional dispersion among the plant species per site was calculated using the packages vegan (Oksanen et al. 2018) and FD (Laliberté et al. 2014) within the statistical environment R (R Core Team 2018). For this purpose, the collated trait information of Uhl et al. (2020) was used. Herb and shrub beta diversity was expressed using the betadisper function for calculating multivariate dispersion (Anderson et al. 2006).

Moth-sampling was done twice per plot, once in early summer (June) and once in late summer (August). We used automated light traps as described by Axmacher & Fiedler (2004), equipped with two 18W light tubes (Sylvania blacklight and Sylvania white blacklight) and powered by 12V dry battery packs. These low-power light sources attract moths mostly from distances of about 10m or less (Truxa & Fiedler 2012). Sampling started at dusk and ended when the battery was finished, which usually was the case after 6-8 hours. We avoided full moon periods, which reduce light trap effectiveness, and bad weather conditions that are known to constrain moth flight activity (Jonason et al. 2014; Yela & Holyoak 1997). Temperature and air humidity were recorded during sampling nights by using data loggers (Lascar electronics, EL-USB-2 RH/TEMP Data Logger), which were placed besides the light traps at breast height. The following morning, caught moths were retrieved and stored in glassine paper bags. Later on, macro- and micromoths were spread (if required) and identified to species level using faunal monographs. Where necessary we dissected genitalia to ascertain species identification.

Data analysis

All local and landscape-scale factors were checked for normality and transformed if necessary. Proportions were logit transformed (Warton & Hui 2011). Moth community data (species counts as well as total individual numbers per plot) were square-root transformed. For moth species diversity, the bias-corrected exponential Shannon diversity index of Chao & Shen (2003) was used (Beck & Schwanghart 2010; Fiedler & Truxa 2012). For moth individual numbers, we first calculated a linear model with the mean temperature and humidity of each sampling night as predictors. From this model, we extracted the residual variation in moth individuals sampled per night, to eliminate the well-known strong influence of microclimate and weather on light-trap catches (Jonason et al. 2014). Moth diversity and residual moth number were compared between PsV and PdC by calculating average values and their standard deviation for each reserve. Residual moth number and moth diversity per site served as response variable in subsequent statistical models.

Altogether, we considered 14 local and 14 landscape factors as possible predictor variables for analysis (Tab. 7.1). First, we performed a PCA, separately for local and landscape factors, to reduce this number of predictors and to avoid collinearity, using the ‘psych’ R package (Revelle 2018). Out of each PCA, we extracted the first 5 PC-axes and named these after their factor loadings for clarity (Appendix 7.2). After that, linear mixed effects models with moth diversity as response variable and the extracted PC-axes values as predictors were calculated using the ‘nlme’ R package (Pinheiro et al. 2019). We included sampling year as random factor. The second random factor was the position of the sites either in PsV or in PdC. For residual moth individual numbers per night, sites were additionally included as random factor, as for every site two nightly catches were available. After testing every predictor separately, we also tested combined models and used a two-sided (forward and backward) stepwise AIC algorithm for model selection using the stepAIC function of the R package ‘MASS’ (Venables & Ripley 2002).

To test whether landscape context might override local negative effects, we assigned our sites to four groups. To delimit these groups, we used the representation of sites along the first two PC-axes and designed four convex hulls, defining which sites belong to which of the four groups (Fig. 7.2). Our aim was to group plots with common site characteristics as expressed by their PC-axes. Plots with high plant and habitat diversity around were deemed to have ‘high habitat quality’. Light-trap sites with low local quality, but high landscape diversity in their surroundings, were allocated into the second group (‘high landscape diversity’). The third group comprised sites with moderate plant and landscape diversity (‘moderate quality’). The fourth group (‘low quality’) represented sites with both, low local and landscape diversity. If favorable landscape context may compensate local negative effects, there should be no difference between the ‘high habitat quality’ group and the ‘high landscape diversity’ group. The groups were tested for differences in their moth species diversity and residual individual number via ANOVA (which is part of the basic statistical package of R).

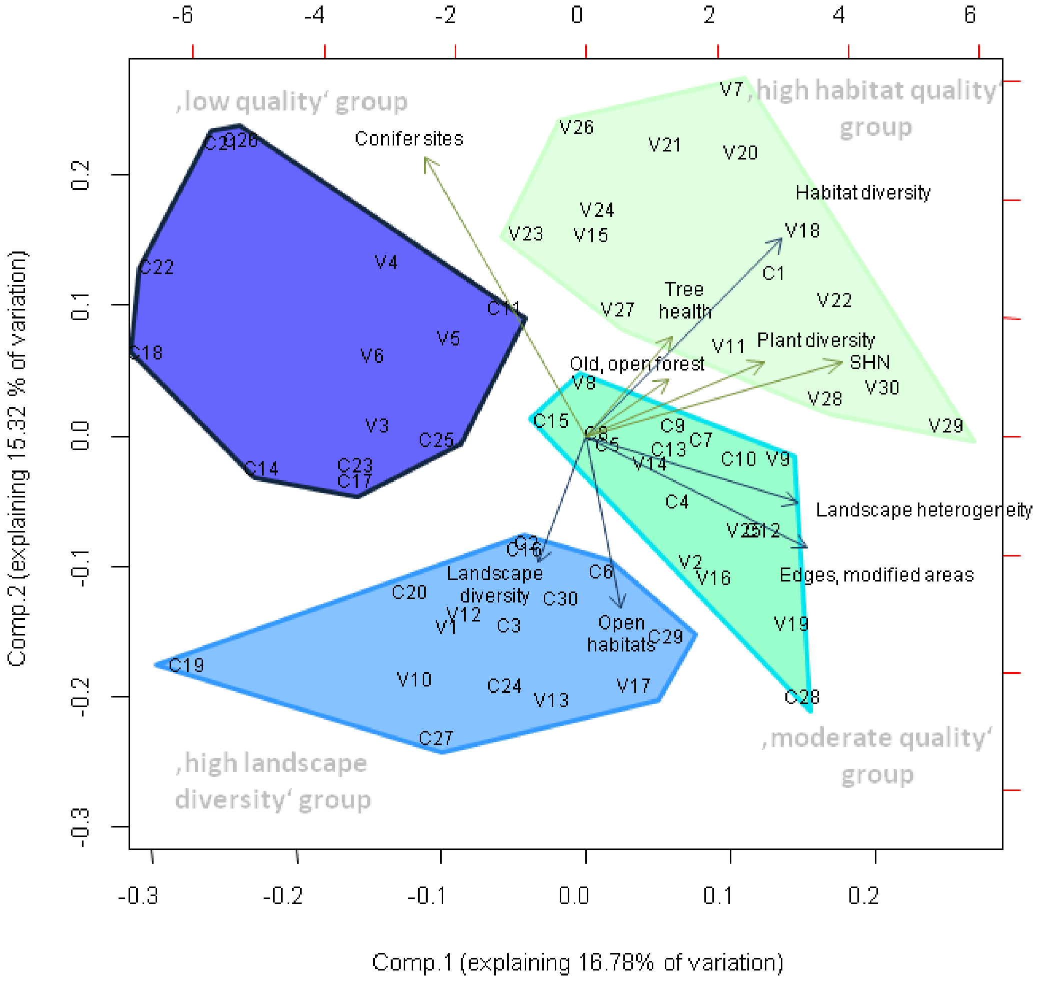

Figure 7.2: PCA ordination plot of the 60 light-trap sites, showing the four defined groups of sites. The shown vectors represent the used environmental variables. Convex hulls mark the groups: ‘high habitat quality’ group = light green, ‘moderate quality’ group= turquoise, ‘high landscape diversity’ group= blue, ‘low quality’ group= dark blue. Vectors referring to local habitat measures are marked as dashed lines, while those referring to landscape measures are solid

Results

In total 23,870 moth individuals were analyzed, which represented 392 species in 32 families. 81 species only were found in PsV, while 52 species were exclusively found in PdC (Appendix 7.1). Of these apparently ‘exclusive’ species, 38 were singletons or uniques in PsV and 22 in PdC, respectively. We observed more than threefold variation in local moth species diversity across sites. Mean local species diversity did not significantly differ between both reserves, although moth assemblages in PsV were on average slightly more diverse than in PdC (PsV: 43.60 ± 10.67, range: 27.38-69.81; PdC: 38.18 ± 9.90, range: 21.87-58.76). The residual variation in moth individual numbers, after accounting for effects of air temperature and humidity on trap catches, also did not show significant differences between PsV (0.86 ± 5.49 referring to on average 227.5 ± 202.6 individuals per nightly sample) and PdC (-0.86 ± 4.02 referring to on average 170.4 ± 130.4 individuals per sample night). As expected, temperature (β=0.25, p=0.004) as well as humidity (β=-0.28, p=0.001) strongly shaped the number of moths captured per night and site.

Among the local factors, the first 5 PC-axes explained 71% of the total measured environmental variation. The first axes mainly describes a gradient from open, dry and warm places to more forested ones, with denser canopy, higher humidity and more soil nutrients. The second one describes forest age and structure, from dense forest stands with lots of young trees to open sites with old, tall trees. Plant taxonomic and functional diversity is represented by the third axis, while the fourth axis indicates the proportion of conifers at the sampling site. The fifth axis is linked to the estimated proportion of dead standing trees and therefore is representing forest and tree health.

The first 5 PC-axes extracted out of the landscape factors explained 84% of the total measured variation. The diversity of natural habitats within a 200m range is captured by the first axes, while the landscape wide diversity (1000 m radius) of natural habitats is represented by the second axis. The third axis indicates a gradient from forest centers to the reserve edges, where also the proportion of modified landscapes around a 1000m radius is increasing. The fourth axis is mainly loaded by the edge density measurements and therefore represents landscape heterogeneity in the surroundings of each light-trap site. Finally, the fifth landscape axis shows how many open sites can be found within a 200m radius around the light traps.

Overall, relationships between local moth species diversity and the 10 factors tested as predictors were rather weak. When factors were tested individually (Appendix 7.3), moth diversity was only significantly and positively related to the gradient from dry and open sites to shady, humid and nutrient rich sites (hereafter called “SHN”), local plant diversity (Fig. 7.3A-B), and to the diversity of natural habitats around light-trap sites (Fig. 7.3C). In a multivariate analysis, only position in the SHN gradient and plant diversity were retained as predictors in the best model (Appendix 7.3). In all cases, these models explained only a small fraction of variance (conditional R² between 0.17 and 0.27).

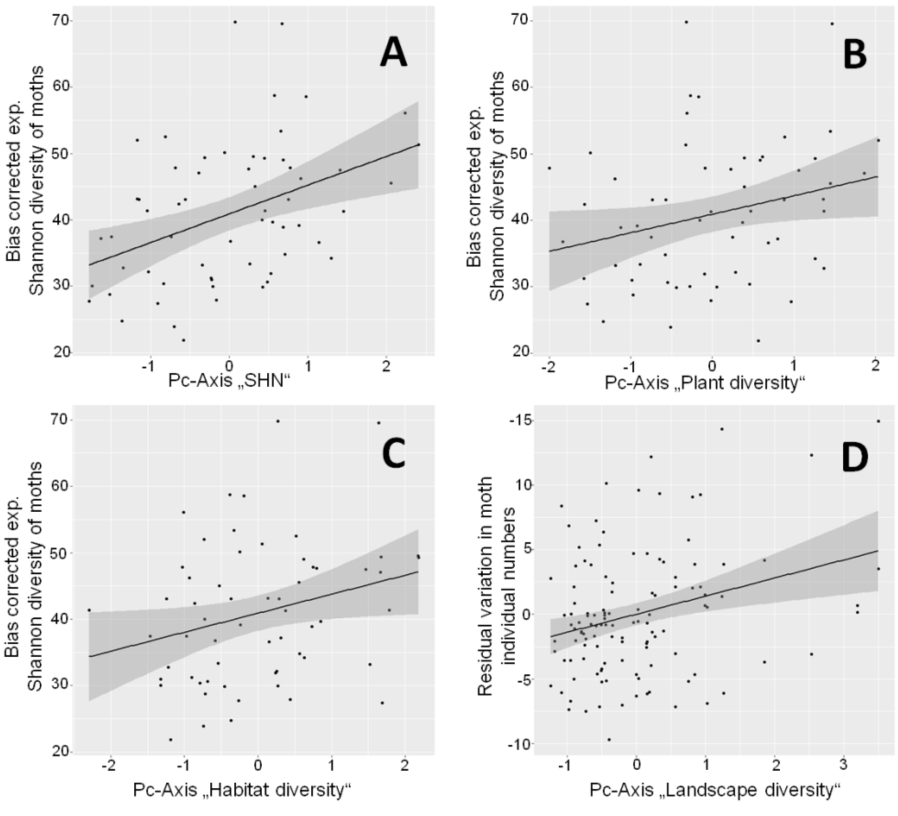

Figure 7.3: Linear models of (A) moth species diversity along the SHN-gradient, (B) moth diversity and the Plant diversity-axis, (C) moth diversity and the habitat diversity-axis and (D) the residual variation in moth numbers captured per site and night and the landscape diversity gradient. In panels A-C each dot represents one of the 60 light-trap sites; in panel D each dot represents one sampling night per site. For details on statistical results see Appendix 7.3

For residual variation in moth numbers sampled per night and site, only landscape diversity had a highly significant positive effect in regression models testing individual factors as potential predictors (Appendix 7.3; Fig. 7.3D). None of the local factors showed a significant correlation with residual moth numbers. The best multivariate model retained the SHN gradient and landscape diversity as relevant predictors. Again, the explanatory power of all models was low (R^2 between 0.00001 and 0.11).

The classification of sites into four groups revealed that 'high habitat quality' sites had on average the highest moth species diversity, followed by the 'moderate quality'-sites, and the 'high landscape diversity'-sites. Lowest moth diversity was found at the 'low quality'-sites (ANOVA: Df = 3;59, F = 3.57, p = 0.02; Fig. 7.4A). In contrast, residual moth numbers showed no significant difference between these groups (ANOVA: Df = 3;119, F = 0.13, p = 0.94, Fig. 7.4B).

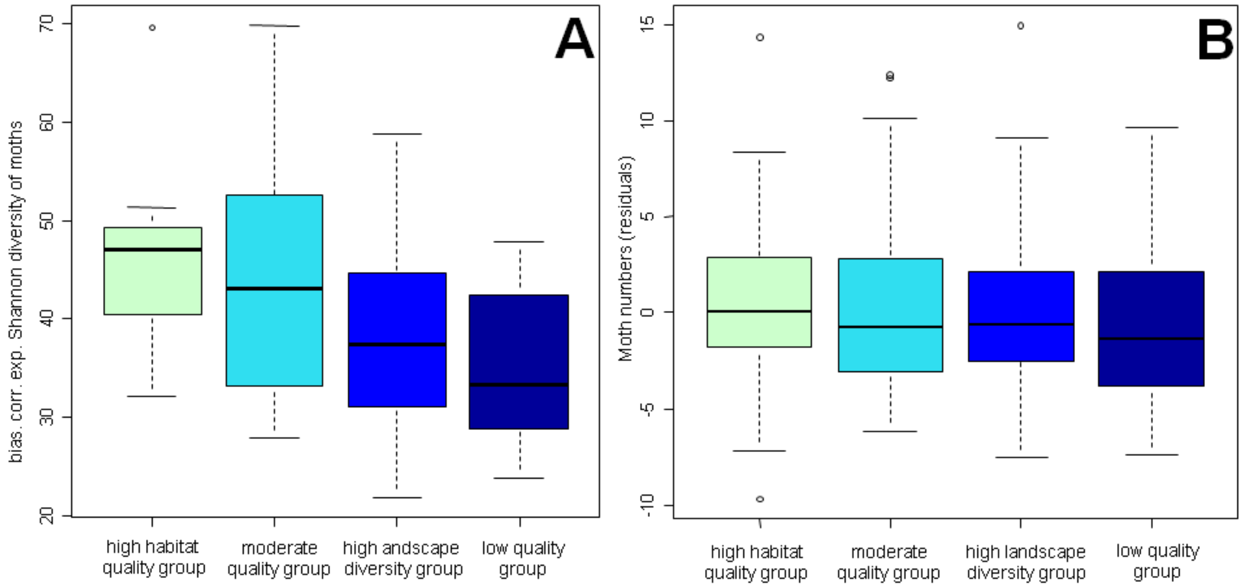

Figure 7.4: Boxplots showing the bias-corrected exponential Shannon diversity values of moths (A) and the residual moth numbers (B) for the four groups of sites: 'high habitat quality' (light green, N=15), 'moderate quality' (turquoise=17), 'high landscape diversity' (blue, N=15) and 'low quality' (dark blue, N=13)

Discussion

Moth species diversity

Our analysis showed that, although there was substantial site-to-site variation in moth diversity across the two studied nature reserves, we could attribute only minor fractions of this variation to factors describing local habitat quality. However, most of the variation could not be explained by any of the observed environmental variables. This might be due to further local attributes like microclimate or natural fluctuations because of predatory pressure. Furthermore, each plot was only sampled twice. As a consequence some singleton species, occurring by chance, can have a major effect on the results. To get a better insight and to reduce this bias, more samples per plot are needed.

By looking at small-scaled diversity patterns, local factors turned out to be far more relevant than descriptors of the landscape context. Moreira et al. (2016) stated that it's unclear if resource availability (plant biomass) or heterogeneity (plant species richness) favor herbivore diversity. Taking into account both local plant diversity and the position of sites in the SHN gradient, our results suggest that number of niches for plant-related insects and plant biomass (which should be higher at SHN sites) together are the most important factors promoting a high insect diversity within the two reserves. The importance of plant richness for Lepidoptera diversity has already been demonstrated for larger-scale diversity patterns (Root et al. 2017) and for agroecosystems (Burgio et al. 2015). Our results suggest that this effect is even observable, when looking at small-scaled changes of plant richness within the same habitat type, viz. oak forest stands. Along the SHN gradient, water and nutrient availability mainly determine vegetation structure and also favor higher moth species diversity. Water and nutrients are the main limiting factors for vegetation in Mediterranean ecosystems (Pérez-Ramos et al. 2012), and are - in this study - linked to higher crown density. Concomitantly, at shadier sites the microclimate changes, being in general cooler than at dry and open localities. In fact, a closed (sub)canopy and heterogeneous forest structure is known to regulate forest microclimate and is capable to buffer even climate change effects such as increasing heat and drought stress (Ehbrecht et al. 2019; Frey et al. 2016). This enhanced above ground biomass and stable microclimatic conditions might also favor more species diversity to occur at higher trophic levels such as in herbivore insect communities.

Habitat diversity around the light trap locations showed only a weak positive correlation with moth diversity. As habitat diversity increases, where there are equally large amounts of grassland, forest and reed areas, our findings might indicate a possible habitat-amount relationship between the number of moth species and the available amount of natural habitats in 200m radius. This “habitat amount hypothesis” has already been supported for forest and meadow moth diversity and the amount of forest and meadow habitats (Merckx et al. 2019). This might also in our case be the main driver of the discovered relationship between habitat and moth diversity. However, the habitat-amount hypothesis is normally only applied to studies regarding one habitat type and the species occupying in such habitats (Fahrig 2013). Expanding this idea, the more suitable habitats (= higher natural habitat diversity) are available in an appropriate scale of effect, the higher local species diversity (=alpha diversity, rather than species richness of a single habitat type) is to be expected.

As Fahrig (2013) states that “habitat amount isn’t everything” and “there is ample evidence that the matrix can influence species richness”, it might also be doubtful to negate any landscape matrix effects like isolation on the study areas. Landscape diversity apparently did not influence small-scaled alpha diversity patterns inside the reserves. However, there might be an effect on all-over-gamma diversity of moths. In fact, Seibold et al. (2019) has shown that insect gamma diversity decreases more at sites, with high amounts of agricultural areas around. Also at our sampling areas the total species richness (viz. gamma diversity) of the two forest reserves is low compared to other Mediterranean forest areas (Infusino et al. 2017). One possible explanation for this might be that PsV and PdC are difficult to colonize for some moth species due to their isolated position amidst human modified areas. Furthermore, both forest reserves are also influenced by abiotic constrains like seaspray, sandy ground and soil salinity as they are situated near the Adriatic coast.

For preserving local diversity, it seems favorable to strengthen structural and plant species rich forests by local extensive conservation management, providing different habitats on the one hand, and developing a near-natural forest structure with uneven aged trees and understory on the other hand. Such structurally rich habitats might also be able to better compensate hot summers and reduced water availability, which will become more and more prevalent in times of climate change, especially in Mediterranean regions.

Moth individual numbers

Local factors did not show any effect on moth individual numbers, clearly contrasting the results with moth diversity as response factor. Yet, other studies well support the influence of local factors like plant richness and management method on insect abundance (Alison et al. 2017, Chisté et al. 2016). This leads us to the assumtion, that only for small-scale local changes, like in our study, correlations might not be detecteble, as abundances are naturally fluctuating to a great extend.

However, landscape-scale characteristics - especially the diversity of natural habitats in 500-1000m radius - were important for moth individual numbers. We only found a correlation between landscape compositional heterogeneity (diversity) and moth abundance, but no effect of landscape configurational heterogeneity (edge density). Landscape configuration is known to affect pollinator abundance (Hass et al. 2018) and functional diversity (Perović et al. 2015) in agroecosystems, where field edges and hedgerows are important habitats influencing metacommunity dynamics and species persistence (Ponisio et al. 2019). For small-scaled diversity patterns in semi-natural forest habitats and nature reserves, however, habitat edges (either between forest and open landscapes or between canals/water and terrestrial habitats) might have a different function. Here, edges could still be suitable habitats for some species, but for others they might rather represent insurmountable barriers. Furthermore, these edges are in between other suitable habitats, whereas agricultural field margins might be the only refuges in between intensively managed arable land.

Concerning landscape compositional heterogeneity, i.e. landscape-scale (500-1000m) habitat diversity, our results might indicate that the habitat amount hypothesis is not only suitable for species diversity, but might also be true for individual numbers, but with differing scales of effect. So, a higher diversity of near-natural habitats in the surroundings may play a role for preserving insect biomass inside nature reserves. Consequently, landscape simplification, although not directly affecting the insect alpha diversity inside nature reserves in our case study, might be a major threat when it comes to insect biomass. This may have repercussions on the capability of reserves to provide the food basis for higher trophic levels, like insectivorous arthropods, birds and bats. Single species mass outbreaks as often observed in intensified agricultural landscapes might not be able to provide stable food resources as such gradations only occur unpredictably over short time periods.

So, for preserving insect biomass, it seems that landscape-scale actions are needed. Enhancing landscape diversity and connectivity between remaining near-natural areas might be crucial for maintaining high insect individual numbers as well as high gamma diversity inside isolated nature reserves. Looking at Mediterranean coastal forest reserves, only very few fragmented patches of these ancient forests remain to the present day (Falcucci et al. 2006), underlining the importance of landscape-scale conservation management for this special biodiversity hotspot region (Myers et al. 2000).

Combining local and landscape variables

Can landscape effects, like high landscape diversity or structural heterogeneity, compensate negative effects of local factors? Of course, a sharp division between local and landscape variables is often not warranted, as there might be inter-correlations such as local nitrogen influx due to landscape-scale agricultural land use (van Dobben & de Vries 2017). However, as the scope of our study was to evaluate the relative importance of different scales of effect, we here tried to conceptually handle local and landscape-scale predictors separately.

Following Tscharntke et al. (2012), favorable landscape structure might even over-compensate poor local habitat quality in terms of biodiversity. For agricultural landscapes, matrix complexity has been shown to enhance biodiversity, as more hedgerows and field margins are important habitats for different insects like pollinators, predators and herbivores (Gallé et al. 2019; Hass et al. 2018). Also diverse management methods, like different mowing strategies enhance agricultural landscape diversity and positively affect insect communities (Fiedler et al. 2017). But how about isolated forest nature reserves embedded in a highly hemerobic landscape? We found highest moth diversity values at the 'high habitat quality' stands, supporting our results from the linear mixed effects models that local factors are most important for moth diversity. Sites of the 'high landscape diversity' group as well as of the 'low quality' group had in contrast lower moth diversity. In our case study, therefore, an 'advantageous' landscape context does not seem to be able to compensate 'low local quality' like low plant and habitat diversity.

Regarding the 'low quality' sites, plots of this group were mainly situated in monotonous conifer forest stands, which can be found in the center of PdC. Here, the planted pine trees are the most characteristic floral elements, with few deciduous trees in between. The lack of other habitat structures such as open sites or reed vegetation in the vicinity of the sampling sites as well as the low local plant species richness might be the main reasons for the low moth diversity observed there. From a conservation perspective, it seems favorable to avoid monotonous forest sites. Structurally heterogeneous and species-rich forests might be much more capable to preserve local insect diversity, especially when other habitat structures like forest clearings (open sites) and water reservoirs (e.g. canals, lakes or reed areas) break up the canopy.The edge-sided 'moderate quality' stands, characterized by medium plant, habitat, and landscape diversity, supported second highest moth diversity. So, contrary to our hypothesis, landscape context did not override local effects, but rather favorable local conditions seem to compensate possible negative effects from surrounding land use. So, edge sided stands were per se not worse than sites in midst of the nature reserves, indicating that also these areas can provide suitable habitats for many moth species.

Conclusion

To understand the complex interplay between multiple factors and species erosion, it is important to understand small-scaled changes in species diversity. In our analysis, mainly local factors seem to be decisive for local diversity patterns. Especially plant richness and above ground biomass, but also the amount of different habitat structures, favors higher moth diversity. In contrast, individual numbers were mainly dependent on landscape compositional heterogeneity. Comparing local quality and landscape context parameters, high landscape diversity is not able to compensate poor local quality. Vice versa, high plant and habitat diversity might offset possible negative influences from surrounding land use practices. Finally, there's a strong need to more precisely zoom into species functional identity and community composition, to evaluate small-scaled changes in natural habitats. From a conservation perspective, local management should focus on maintaining structural and plant species rich habitats as already small-scaled vegetation changes within the same habitat type can significantly influence moth diversity. Monotonous forests, without other habitats breaking up the vegetation structure, seem to be incapable to maintain local insect diversity. Landscape simplification did not affect small-scale insect alpha diversity patterns inside nature reserves, but seems to be decisive for reducing insect gamma diversity and insect biomass, what subsequently might also affect higher trophic levels like birds and bats. So, to guarantee ecosystem function and stabilize food webs, also the landscape-wide diversity of natural habitats and connectivity between near-natural areas has to be considered in conservation management.

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8. From forest to fragment: Compositional differences in coastal forest moth assemblages and their environmental correlates

Abstract

Patterns of β-diversity can provide insight into forces shaping community assembly. We analyzed species-rich insect assemblages in two reserve fragments that had once been part of one contiguous Mediterranean coastal pine forest. Local environments are still similar across both fragments, but their landscape context differs strongly, with one surrounded by intense agricultural land, while the other neighbors the urbanized area of Ravenna. Using 23,870 light-trap records of 392 moth species, and multiple local and landscape metrics, we compared the relative importance of habitat- versus landscape-scale environmental factors for shaping small-scale variation in differentiation and proportional insect β-diversity across 30 sites per reserve.

Moth assemblage composition differed substantially between fragments, most likely due to ecological drift and landscape-scale variation. For proportional β-diversity, especially local forest structure was important. At well developed forest sites, additive homogenization could be observed, whereas the lack of typical forest species at dry, dense, and younger forest sites increased species turnover (subtractive heterogenization). For differentiation β-diversity, local and landscape-scale factors were equally important in both reserves. At the landscape scale (500 m radius around light-trapping sites) the proximity to urban areas and the fraction of human-altered land were most important. At the habitat scale, gradients in soil humidity, nutrient levels and forest structure mattered most, whereas plant diversity had very little explanatory power. Overall, landscape-scale anthropogenic alterations had major effects on moth communities inside the two conservation areas. Yet, even for these parts of one formerly contiguous forest trajectories in community change were remarkably idiosyncratic.

Keywords

Mediterranean insects, β-diversity, species turnover, land use, conservation areas

Introduction

Recently, various studies have reported drastic insect declines across landscape levels (Habel et al. 2019a; van Klink et al. 2020). Human actions like land use change and intensification are major drivers of species losses in urban and agricultural landscapes (Allan et al. 2015; Newbold et al. 2016). Yet, Seibold et al. (2019) and Hallmann et al. (2017) found that severe insect decline is also detectable inside conservation areas. There, local as well as landscape-scale correlates have been shown to be associated with local variation in the diversity of insect communities (Uhl et al. 2020b). Inside nature reserves, anthropogenic actions might indirectly influence population dynamics through fragmentation and isolation effects (Habel & Schmitt 2018; Rossetti et al. 2017), or alter communities by nutrient and pollutant drift (Botías et al. 2016; van Dobben and de Vries 2017). In fact, most conservation areas nowadays exist as isolated fragments, surrounded by human-modified areas. With fragmentation, gene flow between habitat patches can become interrupted (Habel & Schmitt 2018). Some species might not persist on the long run within isolated patches, depending on their life-history traits (Slade et al. 2013). As a result of this directional environmental filtering combined with stochastic ecological drift, anciently connected communities might diverge over time, forming new assemblages with species adapted to survive under the circumstances of the according habitat patch (Vellend 2016).

While the recent insect decline debate is often focusing on species richness and biomass, there is a lack in studies investigating community composition and species turnover. Species composition of ecosystems can give important insights into environmental change (Dornelas et al. 2014; Mendenhall et al. 2012). In fact, impacts on ecosystems primarily are reflected by changes in community composition, as species sharing certain traits might be filtered out and replaced by others (Dornelas et al. 2014; Slade et al. 2013). Losses in α-diversity, in contrast, might only occur with delay, when significant changes in species assemblages might already have impacted ecosystem function (Mori et al. 2018). Changes of the local habitat structure and differing management regimes can affect species composition (for butterflies and moths: Fies et al. 2016; Mangels et al. 2017; Truxa & Fiedler 2012). Furthermore, communities can be altered by landscape-scale changes such as landscape simplification (Gámez-Virués et al. 2015) or increasing anthropogenic influence due to pollution or eutrophication (Uhl et al. 2016; WallisDeVries & van Swaay 2017).

Quantifying the compositional change in communities needs a clear definition, as it is often mixed up with other aspects of β-diversity. In fact, there are various interpretations of β-diversity, leading to multiple β-diversity indices, which address different aspects of compositional variation (Tuomisto 2010a, 2010b). Following its original definition, β-diversity describes a multiplicative or additive partitioning value, by putting α-diversity in context to larger scale γ-diversity (Anderson et al. 2011). Jurasinski et al. (2009) suggested summing up such measures as “proportional diversity” measures. Tuomisto (2010a) in contrast suggested calling the multiplicative partitioning of β-diversity “true beta diversity”, as it is most likely fitting the classical definition, while additive β-diversity should be called “regional diversity excess”. Proportional β-diversity, or true β-diversity, is a correlate to α-diversity, putting the local species diversity in relation to the regional γ-diversity. However, more commonly β-diversity is used in the sense of differentiation diversity i.e. variation in species composition between sites (Anderson et al. 2011; Jurasinski et al. 2009). By partitioning the variation in community structure as a response to environmental factors, differentiation diversity can give insight into how much of observed community change in space or time can be explained by environmental variation (Anderson et al. 2011). We here analyze both, proportional β-diversity and differentiation diversity, in an attempt to unravel the influence of a variety of environmental factors on these two complementary aspects of β-diversity.

First, we want to investigate, how insect assemblages of two anciently connected Mediterranean forest nature reserves nowadays differ in their composition and proportional β-diversity. By analyzing multiple environmental variables, we also try to unravel which ecological filters likely caused this divergence. Second, we are interested in the relative importance of different sets of environmental characters, shaping variation in community composition within each of the two reserves. Especially the potential influence of human actions outside the conservation areas, such as agricultural land use and the proximity to urbanized areas, is considered. Our main research hypotheses therefore are:

- The moth assemblages of the two reserves today differ significantly from another, although both reserves share the same history and provide similar habitats.
- Proportional β-diversity informs about the environmental drivers shaping community assembly on the small scale. A well developed forest structure should provide more niches and therefore favor the occurrence of larger subsets of the regional species pool (additive homogenization). Potential

pollution sources otherwise might cause subtractive heterogenization, as species get lost from the local assemblages.

- Looking at differentiation diversity, effects of both – local and landscape-scale factors – are reflected by the small-scaled moth community composition. However, to understand how these factors shape moth communities, one has to look at the occurrence patterns of individual species and their traits.

As a target group, we selected nocturnal Lepidoptera (‘moths’) since these terrestrial insects are usually rich in species, can easily be sampled using light traps, and reflect a wide variety of bionomic strategies (Slade et al. 2013; Summerville & Marquis 2017). At the same time moths show close functional links to the vegetation of their habitats, mostly through the nutritional demands of their larval stages. Accordingly, a plethora of studies revealed that species composition of moth assemblages usually closely tracks environmental variation down to small spatial scales (Guariento et al. 2020, Habel et al. 2019b; Wölfling et al. 2019).

Methods

Study sites

Our study sites were located within two Mediterranean coastal forest reserves in North-Eastern Italy, near Ravenna. The reserves Pineta san Vitale (hereafter PsV) and Pineta di Classe (herafter PdC) once were part of one big coastal forest area, covering an area of approximately 6000 ha (Malfitano 2002). However, after 1796, deforestation due to land use change and the development of the city and harbor of Ravenna lead to the disappearance of most of the former natural forest area. Nowadays, only about 2000 ha, split up between the two disconnected reserves, remain (Andreatta 2010; Malfitano 2002). As a part of the regional park Po Delta, they both are listed as UNESCO biosphere reserves, and are also partly considered as important bird areas, wetlands of international importance following the convention of Ramsar, and Natura 2000 sites.

The more northern reserve PsV has a total area of about 950 ha and directly neighbors the industrial harbor of Ravenna. To the east, the lagoon Pialassa Baiona forms the border of the reserve, whereas other near-natural wetland areas adjoin to the north and north-west of PsV. In the south-west, agricultural fields and other anthropogenically modified areas neighbor the reserve. The vegetation of PsV mostly consists of mixed oak and pine woods, but also reed areas, open grassland, and riparian forest. Therefore, PsV is a structurally rich near-natural reserve with many different vegetation types, offering typical Mediterranean warm and dry habitats on the one hand, but also riparian and wetland areas with more humid conditions on the other (Merloni & Piccoli 1999).

PdC, the more southern forest reserve, is about 10 km away from PsV, has a total area of about 900 ha, and is mostly surrounded by agricultural areas. Only in the south-east of PdC, near-natural wetland areas adjoin the reserve. As in PsV, the main vegetation type of PdC is mixed oak and pine woods. However, this reserve has not as much structural heterogeneity as PsV and local conditions seem to be drier, as indicated by the vegetation (Uhl et al. 2020a). Additionally, some pine forest parts in the center of PdC are quite monotonous, with impoverished plant diversity and no other habitat structures in their surroundings (Piccoli & Merloni 1999). In the south-west, very dense and young pine forest stands can be found, indicating more recent reforestation activities from about 30 years ago (Enrica Burioli, pers. communication).

Within each of the two reserves, 30 sampling sites (60 sites in total) with on average 821m distance to each other (SD ± 280m) were chosen. By doing so, we wanted to achieve equal distribution of sampling points throughout the reserves. All locations were situated in mixed oak and pine forest to ensure comparability of the habitats where the samples had been taken. Furthermore, sites were selected in such a way that in a radius of about 100m no other vegetation types occurred prominently. Locations had to be accessible by car and were always placed at small forest gaps, so that no bushes and trees could hinder light emission of the light traps used for moth sampling.

Data sampling

We analyzed landscape structure at two different ranges (200m and 500m radius) around each light trap site, based on aerial photographs taken in the year 2017, as provided by Google Maps^{TM}. This was done to see which spatial scale effect of the surrounding landscape was most influential on moth communities. The 200m range represents the small-scale surroundings, while the 500m range stands for the large-scale context extending into the landscape outside of the reserves. Within each perimeter, we quantified landscape elements using the program QGIS (QGIS Development Team 2018). In particular, the proportions of forest, reed and open grassland areas were measured, as well as the proportion of areas covered by open water bodies, agricultural fields, and urban/industrial areas. The latter two ones were summed up as “human-modified areas” in subsequent analyses. Based on the area fractions of forest, reed and grassland areas, the diversity of natural habitat areas was calculated, using the Shannon index. Edge density (in m/ha) served as measure for landscape fragmentation. Additionally, the distance of moth sampling sites to the nearest forest edge, industrial area and water canal was measured.

Vegetation was sampled within five 1x1m² plots for herb layer, and five 5x5m² plots for shrub layer at each site. In each of these herb and shrub layer plots, every plant species was identified and listed in an incidence matrix. Forest structure was analyzed by doing ten point-centered-quarter (PCQ) analyses per sampling site, following Mitchell (2010). Each tree that was included in the PCQ-analysis was identified to species level. Out of the PCQ-data, we were able to calculate forest density (in trees ha^{-1}), cover of deciduous trees (in m²ha^{-1}), cover of conifer trees (in m²ha^{-1}), mean basal area of trees (in m²), and the standard deviation of basal areas. Additionally, canopy density was recorded by using a forest densiometer (Forest densiometers, Robert E. Lemmon, Rapid City). The proportion of dead standing trees was estimated by sight. From the aggregated plant species incidence data (herbs, shrubs, and trees), we calculated plant species richness per plot. As a measure of β-diversity among the vegetation, multivariate dispersion for the herb and shrub layer was calculated for each site (Anderson et al. 2006). Functional dispersion of plants was also calculated, following Laliberté et al. (2014), using the plant incidence data and a matrix with collated trait information as described in Uhl et al. (2020a). Furthermore, plant indicator values after Ellenberg were collected from Pignatti et al. (2005). From these latter data, we calculated a mean indicator value for soil nutrients, humidity and temperature for every light-trap site. Further information on vegetation sampling can be found in Uhl et al. (2020a).

Moths were sampled using automated light traps as described in Axmacher and Fiedler (2004). We used two 18W light tubes (one Sylvania black light and one white black light tube) as light source, powered by 12V dry battery packs. Start of the sampling was at dusk with a sampling duration of 6-8 hours per night. Data collection took place from 2015-2017 in May and June for the early summer moth communities and in August for the late summer moth communities. Each year, we sampled 20 randomly chosen sites out of the 60 locations, avoiding full moon periods and spells of rain, as both these factors may strongly affect flight behavior of moths (Yela & Holyoak 1997). Subsequently, all moths captured in the traps were identified to species level, aggregated per site, and the resulting abundance-weighted species × site matrix served as basis for all explorations of moth diversity (see Uhl et al. 2020b for further details).

Data analysis

As a first step, we analyzed the differences in moth composition between the two anciently connected reserves. This was done by identifying indicator species for each reserve via the ‘indval’ function, as included in the R package ‘labdsv’ (Roberts 2016). We compared environmental variables of PsV and PdC to determine candidate predictors potentially responsible for the divergence of the two forest moth assemblages using Mann-Whitney U-tests, adjusted for multiple comparisons by false discovery rate control (Benjamini & Hochberg 1995; Pike 2011).

For the further analyses of small-scale variation in community composition (differentiation diversity) and proportional β-diversity, we did not use the raw environmental factors, but rather condensed these into principal component axes (PC-axes). This was done to avoid collinearity and to reduce the large number of potential environmental predictors. Principal Component Analyses (hereafter PCA) were performed separately for the local and landscape-scale variables. Assuming that different environmental conditions might be differentially important for the two reserves, we calculated reserve specific local and landscape PCAs for PsV and PdC separately. So in total, four PCAs (local-PsV, local-PdC, landscape-PsV, landscape-PdC) with varimax rotation were performed in the R environment using the package ‘psych’ (Revelle 2018). In the local PCA, 14 factors were included as variables (Appendix 8.2). In the landscape-scale PCA, 8 factors were included (Appendix 8.3). The number of the extracted PC-axes was determined through the Kaiser criterion. The resulting PC-axis scores of sampling sites then served as predictors in linear models and in multivariate ordinations of the local moth communities (see below).

Using the moth community data, we calculated the exponential Shannon α-diversity for each sampling site. Additionally γ-diversity was calculated the same way, but with moth data from all 30 locations per reserve pooled. By doing so, we received two γ-diversity values, referring to either PsV or PdC. As we were especially interested in partitioning diversity into proportional fractions, we decided to use the proportional species turnover (viz. $\beta = 1-\alpha/\gamma$) as measure for proportional β-diversity (Tuomisto 2010a). This β-diversity index is a multiplicative partitioning method defining local assemblages as fractions of the regional species pool. By dividing the observed local species diversity fraction from 1, the index becomes a measure for “turnover”, matching the original definition of β-diversity. So, small values of this β-diversity imply that the local community is nearly as species rich as the entire region (based on large species subsets), while larger values indicate that locally, only minor fractions of the all-over γ-diversity can be found. Small β-values therefore indicate small species turnover, while larger values indicate a rather heterogeneous representation of species across sites.

As the local proportional β-diversity values ($\beta_{observed}$) are all dependent on the regional γ-diversity, there is interdependence between the observed β-diversity values. To correct for the effect of this dependency, we additionally calculated the standardized β_{dev} as suggested by Mori et al. (2014). By using a null model with fixed species occurrence frequencies and randomizing 999 times, we calculated the mean null distribution of β-diversity (β_{null}) and the SD of the null distribution (β_{SD}). The standardized β-diversity β_{dev} is defined as $(\beta_{observed} - \beta_{null})/\beta_{SD}$ and can inform about “the magnitude of deviation from the expected β-diversity in a random assembly process” (Mori et al. 2014).

Standardized β-diversity (β_{dev}) served as response variable in linear models, where the PC-axes of the environmental variables were used as predictors. Models were calculated in the R work space using the ‘nlme’ package (Pinheiro et al. 2018). Best model selection was done via the Akaike information criterion and the 'stepAIC' function of the 'MASS' package (Venables & Ripley 2002). Additionally, we tested for significant differences between the PsV and PdC β-diversity values. Like for the environmental variables, we therefore used the Mann-Whitney U-test.

Looking at differentiation β-diversity, we tested if there is a significant difference between the reserve specific moth communities. For this, a Bray-Curtis similarity matrix was calculated using the square-root transformed abundance data of all 60 sites. The used permutation test was calculated via the 'adonis' function from the package 'vegan' in R (Oksanen et al. 2018). To analyze the potential effect of environmental factors on local moth community composition, we performed a Canonical Analysis of Principal coordinates (CAP) using the 'vegan' package in R (Oksanen et al. 2018). The two reserves here were treated separately. The site scores along the first three PC-axes of the local PCA, served as explanatory variables. From the landscape PCA, site scores of the 'Habitat diversity'-, the 'modified areas'-axis and the 'Distance to industry'-axis were used as predictors. All predictors were z-transformed for standardization. For assessing significance of correlations, we used a PERMANOVA test with 999 randomizations.

Table 8.1: Mean values and standard deviation of the environmental variables measured at 60 light-trapping sites situated in the two forest reserve fragments PsV and PdC in north-eastern Italy. The t/z-values and the p-values of Mann-Whitney U-tests are also given. Results printed in bold face were statistically significant (at $p<0.05$) after table-wise False Discovery Rate correction.

	Reserve PsV	Reserve PdC	t/z-value	p-value
Local site characteristics				
Plant species richness	36.6±5.7	33.0±5.3	-2.47	**0.01**
Functional dispersion of plant species	0.18±0.01	0.18±0.01	-1.38	0.17
Herb layer heterogeneity	0.38±0.1	0.37±0.1	-0.87	0.38
Shrub layer heterogeneity	0.25±0.1	0.25±0.1	-0.73	0.47
Ellenberg indicator "Humidity"	4.2±0.1	4.1±0.1	-1.39	0.16
Ellenberg indicator "Nutrients"	4.4±0.2	4.2±0.2	-1.86	0.06
Ellenberg indicator "Temperature"	6.5±0.1	6.5±0.07	-0.94	0.35
Forest density (mean trees/ha)	308.3±121.1	345.5±103.0	-1.53	0.13
Canopy density (in %)	64.3±13.8	65.4±14.8	-0.34	0.73
Cover of deciduous trees (m^2ha^{-1})	11.8±7.1	11.3±5.4	-0.29	0.77
Cover of conifer trees (m^2ha^{-1})	12.9±7.4	13.8±8.2	-0.29	0.77
Mean basal area (in cm^2ha^{-1})	897.5±357.4	755.4±238.4	-1.42	0.16
Standard deviation of basal area	1107.4±411.7	946.3±327.9	-1.78	0.08
% dead standing trees	8.4±8.2	11.4±11.3	-1.09	0.28
Landscape-level characteristics				
Distance to reserve edge (in m)	424.6±264.9	419.5±275.0	-0.14	0.89
Distance to canal (in m)	188.5±218.2	593.3±476.7	-4.07	**<0.001**
Distance to industry (in m)	4035.1±1186.9	13583.0±1556.5	-6.65	**<0.001**
Diversity of natural habitats (200m)	0.40±0.19	0.15±0.20	-4.48	**<0.001**
Edge density (500m)	62.3±21.0	43.4±33.3	-2.61	**0.01**
Proportion of reed (200m)	0.09±0.10	0.02±0.10	-3.70	**<0.001**
Proportion of grassland (200m)	0.04±0.10	0.01±0.02	-2.49	**0.01**
Proportion of modified areas (500m)	0.08±0.12	0.13±0.14	-1.61	0.11

Results

In total, we found 23870 individuals of 392 moth species. 259 of these species (66.1%) were found in both reserve fragments, while 81 species (38 of which were singletons) only occurred in PsV, and 52 species (22 singletons) were exclusive to PdC. So, for PsV we found 340 species, while in PdC only 311 species were recorded. The exponential bias-corrected Shannon α-diversity for all sites was on average higher in PsV (43.6±10.7) than in PdC (38.2±9.9). However, this difference was just not significant (z=-1.81, p=0.07). γ-diversity of both reserve fragments, expressed by the same metric, reached roughly equal values (PsV: 75.2, PdC: 77.9).

Typical moth species of PsV, extracted via the indval-function, included specialist oak feeders like *Teleiodes luculella* and *Acrobasis consociella*, but also the highly polyphagous *Clepsis consimilana* and *Ligdia adustata* (host-specific to Euonymus shrubs) emerged as indicators. For PdC, the moss-feeding *Eudonia mercurella*, the pine herbivore *Macaria liturata*, and the oak feeder *Spatalia argentina* were characteristic. All indicator species, having a probability of >0.05 to preferentially appear in only one reserve fragment, are listed in Appendix 8.1.

Of the local environmental variables, only plant diversity differed significantly between the two reserves, being on average higher at sites in PsV. Trees also were on average larger and the forest was more heterogeneous there. In contrast, we found more trees/ha and on average more dead wood in PdC, yet all these differences were statistically not significant. At the landscape level, sampling sites in PsV had significantly higher habitat and landscape diversity and contained more reed areas. Furthermore, in PsV there are more water canals, as shown by smaller distances from each sampling site to the closest canal (Tab. 8.1).

Multivariate description of site characters

The PsV-local-PCA resulted in five PC-axes with eigenvalues >1.00, together explaining 76% of variation. Axes were named after their main factor loadings to facilitate interpretation (Appendix 8.2). The PdC-local-PCA also resulted in five PC-axes to be selected, explaining 77% of variation. In contrast to the PsV-PCA, the factor loadings of the five PC-axes were sorted differently, leading us to attribute alternative axis names to them (Tab. 8.2). In the landscape-PCA, the four first axes explained 84% of the variation in PsV. In PdC, only two axes were extracted, following the Kaiser criterion. However, these two axes explained 70% of variation (Tab.8.2, Appendix 8.3 for factor loadings).

Table 8.2: Names of the ordination axes (Eigenvalues >1.00) resulting from the different PCAs in order to condense raw variables. Proportions of explained variation are given in brackets behind each axis.

PCA of local factors						**Total expl. variation**
	PC-Axis 1	**PC-Axis 2**	**PC-Axis 3**	**PC-Axis 4**	**PC-Axis 5**	
PsV	Old, open forest (20%)	Plant diversity (18%)	Humidity nutrient gradient (17%)	Herb-layer heterogeneity (12%)	Tree health (8%)	76%
PdC	Humidity nutrient gradient (25%)	Dense, young forest (16%)	Conifer cover (15%)	Heterogeneous warm forest (12%)	Plant diversity (10%)	77%

Table 8.2 (continued): Names of the ordination axes (Eigenvalues >1.00) resulting from the different PCAs in order to condense raw variables. Proportions of explained variation are given in brackets behind each axis.

PCA of landscape factors						**Total expl. variation**
	PC-Axis 1	**PC-Axis 2**	**PC-Axis 3**	**PC-Axis 4**	**PC-Axis 5**	
PsV	Habitat diversity (31%)	Modified areas (29%)	Open habitats (21%)	Distance to industry (19%)	-	84%
PdC	Habitat diversity (41%)	Distance to edges (28%)	-	-	-	70%

Proportional β-diversity of moths

In both reserves there was strong variance in proportional moth β-diversity between individual sampling sites. In PsV proportional β-diversity ranged from 0.18 to 0.68 (mean: 0.52±0.10). Smallest values were found at sites V16 and V20, located in the southern middle of the reserve, whereas we observed highest values in the north of the reserve, at sites V6, V1 and V2 (Fig. 8.1). For PdC, values ranged between 0.40 and 0.83 (Mean: 0.60±0.11), showing in general higher proportional β-diversity, with smallest values at sites C7 and C8, and the highest value at C22 (Fig. 8.1). Overall, PsV had significantly lower proportional β-diversity compared to PdC (t=-2.88, p=0.01). So, inside PdC there was a substantially higher species turnover from site to site than in PsV. For assessing the potential influence of environmental variables on proportional β-diversity we first calculated two full linear models, separately for PsV and for PdC,

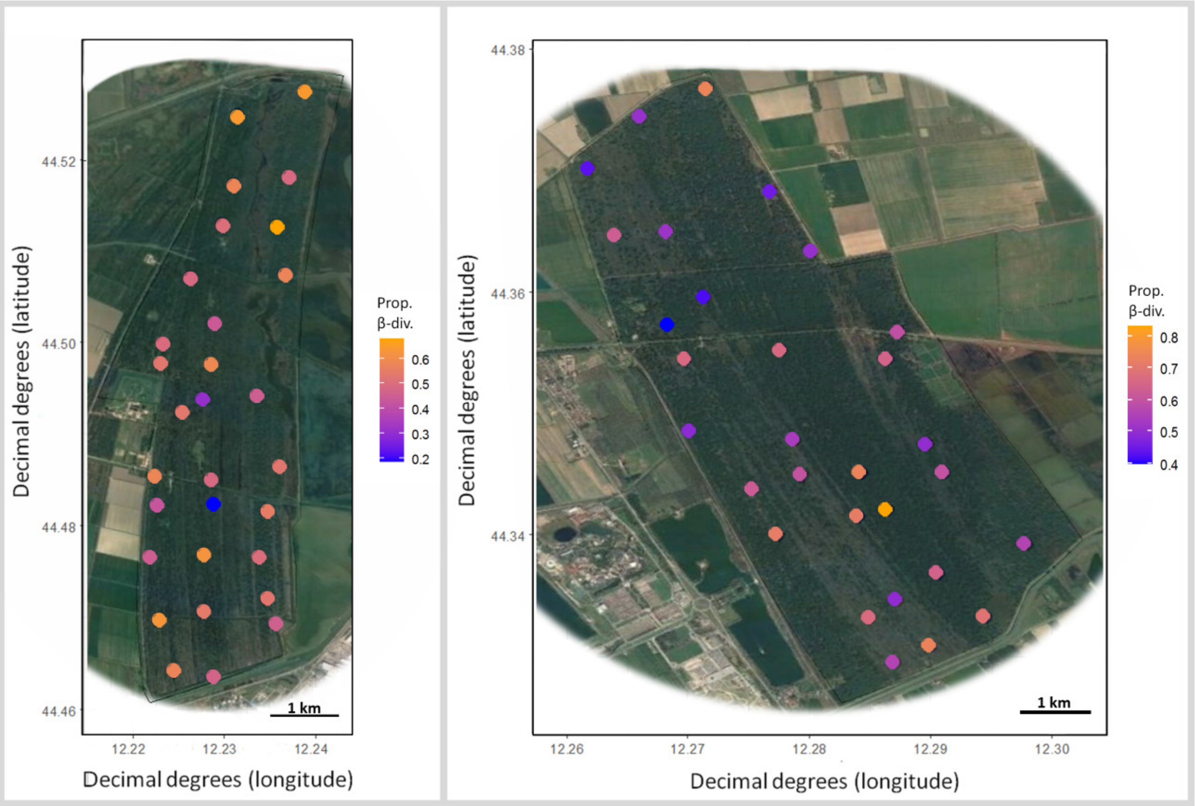

Figure 8.1: Distribution of the proportional β-diversity values of moth assemblages across the 60 sites in the two forest fragments, indicated by a color gradient. Orange= high proportional β-diversity, blue= low proportional β-diversity. Modified maps are based on Google^{TM} satellite images. Left: Pineta san Vitale; right: Pineta di Classe

including all predictors extracted through the respective PCAs. In these models, standardized β-diversity β_{dev} was used as response variable. Through model selection via AIC, we then found the best models for PsV and PdC, respectively. In PsV, the PC-axis 'Plant diversity' (t=-2.37, beta-coefficient=-0.51, p=0.03), the 'Humidity-nutrient-gradient' (t=-2.33, beta-coefficient=-0.42, p=0.03), the PC-axis 'Modified areas' (t=2.10, beta-coefficient=0.43, p=0.05) and 'Open habitats' (t=-1.53, beta-coefficient=-0.29, p=0.14) were included in the best model. Proportional β-diversity was lower at shady, nutrient rich sites that provided high plant species richness (Fig. 8.2). Modified areas in the surroundings otherwise led to increased species turnover. This best model had an adjusted R^2 value of 0.19. For PdC, the PC-axes 'Humidity-nutrient-gradient' (t=-3.37, beta-coefficient=-0.48, p=0.002), 'Dense, young forest' (t=2.11, beta-coefficient=0.30, p=0.05), 'Conifer cover' (t=-2.65, beta-coefficient=-0.38, p=0.01) and 'Heterogeneous warm forest' (t=1.34, beta-coefficient=0.19, p=0.19) were included in the best model. These four predictors altogether explained 42% of the among-site variation in proportional β-diversity of moth assemblages. Conversely, proportional β-diversity in PdC therefore was lower at shady, humid and nutrient rich sites (Fig. 8.2), but was also decreasing with an open, old-grown forest structure and more pine trees around. So, old grown conifer sites on humid and nutrient rich ground had lower moth species turnover than younger, dry and dense forest sites.

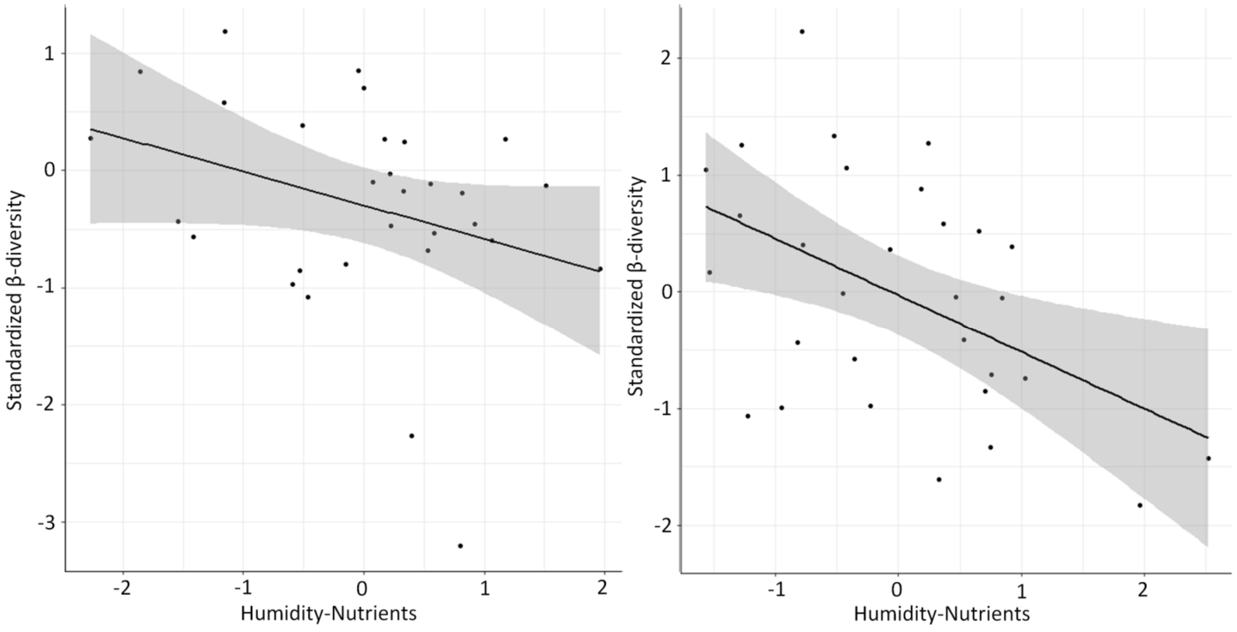

Figure 8.2: Bivariate correlations of proportional moth β-diversity with the two environmental factors which explained most of the variation in linear regression models. In the reserves Pineta san Vitale (left) and Pineta di Classe (right) the humidity-nutrient gradient was included in the best model. Grey shaded areas indicate the 95% confidence intervals of each model (black line)

Differentiation diversity of moths

Moth species composition differed significantly between PsV and PdC (PERMANOVA test: R^2=0.12, $F_{1;58}$ =7.61, p=0.001). This faunal distinction was mainly due to differences in relative species abundances between the two reserve fragments, while only a few species beyond the many singletons were exclusive to either PsV or PdC, respectively. In CAP analyses, local and landscape-scale variables explained more or less equal fractions of variation in moth community composition (Tab. 8.3). For PsV, 13.4% of the variation could be attributed to local factors, while 12.9% were explained by landscape factors.

Here, we found the distance to the nearest industrial plant being a significant predictor of moth community composition, explaining about 5% of the total variation. The position of sites along the humidity-nutrient gradient also turned out to significantly shape moth species composition. Altogether, about 26.3% of the variation in moth community composition could be attributed to the investigated predictors (Tab. 8.3, Fig. 8.3).

For PdC, the outcome of the constrained ordination analysis was remarkably different. 20.9% of the variation in the moth community could be explained by three local factors, all of which significantly shaping moth assemblages (Tab. 8.3). Additional 9.2% of the variation was attributable to two landscape-scale variables. Here, the 'Distance to forest edges' was a significant factor shaping moth community composition. In total, we were able to explain a slightly larger fraction (30.13%) of the variation in moth assemblage composition by the selected environmental descriptors in this second reserve fragment (Tab. 8.3, Fig. 8.3). Overall, the environmental factors that emerged as relevant correlates of local moth species composition varied strikingly between the two forest fractions.

Table 8.3: Results of PERMANOVA tests, checking for correlations between environmental variables and local moth community composition across 30 sites per reserve. Percentages of explained variation by each environmental variable (PC-axes) in the CAP analyses are given as well as p-values (based on 999 permutations). Results printed in bold face were statistically significant (at p<0.05) after table-wise False Discovery Rate correction.

Reserve PsV			
	Factor	Explained variation	p-value
Local factors	Humidity-Nutrients	5.47%	**0.01**
	Old, open forest	4.26%	0.11
	Plant diversity	3.64%	0.25
Landscape factors	Habitat diversity	3.49%	0.31
	Modified areas	4.10%	0.14
	Distance to industry	5.33%	**0.02**
total		26.28%	
Reserve PdC			
Local factors	Conifer cover	7.03%	**0.001**
	Dense, young forest	6.98%	**0.004**
	Humidity-Nutrients	6.89%	**0.003**
Landscape factors	Habitat diversity	4.23%	0.07
	Distance to edges	5.01%	**0.02**
total		30.13%	

Discussion

The anciently connected forest areas of PsV and PdC nowadays show still similar basic environmental conditions. Most local site characters did not differ remarkably, although we found minor dissimilarity in plant diversity, forest structure and composition. Assuming that both forest patches basically are formed by the same environmental prerequisites (e.g. sandy underground, Mediterranean coastal climate), have a sufficiently large area and a quite compact shape, the preservation of the natural local habitats seems guaranteed (Petrášová-Šibíková et al. 2017). However, the current landscape context of both reserve fragments is very dissimilar. In PsV, there are more water canals than in PdC, indicating higher water availability. In fact, PsV is characterized by more humidity-indicating plants, while typical PdC plant species are affiliated with dry and warm conditions (Uhl et al. 2020a). Furthermore, sites in PsV are surrounded by much more near-natural areas – especially reed – resulting in higher landscape diversity, while the landscape context of sites situated in PdC is quite impoverished and simplified. This higher landscape diversity might be one reason for the higher moth species richness and α-diversity in PsV, compared to PdC (Uhl et al. 2020b), underlining the importance of landscape diversity for regional species richness in isolated conservation areas (Seibold et al. 2019).

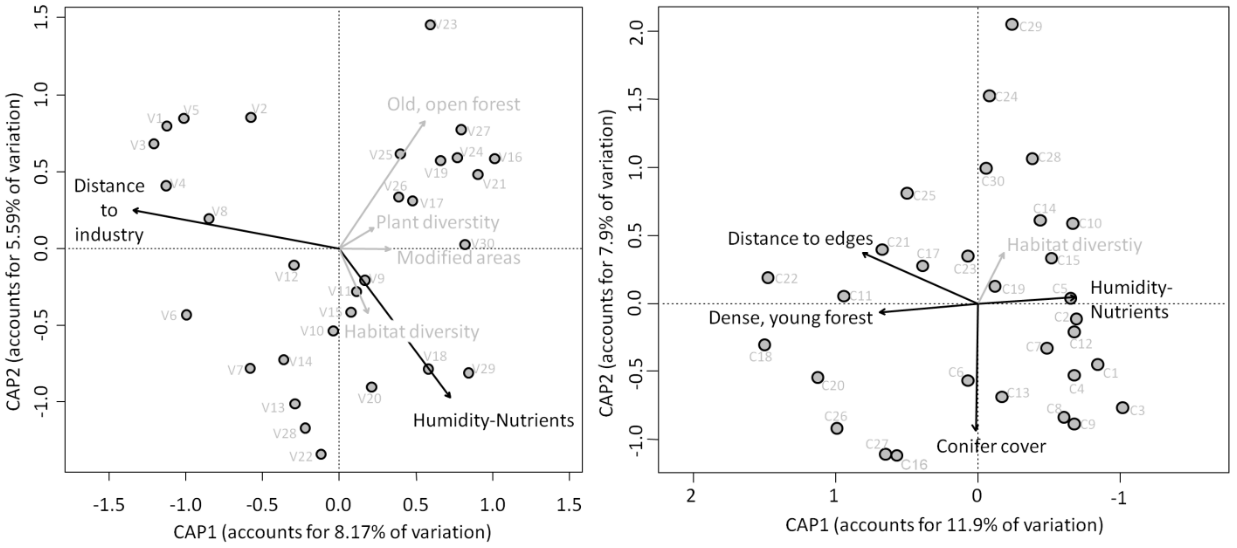

Figure 8.3: Canonical analysis of principal coordinates, separately for PsV (left) and PdC (right) moth communities. Environmental variables (the first three PC-axes of the local PCA, and selected PC-axes of the landscape PCA) are included as vectors. Significant predictors are colored in black, while those with minor effects on moth communities are colored grey. The results of the PERMANOVA, testing for how much of the variation in community composition is explained by the predictors and which of them had significant influences, are given in Table 8.3

Proportional β-diversity

As a measure of diversity partitioning, proportional β-diversity can reveal the spatial scaling of diversity loss across sites (Socolar et al. 2016), however studies of β-diversity are much less common than investigations on species richness or α-diversity (Mori et al. 2018). With increasing proportional β-diversity (i.e. ever smaller species subsets), local communities become more heterogeneous, indicating subtractive heterogenization by the loss of ubiquitous species. Declining proportional β-diversity (larger species subsets), in contrast indicates community homogenization as rare species becoming more widespread (additive homogenization: Socolar et al. 2016). Analyzing β-diversity on a landscape scale can furthermore reveal the processes of additive heterogenization, so increased turnover that is based on higher regional γ-diversity, and subtractive homogenization, meaning the disappearance of rare species on the landscape level (Socolar et al. 2016, Fig. 8.4). These latter two mechanisms describe the known covariance of β-diversity and γ-diversity patterns, viz. the logical dependence of higher regional diversity favoring higher landscape-wide species turnover (Ulrich et al. 2016). Hence, additive heterogenization and subtractive homogenization cannot be found, when communities within one region are compared, as higher turnover mathematically is based on smaller species subsets. For insect communities, there are only few β-diversity studies, mainly focusing on aquatic (Hepp et al. 2012, McCreadie & Adler 2018) and tropical insect communities (Beck et al. 2012, Kitching et al. 2013, Novotny et al. 2007) or conducted at much larger geographical scales (Chesters et al. 2019). Smaller-scale variation in β-diversity, especially in fragmented conservation areas, however is until today only poorly understood.

Comparing the two reserve fragments, moth assemblages in PsV were more homogenized with lower species turnover between sites. Since PsV comprises more different habitat types (Merloni & Piccoli 1999), one first might have expected the contrary. However, these diverse habitat structures and a well developed forest understory can be found all over the reserve. In PdC, in contrast, some sites resemble

PsV locations by their forest structure and their landscape context while other areas are structurally impoverished. At these locations a near-natural forest structure is still lacking, as well as any habitats other than mixed oak-pine stands in their vicinity. Since sites in PsV also harbor on average higher local moth species richness, we conclude that additive homogenization might have caused the lower species turnover in this northern reserve. Moth species that occurred rarely in PdC might be quite common in PsV, enhancing its mean α-diversity per site and reducing species turnover between sites.

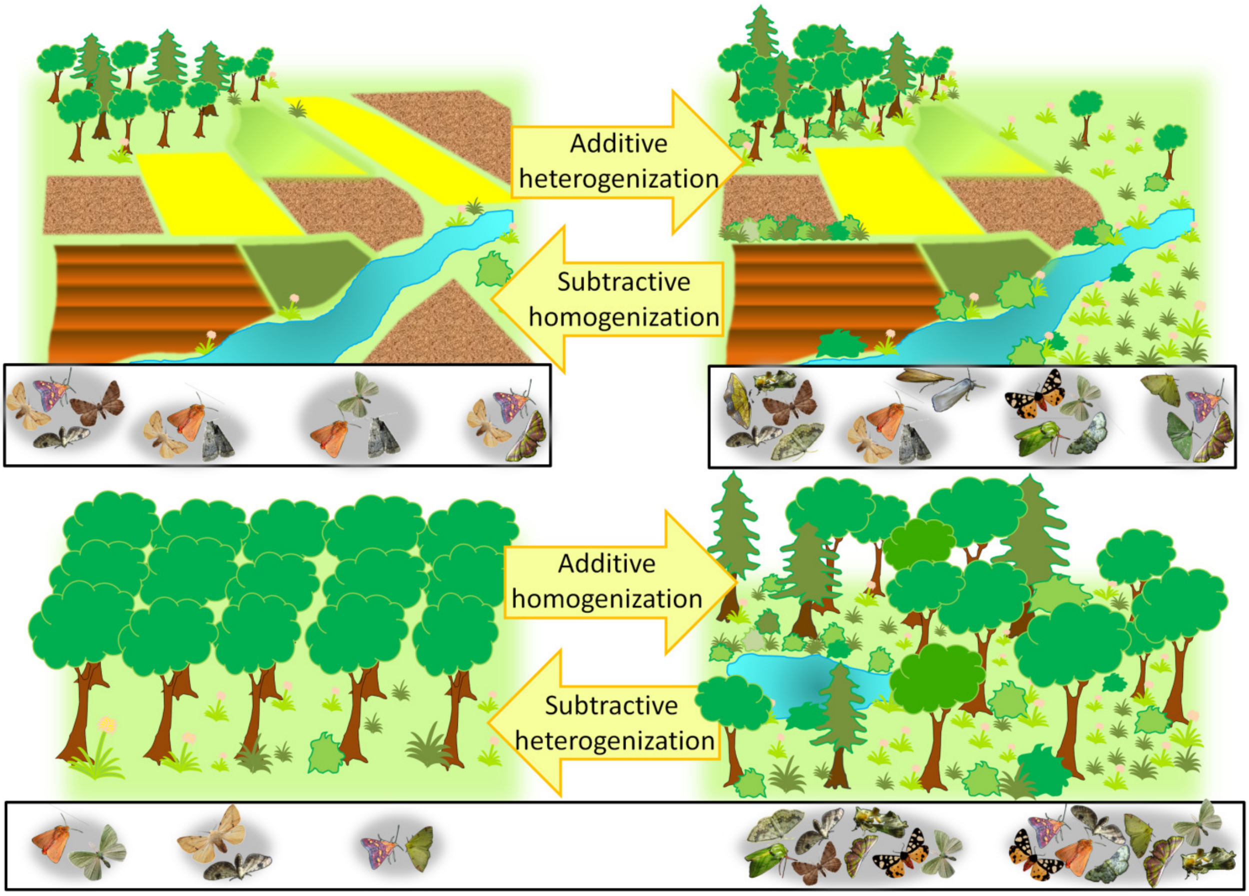

Figure 8.4: Schematic overview of the four processes that explain changes in β-diversity, following Socolar et al. (2016). Additive heterogenization and subtractive homogenization are acting on the landscape level and describe that with a declining regional species pool (represented by the white boxes, upper part), species turnover is also declining. So, in ever smaller species subsets (indicated by the grey background) the chance to observe the same species becomes higher. Additive homogenization and subtractive heterogenization, in contrast, are processes that are found when species subsets within one species pool (represented by only one white box, below) are compared. Within a forest, larger subsets of the species pool can be found where more niches are available, leading to lower proportional β-diversity.

Fitting to this assumption, proportional β-diversity in PdC was lower at shady, humid and nutrient-rich sites, negatively correlated to an increasing cover of conifer trees and to a more open, old-grown forest structure. So, larger diversity subsets in PdC occurred at well developed forest sites, most resembling the ecological conditions of the PsV sites. In PsV, we observed the same correlation: Species turnover decreased along the 'Humidity-nutrient gradient', and with increasing plant diversity. Other local factors like the 'Old, open forest'-axis were not included the best PsV model, although this factor was an equivalent for the 'Dense, young forest'-axis in PdC. The PsV forest structure had overall less variance across sites compared to PdC. Very dense, young forest stands are missing here, and at most sites the amount of conifer and deciduous tree biomass is balanced. The gradient from younger, dense forest stands to old-grown open forest sites therefore is less pronounced than in PdC, what might be the reason for this factor being less relevant in PsV.

Forest succession is known to play a key role for insect communities. Looking at β-diversity, Miller and terHorst (2012) found that with ongoing succession there is a decreasing species turnover, supporting our own observations. Our study, however, furthermore points out, that additive homogenization seems to be key the process driving the decline in species turnover at near-natural forest sites. Formulated from another point of view, subtractive heterogenization, viz. the local lack of otherwise ubiquitous forest species at dense, young forest sites, may have caused the observed pattern (Fig. 8.4). So, additive homogenization and subtractive heterogenization here describe the same process, but in opposite directions (Fig. 8.4). However, this is only true for the interpretation of spatial analyses, as in time series, the direction of change from ancient to recent communities is fixed.

Landscape-scale aspects were not included in the best PdC-model. However, for PsV the 'Open habitats'-axis and the 'Modified areas'-axis seem to affect proportional β-diversity at least to some extent. The presence of open grasslands reduced species turnover, favoring additive homogenization through the establishment of specialized species in local communities. Near-natural habitat structures like open grasslands therefore can play a crucial role for insect β-diversity inside forests, as they break up the homogenous forest structure and provide more niches for different insects. In agricultural landscapes, Landis (2017) reviewed the important role of landscape complexity for maintaining high diversity and related ecosystem services. Our results furthermore corroborate the value of particular landscape structures for increasing species diversity inside conservation areas.

In contrast, we found higher species turnover between sites (smaller subsets) when an increasing amount of agricultural and urban areas was measured in the surroundings. This can indicate that (1) some species are missing at sites with more modified areas around (subtractive heterogenization), or – formulated again from another point of view (2) some species become more common, when no anthropogenic land use in the surroundings can be found (additive homogenization) (Socolar et al. 2016). Human actions on the landscape scale can influence nature reserves indirectly, through the drift of pesticides (Zivan et al. 2016) or the influx of nutrients from surrounding agricultural landscapes. Nutrient input can alter vegetation structure (Uhl et al. 2020a) and also might reduce food plant quality for insects (Kurze et al. 2018). Additionally, light pollution can be enhanced when more urban areas are surrounding the sampling site. Artificial light at night has major effects on nocturnal insect communities, disrupts the development of insects at different life stages (Boyes et al. 2020), affects their fitness directly by reducing optical efficiency and orientation, and desynchronizes their internal clock (Owens & Lewis 2018). So, there are multiple possible reasons that might explain the observed patterns in β-diversity. Therefore, further studies are needed to more precisely unravel the effects of landscape-scale anthropogenic actions on nature reserves.

Differentiation diversity

In contrast to proportional β-diversity, differentiation diversity is not a diversity partitioning metric, but can be used to study the drivers of species composition (Jurasinski et al. 2009). Even though local site characteristics were rather similar between the two reserve fragments and there is a large basic moth species pool both reserves have in common, we found highly significant differences in moth species composition between PsV and PdC. Some species clearly are bound to the occurrence of particular food plants, e.g. *Eutelia adulatrix* exclusively occurs in PdC, because its larval food plant *Cotinus coggygria* can only be found there. As the two reserves have a quite diverged plant community in terms of species composition (Uhl et al. 2020a), this might explain some of the compositional differences in PsV and PdC moth communities. Other studies have established the influence of plant diversity on moth diversity (Root et al. 2017), and in fact also in the two study areas, a higher plant richness at the site scale level enhances local moth diversity (Uhl et al. 2020b). However, assuming that the particular composition of plant communities is often more important for local assemblages of herbivorous insects than the absolute number of plant species (Gavish et al. 2019, Kemp et al. 2017), this might be one reason for local predictors like the 'Plant richness'-Axis failing to explain differences in moth community composition. From the landscape-level point of view, the presence of more reed areas in PsV might explain the occurrence of some specialist reed herbivores like *Phragmataecia castaneae* and *Schoenobius gigantella* as indicator species of PsV. The faunal differentiation between the two forest fragments is in line with the landscape-divergence hypothesis formulated by Laurance et al. (2007) who predicted that local communities tend to diverge when surrounded by different landscapes, even if the local conditions are not that different. Besides environment-driven deterministic processes, also ecological drift likely has contributed to differences in the moth communities (Gilbert & Levine 2017, Mori et al. 2018). As only few of the recognized indicator species were exclusively found in one reserve, we conclude that for most species it was the difference in their abundances rendering them a statistical indicator for either PsV or PdC.

Small-scale insect community composition within the two reserve fragments was substantially influenced by local as well as landscape-scale factors, with roughly equal importance of both scales of effect. Accordingly, moths were again confirmed as suitable target organisms for small-scale analyses with distances of only about 500m between sampling sites (Slade et al. 2013), although they are considered to be a quite mobile insect group. In contrast, other insect groups failed to reflect variation in vegetation structure and other environmental factors (Kemp et al. 2017). Emphasizing the importance of water and nutrient availability for Mediterranean plant and insect communities, only the humidity-nutrient gradient emerged as a significant predictor of moth species composition in both reserves. This PC-Axis well reflected the gradient from dry and warm sites to shady, humid and nutrient-rich forest locations with a rather dense canopy layer. However, 'nutrient-rich' does not mean that these sites were really eutrophic, as the highest average nutrient indicator values derived from the local vascular plant species lists in both reserves never exceeded a value of 5.51 (at location C1), indicating only moderate absolute nutrient availability. More likely, we interpret this PC-Axis as referring to a natural succession gradient. In a near-natural forest, shady sites with well developed sub-canopy layer, built up by small trees and shrubs, can regulate the local microclimate by buffering hot temperatures in summer as well as cold winter days (Prévosto et al. 2020). Furthermore, the forest humus layer ensures nutrient and water availability and again guarantees stable environmental conditions. These stable conditions, together with the structural richness of such near-natural forest sites positively affect moth taxonomic and functional diversity (Uhl et al. 2020b, Uhl et al. unpublished data). That this also translates into an effect on community composition was therefore not surprising. Other forest structure components (like forest density and age, or conifer cover), however, only were significant predictors of variation in moth species composition in PdC. We again attribute this outcome to the reduced variance in PsV forest structure, where very dense, young forest stands and monotonous conifer sites were missing.

On the landscape scale, especially the two anthropogenic influences emerged as significant predictors shaping moth communities inside the forest reserves. For sites in PsV, the distance to urbanized areas turned out to significantly affect differentiation β-diversity. Uhl et al. (2016) earlier demonstrated that the abundance of twelve ecologically informative micro-moth species was declining in the vicinity of the industrial plants in PsV, whereas only four species became more abundant there. Also in the present study some moth species were becoming significantly less abundant along the 'distance to industry'-Axis within PsV. For example *Carpatolechia aenigma* (r=0.57, p<0.001) and also *Acrobasis consociella* (r=0.42, p=0.02) were less abundant in vicinity to the industrial harbor. Larvae of these species feed on oak trees, which occur at all our study sites. The absence of these oak feeders in the south of PsV therefore might indicate locally poor food plant quality, as oaks near the industrial plants tend to have lower crown densities, indicating reduced fitness (Uhl & Wölfling 2015). Interestingly, some further specialized oak feeders were only observed in PdC. For example, *Catocala conversa* and *Spatalia argentina* never showed up in PsV during three summers of intense light-trapping efforts although local conditions seem favorable for both species. Furthermore, *Spatalia argentina* formerly occurred in PsV, as there are voucher specimens in old collections from around 1950 (Mirko Wölfling, unpublished observations). The current absence of these species might hint to some constraints acting on oak-feeding moth species in PsV. Our present study therefore confirms earlier findings of Uhl et al. (2016) on micromoths, but more concisely points out that the observed community shifts do not mainly refer to changes in local vegetation (Uhl et al. 2016), but seem to be influenced by landscape-scale drivers, indirectly affecting the food plant quality. The 'Distance to industry'-gradient, however, may also be influenced by other landscape structures that were not analyzed. In the north of PsV, large reed areas exist. Though, they were not represented by any of the landscape factors, as they were too far away from the sampling sites. The proximity and amount of reed areas might have influenced the abundance of moths affiliated with *Phragmites australis* or aquatic plants, which were more likely to occur in the north of PsV. As an example, the aquatic species *Acentria ephemerella* (r=0.40, p=0.03) and also the reed affiliated species *Leucania obsoleta* (r=0.49, p=0.006) were significantly correlated to the 'Distance to industry'-axis.

Looking at PdC, another anthropogenic landscape factor significantly affected moth communities. The distance to forest edges, which also represented a decreasing proportion of human-modified areas in the surroundings of the sampling sites, significantly shaped moth assemblages. The small differences in species composition here can be explained by possible spill-over of moths from surrounding ruderal or agricultural areas. Potential pest species like *Ostrinia nubilalis* (r=-0.58, p<0.001) and *Agrotis ipsilon* (r=-0.60, p<0.001) became significantly more abundant at PdC forest edges. Same was observed for *Dypterygia scabriuscula* (r=-0.65, p<0.001) and *Timandra comae* (r=-0.59, p<0.001), which both are feeding on *Rumex* species at ruderal sites as larvae. Conversely, forest species like *Macaria liturata* (r=0.40, p=0.03) or *Scoparia basistrigalis* (r=0.50, p=0.004), become less abundant at edge sided locations. Similar landscape-modulated edge effects on moth community composition were also described by Fuentes-Montemayor et al. (2012) who found especially woodland species to be dependent on larger forest fragments and forest centers. In small woodland patches and edges, forest species seem to be replaced by generalist species, confirming the species-replacement-hypothesis sensu Summerville and Crist (2003). So, anthropogenically induced modifications on landscape scale, like land use intensification or landscape simplification, do not only affect communities on site, but also more distant biota inside nature reserves. Our study shows that these landscape-scale effects are also detectable via small-scaled variation in community composition inside two forest nature reserve fragments. For the conservation of specialized forest species, it therefore seems especially important to preserve larger fragments of near-natural forest, with fewer edges between reserve and modified areas. Structural heterogeneity within the forest, through the presence of other habitat structures like open grassland areas, furthermore can stabilize local communities and counteract biodiversity decline.

Concluding remarks

Our results show that the variation of proportional β-diversity strongly depended on site-specific environmental gradients. The stronger these gradients are pronounced, the more likely they are to be reflected by proportional β-diversity and species turnover. The strength of gradients therefore always determines their importance for insect community composition and should always be considered when ecological data are interpreted.

Landscape attributes again emerged as important for the integrity of biota in forest fragments. Even in mobile insects such as moths, small-scaled community variation turned out to be related to both, local and landscape-scale environmental factors. In our study, a near-natural forest structure came up as the most important factor on the local scale, while on the landscape scale, human modifications severely influenced community assembly of moths within nature reserves. Human actions therefore do not end at the field border and their effects on nearby protected natural habitats always need to be considered in conservation management.

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9. Qualitative and quantitative loss of habitat at different scales affects functional moth diversity

Abstract

1. Land use change has led to large-scale insect decline, threatening ecosystem resilience through reduced functional diversity. Even in nature reserves, losses in insect diversity have been detected. Hereby, changes in local habitat quality and landscape-scale habitat quantity can play a role driving functional diversity erosion.

2. Our aim was to analyze how local and landscape-scale factors simultaneously affect functional insect diversity. Therefore, we sampled moths in two Italian coastal forest reserves at 60 sites. Our focus was on functional richness, redundancy and niche occupation, being important for ecosystem resilience, following the insurance-framework. Ecological information of 387 species and 14 traits was used to analyze functional diversity. Twenty-five functional groups were recognized and used to estimate niche occupation and redundancy. Fourteen local and 12 landscape-scale factors were measured and condensed by using Principal Components Analysis. The resulting PC-axes served as predictors in linear mixed effects models.

3. Functional richness, redundancy and niche occupation of moths were lower at sites with low habitat quality and quantity, indicating reduced ecosystem resilience. Especially landscape diversity and habitat structure, viz. a humidity-nutrient gradient, but also plant diversity, were promoting functional richness. Landscape fragmentation, indicating increased impermeability for insects, reduced local functional richness, redundancy and niche occupation.

4. Local habitat quality and landscape-wide habitat quantity are both important for maintaining functional insect diversity inside reserves. Therefore, small and isolated nature reserves might fail in preserving biodiversity and ecosystem functions through adverse effects acting from the surrounding landscape structure and configuration.

Keywords

Landscape diversity, local factors, functional redundancy, Lepidoptera, functional richness, isolated nature reserves, Mediterranean

Introduction

Changing environmental conditions due to human activities can be ever more challenging for the communities inhabiting the few remaining near-natural areas. Land use change, especially intensified management practices and habitat fragmentation, in fact are currently the most important drivers of biodiversity decline (Newbold et al. 2015). However, maintaining species rich communities is crucial for ecosystem functioning as biodiversity enhances ecosystem multifunctionality (Allan et al. 2015; Diaz et al. 2007), is linked to ecosystem productivity (Duffy et al. 2017) and to ecosystem resilience (Mori et al. 2013; Oliver et al. 2015). Yachi & Loreau (1999) theoretically investigated the relationship between species richness and ecosystem function by formulating the ‘insurance hypothesis’. This hypothesis was repeatedly supported (Isbell et al. 2018; Oliver et al. 2015), indicating the importance of species richness and functional redundancy for the resilience of ecosystem function. Basically, functional redundancy ensures that even if some species vanish because of disturbance or stochastic effects, other ones might occupy sufficiently similar ecological niches and so maintain the function of the whole ecosystem. As species richness alone cannot inform about which functional niches are occupied by how many species (Lewis et al. 2014), measures of functional diversity have become an important tool for community ecology research (Gagic et al. 2015; Mason & De Bello 2013). Different functional aspects of species here can give important insight into how species react to disturbance (response traits), and how they affect ecosystem processes (effect traits). This response-effect trait framework has been described by Suding et al. (2008) and was, similar to other functional diversity approaches, first introduced in plant community research (Allan et al. 2015; Diaz et al. 2007).

However recently, functional diversity has also become more common in insect studies (Greenop et al. 2018; Guariento et al. 2020; Woodcock et al. 2019). Insects as a very species-rich group occupy multiple important niches that guarantee ecosystem functions and services, such as pollination, decomposition, herbivory and predation, as well as food supply for higher trophic levels (Beck & McCain 2020; Greenop et al. 2018; Woodcock et al. 2019). At the same time, insect decline over the last decades can be observed at multiple scales (Habel et al. 2019a, b; Seibold et al. 2019) and has become a topic of public interest (Leather 2018; Saunders 2019). The drastic decline in insect abundances and diversity is an alarming sign of overexploiting our natural environment at the cost of biodiversity and ecosystem function (Woodcock et al. 2014, 2019). Insect diversity decreases due to intensive local management (Chisté et al. 2016; Mangels et al. 2017) and large-scale landscape simplification (Gámez-Virués et al. 2015; Merckx et al. 2012a), and is accompanied by reduced species turnover across landscapes (Merckx & Van Dyck 2019). This finally leads to decreasing landscape-wide gamma diversity and an all over homogenized species pool mainly consisting of generalist species (Clavel et al. 2011; Piano et al. 2020; Seibold et al. 2019). So, when dividing land use factors into different spatial scales of effect, insect decline seems to be driven by loss in local habitat quality as well as landscape-wide habitat quantity.

Habitat quantity describes the amount of habitable area available for subsets of species in a certain range of effect. The definition of a 'habitat' always depends on the focal species and its demands on the environment. For example, the amount of forested area in a 1000m range around a focal site might influence the number of forest species to be found there (Fahrig 2013). Taking this paradigm to the next spatial level, higher landscape-level habitat diversity might positively affect taxonomic and functional diversity of local assemblages. With more different habitat types around a focal site, more functional niches are available which sustain a larger regional species pool (Merckx et al. 2019; Woodcock et al. 2014). This determines how many species on the local level, as a subset of the regional pool, can be found (Tscharntke et al. 2012). Further proxies of habitat quantity might be the total amount of semi-natural habitats in the vicinity of the focal site, or - in reverse - how much area around has been modified by land use (e.g. agriculture or buildings), and might therefore no longer be habitable to most biota.

Similar to habitat quantity, also the definition of quality always depends on the requirements of the target organisms. Therefore, quality is nearly impossible to define for a whole community consisting of different species with different needs (Dennis et al. 2014). Nevertheless, for terrestrial insects - especially pollinators and herbivores, which have a long history of co-evolution with plants (Macior 1971) - a high quality site might be marked by high plant species richness and high structural complexity of its vegetation. Looking for example at forest habitats, a near-natural forest structure with unevenly aged trees, a substantial understory layer, and a certain amount of deadwood might for many species be of higher quality than evenly aged, dense, young forest stands which are planted for a maximum gain in timber production (Thorn et al. 2015).

As insect decline is not only known from agricultural areas with intensive management (Fiedler et al. 2017; Mangels et al. 2017), but also in conservation areas (Seibold et al. 2019), the focus of our study was to simultaneously unravel the roles of small-scaled differences in local habitat quality and landscape-wide habitat quantity for functional moth diversity inside nature reserves. We here define how these two scales might be circumscribed, and correlate them to the functional diversity of moths as a species-rich insect group, which often has been used as indicators of ecological integrity of biota (Merckx et al. 2012a; Uhl et al. 2016). We emphasize that our focus here lies on small-scaled changes within nature reserves, rather than on overall changes in gamma diversity between different areas under study embedded in a larger landscape unit. Detecting these small-scale changes along habitat quality and quantity gradients within conservation areas might be crucial for ameliorating conservation management practices, aiming to preserve intact and species rich ecosystems.

For analyzing functional diversity, different indices have been developed. Functional diversity measures can be separated into three main categories: Functional richness (hereafter FRic), evenness (hereafter FEve) and divergence (hereafter FDiv; Mouchet et al. 2010). All three facets of functional diversity have to be considered as no single index of functional diversity gives full insight into all aspects (Mouchet et al. 2010). However, as the focus of our study lies on the importance of functional richness for ecosystems, mainly measures related to this aspect of functional diversity will be considered. As FRic is sensitive to outliers (Laliberté & Legendre, 2010) and only takes into account the most extreme trait values (Mouchet et al. 2010), we further explore how species in local communities are distributed across the available trait space by investigating trait space occupation and functional redundancy. Results for FEve, FDiv and functional dispersion (hereafter FDis) will also be presented, but will not be discussed in detail.

For plants, FRic of communities has been shown to depend on local management (Niu et al. 2016) and also landscape-scale land use (Bruno et al. 2016). Furthermore, the management type in farmlands affects butterfly functional richness (Goded et al. 2019). Concerning the proportion of occupied niches, diverse landscape and structurally rich habitats should provide more niches which can be occupied by different species. For functional redundancy, an effect of local land use (Laliberté et al. 2010) and landscape-scale heterogeneity (Feit et al. 2019) has already been found in agricultural landscapes. So, the main hypotheses for our study are:

- Both local habitat quality and landscape-scale quantity determine FRic and functional redundancy of local insect communities.
- Niche occupation is related to landscape diversity and the structural complexity of the habitats, as with more heterogeneity, more niche options are available.
- FEve is positively correlated with landscape diversity, as with more diverse near-natural habitat areas, occupancy of functional niches should be more evenly distributed.
- FDis, as a measure of functional specialization, depends on habitat quality and quantity, like FRic.

Methods

Study areas

Our study sites were situated in two isolated forest reserves in north-eastern Italy, near the city of Ravenna. Both reserves – Pineta san Vitale (hereafter PsV) and Pineta di Classe (hereafter PdC) – are today of high legal conservation concern, as they are part of the regional park Po Delta, listed as UNESCO biosphere reserves, are protected as Natura 2000 sites and as important bird area.

The two forests – which were connected until the 18th century – were planted on paleodunes and used for pine nut harvest, cattle grazing and wood production (Andreatta 2010). With the abandonment of these extensive management practices the pinewoods developed, due to natural succession, towards a semi-natural forest structure (Wölfling et al. 2019). In parallel, agricultural intensification and urbanization in the surroundings lead to ongoing fragmentation and isolation, such that of the initial 6000ha forest area less than 2000ha, split up between PsV (950ha) and PdC (900ha), remain to the present (Andreatta 2010; Malfitano 2002). Today, the main habitat type inside the reserves is a mix of oak and pine forest, but also other vegetation types like riparian forests, reed areas and open grasslands can be found (Uhl et al. 2020a).

The areas around the two reserves are dominated by intensive agriculture (in the case of PdC), the industrial harbor of Ravenna to the south of PsV, and some other protected natural areas in the north of PsV. These different landscape surroundings as well as small-scaled variation in the local vegetation form the basis of our present investigations on correlations between local functional diversity of insects, habitat quality and quantity.

Data collection

We chose 60 sites (30 in each reserve) equally distributed throughout the study area (Fig. 9.1). Distances between sites were rather low with about 500m between neighbouring light trap sites. All sites were situated in mixed forest and were accessible by one of the numerous forest paths. Sampling took place from 2015 to 2017, with 20 randomly chosen sites visited per year.

Figure 9.1: Map showing the 60 study sites (white circles) within the two investigation areas in NE Italy (left: Pineta san Vitale, right: Pineta di Classe). The map is based on Google Maps™ satellite images and modified via QGIS. The coordinates of the two reserves are: 44°27’48.09’’ - 44°31’39.15’’ N; 12°13’01.08’’- 12°14’16.97’’ O (Pineta san Vitale), 44°19’35.00’’ - 44°22’36.35’’ N; 12°15’35.51’’ – 12°18’04.46’’ O (Pineta di Classe)

For surveying vegetation structure, we sampled each site with five 1x1m² plots in the herb layer, and five 5x5m² plots in the shrub layer. This was done in spring and early summer (April-June), when many species were in flower and so more easy to identify. Within these plots, every vascular plant species was identified and recorded. Forest structure was analyzed by doing 10 point-centered-quarter analyses per site, following Mitchell (2010). The point-centered-quarter analysis is a non-plot-based sampling technique for analyzing forest structure, where the distance to the four nearest trees is measured. Additionally, for each of the recorded trees its diameter at breast height, height and species identity was noted. With these data, we were able to calculate proxies for forest density (in trees/ha), forest cover of deciduous and conifer trees (in m²/ha), mean basal areas of trees (as a proxy for forest age) and the standard deviation of basal areas (as a proxy for age heterogeneity). Across all plant species found at a location, mean Ellenberg indicator values for humidity, soil nutrients, temperature and light were calculated. For the functional analysis of plants, we established a trait matrix containing 46 different functional aspects like family affiliation, mode of seed dispersal, root type or leaf structure (Appendix 6.2). We then calculated functional dispersion among plant species per site using the packages FD (Laliberté & Legendre 2010) and vegan (Oksanen et al. 2018) in the statistical R environment (R Core Team 2018). Additionally, we quantified compositional herb and shrub heterogeneity (beta diversity) using the betadisper function for multivariate dispersion (Anderson et al. 2006). Further details on the vegetation sampling can be looked up in Uhl et al. (2020a).

At the landscape level, we analyzed two different scales of effect: the close vicinity around the sampling locations (200m buffer) and the larger-scale landscape context (1000m buffer) around each light trap location. The 200m buffer hereby was mainly describing habitat quantity inside the conservation areas, while the 1000m scale was strongly influenced by landscape elements outside the reserves. Therefore, the two scales - which are not correlated - were considered as revealing complementary aspects of the landscape context of our study sites. For the analysis, we used the program QGIS (QGIS Development Team 2018) and satellite images taken from the two forest areas in 2017, as provided by Google Maps™. In total, six different landscape elements were defined: forested area, open grassland, reed vegetation, open waterbodies, urban/industrial areas, and arable fields. From the area fractions of the first four landscape elements, we calculated the Shannon diversity of natural habitats, while the last two landscape elements were summed up as ‘proportion of modified areas’. At the small-scale (viz. 200m), only the proportion of open and reed areas, as well as the diversity of natural habitats was used for further analyses, as other structural elements like open water and human-modified land were mostly missing within this radius. The proportion of forest area was also discarded, as it was inversely proportional to the other measured structures. For the wider landscape level (1000m), we included the proportion of forest, open and reed areas as well as the proportion of modified areas around the moth collection sites. Additionally, landscape Shannon diversity of natural habitats and edge density (as a proxy for landscape fragmentation, in m/ha) within 1000m radius were considered. Furthermore, we measured the distance from each light trap site to the nearest forest edge, water canal and industrial plant.

Moth sampling took place in June and in August. So, two samples of each site were available, representing the early summer and late summer moth aspect. For the following analysis, we pooled these two samples to get one species abundance list per site. We used automated light traps as described in Axmacher and Fiedler (2004), equipped with two 18W tubes (Sylvania Blacklight and White Blacklight) powered by 12V dry battery packs. Start of moth sampling was at dusk, with a sampling duration of about 5-8 hours. As moths normally are on the wing until midnight and only few individuals are active after the dew point is reached (personal observations), we assume that minor differences in sampling time per night did not affect the outcome. All Lepidopterans found in the traps were subsequently mounted and identified to species level using faunal monographs. Where necessary, we dissected genitalia for identification.

For functional diversity analysis, 50 ecological characters were collated, scoring 14 different physiological, behavioral and ecological traits. Traits to describe the physiological and phenological characteristics of species were: mean forewing length, the presence of a proboscis, voltinism, and the overwintering stage. Behavioral traits comprised larval sociality, activity time of day of adults, and migratory behavior. Ecological traits were: the degree of larval food specialization, identity of larval food plant families (taking into account 16 frequently used plant families), development in beehives, food plant type (deciduous trees, conifers, grasses, herbs, inside fruits, on lichens/algae, fungi, mosses, detritus, water plants, in wood, or root feeding), larval feeding mode (endophagous, ectophagous, or semi-concealed between folded leaves), preferred habitat type (forest, shrub, grass, reed), and the northern limit of the distribution area in Europe. Details on scoring of the traits and sources of data can be found in Appendix 9.2.

Using this broad array of traits, we primarily aimed to achieve an integrative description of the ecological needs of all sampled moth species. Most information can be considered as response traits, yet the segregation of effect from response traits for moths remains controversial. Some characteristics like body size or the number of generations per year must be considered both, effect and response trait. Indeed both concepts may overlap (Suding et al. 2008). Many unequivocal effect traits like pollination efficiency or nutritional value for birds and bats remain unknown for practically all species. As a consequence, we decided not to partition our analyses arbitrarily between putative response and effect traits.

Data analysis

Where appropriate, environmental data were transformed to approximate a normal distribution. Proportions like tree crown density and landscape element quantity were logit transformed (Warton & Hui, 2011). After that, we performed a PCA with all 14 local variables to avoid collinearity. The resulting first five PC-axes served as environmental predictors in subsequent linear mixed effects models (LMMs). The same procedure was applied to the 12 landscape descriptors (see also Uhl et al., 2020b; Appendix 9.3).

For the functional diversity analysis, a dendrogram of species according to their trait scores, based on Gower dissimilarities and Ward clustering, was calculated. Using this dendrogram, we defined and named different functional groups, to better understand the occupancy of functional trait space in the moth communities. We defined the critical threshold for separating groups after visual inspection of the species clusters following their ecological characteristics (Appendix 9.4). With a distance threshold of 0.3 we assessed whether these so defined groups differed significantly from another by performing a Permanova test with 999 permutations, as implemented in the ‘vegan’ package in R (Oksanen et al. 2018). Proportional local trait space occupation was calculated for each sampling site by dividing the number of locally represented functional groups of moths through the total number of functional groups that was found throughout PsV and PdC together. Trait space occupancy therefore is a proportional value and was logit transformed for inclusion in LMMs. As a measure of functional redundancy, we calculated the mean number of species present in each functional group per site. The remaining standard functional diversity measures were calculated using the package ‘FD’ (Laliberté & Legendre 2010). Contrary to trait space occupation and functional redundancy measurement, the calculation of FRic, FEve, FDiv and FDis was done using a convex hull volume approach with the ‘dbFD’ function.

FRic is defined as the convex hull volume on trait space (Villéger et al. 2008). It therefore is only dependent on species trait values and not abundance-weighted. FEve describes the distribution of species in trait space. It normally is calculated as the equalness of distributions of the species among the minimum spanning tree in trait space (Villéger et al. 2008). When weighted by abundance, FEve describes two different components, the regularity of species distribution in trait space and the homogeneity of species abundances (Legras & Gaertner 2018). Without weighting, only species distribution is considered. So, as FEve is composed of these two components this index sometimes fails in reflecting real functional evenness (Legras & Gaertner 2018). Hence, we followed the suggestion of Legras & Gaertner (2018) and computed abundance-weighted as well as unweighted versions of FEve to better understand the contribution of its two components. FDiv captures the deviance of individual species to the trait space center, weighted by abundance (Villéger et al. 2008). It therefore represents niche differentiation and indicates the degree of competition among abundant species (Mason et al. 2005; Mouchet et al. 2010). Independently from these three aspects, FDis represents a functional pendant to the taxonomic species diversity indices, as it reflects the abundance-weighted dispersion of species in trait space (Laliberté & Legendre 2010). Following Bellwood et al. (2005), who defined ‘functional specialization’ as ‘the relative distance of a species from the centroid’, FDis - as it is calculated through the abundance-weighted mean distance between the species and the functional trait space centroid (Laliberté & Legendre 2010) - might also be interpreted as “mean functional specialization” of a community.

We used the seven different functional diversity indices as response variable in linear mixed effects models, done with the ‘nlme’ package (Pinheiro et al. 2018). Reserve affiliation served as random factor. We first constructed full models without interactions between predictors and then selected the best model for each functional diversity index by using the Akaike information criterion (AIC) with the stepAIC function in the MASS R package (Venables & Ripley 2002). The statistical routine of stepAIC selects the best model by stepwise adding and removing predictors to the initial model and checking for the resulting AIC values. The residuals of the resulting best models were then checked for spatial autocorrelation using Moran’s I test. As spatial autocorrelation never was an issue, no further correction approaches were needed. Additionally, bivariate models for each response variable with every predictor separately were performed to check for any relationships that might be hidden within the model selection approaches.

Results

We analyzed 23375 moth individuals, representing 387 species in 27 families. The 5 PC-axes of each of the two PCAs explained 71% (local factors) and 84% (landscape factors) of the total measured variation, respectively. To facilitate understanding, we named these PC-axes following their major factor loadings (Appendix 9.3). For the local factors, the first ‘Humidity-nutrient gradient’-Axis describes a gradient from drier and nutrient poor locations with open canopy, to sites with denser foliage, where soil humidity and nutrient availability is higher. The second axis was mainly loaded by forest age and density and therefore is called ‘Old, open forest’. The third axis (‘Plant diversity’) mirrors increasing plant species richness and plant functional diversity. The fourth ‘Conifer cover’ axis shows the gradient from sites with low to high amount of conifer biomass contributing to the forest stands. Additionally, conifer sites were characterized by a more heterogeneous herb layer. The fifth axis (‘Tree health’) reflects the decreasing number of dead trees at a location.

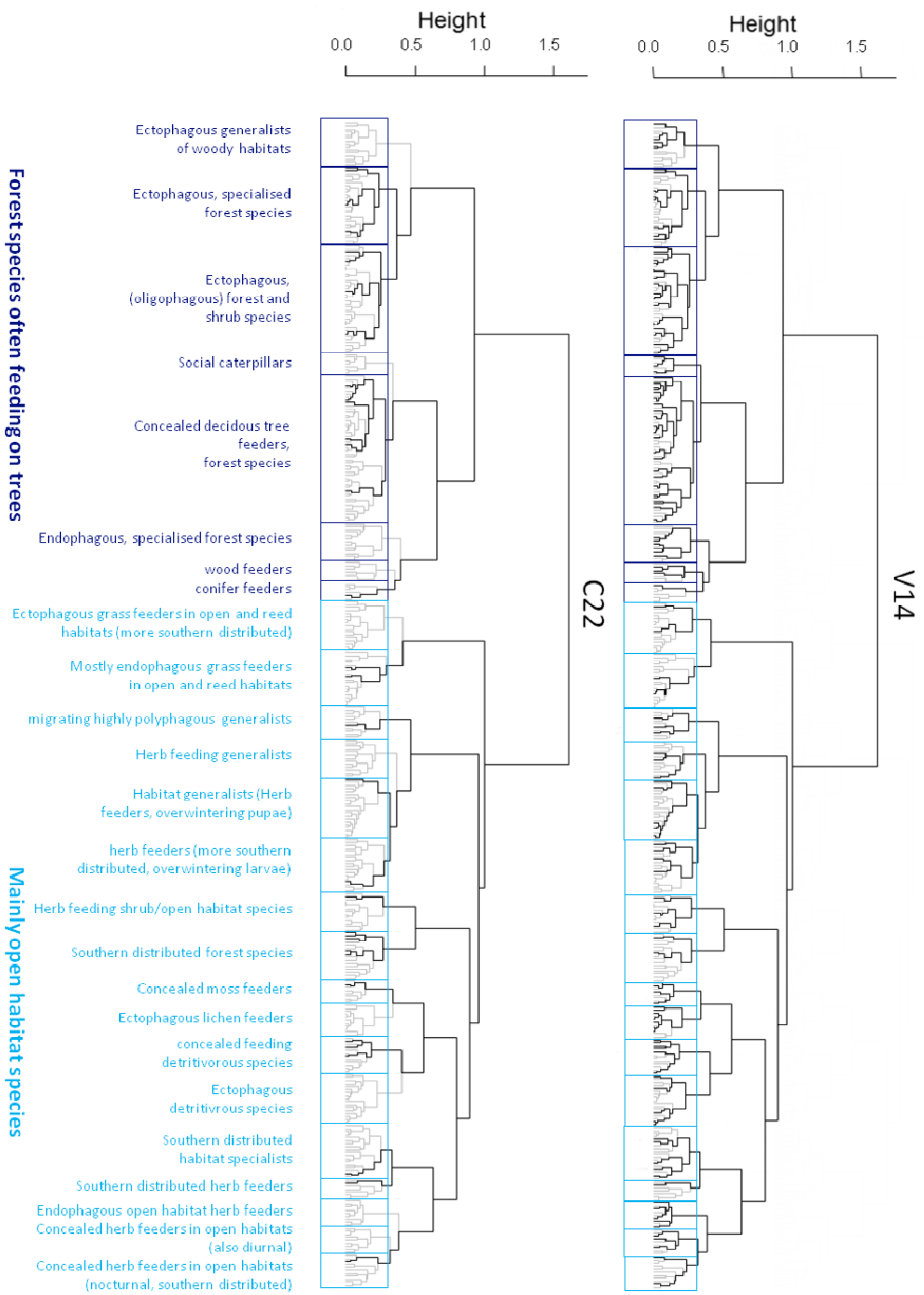

Figure 9.2: Functional dendrogram of the whole observed moth species pool (387 species) in the two pine forest reserves in NE Italy. The two most extreme local moth communities are depicted exemplarily. Upper panel: a species rich 'high quality' plot (V14) with multiple species represented in most functional groups. Lower panel: a species poor plot (C22) with few or even no species representing most functional groups. Species present at each site are indicated by black lines. Statistically significant sub-clusters after a PERMANOVA (accepted as functional groups in this study) are shown as blue boxes. Different colors indicate the two main sections of species that generally partition the functional dendrogram into moths of woodland (dark blue) and open habitats (light blue), respectively.

For the landscape PCA, the first axis 'Habitat diversity' refers to the diversity of near-natural habitats close to the sampling sites (radius of 200m). The vicinity to industrial plants is also represented by this axis. The second axis 'Anthropogenic influence' shows the gradient from reserve centers with many natural areas around to the forest edges, where increasingly modified areas in a 1000m range around the sampling site can be found. The third axis 'Landscape diversity' reflects an increasing diversity of natural habitats in a 1000m radius. 'Landscape fragmentation' mainly represents the landscape-wide edge density, while the fifth axis 'Open habitats' describes the proportion of open habitats within 200m around the sampling locations.

The functional dendrogram of moths shows two main sections, with one containing mainly forest dwelling species dependent on trees (e.g. larvae feeding on foliage of trees or developing in wood), and the other mostly consisting of open habitat species with other larval feeding habits (most of them feeding on herbs, but also including grass, moss and lichen feeders). These sections further split up into 25 functional groups (8 in the first forest species section, 17 in the second section) which were significantly different from each other ($R^2=0.71$, $p=0.001$). The functional groups and the whole dendrogram are presented Appendix 9.4. Each functional group comprised 6 to 49 species (mean: 15.5 ± 9.7), indicating substantial functional redundancy in the regional moth fauna. The largest unit (49 species) comprises forest species which develop as concealed feeders on deciduous trees, while the smallest unit (6 species) contains all conifer-feeding species. Based on these units, proportional trait space occupation and mean functional redundancy per site were calculated. Highest mean functional redundancy was found at site V14 (proportional niche occupation: 100%, mean functional redundancy: 5.12 species per functional group), while C22 had lowest values (trait space occupation: 60%, mean functional redundancy: 1.32 species; Fig. 9.2). On average, we found 2.96 species per functional group at each site.

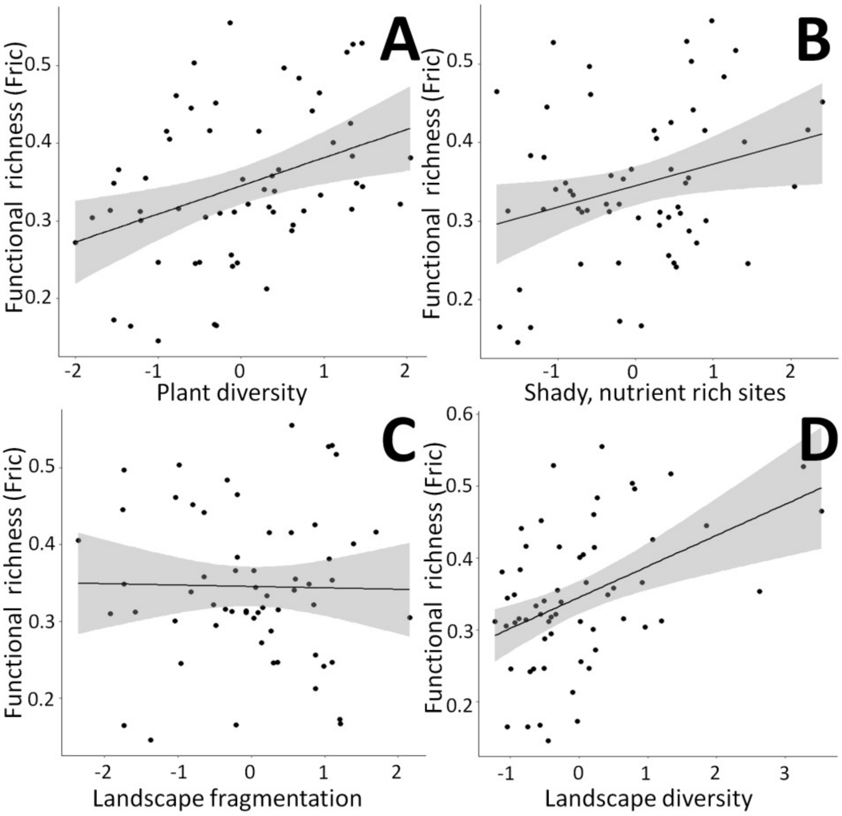

Figure 9.3: Linear bivariate regressions showing the relationships between moth functional richness (FRic) and a) Plant diversity, b) Shady, humid, nutrient rich sites, c) Landscape fragmentation and d) Landscape diversity. The detailed results of the linear mixed effects models (shown as black line and shaded area) can be looked up in Appendix 9.5

Detailed results of the bivariate linear mixed effects models can be found in Appendix 9.5. Moran's I statistic revealed no spatial autocorrelation within the residuals of the best models, selected via AIC. We observed significant positive relationships between FRic and 'Plant diversity', the 'Humidity-nutrient gradient' and 'Landscape diversity' (Fig. 9.3a-b and d), which were - together with 'Landscape fragmentation' (Fig. 9.3c) - combined in the best model (Tab. 9.1). Altogether, these factors explained roughly 50% of the total variation. The best model for proportional trait space occupation comprised six predictors, of which 'Plant diversity', the 'Humidity-nutrient gradient', 'Landscape diversity' (Fig.9.4a-b and d) and the 'Old, open forest'-Axis were positively correlated, while 'Tree health' (Fig. 9.4c) and 'Landscape fragmentation' were negatively correlated with the response variable (Tab. 9.1). Here, 43% of the total variation could be explained. Looking at functional redundancy, four factors, viz. 'Plant diversity', the 'Humidity-nutrient gradient', 'Landscape diversity' (all three positively correlated, Fig. 9.5a-b and d) and 'Landscape fragmentation' (negatively correlated, Fig. 9.5c) were included in the best model (Tab. 9.1). The model explained 47% of the total variation.

For FEve, we observed differences in the behavior between the abundance weighted and un-weighted index versions. The best model for abundance weighted FEve revealed 'Landscape diversity', the 'Humidity-nutrient gradient' (both negatively correlated) and 'Landscape fragmentation' (positive correlation) as significant predictors (Tab. 9.1). Twenty-one percent of the total variation could be explained by this model. Without abundance weighting, the best model for FEve (viz. the regularity of species distribution) combined the 'Humidity-nutrient gradient', 'Plant diversity' (both positively correlated) and 'Landscape fragmentation' (negative relationship) as predictors (Tab. 9.1). The model captured

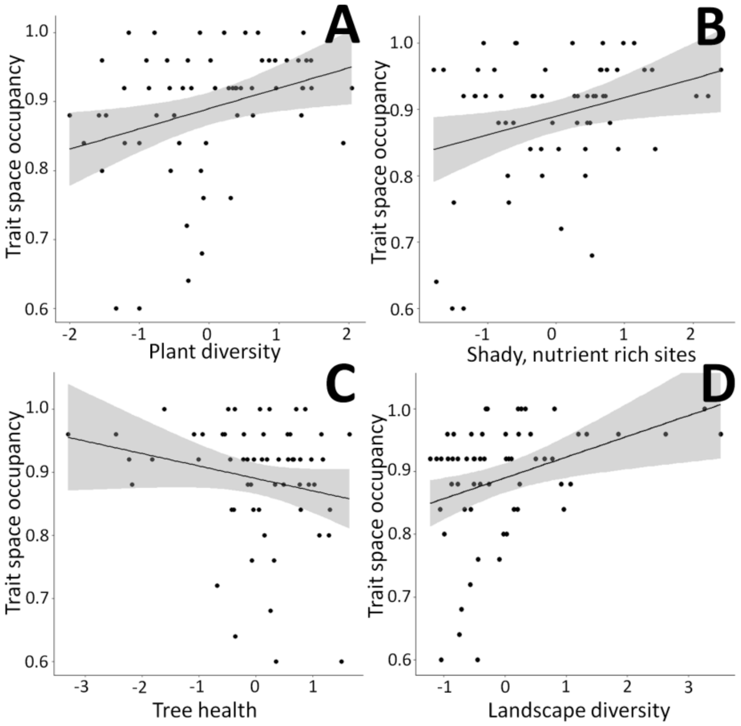

Figure 9.4: Linear bivariate regressions showing the relationships between trait space occupancy and the PC axes depicting a) Plant diversity, b) Shady, humid, nutrient rich sites, c) Tree health and d) Landscape diversity. The detailed results of the linear mixed effects models (shown as black line and shaded area) can be looked up in Appendix 9.5

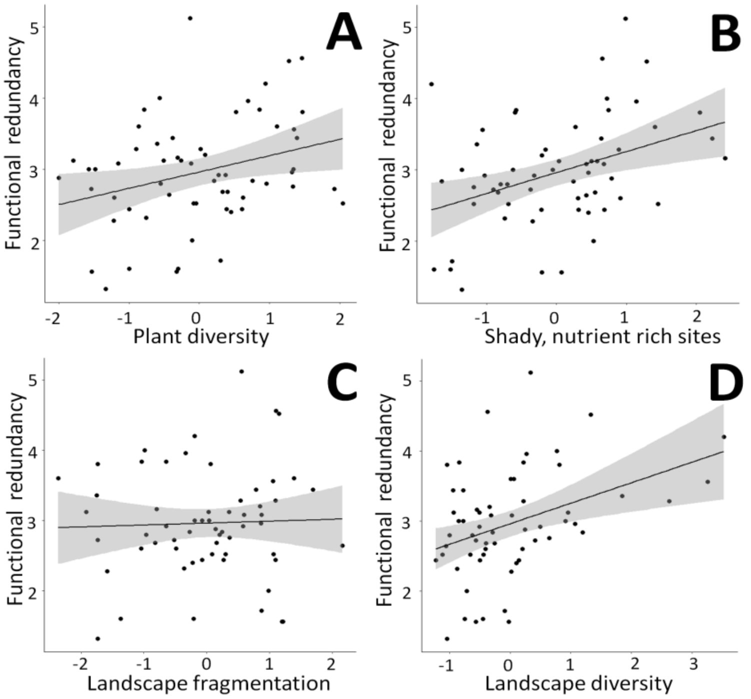

Figure 9.5: Linear bivariate regressions showing the relationships between functional redundancy and a) Plant diversity, b) Shady, humid, nutrient rich sites, c) Landscape fragmentation and d) Landscape diversity. Detailed results of the linear mixed effects models (shown as black line and shaded area) can be looked up in Appendix 9.5

26% of the total variation. FDiv and FDis were not correlated to any of the tested factors in single predictor models (Appendix 9.5). Multivariate models for FDiv and FDis only had small R^2 values and therefore explained but minor fractions of variation (Tab. 9.1).

Table 9.1: Best models for seven different functional diversity indices (as response variables) and multiple predictors tested simultaneously, selected via AIC. Reserve ID was included as random factor in each model.

Response	predictors	t-value	p-value	Beta-coefficient	Marginal R^2	Conditional R^2
FRic	Landscape diversity	5.45	<0.001	0.52	0.50	0.50
	Landscape fragmentation	-2.47	0.02	-0.25		
	Shady, nutrient rich sites	4.61	<0.001	0.46		
	Plant diversity	4.25	<0.001	0.42		
Trait space occupancy	Landscape diversity	4.44	<0.001	0.46	0.43	0.43
	Landscape fragmentation	-2.13	0.04	-0.24		
	Shady, nutrient rich sites	3.79	<0.001	0.41		
	Old, open forest	1.99	0.05	0.21		
	Plant diversity	3.18	0.003	0.34		
	Tree health	-1.87	0.07	-0.19		
Functional redundancy	Landscape diversity	4.90	<0.001	0.49	0.47	0.47
	Landscape fragmentation	-1.84	0.07	-0.19		
	Shady, nutrient rich sites	5.25	<0.001	0.54		
	Plant diversity	3.27	0.002	0.33		
FDis	Shady, nutrient rich sites	-1.16	0.25	-0.15	0.06	0.18
	Plantdiv	1.76	0.08	0.22		
FEve (weighted)	Landscape diversity	-2.40	0.02	-0.30	0.16	0.21
	Landscape fragmentation	2.16	0.04	0.27		
	Shady, nutrient rich sites	-2.35	0.02	-0.30		
FEve (un-weighted)	Landscape fragmentation	-2.55	0.01	-0.32	0.22	0.26
	Shady, humid nutrient rich sites	3.17	0.002	0.38		
	Plant diversity	2.77	0.01	0.33		
FDiv	Anthropogenic influence	1.54	0.13	0.22	0.13	0.13
	Open habitats	-1.39	0.17	-0.18		
	Shady, nutrient rich sites	-1.57	0.12	-0.21		
	Conifer sites	1.47	0.15	0.21		

Discussion

We analyzed multiple environmental gradients and their influence on various aspects of functional diversity of a species-rich group of insects within two nature reserves. Especially FRic and niche occupation may give insight into the possible multifunctionality of the local ecosystem, as we infer that with higher niche occupation, the function of the local ecosystem is guaranteed. Functional redundancy, on the other hand, can be seen as an indicator for ecosystem resilience (Feit et al. 2019), as with more species occupying the same functional group, it is less likely that the loss of single species immediately leads to a loss of functioning ('insurance hypothesis': Yachi & Loreau 1999). Conversely, any further loss of species at sites with already low functional redundancy may directly translate into the reduction of ecosystem functionality, as some functional groups are then no longer occupied.

The functional group divisions of moth species clearly reflected the different habitat structures available to these insects in the study area, mainly consisting of forest sites, but also reed and open habitat patches. Overall, the 387 moth species recorded covered a wide range in functional trait space and could be grouped into 25 clusters according to a multitude of trait data. The by far biggest of these groups consisted of forest species, whose caterpillars live concealed on deciduous trees. In contrast, conifer feeders, species living inside wood and moths with caterpillars living gregariously had lowest species numbers. The presence of various moss and lichen feeders as well as over 25 detritivorous species also mirrors the wide variety of feeding niches available to Lepidopterans in the two studied reserves. Such a broad representation of functional niche space is typical for Lepidoptera in a near-natural forest area (Summerville & Crist 2003; Thorn et al. 2015). Moreover, substantial redundancy has been observed elsewhere in species-rich assemblages of temperate-zone forest moths (Truxa & Fiedler 2016).

Niche occupation at all 60 sites was never less than 60%, and every niche was on average occupied by three species per site. Yet, in PdC niche occupation and functional redundancy was in general lower than in PsV, what mirrors the reduced habitat structural richness, compared to PsV. Some of the PdC sites are completely dominated by monotonous pine forest stands. Open grassland or reed vegetation was largely missing, particularly in the center of the reserve. This lack of alternative habitats seems decisive for the absence of species like *Laelia coenosa* and *Schoenobius gigantella* which are bound to reed areas. We therefore conclude that habitat mosaics within conservation areas significantly enhance functional redundancy on site and therefore ameliorate local ecosystem resilience. These findings are in line with previous studies pointing out the importance of local environmental heterogeneity for ecosystem resilience (Oliver et al., 2015). Functional redundancy within moth assemblages was especially low at six locations (one of them situated in PsV, five in PdC). With a value below two, these moth communities showed almost no redundancy as every functional group was on average only occupied by one species, if at all. This was not only true for functional groups comprising species bound to special habitats, but also for typical forest moth groups (Fig. 9.2, Appendix 9.4). At these impoverished sites, any further erosion in species richness might directly affect ecosystem resilience as some niches would become vacant. Most of these functionally impoverished locations were surrounded by monotonous landscapes and were locally characterized as nutrient-poor, dry forest stands. Importantly, low landscape diversity values at these sites were not driven by land use outside the reserves – which was represented by the 'Anthropogenic influence'-Axis – but by the monotonous habitat structure inside the reserves. Especially the five functionally most impoverished moth assemblages in PdC were located near the reserve center, where only few other near-natural habitats were breaking up the pine stands.

For our small-scaled analyses of functional diversity patterns within two reserves, we had to consider possible spatial autocorrelation between our sampling sites. However, we found no spatial autocorrelation within the residuals of our multivariate regression models. Looking at the R^2 values of the models, up to 50% of the variation within our data could be explained. The residual variation might have been driven by local microclimatic and weather conditions, which are known to strongly affect moth flight-to-light-behavior (Jonason et al. 2014). Furthermore, there might have been some bias because of the yearly fluctuations in moth species abundances, as data sampling was split up over three years.

Within the multivariate models, only four of the ten candidate predictors (five local and five landscape-scale PC-axes), representing 28 condensed raw variables, had a major effect on functional diversity of insect assemblages, as these four factors were included in the best models selected via AIC. 'Landscape diversity' and the local 'Humidity-nutrient gradient' were the strongest predictors for functional richness, redundancy and niche occupation among moths, as indicated by their beta coefficients. At shady sites with humid and nutrient-rich soils, surrounded by diverse near-natural landscapes within 1000m radius, we found in general more niches to be occupied by moths, more species per functional group and – in consequence – higher functional richness. Furthermore, plant diversity (positively) and landscape fragmentation (negatively) always played a role in the best models. Previous findings already showed that moth taxonomic species richness and diversity is promoted by near-natural vegetation and large-scale landscape structure (Botham et al. 2015; Merckx et al. 2012b; Root et al. 2017). By including also functional species traits, our results demonstrate that these proxies of habitat quality and quantity also affect community attributes that potentially translate into ecosystem multifunctionality and resilience.

As we were looking at multiple local and landscape-scale predictors simultaneously, we furthermore were able to compare the influence of different scales of effect for functional moth diversity. Accordingly, large-scale landscape diversity (within 1000m radius) and the local humidity-nutrient gradient seem to play equally important roles, followed by plant diversity and finally landscape fragmentation. The smaller scale habitat diversity (within 200m radius) in contrast seems to have only minor effects on functional diversity and was never included in the best multivariate models. With regard to habitat quantity at the landscape scale, landscape diversity was the most important predictor for our measures of insect functional diversity. The more different, near-natural habitat areas were available within a 1000m radius around the light-trapping sites, the more functionally rich was the local moth community, comprising higher niche occupation and increased functional redundancy. So, surrounding landscape diversity affected community attributes related to ecosystem function (occupancy) and resilience (redundancy) inside protected nature reserves. Positive effects of landscape-scale diversity on functional redundancy have already been found in agricultural systems (Feit et al. 2019). However, to our knowledge there was to date no evidence on the landscape context also influencing the functional richness of insects inside nature reserves. Nevertheless, effects of landscape context on local insect biomass and diversity (Seibold et al. 2019) might have indicated such a correlation to exist.

Besides the diversity of near-natural habitats around the reserves, also the shape and structure of landscape elements influenced moth functional richness. Sites surrounded by a landscape with higher edge density had in general lower functional redundancy, fewer occupied niches and in consequence lower functional richness. More landscape edges can affect how species disperse throughout a region (Collinge & Palmer 2002) or influence a habitat’s microclimate through edge effects (Schmidt et al. 2017). The effect of large-scale landscape configuration and connectivity on ecosystem functionality and especially on the biodiversity-ecosystem functioning relationship has been shown in various studies (Liu et al. 2018). However, the influence of landscape fragmentation on moth functional diversity was much less pronounced than the effect of landscape diversity. This indicates that possible barriers to species movements in the landscape – even though playing a major role for functional richness – are less important than the availability of near-natural habitats in the vicinity (Merckx et al. 2019). So, altogether, landscape compositional (viz. landscape diversity) and configurational (viz. landscape fragmentation) heterogeneity were driving the functional diversity of moth communities inside the studied nature reserves, with composition being more important than configuration. Perović et al. (2015) investigated these two aspects of landscape heterogeneity in grassland areas and found landscape composition to affect butterfly taxonomic diversity, while configuration only seemed to play a role for functional composition. Contrastingly, in studies on agri-environmental schemes, only configurational heterogeneity and not crop diversity (as a measure for landscape composition) influenced pollinators (Hass et al. 2018). The importance of composition and configuration therefore is strongly dependent on the focal ecosystem and seems also to vary among groups of organisms that are studied. In agricultural areas for example, unmanaged edges and hedgerows can serve as important microhabitats for insects (Merckx et al. 2012a), whereas edges in forest habitats can represent insurmountable barriers for some forest species (Slade et al. 2013).

Other landscape-scale predictors did not substantially affect moth functional diversity, although we had expected some correlations to occur with the small-scaled 'Habitat diversity'-Axis or the 'Anthropogenic influence' gradient. It seems that directly neighboring surroundings within 200m radius were by far not as important for the functional integrity of local moth assemblages as larger-scale availability of different natural habitats (Merckx et al. 2012a, 2018). Perhaps the rather high mobility of many moths here plays a role and leads to small-scale neighborhoods being not as important as the wider surroundings. For the 'Anthropogenic influence'-Axis, we had expected some negative correlations, as other studies already have shown that intensified land use in the vicinity of conservation areas also affects nearby natural habitats (Seibold et al., 2019). However, for the two coastal nature reserves, surrounding agriculture and industrial areas seem to play minor roles in their immediate vicinity. Perhaps, separate consideration of the two reserves might yield different results, as for PsV some relationships between the proximity of industrial areas and local micro-moth FD inside this reserve have already been established (Uhl et al. 2016). Anthropogenic influences might therefore affect biodiversity punctually and have to be investigated individually for each reserve. More generally, however, our results indicate that the two rather big natural areas are able to preserve insect biodiversity to some extent. By further ameliorating the diversity of natural habitats inside the reserves or the connectivity between natural areas of different habitat structures, conservation efforts could be even more successful.

As expected, local habitat quality was always important for moth communities. Mainly two specific predictors emerged as relevant: The 'Humidity-nutrient gradient' and 'Plant diversity'. In the two nature reserves under study, the first of these factors describes successional stages of forest development, which once started as rather open pine plantations and since then have developed towards a near-natural forest vegetation (Wölfling et al. 2019). At some places in the reserves, the dry and open structure of the ancient plantations is still visible, whereas other locations are nowadays characterized by forest offering shady and more humid habitat conditions for insects. The availability of water and nutrients is in general a limiting factor for vegetation in coastal Mediterranean ecosystems (Pérez-Ramos et al. 2012). Here, natural succession can also play an important role for the natural water cycle, as shadier sites retain more humid soils by reducing direct sun light (Von Arx et al. 2012). The retention of water is especially important for Mediterranean ecosystems being prone to increasing drought events in terms of climate change (Barredo et al. 2016). Besides these positive effects for water management, shady sides can also stabilize microclimatic conditions (Kovács et al. 2017). Structurally rich forests and stable microclimate, arising from secondary succession, might finally result in more insect species being able to inhabit such places, enhancing functional richness and therefore also ameliorating ecosystem functionality. Additionally, plant diversity played a role for maintaining a functionally rich insect community. Obviously, the more different plant species grow at a location, the more herbivorous insect species may find suitable food resources at this site. This positive effect of plant richness on moth species diversity has already been observed for different forest management regimes (Root et al. 2017) and for small-scaled site-to-site variation in the same two forest reserves as investigated here (Uhl et al. 2020b).

Contrary to expectation, all other descriptors of local habitat conditions, such as 'Conifer cover', 'Tree health' and 'Old, open forest', did not substantially affect FRic and redundancy, although the latter two were included in the best model for niche occupancy. Niche occupation was declining where fewer dead standing trees were found. This might underline the importance of deadwood for forest ecosystems, as decaying wood material itself is a food resource for some insect species (Gossner et al. 2013). Decaying trees that remain standing upright inside a forest contribute to the formation of forest gaps which in turn facilitate more herb and shrub species to grow. Indeed, old open forest sites had more niches occupied by moths than younger and dense forest stands, indicating that with growing forest age, more niches become available and subsequently more insect species are able to establish and occupy these habitat structures (Schowalter 2017). However, these relationships that are rather well documented for relationships between insect species richness and vegetation succession in many other systems, only described minor fractions of variation in moth functional diversity in our study and were far less important than plant richness and the humidity-nutrient gradient.

All together, our results underline the equally strong importance of habitat quality and quantity aspects for the functional integrity of communities within nature reserves. For preserving local biodiversity and counteracting insect loss, there are mainly two conclusions that can be derived from our results. First, local management should aim at increasing the diversity of near-natural habitats within and beyond the boundaries of reserves. This is important for ameliorating functional redundancy and therefore ecosystem resilience on site. Especially for woodland habitats, maintaining structurally-rich, old-grown forests with diverse understory, forest gaps and high plant species richness can contribute to preserving insect biodiversity, which in turn is essential for terrestrial ecosystem functionality (Weisser & Siemann 2013). Second, our results show that local management needs to be supported by landscape-scale actions, even if conservation areas are relatively large. Ameliorating the diversity of near-natural landscape elements and simultaneously reducing landscape fragmentation can enhance the functional richness of local insect communities. The importance of landscape-scale actions to promote diverse habitats and connectivity is therefore crucial for conservation success, as local management alone can likely not preserve biodiversity in isolated nature reserves in the long run.

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10. Synopsis

In recent years, a multitude of studies reported on losses in insect biomass, numbers and regional γ-diversity (Bell et al. 2020; Hallmann et al. 2017; Seibold et al. 2019), followed by general conclusions and reviews about the possible drivers of insect decline (Habel et al. 2019b; Sánchez-Bayo & Wyckhuys 2019). Insect assemblages have turned out many times to very sensitively reflect environmental quality of habitats, and especially multiple studies on communities of nocturnal moths have turned out fruitful in that regard (Habel et al. 2019c; Slade et al. 2013; Uhl et al. 2016). My thesis work contributes to the understanding of how insects are affected by environmental gradients in isolated conservation areas, as I was not only analyzing multiple factors simultaneously, but also a variety of different aspects of biodiversity, viz. small-scaled α-diversity patterns, various β-diversity measures and functional diversity aspects of plants as well as moths.

The importance of the different spatial scales of effect varied depending on the diversity measure that was analyzed. As expected by one of my hypotheses, I found more moth species in PsV than in PdC, indicating that the higher landscape diversity surrounding PsV positively affects the γ-diversity of this reserve. Higher local plant diversity and a near-natural forest structure enhanced local moth α-diversity within my study areas, supporting my fourth hypothesis. So, for inventory diversity measures, I found small-scaled moth α-diversity to depend on small-scaled variables, while γ-diversity patterns seem to be influenced by larger-scale landscape attributes (Fig. 10.1). In fact, this relationship was hypothesized and tested by Gavish et al. (2019), who stated that the response type most strongly is related to the equivalent factor type (scale-matching hypothesis). However, this assumption seems only partly corroborated, as the number of locally observed moth individuals was mainly correlated to landscape diversity but not to any of the small-scaled local factors. Of course, it is always important to consider the strength of the investigated gradients. In my analyses landscape diversity differed from locations with only one habitat type around to light trap sites with diverse near-natural areas in the surroundings. Vascular plant species richness in contrast always ranged between 23-47 species per site and all sampled locations were situated within the same forest type. Studies that considered different habitats across sites with a larger variance in plant richness repeatedly found substantial effects of plant diversity on insect abundance (Alison et al. 2017; Chisté et al. 2016). But, if the strength of the observed environmental gradient has this strong effect, how can we assume that the scale-matching hypothesis is right? Another problem is that α- and γ-diversity are not independent from each other. Both of these measures describe basically the same component and only differ in the spatial scale that is considered (Jurasinski et al. 2009). By definition, α-diversity is always a subset of the regional species pool (γ-diversity).

In fact, inventory measures have further limitations concerning biodiversity change (Hillebrand et al. 2018). Species richness as well as α- and γ-diversity can remain stable, although the composition of species might already have changed due to environmental constraints (Mori et al. 2018). Therefore, it is always important to also take a look at species composition and functional diversity. Of course, the analysis of functional characteristics always depends on the availability of information. For insects we often lack the information to build up a species traits matrix, which is necessary for functional analyses. However, for European Lepidoptera there is quite a good knowledge about their ecological needs and characteristics, making them again useful target organisms for ecological analyses. In my thesis differentiation diversity (species composition) as well as functional characteristics like functional richness, redundancy and niche occupation were influenced by both, local and landscape-scale aspects (Chapter 8 and 9, Fig. 10.1), confirming the fifth and sixth hypothesis. Especially habitat quality (like forest structure on the local scale) and habitat quantity (the diversity of near-natural habitats on the regional scale) affected species composition and functional diversity. The effect of large-scale surroundings, including areas outside the reserves, turned out as one of the most important factors determining functional richness and redundancy of moths within the conservation areas (Chapter 9). Species composition and functional characteristics derived from species traits here once again proved their great suitability for detecting responses to environmental change, and hence should always be considered, when talking about insect decline and how to counteract diversity loss.

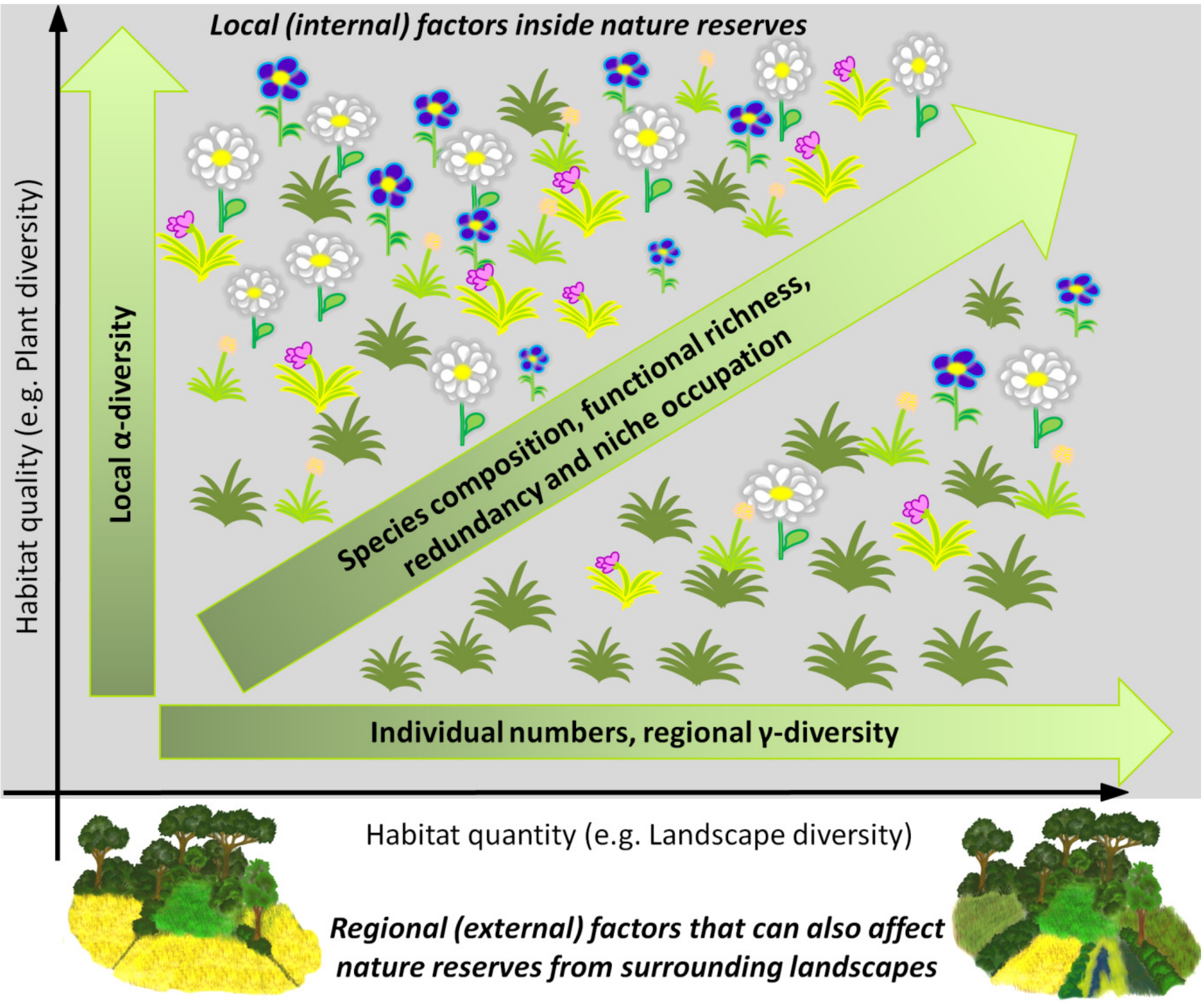

Figure 10.1: Summary of how local (grey background) and regional (white background) factors influence different aspects of biodiversity in isolated nature reserves embedded in a cultivated landscape. Symbols of plants schematically indicate a gradient from low (lower part) to high (upper part) plant diversity, while the small icons of landscapes resemble a gradient from low (left) to high (right) landscape diversity. The shading of the arrows indicates low (dark green) to high (bright green) diversity.

So, which factors are really important for biodiversity and how can we counteract further insect declines? The great variety of different ecosystems – each of which having their own peculiarities – makes it difficult to find an all-fits-one solution for preserving biodiversity. The importance of different factors furthermore can vary depending on the focal organisms of interest. However, the growing scientific knowledge in this topic has drawn a comprehensive picture of the multiple factors acting on different ecosystems and their biodiversity.

Land use change is often viewed as the major factor contributing to large-scale insect γ-diversity loss. With the disappearance of hedgerows and field margins, landscape simplification impacts insect abundance (Hass et al. 2018) and diversity (Gallé et al. 2019; Perović et al. 2015, Fig. 10.2). Insect species richness of remaining near-natural areas is also indirectly impacted through habitat fragmentation (Rossetti et al. 2017), which is composed of two key factors: The loss of habitat and the isolation of remaining near-natural areas, both reducing biodiversity and ecosystem function (Haddad et al. 2015, Fig. 10.2). Isolation effects on the one hand can affect species dispersion success between habitats, especially discriminating against specialized and often less mobile species (Slade et al. 2013). But also in generalist species, disrupted gene flow between populations can lead to local extinctions (Habel & Schmitt 2018). On the other hand, the persistence of species is bound to the amount of suitable near-natural habitats on the landscape scale (Merckx et al. 2019). The so called habitat-amount hypothesis (Fahrig 2013), which describes this relationship between species occurrences and habitat amount, however always was focusing on one habitat type. Hence, no assumptions for local α-diversity and its dependence on the landscape-scale diversity of different near-natural habitats were made. In Chapter 7 I found α-diversity of moths inside the conservation areas to correlate with the diversity of near-natural areas within 200m radius. Furthermore, increasing landscape diversity within 1000m radius had a positive effect on moth individual numbers and was the most important factor related to functional richness inside the conservation areas (Chapter 9). Landscape diversity can therefore be a decisive factor, when it comes to the preservation of regional insect diversity, functional richness and abundance. As moths do not only provide pollination as ecosystem service, but also serve as food for birds and bats or as resources for a multitude of arthropod parasitoid and predators, this landscape diversity effect might also transfer to higher trophic levels.

Besides these landscape-scale effects on biodiversity, also small-scaled local environmental gradients can shape insect communities. As written earlier, moth α-diversity was mainly influenced by local conditions inside my study areas. The humidity-nutrient gradient, which mainly reflects some kind of natural succession gradient within my study areas, was the most important factor shaping local α-diversity patterns of insects (Chapter 7, Fig. 10.2). At shady, humid and nutrient rich sites with high plant diversity, there was higher moth species diversity (Chapter 7), as accompanied by increased functional richness and redundancy (Chapter 9). These patterns were also observable when I analyzed proportional β-diversity in PsV and PdC. Well developed near-natural forest sites were colonized by significantly larger fractions of the regional species pool, confirming my fifth hypothesis on local attributes being determinant for proportional diversity. This indicates additive homogenization, i.e. the co-occurrence of more species (larger species subsets in relation to the regional species pool), as with the diverse vegetation structures more niches become available. This is not only true for forest reserves, but can also be observed in managed forests. In fact, Knuff et al. (2020) found structural richness in managed forests to enhance insect diversity. So, forest management can have major effects on insect diversity (Thorn et al. 2015) and community composition (Gossner et al. 2013; Truxa & Fiedler 2012, Fig. 10.2). We therefore have to rethink the way we are arranging woodland habitats. Removing old trees and deadwood with the goal of "preserving a healthy and regenerating forest" counteracts biodiversity conservation. Same must be said about removing understory vegetation like shrubs and small trees for better accessibility and simultaneously planting trees very densely without keeping forest gaps. Also within my investigation areas, young and dense forest sites were colonized by only minor fractions of the regional moth community (Chapter 8). Without a near-natural forest structure that is build through natural succession, we risk to lose the forest's self-regulating microclimate (Kovács et al. 2017; Prévosto et al. 2020) and its ecosystem multifunctionality, as indicated by reduced moth functional richness and lower redundancy at dense, young forest sites (Chapter 9).

Taking all these findings into account, local and landscape-scale effects together are shaping moth communities inside conservation areas. However, some of my analyzed factors draw attention on the difficulty to discriminate against what is local and what is a landscape factor. Especially landscape-scale anthropogenic actions can not only affect biota on site, but also impact more distant ecosystems. Looking at human dominated areas, we have quite a good knowledge about the impacts of anthropogenic actions on biodiversity. Urbanization as such – so the loss of habitats because of surface sealing – has major impacts on species composition and richness (Fig. 10.2). Biotic homogenization often can be found in urban areas, where the lack of various specialist species makes communities more similar and reduces species turnover (Knop 2016; Merckx & van Dyck 2019). With increasing urbanization, also light pollution becomes a problem not only for insects on site, but also for the biotic communities living along wider ranges. Artificial light at night is in the suspicion of negatively influencing nocturnal insects on the large scale by desynchronizing their internal clock, reducing their fitness, and disrupting their optical efficiency (Owens & Lewis 2018, Fig. 10.2). Furthermore the loss of dark nights can act on different life stages and so disrupt insect development in many ways (Boyes et al. 2020). These physiological findings are supported by long-term in-field observations on community level in other regions, as moth species with phototactic behavior seem more prone to decrease in their population size than diurnal ones or species without light affinity (van Langevelde et al. 2018; Owens et al. 2019). Finally, ecological interactions like pollination (Knop et al. 2017; Macgregor et al. 2015) and top-down control by parasitoids (Sanders et al. 2018) can be affected by artificial light at night. Another problem that might not only influence local communities, but also insect diversity and composition of surrounding areas, is airborne industrial pollution. In my analyses in one of the two forest fragments (PsV) situated close to an urban area, I repeatedly found species turnover along the distance to industry gradient, with fewer oak feeders near the industrial harbor of Ravenna (Uhl et al. 2016, Chapter 9), likely due to reduced host plant quality (Uhl & Wölfling 2015). So here, urban areas in the surroundings seem to affect the communities of nearby conservation areas.

Agricultural areas are another example for human dominated areas, where economic management can have major effects on local and landscape-scale biodiversity. The intensification of agricultural practices threatens biodiversity (Chisté et al. 2016; Habel et al. 2019a; Mangels et al. 2017), changes community composition (Mangels et al. 2017) and leads to the loss of specialist species (Gámez-Virués et al. 2015, Fig. 10.2). The use of pesticides additionally can have lethal and sublethal effects on a majority of non-target arthropods (Pisa et al. 2014), including pollinators and beneficial insect-pest predators (Krupke et al. 2017; McArt et al. 2017; Monteiro et al. 2013). By the loss of pollinators (Hass et al. 2018) and reduced natural pest control (Rusch et al. 2016), intensive agricultural practices hereby extinguish the ecosystem services on which they are dependent on. Besides these direct local consequences, pesticide drift can be detected over wide ranges (Zivan et al. 2016) and also affect biota in nearby habitats (Botías et al. 2019, Fig. 10.2). Talking about drift, also fertilizers do not stay on the agricultural target area, but are known to impact water systems (Swaney et al. 2012, Fig. 10.2) and contribute to the airborne NOx content (Almaraz et al. 2018). As van Dobben and de Vries (2017) found out that nitrogen deposition altered the understory vegetation structure of managed forests across Europe, it was also conceivable that nutrient influx could be observed in conservation areas. In Chapter 6, I indeed found correlations between mean plant nutrient indicator values and the proportion of agricultural areas in the surroundings, confirming my second hypothesis. The use of fertilizers in agricultural areas therefore seems to alter plant communities of conservation areas (Fig. 10.2). Elevated nitrogen concentrations, however, might not only change plant species composition, but might also impact food plant quality (Kurze et al. 2018) and thereby alter plant-herbivore interactions (Li et al. 2016). In fact, the correlation between the proportion of agricultural areas and species composition was not only observable in plants, but also in PdC moth communities (Chapter 8). Finally, anthropogenic land use can not only change plant species composition towards nitrogen indicating species, but also replace plant species of restricted distributional ranges by cosmopolitan species (Chapter 6). These findings stand in contrast to my first hypothesis, as I originally was expecting, that plant communities inside PsV are not a priory affected by the landscapes outside the reserves.

So, it is not only the local management that matters, but also the larger-scale anthropogenic land use that influences biodiversity over direct and indirect pathways. In conclusion, we urgently have to finish thinking within borders. Conservation areas, that have been defined to preserve local biota, might fail in keeping the original species diversity, when intensive agriculture and land use change alters the landscape structure around. Admitting that nature reserves are not disconnected from their landscape context is the first step for a more effective management policy that can counteract insect declines. My results concerning proportional and differentiation β-diversity finally draw attention on the specific influences that can affect biodiversity on site (Chapter 8). Human actions on the landscape scale acted quite idiosyncratically on the focal investigation area, as shown by the two most important factors influencing moth β-diversity in PsV and PdC, respectively. For PsV, it was the distance to the nearest industrial plants that mainly shaped moth community composition, while in PdC it was the amount of agricultural areas in the surroundings. These changes, however, were only observable within differentiation diversity, but not in proportional β-diversity, contrasting my seventh hypothesis. So, although both reserves have a lot in common and share a long history, when they developed from one continuous coastal forest, their moth communities today seem influenced by different factors acting from their surroundings. Based on this knowledge, the importance of local case studies and individual observations for preserving species diversity is underlined. Meta-studies and generalizations cannot always provide us with the specific insights into the determining factors that might mainly shape, and threaten, communities of the focal areas of interest.

As a last point, human activities have not only altered landscapes on the large scale, but also undeniably influenced the worlds' climate (Ripple et al. 2019). Changing climatic conditions can shift distributional ranges of species (Breed et al. 2012) and threaten certain taxa due to habitat loss (Stuhldreher and Fartmann 2018). When the microclimatic conditions change, many species might lose suitable habitats within protected areas. Shifting distributional ranges therefore can undermine conservation efforts and will become a major problem if no actions to counteract climate change are taken by policy makers (Araújo et al. 2011).

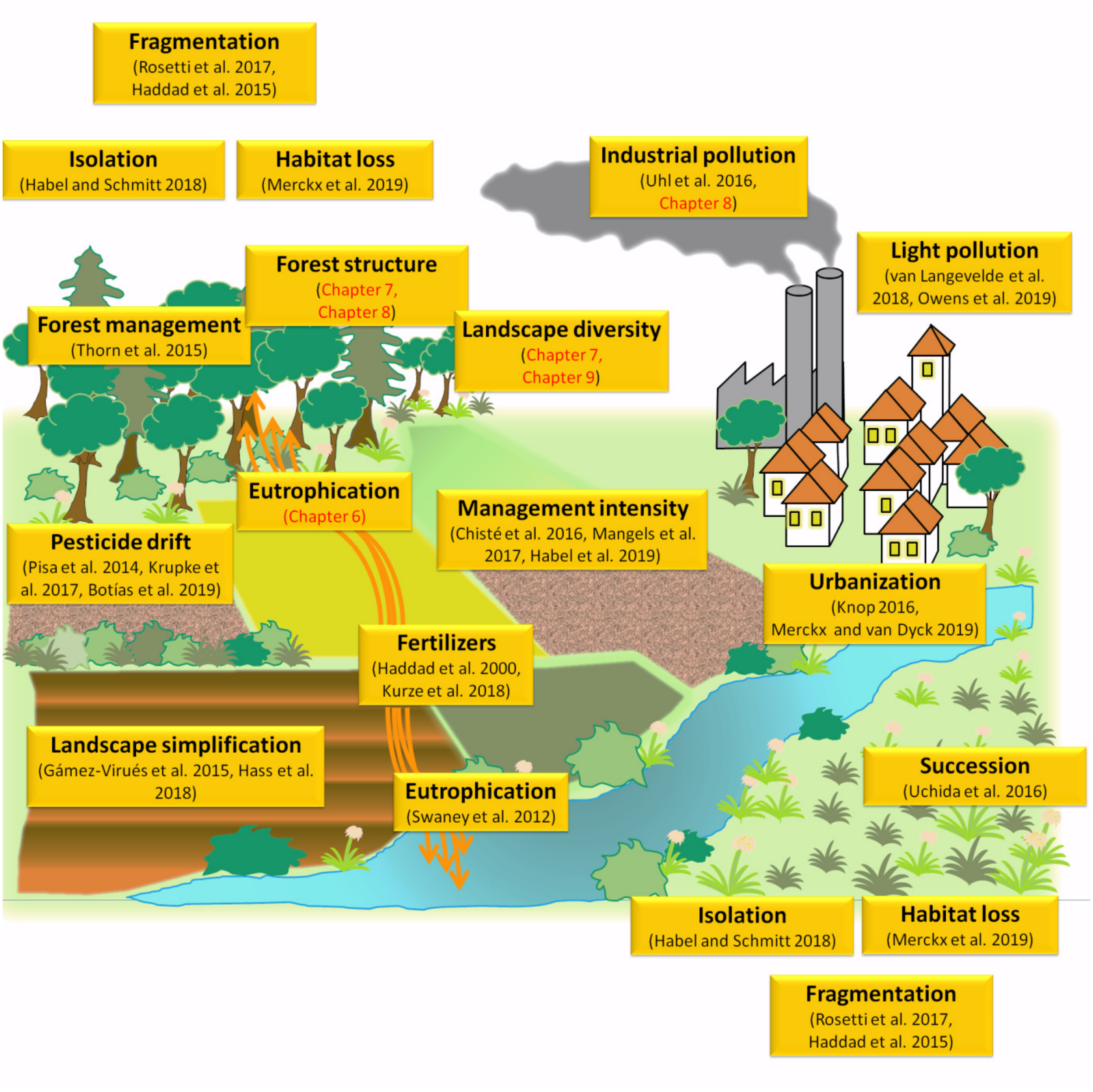

Figure 10.2: Schematic overview of the multiple drivers of insect decline. Pathways supported also through findings of my thesis are marked in red. The two components of fragmentation (isolation and habitat loss) can affect grassland as well as forest habitats. Therefore, these aspects can be found twice (in the upper left of the picture, indicating forest fragmentation, and in the lower right, indicating fragmentation of semi-natural grasslands).

So, are anthropogenic actions always to blame and do we inevitably push biodiversity beyond its planetary boundaries (Newbold et al. 2016)? This should not be the final impression one should have. Humans are part of the world's ecosystems and have always influenced how terrestrial landscapes look like, at least since the Neolithic revolution (Yerkes et al. 2012). The complete abandonment of extensive management practices can reduce biodiversity in a similar manner, as land use intensification does. This can for example be seen in Mediterranean landscapes, where land abandonment leads to large-scale reforestation due to natural succession (Geri et al. 2010, Fig. 10.2). Biodiversity-rich semi-natural grasslands and heath areas as a consequence are disappearing, and with them survival of a variety of specialized species is also at stake (Falcucci et al. 2006; Uchida et al. 2016). When extensively used semi-natural grasslands experience intensification in management, the same can be observed: Specialized insect species disappear and biodiversity declines (Uchida et al. 2016). Managing landscapes extensively by keeping a diverse landscape mosaic with a mix of different extensive grassland management practices can therefore preserve or even enhance insect biodiversity (Bonari et al. 2017; Fiedler et al. 2017). These assumptions are widely accepted in the scientific community and are not only true for grassland ecosystems, but also for forest habitats. The loss of open woodlands and mature forest can be described as "erasing a European biodiversity-hotspot" (Miklín & Čížek 2014) as both, intensifying forest management practices and no-intervention approaches in forest nature reserves can contribute to biodiversity decline (Sebek et al. 2015; Spitzer et al. 2008). As open structures within forests vanish, plant communities become impoverished, favoring mainly species of humid and nutrient-rich conditions (Hédl et al. 2010). Such a succession effect of course also affects the woodland insect communities (Sebek et al. 2015; Spitzer et al. 2008) and has led to open forest specialists being one of the most endangered insect groups in Central Europe (Dolek et al. 2018; Spitzer et al. 2008).

In line with this, structural richness within the analyzed forest reserves, viz. the existence of other habitat structures like forest gaps and wetland areas, positively affected moth α-biodiversity (Chapter 7). To maintain open areas within my investigation area, horses are now kept in PsV. This kind of conservation management, including large herbivores as ecosystem engineers, is suggested by computer simulations (Schulze et al. 2018), was also successful in other woodland habitats (Garrido et al. 2020) and has shown to support insect conservation (Garrido et al. 2019). These findings raise the question, if also managed forests should be combined with other land use practices, such as cattle grazing, to ameliorate the situation for insect diversity. This is especially important, when considering the history of European forests that were ever since shaped first by native mega-herbivores and later on by domestic grazers. Therefore many forest species until today are dependent on habitat structures that are built by large herbivores (Bengtsson et al. 2000; Spitzer et al. 2008). Where no large herbivores are left, extensive traditional practices of woodland use can help maintaining diverse insect communities. Examples for such extensive management methods are coppicing and coppice with standard. In coppice woodlands, small trees are frequently cut down, leading to multiple shoots re-growing from the stem. Coppice with standard describes the combined management of coppicing with woodland pasture and some old-grown trees in between. Both of these practices can enhance species richness and promote especially endangered species (Dolek et al. 2018; Fartmann et al. 2013; Freese et al. 2006; Müller-Kroehling et al. 2020).

In summary, preserving a near-natural, old-grown forest does not mean to exclude all kinds of forest management. Like indicated above, it's worth a thought to reintroduce historic, extensive management practices, where old trees and bushes are kept, as well as open grassland habitats, that can be used e.g. as woodland pasture. By doing so, the landscape-scale diversity of different near-natural habitats is kept high and contributes to the preservation of a high regional insect γ-diversity. Furthermore, by the maintenance of open-grown trees and woodland pastures one of the diversity-hotspot habitats of Europe can be promoted, also boosting the species-rich communities of these habitat structures (Sebek et al. 2016).

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12. Appendix

Appendix 6.1: Plant species incidence matrix (Part 1: Species A-Er, Plot V1-V15)

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14	V15
Acer_campestre	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Achillea_millefolium_aggr	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Aegonychon_purpurocaeruleum	0	0	0	0	0	0	0	0	1	1	0	1	0	0	0
Agrimonia_eupatoria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ailanthus_altissima	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ajuga_chamaepitys	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ajuga_reptans	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Alliaria_petiolata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Alnus_glutinosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anacamptis_coriophora	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anacamptis_morio	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Anacamptis_pyramidalis	0	0	1	0	1	0	0	0	0	0	0	0	1	1	0
Anisantha_sterilis	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0
Anthemis_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anthoxanthum_odoratum	1	1	1	1	0	0	0	0	0	0	0	0	0	0	1
Aphanes_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Arabidopsis_thaliana	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Arabis_sagittata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Arenaria_serpyllifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aristolochia_clematitis	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
Aristolochia_rotunda	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0
Arum_italicum	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0
Asparagus_acutifolius	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1
Asparagus_officinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Asperula_laevigata	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
Avena_fatua	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Ballota_nigra	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Bellis_perennis	0	1	0	1	0	0	1	1	0	0	1	1	1	1	1
Berberis_vulgaris	0	0	0	0	0	0	0	1	0	0	0	0	1	0	1
Brachypodium_phoenicoides	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
Brachypodium_sylvaticum	0	1	0	1	0	0	1	0	1	0	0	0	0	1	1
Bromus_erecta	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0
Calystegia_sepium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Campanula_rapunculus	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Cardamine_hirsuta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carduus_pycnocephalus	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
Carex_acuta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carex_acutiformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carex_distans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carex_flacca	0	1	0	1	1	1	0	0	0	0	0	1	0	0	1
Carex_liparocarpos	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carpinus_betulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Celtis_australis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Centaurea_nigrescens	0	1	0	1	0	1	1	1	0	0	0	1	0	0	0
Centaurium_erythraea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cerastium_brachypetalum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cerastium_fontanum	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Cerastium_glomeratum	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Cerastium_semidecandrum	1	1	1	0	0	1	0	0	0	1	0	1	0	1	1
Chaerophyllum_temulum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cichorium_intybus	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0
Cirsium_arvense	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Clematis_flammula	0	1	0	1	0	0	0	0	1	0	0	1	0	0	1
Clinopodium_vulgare	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Convolvulus_arvensis	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Cornus_mas	0	0	0	0	0	1	0	0	1	0	1	1	0	0	0
Cornus_sanguinea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cotinus_coggygria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Crataegus_monogyna	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Crepis_capillaris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Crepis_foetida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cynoglossum_officinale	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Dactylis_glomerata	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Daucus_carota	0	1	0	0	0	0	1	0	0	0	0	1	1	0	0
Dioscorea_communis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Diplotaxis_tenuifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Echium_vulgare	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Elaeagnus_angustifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Equisetum_ramosissimum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Erigeron_sumatrensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Erodium_cicutarium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eryngium_campestre	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 6.1: Plant species incidence matrix (Part 2: Species Eu-Pop, Plot V1-V15)

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14	V15
Euonymus_europaeus	0	1	0	1	0	0	0	0	1	1	1	1	1	1	1
Eupatorium_cannabinum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euphorbia_cyparissias	1	1	1	0	1	0	1	0	0	1	0	1	1	1	1
Euphorbia_helioscopia	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Frangula_alnus	0	0	0	0	0	0	0	1	0	1	1	0	0	1	1
Fraxinus_angustifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fraxinus_excelsior	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fraxinus_ornus	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1
Galium_aparine	1	0	0	1	0	0	1	0	1	0	1	0	1	0	0
Galium_mollugo	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0
Genista_tinctoria	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0
Geranium_columbinum	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Geranium_dissectum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Geranium_molle	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0
Geranium_purpureum	1	0	1	0	0	0	1	0	1	1	0	0	1	0	1
Geranium_robertianum	0	0	0	0	1	0	1	0	1	0	1	0	0	0	0
Geum_urbanum	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0
Gladiolus_italicus	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Glechoma_hederacea	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Hedera_helix	0	1	0	0	0	1	1	1	1	0	1	1	1	0	1
Helianthemum_jonium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Helianthemum_nummularium	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0
Helminthotheca_echioides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hippocrepis_emerus	0	1	0	0	0	1	0	1	0	1	0	1	1	1	1
Hordeum_murinum	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Humulus_lupulus	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Hypericum_perforatum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hypochaeris_radicata	1	0	1	1	1	0	1	0	0	0	0	0	0	0	0
Inula_salicina	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
Iris_foetidissima	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Jacobaea_erratica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Juniperus_communis	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0
Knautia_integrifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Lamium_purpureum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lathyrus_sphaericus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lepidium_campestre	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Ligustrum_vulgare	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
Linum_bienne	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lonicera_caprifolium	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
Lonicera_japonica	0	0	0	1	0	0	1	0	0	1	0	0	0	0	0
Lotus_corniculatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Luzula_campestris	1	1	0	1	0	0	0	0	1	0	0	0	0	1	1
Lycopus_europaeus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Malus_pumila	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Melilotus_indicus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mentha_aquatica	0	0	0	1	0	0	0	1	0	0	1	0	1	1	1
Myosotis_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Myosotis_ramosissima	1	0	0	0	1	0	0	0	0	0	0	0	0	1	0
Myosoton_aquaticum	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
Neotinea_tridentata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ochlopoa_annua	0	0	0	0	0	0	1	0	1	0	1	1	1	1	0
Onopordum_acanthium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ornithogalum_orthophyllum	0	0	0	1	0	0	0	0	0	0	0	1	1	1	1
Oxalis_corniculata	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Oxalis_dillenii	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Phillyrea_angustifolia	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Phillyrea_latifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phragmites_australis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pinus_halepensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pinus_nigra	1	0	1	0	1	0	1	1	1	0	1	0	0	0	1
Pinus_pinaster	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pinus_pinea	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
Pinus_sylvestris	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Plantago_coronopus	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Plantago_lanceolata	1	1	1	1	1	0	1	0	0	0	0	1	0	1	1
Plantago_major	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0
Plantago_media	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Platanthera_chlorantha	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Poa_bulbosa	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1
Poa_pratensis	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0
Polygala_comosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Populus_alba	0	1	0	0	1	1	1	0	1	1	1	1	1	1	1
Populus_nigra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 6.1: Plant species incidence matrix (Part 3: Species Pot-Z, Plot V1-V15)

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14	V15
Potentilla_hirta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Potentilla_reptans	0	0	0	1	0	1	0	1	0	1	1	1	0	0	0
Prunella_laciniata	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Prunella_vulgaris	0	0	0	0	0	1	1	1	0	0	0	1	1	1	1
Prunus_avium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Prunus_spinosa	0	1	0	1	1	0	0	1	1	1	1	1	0	1	0
Pteridium_aquilinum	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0
Pyracantha_coccinea	0	1	0	0	0	0	0	0	0	1	0	0	0	1	1
Pyrus_communis	0	0	0	0	0	1	0	0	0	0	0	1	0	1	1
Quercus_ilex	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Quercus_robur	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ranunculus_bulbosus	0	0	0	1	0	1	1	1	1	1	1	1	1	1	1
Ranunculus_parviflorus	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0
Ranunculus_polyanthemos	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Ranunculus_sardous	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Raphanus_raphanistrum	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
Reseda_alba	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhamnus_alaternus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhamnus_cathartica	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Robinia_pseudoacacia	1	0	0	0	0	0	1	0	1	0	1	0	0	0	0
Rosa_canina	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Rubia_peregrina	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0
Rubus_ulmifolius	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
Ruscus_aculeatus	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Salvia_verbenaca	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sambucus_nigra	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Sanguisorba_minor	1	0	1	0	1	0	0	0	1	0	0	0	0	0	1
Scabiosa_columbaria	1	0	0	0	0	0	0	0	0	1	0	0	0	0	1
Scabiosa_triandra	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sedum_sexangulare	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Serapias_vomeracea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sherardia_arvensis	1	1	0	1	0	0	1	0	1	1	1	1	1	1	1
Silene_latifolia	0	0	1	0	0	0	1	0	0	1	0	0	1	1	0
Silene_viridiflora	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Silene_vulgaris	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0
Sisymbrium_officinale	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Sonchus_arvensis	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
Sonchus_asper	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0
Sorbus_domestica	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Stachys_officinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stellaria_media	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Stellaria_pallida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Symphytum_bulbosum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Symphytum_officinale	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tamarix_gallica	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Taraxacum_spec	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0
Teucrium_chamaedrys	1	0	1	1	1	0	0	0	1	1	0	1	0	1	1
Teucrium_scordium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thlaspi_alliaceum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thymus_pulegioides	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Torilis_nodosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trifolium_nigrescens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trifolium_repens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tripolium_pannonicum	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Ulmus_laevis	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0
Valerianella_locusta	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Veronica_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Veronica_hederifolia	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Veronica_officinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Veronica_persica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Viburnum_lantana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Viburnum_opulus	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Vicia_sativa	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Vicia_villosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Vincetoxicum_hirundinaria	0	0	0	0	0	1	0	0	0	1	0	1	1	1	0
Viola_hirta	0	0	0	0	0	0	1	0	0	1	1	1	1	0	0
Viola_odorata	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
Viola_reichenbachiana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 6.1: Plant species incidence matrix (Part 4: Species A-Er, Plot V16-V30)

	V16	V17	V18	V19	V20	V21	V22	V23	V24	V25	V26	V27	V28	V29	V30
Acer_campestre	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Achillea_millefolium_aggr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Aegonychon_purpurocaeruleum	0	0	0	0	1	0	1	0	0	1	1	0	0	0	0
Agrimonia_eupatoria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ailanthus_altissima	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ajuga_chamaepitys	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ajuga_reptans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Alliaria_petiolata	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
Alnus_glutinosa	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Anacamptis_coriophora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anacamptis_morio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anacamptis_pyramidalis	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0
Anisantha_sterilis	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0
Anthemis_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anthoxanthum_odoratum	1	0	0	1	0	1	0	1	1	0	0	1	1	1	1
Aphanes_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Arabidopsis_thaliana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Arabis_sagittata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Arenaria_serpyllifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aristolochia_clematitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aristolochia_rotunda	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Arum_italicum	0	0	0	1	1	0	1	0	0	0	1	0	0	0	0
Asparagus_acutifolius	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1
Asparagus_officinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Asperula_laevigata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Avena_fatua	0	0	0	0	0	1	1	1	1	0	0	1	1	1	1
Ballota_nigra	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
Bellis_perennis	1	1	1	0	1	1	1	1	1	0	1	0	1	1	1
Berberis_vulgaris	0	0	1	0	0	1	0	1	1	1	1	1	0	0	1
Brachypodium_phoenicoides	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0
Brachypodium_sylvaticum	0	1	1	0	1	1	0	0	1	1	0	1	1	0	0
Bromus_erecta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Calystegia_sepium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Campanula_rapunculus	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0
Cardamine_hirsuta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carduus_pycnocephalus	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0
Carex_acuta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carex_acutiformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carex_distans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Carex_flacca	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0
Carex_liparocarpos	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carpinus_betulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Celtis_australis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Centaurea_nigrescens	0	1	0	0	0	0	0	0	0	0	1	1	1	1	1
Centaurium_erythraea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cerastium_brachypetalum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cerastium_fontanum	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0
Cerastium_glomeratum	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Cerastium_semidecandrum	1	1	1	0	0	0	0	1	0	0	0	0	0	0	1
Chaerophyllum_temulum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cichorium_intybus	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Cirsium_arvense	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Clematis_flammula	0	0	1	1	0	0	1	1	0	1	1	0	1	1	0
Clinopodium_vulgare	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Convolvulus_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cornus_mas	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0
Cornus_sanguinea	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Cotinus_coggygria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Crataegus_monogyna	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1
Crepis_capillaris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Crepis_foetida	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0
Cynoglossum_officinale	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dactylis_glomerata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Daucus_carota	0	1	0	0	1	1	0	0	0	0	1	1	1	1	0
Dioscorea_communis	0	0	0	0	0	0	1	0	0	1	0	0	1	0	0
Diplotaxis_tenuifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Echium_vulgare	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Elaeagnus_angustifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Equisetum_ramosissimum	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Erigeron_sumatrensis	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Erodium_cicutarium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eryngium_campestre	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 6.1: Plant species incidence matrix (Part 5: Species Eu-Pop, Plot V16-V30)

	V16	V17	V18	V19	V20	V21	V22	V23	V24	V25	V26	V27	V28	V29	V30
Euonymus_europaeus	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1
Eupatorium_cannabinum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euphorbia_cyparissias	1	1	0	1	0	0	1	1	0	1	0	0	0	1	1
Euphorbia_helioscopia	0	1	0	0	1	0	1	1	1	0	0	0	1	1	0
Frangula_alnus	0	0	1	0	0	0	1	1	0	1	0	0	1	1	0
Fraxinus_angustifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fraxinus_excelsior	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fraxinus_ornus	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0
Galium_aparine	0	0	0	1	1	0	1	1	1	1	1	1	0	1	1
Galium_mollugo	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0
Genista_tinctoria	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Geranium_columbinum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Geranium_dissectum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Geranium_molle	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Geranium_purpureum	0	0	0	1	0	0	1	0	1	0	0	0	0	1	0
Geranium_robertianum	1	0	0	0	1	0	0	0	0	0	1	0	1	0	0
Geum_urbanum	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Gladiolus_italicus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Glechoma_hederacea	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Hedera_helix	1	0	0	0	1	1	1	0	1	1	1	1	1	1	1
Helianthemum_jonium	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Helianthemum_nummularium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Helminthotheca_echioides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hippocrepis_emerus	0	0	1	0	0	1	0	1	1	1	0	1	0	0	0
Hordeum_murinum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Humulus_lupulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hypericum_perforatum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hypochaeris_radicata	0	0	0	0	1	1	0	0	1	0	0	0	1	1	1
Inula_salicina	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Iris_foetidissima	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Jacobaea_erratica	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0
Juniperus_communis	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Knautia_integrifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lamium_purpureum	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Lathyrus_sphaericus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lepidium_campestre	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
Ligustrum_vulgare	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Linum_bienne	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0
Lonicera_caprifolium	0	0	0	0	0	0	1	0	1	0	1	0	1	0	0
Lonicera_japonica	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
Lotus_corniculatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Luzula_campestris	1	1	0	1	0	1	1	0	1	1	0	1	1	0	0
Lycopus_europaeus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Malus_pumila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Melilotus_indicus	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Mentha_aquatica	1	1	1	1	0	0	0	0	0	0	0	0	0	0	1
Myosotis_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Myosotis_ramosissima	1	0	0	1	0	0	0	1	0	0	0	0	0	0	1
Myosoton_aquaticum	0	0	0	1	1	0	1	0	1	0	1	1	0	0	0
Neotinea_tridentata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ochlopoa_annua	0	1	1	0	0	0	0	0	0	1	1	0	0	0	0
Onopordum_acanthium	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Ornithogalum_orthophyllum	0	1	1	1	0	0	0	0	1	0	0	1	0	1	1
Oxalis_corniculata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oxalis_dillenii	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Phillyrea_angustifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phillyrea_latifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phragmites_australis	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Pinus_halepensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pinus_nigra	1	0	0	1	1	0	1	1	0	1	0	0	0	0	0
Pinus_pinaster	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Pinus_pinea	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1
Pinus_sylvestris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Plantago_coronopus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Plantago_lanceolata	1	1	1	0	0	0	0	0	1	1	0	1	1	1	1
Plantago_major	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0
Plantago_media	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Platanthera_chlorantha	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
Poa_bulbosa	0	1	1	1	1	0	1	1	1	0	1	0	1	0	1
Poa_pratensis	0	0	1	0	0	0	1	0	0	0	0	1	1	0	1
Polygala_comosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Populus_alba	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1
Populus_nigra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 6.1: Plant species incidence matrix (Part 6: Species Pot-Z, Plot V16-V30)

	V16	V17	V18	V19	V20	V21	V22	V23	V24	V25	V26	V27	V28	V29	V30
Potentilla_hirta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Potentilla_reptans	0	1	1	0	0	0	0	0	0	0	0	0	1	1	1
Prunella_laciniata	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Prunella_vulgaris	0	1	1	0	0	0	0	0	0	0	0	1	1	0	0
Prunus_avium	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
Prunus_spinosa	0	1	1	1	1	1	1	0	0	1	1	1	1	1	1
Pteridium_aquilinum	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Pyracantha_coccinea	0	0	1	1	0	0	0	0	0	1	0	1	0	0	0
Pyrus_communis	0	0	0	0	0	0	0	1	1	1	0	0	0	1	1
Quercus_ilex	0	0	0	1	0	0	1	0	0	1	0	0	1	0	0
Quercus_robur	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ranunculus_bulbosus	1	1	1	1	1	1	1	1	1	0	0	0	1	1	1
Ranunculus_parviflorus	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ranunculus_polyanthemos	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
Ranunculus_sardous	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Raphanus_raphanistrum	0	0	0	0	0	0	0	1	1	0	0	0	1	0	0
Reseda_alba	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhamnus_alaternus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhamnus_cathartica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Robinia_pseudoacacia	0	0	0	0	1	0	1	1	0	0	0	0	0	1	1
Rosa_canina	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Rubia_peregrina	0	0	0	1	1	1	0	0	0	0	0	1	1	0	0
Rubus_ulmifolius	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ruscus_aculeatus	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Salvia_verbenaca	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sambucus_nigra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sanguisorba_minor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scabiosa_columbaria	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Scabiosa_triandra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sedum_sexangulare	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Serapias_vomeracea	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Sherardia_arvensis	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Silene_latifolia	0	0	0	1	1	1	1	0	0	1	0	0	0	1	0
Silene_viridiflora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Silene_vulgaris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sisymbrium_officinale	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sonchus_arvensis	1	0	0	0	1	1	0	0	0	0	0	0	0	1	0
Sonchus_asper	0	0	0	0	1	1	0	0	0	0	0	1	0	0	0
Sorbus_domestica	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Stachys_officinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stellaria_media	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0
Stellaria_pallida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Symphytum_bulbosum	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Symphytum_officinale	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0
Tamarix_gallica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Taraxacum_spec	0	1	1	0	0	1	0	0	0	1	0	1	0	0	1
Teucrium_chamaedrys	1	0	0	1	0	0	0	1	1	1	0	0	0	0	0
Teucrium_scordium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thlaspi_alliaceum	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Thymus_pulegioides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Torilis_nodosa	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Trifolium_nigrescens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trifolium_repens	1	1	1	0	0	0	0	0	0	0	0	0	0	0	1
Tripolium_pannonicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ulmus_laevis	1	1	0	1	1	0	1	0	1	1	1	1	1	1	1
Valerianella_locusta	1	0	0	0	0	0	1	1	0	0	0	0	0	0	1
Veronica_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Veronica_hederifolia	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0
Veronica_officinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Veronica_persica	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Viburnum_lantana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Viburnum_opulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vicia_sativa	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Vicia_villosa	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Vincetoxicum_hirundinaria	0	0	0	0	1	0	0	0	1	1	0	0	0	0	0
Viola_hirta	0	1	1	0	1	0	0	0	0	1	1	0	0	1	0
Viola_odorata	1	0	0	1	0	1	1	0	1	0	0	0	0	0	0
Viola_reichenbachiana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 6.1: Plant species incidence matrix (Part 7: Species A-Er, Plot C1-C15)

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15
Acer_campestre	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0
Achillea_millefolium_aggr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aegonychon_purpurocaeruleum	1	1	1	1	1	1	0	1	1	1	1	1	0	1	1
Agrimonia_eupatoria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ailanthus_altissima	1	0	0	0	0	0	0	1	0	0	0	1	0	0	0
Ajuga_chamaepitys	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ajuga_reptans	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Alliaria_petiolata	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Alnus_glutinosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anacamptis_coriophora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anacamptis_morio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anacamptis_pyramidalis	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Anisantha_sterilis	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Anthemis_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Anthoxanthum_odoratum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aphanes_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Arabidopsis_thaliana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Arabis_sagittata	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Arenaria_serpyllifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aristolochia_clematitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aristolochia_rotunda	1	1	0	0	0	0	0	0	0	0	0	1	1	0	0
Arum_italicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Asparagus_acutifolius	0	0	1	1	1	1	0	1	1	1	1	1	1	1	1
Asparagus_officinalis	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Asperula_laevigata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Avena_fatua	1	1	0	0	0	1	0	0	1	0	0	0	0	0	0
Ballota_nigra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bellis_perennis	1	1	1	1	0	1	1	1	1	0	1	1	0	0	0
Berberis_vulgaris	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1
Brachypodium_phoenicoides	0	0	0	0	0	1	0	0	1	0	1	1	0	1	0
Brachypodium_sylvaticum	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0
Bromus_erecta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Calystegia_sepium	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Campanula_rapunculus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cardamine_hirsuta	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carduus_pycnocephalus	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
Carex_acuta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carex_acutiformis	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Carex_distans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carex_flacca	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0
Carex_liparocarpos	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
Carpinus_betulus	0	0	0	0	0	0	1	0	0	1	0	0	0	1	0
Celtis_australis	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Centaurea_nigrescens	0	1	0	0	1	1	0	0	0	0	0	1	0	1	0
Centaurium_erythraea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cerastium_brachypetalum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cerastium_fontanum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cerastium_glomeratum	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0
Cerastium_semidecandrum	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Chaerophyllum_temulum	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cichorium_intybus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cirsium_arvense	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Clematis_flammula	0	0	0	0	1	1	0	1	1	0	1	0	1	1	0
Clinopodium_vulgare	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Convolvulus_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cornus_mas	1	0	0	1	1	0	0	0	0	0	1	0	0	0	0
Cornus_sanguinea	0	1	0	0	0	0	0	1	0	0	0	0	1	0	0
Cotinus_coggygria	0	0	1	1	0	0	0	0	0	1	0	0	0	1	1
Crataegus_monogyna	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
Crepis_capillaris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Crepis_foetida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cynoglossum_officinale	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Dactylis_glomerata	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Daucus_carota	0	0	1	1	1	0	0	0	0	0	0	0	1	0	0
Dioscorea_communis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Diplotaxis_tenuifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Echium_vulgare	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Elaeagnus_angustifolia	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Equisetum_ramosissimum	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Erigeron_sumatrensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Erodium_cicutarium	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Eryngium_campestre	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0

Appendix 6.1: Plant species incidence matrix (Part 8: Species Eu-Pop, Plot C1-C15)

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15
Euonymus_europaeus	1	1	1	1	1	0	1	1	1	0	1	0	0	0	1
Eupatorium_cannabinum	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Euphorbia_cyparissias	1	0	0	1	1	0	0	1	1	1	1	0	1	1	1
Euphorbia_helioscopia	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0
Frangula_alnus	0	0	0	0	0	0	0	0	0	1	0	1	1	1	1
Fraxinus_angustifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Fraxinus_excelsior	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fraxinus_ornus	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Galium_aparine	1	0	1	0	1	0	1	1	1	1	1	1	0	1	1
Galium_mollugo	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Genista_tinctoria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Geranium_columbinum	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
Geranium_dissectum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Geranium_molle	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Geranium_purpureum	0	0	1	0	0	1	0	1	0	0	0	1	1	0	0
Geranium_robertianum	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Geum_urbanum	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Gladiolus_italicus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Glechoma_hederacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hedera_helix	1	0	1	1	1	1	1	0	1	0	1	1	0	0	0
Helianthemum_jonium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Helianthemum_nummularium	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Helminthotheca_echioides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hippocrepis_emerus	0	1	1	0	1	0	0	1	1	0	0	0	0	1	1
Hordeum_murinum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Humulus_lupulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hypericum_perforatum	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Hypochaeris_radicata	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Inula_salicina	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Iris_foetidissima	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Jacobaea_erratica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Juniperus_communis	0	0	0	0	1	0	0	0	1	0	1	0	0	0	0
Knautia_integrifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lamium_purpureum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lathyrus_sphaericus	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Lepidium_campestre	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ligustrum_vulgare	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Linum_bienne	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lonicera_caprifolium	1	0	0	0	0	0	1	0	0	0	0	1	0	0	1
Lonicera_japonica	0	0	1	0	0	1	0	0	1	0	0	0	0	0	0
Lotus_corniculatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Luzula_campestris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lycopus_europaeus	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Malus_pumila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Melilotus_indicus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mentha_aquatica	1	0	1	0	1	0	0	1	0	1	1	0	1	1	1
Myosotis_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Myosotis_ramosissima	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0
Myosoton_aquaticum	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Neotinea_tridentata	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0
Ochlopoa_annua	0	0	0	0	0	1	0	1	0	0	0	1	0	1	0
Onopordum_acanthium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ornithogalum_orthophyllum	0	0	0	0	1	1	0	1	1	1	0	1	1	1	0
Oxalis_corniculata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oxalis_dillenii	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Phillyrea_angustifolia	0	0	1	0	0	1	0	0	1	0	1	0	0	0	1
Phillyrea_latifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phragmites_australis	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Pinus_halepensis	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Pinus_nigra	0	1	0	0	1	0	1	1	1	1	1	0	1	0	1
Pinus_pinaster	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0
Pinus_pinea	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
Pinus_sylvestris	0	0	1	0	0	0	0	1	0	0	0	0	1	0	0
Plantago_coronopus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Plantago_lanceolata	0	1	0	0	1	1	0	1	1	0	1	0	0	1	0
Plantago_major	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Plantago_media	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Platanthera_chlorantha	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Poa_bulbosa	1	0	0	0	1	1	0	0	1	0	0	0	1	0	0
Poa_pratensis	1	0	0	0	0	1	0	0	1	0	0	0	0	0	0
Polygala_comosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Populus_alba	1	1	0	1	1	1	0	0	0	1	0	0	0	1	0
Populus_nigra	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0

Appendix 6.1: Plant species incidence matrix (Part 9: Species Pot-Z, Plot C1-C15)

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15
Potentilla_hirta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Potentilla_reptans	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Prunella_laciniata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Prunella_vulgaris	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0
Prunus_avium	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0
Prunus_spinosa	1	0	0	1	1	0	0	0	1	0	0	1	1	0	1
Pteridium_aquilinum	0	0	0	1	1	0	0	1	0	1	0	0	0	1	0
Pyracantha_coccinea	1	1	1	1	1	1	0	1	1	0	0	1	0	0	0
Pyrus_communis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Quercus_ilex	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Quercus_robur	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ranunculus_bulbosus	1	0	0	0	1	1	0	0	1	0	0	1	0	1	0
Ranunculus_parviflorus	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Ranunculus_polyanthemos	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ranunculus_sardous	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0
Raphanus_raphanistrum	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Reseda_alba	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhamnus_alaternus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhamnus_cathartica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Robinia_pseudoacacia	0	0	1	0	0	0	0	0	1	0	0	1	0	0	0
Rosa_canina	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
Rubia_peregrina	0	1	1	1	0	0	0	0	0	0	1	0	0	1	0
Rubus_ulmifolius	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1
Ruscus_aculeatus	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
Salvia_verbenaca	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sambucus_nigra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sanguisorba_minor	0	0	1	0	0	0	0	0	0	0	1	0	1	0	0
Scabiosa_columbaria	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
Scabiosa_triandra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sedum_sexangulare	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Serapias_vomeracea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sherardia_arvensis	1	1	1	1	1	1	1	1	1	0	0	0	1	0	0
Silene_latifolia	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Silene_viridiflora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Silene_vulgaris	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0
Sisymbrium_officinale	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sonchus_arvensis	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0
Sonchus_asper	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Sorbus_domestica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stachys_officinalis	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
Stellaria_media	1	0	0	0	1	1	0	0	1	0	0	0	0	0	0
Stellaria_pallida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Symphytum_bulbosum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Symphytum_officinale	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Tamarix_gallica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Taraxacum_spec	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0
Teucrium_chamaedrys	0	0	0	0	1	1	0	0	1	0	1	0	1	1	0
Teucrium_scordium	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Thlaspi_alliaceum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thymus_pulegioides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Torilis_nodosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trifolium_nigrescens	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Trifolium_repens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tripolium_pannonicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ulmus_laevis	1	1	0	1	1	1	1	0	0	1	0	0	0	0	1
Valerianella_locusta	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Veronica_arvensis	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Veronica_hederifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Veronica_officinalis	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Veronica_persica	1	0	1	0	0	0	1	0	1	0	0	0	0	0	0
Viburnum_lantana	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Viburnum_opulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vicia_sativa	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Vicia_villosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vincetoxicum_hirundinaria	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Viola_hirta	0	1	1	0	0	1	1	0	0	0	0	0	0	1	0
Viola_odorata	1	0	0	1	0	0	0	1	1	1	1	1	0	0	1
Viola_reichenbachiana	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0

Appendix 6.1: Plant species incidence matrix (Part 10: Species A-Er, Plot C16-C30)

	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30
Acer_campestre	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Achillea_millefolium_aggr	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Aegonychon_purpurocaeruleum	0	1	0	0	1	1	1	1	1	1	0	0	1	1	1
Agrimonia_eupatoria	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Ailanthus_altissima	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ajuga_chamaepitys	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ajuga_reptans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Alliaria_petiolata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Alnus_glutinosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anacamptis_coriophora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anacamptis_morio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anacamptis_pyramidalis	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anisantha_sterilis	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Anthemis_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anthoxanthum_odoratum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aphanes_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Arabidopsis_thaliana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Arabis_sagittata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Arenaria_serpyllifolia	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Aristolochia_clematitis	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Aristolochia_rotunda	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
Arum_italicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Asparagus_acutifolius	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1
Asparagus_officinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Asperula_laevigata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Avena_fatua	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ballota_nigra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bellis_perennis	0	0	1	1	1	1	1	0	1	1	0	0	1	1	0
Berberis_vulgaris	1	1	1	1	0	0	1	1	0	1	1	1	0	0	0
Brachypodium_phoenicoides	1	1	1	1	0	1	1	1	0	1	0	0	1	0	1
Brachypodium_sylvaticum	0	1	1	0	1	0	1	0	1	0	0	0	1	1	1
Bromus_erecta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Calystegia_sepium	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Campanula_rapunculus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cardamine_hirsuta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carduus_pycnocephalus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carex_acuta	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Carex_acutiformis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carex_distans	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Carex_flacca	0	1	0	0	1	0	0	1	1	0	1	0	0	1	1
Carex_liparocarpos	1	0	0	0	1	1	0	0	1	1	1	1	1	0	1
Carpinus_betulus	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Celtis_australis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Centaurea_nigrescens	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Centaurium_erythraea	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Cerastium_brachypetalum	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
Cerastium_fontanum	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Cerastium_glomeratum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cerastium_semidecandrum	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0
Chaerophyllum_temulum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cichorium_intybus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cirsium_arvense	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Clematis_flammula	1	1	1	0	1	1	1	0	0	0	1	0	0	1	0
Clinopodium_vulgare	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Convolvulus_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cornus_mas	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
Cornus_sanguinea	0	0	0	0	0	0	1	1	1	1	0	0	0	0	1
Cotinus_coggygria	0	1	1	1	0	1	1	1	1	1	0	0	0	0	0
Crataegus_monogyna	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Crepis_capillaris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Crepis_foetida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cynoglossum_officinale	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dactylis_glomerata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Daucus_carota	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Dioscorea_communis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Diplotaxis_tenuifolia	0	1	1	0	0	1	0	0	0	0	1	0	0	0	0
Echium_vulgare	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Elaeagnus_angustifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Equisetum_ramosissimum	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Erigeron_sumatrensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Erodium_cicutarium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eryngium_campestre	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 6.1: Plant species incidence matrix (Part 11: Species Eu-Pop, Plot C16-C30)

	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30
Euonymus_europaeus	0	1	0	0	0	0	0	1	0	0	0	0	1	0	0
Eupatorium_cannabinum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euphorbia_cyparissias	1	1	1	1	1	0	1	1	0	1	0	1	1	1	1
Euphorbia_helioscopia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Frangula_alnus	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0
Fraxinus_angustifolia	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
Fraxinus_excelsior	0	0	0	0	0	1	0	0	0	1	0	0	1	0	1
Fraxinus_ornus	0	1	0	0	0	0	0	0	0	1	0	1	1	1	0
Galium_aparine	1	0	0	0	0	1	0	1	0	0	0	1	1	0	0
Galium_mollugo	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Genista_tinctoria	0	0	1	0	0	1	1	0	1	1	1	1	1	0	1
Geranium_columbinum	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Geranium_dissectum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Geranium_molle	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Geranium_purpureum	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Geranium_robertianum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Geum_urbanum	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Gladiolus_italicus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Glechoma_hederacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hedera_helix	0	1	1	0	0	0	1	0	1	1	1	1	1	1	0
Helianthemum_jonium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Helianthemum_nummularium	0	1	0	0	1	0	0	0	0	0	0	1	0	0	0
Helminthotheca_echioides	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
Hippocrepis_emerus	0	0	0	0	0	0	1	0	0	0	1	1	0	0	1
Hordeum_murinum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Humulus_lupulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hypericum_perforatum	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Hypochaeris_radicata	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Inula_salicina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Iris_foetidissima	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0
Jacobaea_erratica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Juniperus_communis	0	1	1	0	0	0	0	0	0	1	1	1	0	0	1
Knautia_integrifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lamium_purpureum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lathyrus_sphaericus	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lepidium_campestre	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ligustrum_vulgare	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1
Linum_bienne	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lonicera_caprifolium	0	0	0	1	0	1	0	0	0	1	0	0	0	0	1
Lonicera_japonica	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Lotus_corniculatus	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Luzula_campestris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lycopus_europaeus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Malus_pumila	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Melilotus_indicus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mentha_aquatica	1	0	0	0	1	0	0	1	0	0	0	1	0	0	0
Myosotis_arvensis	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0
Myosotis_ramosissima	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Myosoton_aquaticum	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Neotinea_tridentata	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Ochlopoa_annua	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Onopordum_acanthium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ornithogalum_orthophyllum	0	1	0	1	0	0	0	1	1	0	0	0	1	1	1
Oxalis_corniculata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oxalis_dillenii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phillyrea_angustifolia	0	1	1	1	1	1	1	1	0	1	1	1	0	0	1
Phillyrea_latifolia	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Phragmites_australis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pinus_halepensis	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pinus_nigra	1	1	0	0	1	0	0	0	0	0	0	1	0	0	0
Pinus_pinaster	1	0	0	1	0	0	1	0	0	0	1	1	1	0	0
Pinus_pinea	0	1	1	1	0	1	1	1	0	1	1	1	0	1	1
Pinus_sylvestris	1	0	0	1	1	0	0	0	0	0	0	1	0	0	0
Plantago_coronopus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Plantago_lanceolata	0	0	0	1	0	0	0	1	1	0	0	0	0	0	0
Plantago_major	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Plantago_media	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Platanthera_chlorantha	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Poa_bulbosa	0	1	0	0	0	1	0	0	1	0	0	0	1	0	0
Poa_pratensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Polygala_comosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Populus_alba	0	1	0	0	0	1	0	0	1	1	0	1	1	1	0
Populus_nigra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 6.1: Plant species incidence matrix (Part 12: Species Pot-Z, Plot C16-C30)

	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30
Potentilla_hirta	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
Potentilla_reptans	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0
Prunella_laciniata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Prunella_vulgaris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Prunus_avium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Prunus_spinosa	1	0	0	1	1	0	0	1	0	0	0	1	0	0	0
Pteridium_aquilinum	1	1	0	0	1	1	0	1	0	0	0	1	0	0	0
Pyracantha_coccinea	0	0	0	1	0	0	0	1	1	1	1	1	0	1	1
Pyrus_communis	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Quercus_ilex	1	1	1	1	1	1	1	1	0	1	1	1	0	0	1
Quercus_robur	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ranunculus_bulbosus	0	0	0	0	1	0	0	0	1	1	0	0	1	1	0
Ranunculus_parviflorus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ranunculus_polyanthemos	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ranunculus_sardous	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Raphanus_raphanistrum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Reseda_alba	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Rhamnus_alaternus	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Rhamnus_cathartica	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Robinia_pseudoacacia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rosa_canina	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
Rubia_peregrina	0	0	1	0	0	0	0	0	0	1	1	0	1	1	1
Rubus_ulmifolius	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1
Ruscus_aculeatus	0	1	1	1	0	1	1	0	1	1	1	1	0	1	1
Salvia_verbenaca	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Sambucus_nigra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sanguisorba_minor	1	0	0	0	1	0	1	0	0	0	0	1	0	0	0
Scabiosa_columbaria	0	0	0	1	1	0	0	0	0	0	0	1	0	0	0
Scabiosa_triandra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sedum_sexangulare	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Serapias_vomeracea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sherardia_arvensis	1	0	1	0	0	1	1	0	1	1	1	1	1	0	0
Silene_latifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Silene_viridiflora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Silene_vulgaris	1	0	1	0	1	1	1	0	0	0	0	1	1	0	0
Sisymbrium_officinale	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sonchus_arvensis	0	0	1	0	0	0	0	0	0	0	1	1	0	0	0
Sonchus_asper	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sorbus_domestica	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Stachys_officinalis	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Stellaria_media	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stellaria_pallida	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Symphytum_bulbosum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Symphytum_officinale	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tamarix_gallica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Taraxacum_spec	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Teucrium_chamaedrys	1	1	1	0	1	1	1	1	1	1	1	1	1	0	1
Teucrium_scordium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thlaspi_alliaceum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thymus_pulegioides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Torilis_nodosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trifolium_nigrescens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trifolium_repens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tripolium_pannonicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ulmus_laevis	1	0	0	0	1	1	0	0	1	1	0	0	1	1	0
Valerianella_locusta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Veronica_arvensis	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0
Veronica_hederifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Veronica_officinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Veronica_persica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Viburnum_lantana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Viburnum_opulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vicia_sativa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vicia_villosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vincetoxicum_hirundinaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Viola_hirta	0	0	0	0	1	1	0	0	1	1	0	1	1	0	0
Viola_odorata	0	1	0	1	0	0	0	1	0	0	1	0	0	1	0
Viola_reichenbachiana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Appendix 6.2: Plant trait matrix (Part 1: Species A-E, Traits “yearly phenology” - “Plant height”)

Species	annual	biennal	perennial	spinescense	lifeform	N fixation	resin (0/1)	latex (0/1)	storage organ (rhizome, bulb etc.)	taproot	Plant height (cm)
Acer_campestre	0	0	1	0	tree	0	0	0	0	0	500
Achillea_millefolium_aggr	0	0	1	0	forb	0	0	0	1	0	60
Aegonychon_purpurocaeruleum	0	0	1	0	forb	0	0	0	1	0	50
Agrimonia_eupatoria	0	0	1	0	forb	0	0	0	1	0	60
Ailanthus_altissima	0	0	1	0	tree	0	0	0	0	0	1500
Ajuga_chamaepitys	0.5	0.5	0	0	forb	0	0	0	0	0	20
Ajuga_reptans	0	0	1	0	forb	0	0	0	1	0	15
Alliaria_petiolata	0	0.5	0.5	0	forb	0	0	0	0	1	80
Alnus_glutinosa	0	0	1	0	tree	1	0	0	0	0	2000
Anacamptis_coriophora	0	0	1	0	forb	0	0	0	1	0	30
Anacamptis_morio	0	0	1	0	forb	0	0	0	1	0	40
Anacamptis_pyramidalis	0	0	1	0	forb	0	0	0	1	0	50
Anisantha_sterilis	1	0	0	0	graminoid	0	0	0	0	0	40
Anthemis_arvensis	1	0	0	0	forb	0	0	0	0	0	50
Anthoxanthum_odoratum	0	0	1	0	graminoid	0	0	0	0	0	60
Aphanes_arvensis	1	0	0	0	forb	0	0	0	0	0	30
Arabidopsis_thaliana	0.5	0.5	0	0	forb	0	0	0	0	0	15
Arabis_sagittata	0	0	1	0	forb	0	0	0	0	0	60
Arenaria_serpyllifolia	0.5	0.5	0	0	forb	0	0	0	0	0	15
Aristolochia_clematitis	0	0	1	0	forb	0	0	0	1	0	100
Aristolochia_rotunda	0	0	1	0	forb	0	0	0	1	0	40
Arum_italicum	0	0	1	0	forb	0	0	0	1	0	40
Asparagus_acutifolius	0	0	1	1	vine	0	0	0	1	0	150
Asparagus_officinalis	0	0	1	0	forb	0	0	0	1	0	150
Asperula_laevigata	0	0	1	0	forb	0	0	0	0	0	80
Avena_fatua	1	0	0	0	graminoid	0	0	0	0	0	100
Ballota_nigra	0	0	1	0	forb	0	0	0	1	0	60
Bellis_perennis	0	0	1	0	forb	0	0	0	1	0	15
Berberis_vulgaris	0	0	1	1	shrub	0	0	0	0	0	200
Brachypodium_phoenicoides	0	0	1	0	graminoid	0	0	0	1	0	60
Brachypodium_sylvaticum	0	0	1	0	graminoid	0	0	0	0	0	50
Bromus_erecta	0	0	1	0	graminoid	0	0	0	0	0	60
Calystegia_sepium	0	0	1	0	vine	0	0	0	1	0	120
Campanula_rapunculus	0	1	0	0	forb	0	0	0	0	1	100
Cardamine_hirsuta	0.5	0.5	0	0	forb	0	0	0	0	0	25
Carduus_pycnocephalus	0	1	0	1	forb	0	0	0	0	1	60
Carex_acuta	0	0	1	0	graminoid	0	0	0	1	0	150
Carex_acutiformis	0	0	1	0	graminoid	0	0	0	1	0	100
Carex_distans	0	0	1	0	graminoid	0	0	0	0	0	80
Carex_flacca	0	0	1	0	graminoid	0	0	0	1	0	50
Carex_liparocarpos	0	0	1	0	graminoid	0	0	0	1	0	30
Carpinus_betulus	0	0	1	0	tree	0	0	0	0	0	1500
Celtis_australis	0	0	1	0	tree	0	0	0	0	0	1000
Centaurea_nigrescens	0	0	1	0	forb	0	0	0	0	0	100
Centaurium_erythraea	0	1	0	0	forb	0	0	0	0	0	50
Cerastium_brachypetalum	1	0	0	0	forb	0	0	0	0	0	30
Cerastium_fontanum	0	0	1	0	forb	0	0	0	0	0	20
Cerastium_glomeratum	1	0	0	0	forb	0	0	0	0	0	30
Cerastium_semidecandrum	0.5	0.5	0	0	forb	0	0	0	0	0	20
Chaerophyllum_temulum	0.5	0.5	0	0	forb	0	0	0	1	0	140
Cichorium_intybus	0	0	1	0	forb	0	0	1	0	1	120
Cirsium_arvense	0	0	1	1	forb	0	0	0	1	0	150
Clematis_flammula	0	0	1	0	vine	0	0	0	0	0	500
Clinopodium_vulgare	0	0	1	0	forb	0	0	0	0	0	60
Convolvulus_arvensis	0	0	1	0	vine	0	0	0	1	0	50
Cornus_mas	0	0	1	0	shrub	0	0	0	0	0	500
Cornus_sanguinea	0	0	1	0	shrub	0	0	0	0	0	400
Cotinus_coggygria	0	0	1	0	shrub	0	0	1	0	0	500
Crataegus_monogyna	0	0	1	1	shrub	0	0	0	0	0	500
Crepis_capillaris	0.5	0.5	0	0	forb	0	0	1	0	1	100
Crepis_foetida	0.5	0.5	0	0	forb	0	0	1	0	1	40
Cynoglossum_officinale	0	1	0	0	forb	0	0	0	0	1	80
Dactylis_glomerata	0	0	1	0	graminoid	0	0	0	0	0	120
Daucus_carota	0	1	0	0	forb	0	0	0	1	0	60
Dioscorea_communis	0	0	1	0	vine	0	0	0	1	0	400
Diplotaxis_tenuifolia	0	0	1	0	forb	0	0	0	0	1	50
Echium_vulgare	0	1	0	0	forb	0	0	0	0	1	80
Elaeagnus_angustifolia	0	0	1	0	tree	1	0	0	0	0	500
Equisetum_ramosissimum	0	0	1	0	forb	0	0	0	1	0	100
Erigeron_sumatrensis	0.5	0.5	0	0	forb	0	0	0	0	0	150
Erodium_cicutarium	0.5	0.5	0	0	forb	0	0	0	0	0	20
Eryngium_campestre	0	0	1	1	forb	0	0	0	0	1	40
Euonymus_europaeus	0	0	1	0	shrub	0	0	1	0	0	500
Eupatorium_cannabinum	0	0	1	0	forb	0	0	0	0	0	150
Euphorbia_cyparissias	0	0	1	0	forb	0	0	1	0	0	40
Euphorbia_helioscopia	1	0	0	0	forb	0	0	1	0	0	40

Appendix 6.2: Plant trait matrix (Part 2: Species F-Pr, Traits “yearly phenology” - “Plant height”)

Species	annual	biennal	perennial	spinescense	lifeform	N fixation	resin (0/1)	latex (0/1)	storage organ (rhizome, bulb etc.)	taproot	Plant height (cm)
Frangula_alnus	0	0	1	0	shrub	0	0	0	0	0	300
Fraxinus_angustifolia	0	0	1	0	tree	0	0	0	0	1	1500
Fraxinus_excelsior	0	0	1	0	tree	0	0	0	0	1	2000
Fraxinus_ornus	0	0	1	0	tree	0	0	0	0	1	1000
Galium_aparine	1	0	0	0	vine	0	0	0	0	0	120
Galium_mollugo	0	0	1	0	shrub	0	0	0	0	0	100
Genista_tinctoria	0	0	1	0	shrub	1	0	0	0	0	40
Geranium_columbinum	1	0	0	0	forb	0	0	0	0	1	60
Geranium_dissectum	1	0	0	0	forb	0	0	0	0	1	40
Geranium_molle	1	0	0	0	forb	0	0	0	0	1	25
Geranium_purpureum	0.5	0.5	0	0	forb	0	0	0	0	1	20
Geranium_robertianum	0.5	0.5	0	0	forb	0	0	0	0	1	40
Geum_urbanum	0	0	1	0	forb	0	0	0	1	0	100
Gladiolus_italicus	0	0	1	0	forb	0	0	0	1	0	60
Glechoma_hederacea	0	0	1	0	forb	0	0	0	0	0	30
Hedera_helix	0	0	1	0	vine	0	0	0	0	0	1500
Helianthemum_jonium	0	0	1	0	forb	0	0	0	0	0	30
Helianthemum_nummularium	0	0	1	0	forb	0	0	0	0	0	30
Helminthotheca_echioides	0.5	0.5	0	0	forb	0	0	1	0	1	60
Hippocrepis_emerus	0	0	1	0	shrub	1	0	0	0	0	200
Hordeum_murinum	1	0	0	0	graminoid	0	0	0	0	0	40
Humulus_lupulus	0	0	1	0	vine	0	0	0	1	0	600
Hypericum_perforatum	0	0	1	0	forb	0	0	0	1	0	80
Hypochaeris_radicata	0	0	1	0	forb	0	0	1	0	1	50
Inula_salicina	0	0	1	0	forb	0	0	0	0	1	40
Iris_foetidissima	0	0	1	0	forb	0	0	0	1	0	100
Jacobaea_erratica	0	1	0	0	forb	0	0	0	0	0	80
Juniperus_communis	0	0	1	1	shrub	0	0	0	0	1	300
Knautia_integrifolia	1	0	0	0	forb	0	0	0	0	1	60
Lamium_purpureum	0.5	0.5	0	0	forb	0	0	0	0	0	20
Lathyrus_sphaericus	1	0	0	0	forb	1	0	0	0	0	50
Lepidium_campestre	1	0	0	0	forb	0	0	0	0	0	80
Ligustrum_vulgare	0	0	1	0	shrub	0	0	0	0	0	300
Linum_bienne	0	1	0	0	forb	0	0	0	0	0	30
Lonicera_caprifolium	0	0	1	0	vine	0	0	0	0	0	300
Lonicera_japonica	0	0	1	0	vine	0	0	0	0	0	1000
Lotus_corniculatus	0	0	1	0	forb	1	0	0	0	1	40
Luzula_campestris	0	0	1	0	graminoid	0	0	0	0	0	25
Lycopus_europaeus	0	0	1	0	forb	0	0	0	1	0	100
Malus_pumila	0	0	1	0	tree	0	0	0	0	0	500
Melilotus_indicus	1	0	0	0	forb	1	0	0	0	0	50
Mentha_aquatica	0	0	1	0	forb	0	0	0	1	0	30
Myosotis_arvensis	0.5	0.5	0	0	forb	0	0	0	0	0	30
Myosotis_ramosissima	1	0	0	0	forb	0	0	0	0	0	20
Myosoton_aquaticum	0	0	1	0	forb	0	0	0	1	0	40
Neotinea_tridentata	0	0	1	0	forb	0	0	0	1	0	40
Ochlopoa_annua	0.5	0.5	0	0	graminoid	0	0	0	0	0	10
Onopordum_acanthium	0	1	0	1	forb	0	0	0	0	1	150
Ornithogalum_orthophyllum	0	0	1	0	forb	0	0	0	1	0	15
Oxalis_corniculata	0	0	1	0	forb	0	0	0	1	0	30
Oxalis_dillenii	0.333	0.333	0.3333	0	forb	0	0	0	0	1	20
Phillyrea_angustifolia	0	0	1	0	shrub	0	0	0	0	0	300
Phillyrea_latifolia	0	0	1	0	shrub	0	0	0	0	0	300
Phragmites_australis	0	0	1	0	graminoid	0	0	0	1	0	250
Pinus_halepensis	0	0	1	0	tree	0	1	0	0	1	2000
Pinus_nigra	0	0	1	0	tree	0	1	0	0	1	2000
Pinus_pinaster	0	0	1	0	tree	0	1	0	0	1	2000
Pinus_pinea	0	0	1	0	tree	0	1	0	0	1	2000
Pinus_sylvestris	0	0	1	0	tree	0	1	0	0	1	3000
Plantago_coronopus	0	0	1	0	forb	0	0	0	0	1	30
Plantago_lanceolata	0	0	1	0	forb	0	0	0	0	1	50
Plantago_major	0	0	1	0	forb	0	0	0	0	1	30
Plantago_media	0	0	1	0	forb	0	0	0	0	1	60
Platanthera_chlorantha	0	0	1	0	forb	0	0	0	1	0	50
Poa_bulbosa	0	0	1	0	graminoid	0	0	0	0	0	30
Poa_pratensis	0	0	1	0	graminoid	0	0	0	1	0	50
Polygala_comosa	0	0	1	0	forb	0	0	0	1	0	30
Populus_alba	0	0	1	0	tree	0	0	0	0	0	3000
Populus_nigra	0	0	1	0	tree	0	0	0	0	0	2500
Potentilla_hirta	0	0	1	0	forb	0	0	0	0	0	30
Potentilla_reptans	0	0	1	0	forb	0	0	0	0	0	20
Prunella_laciniata	0	0	1	0	forb	0	0	0	0	0	25
Prunella_vulgaris	0	0	1	0	forb	0	0	0	0	0	20
Prunus_avium	0	0	1	0	tree	0	0	0	0	0	1500
Prunus_spinosa	0	0	1	1	shrub	0	0	0	0	0	300

Appendix 6.2: Plant trait matrix (Part 3: Species Ps-Z, Traits “yearly phenology” - “Plant height”)

Species	annual	biennal	perennial	spinescense	lifeform	N fixation	resin (0/1)	latex (0/1)	storage organ (rhizome, bulb etc.)	taproot	Plant height (cm)
Pteridium_aquilinum	0	0	1	0	fern	0	0	0	1	0	200
Pyracantha_coccinea	0	0	1	1	shrub	0	0	0	0	0	200
Pyrus_communis	0	0	1	1	tree	0	0	0	0	1	500
Quercus_ilex	0	0	1	0	tree	0	0	0	0	1	1000
Quercus_robur	0	0	1	0	tree	0	0	0	0	1	2000
Ranunculus_bulbosus	0	0	1	0	forb	0	0	0	1	0	50
Ranunculus_parviflorus	1	0	0	0	forb	0	0	0	0	0	20
Ranunculus_polyanthemos	0	0	1	0	forb	0	0	0	0	0	80
Ranunculus_sardous	1	0	0	0	forb	0	0	0	0	0	30
Raphanus_raphanistrum	1	0	0	0	forb	0	0	0	0	1	60
Reseda_alba	0.333	0.333	0.3333	0	forb	0	0	0	0	1	80
Rhamnus_alaternus	0	0	1	0	shrub	0	0	0	0	1	500
Rhamnus_cathartica	0	0	1	1	shrub	0	0	0	0	1	500
Robinia_pseudoacacia	0	0	1	1	tree	1	0	0	0	1	2000
Rosa_canina	0	0	1	1	shrub	0	0	0	0	1	200
Rubia_peregrina	0	0	1	0	vine	0	0	0	0	1	250
Rubus_ulmifolius	0	0	1	1	shrub	1	0	0	0	0	150
Ruscus_aculeatus	0	0	1	1	shrub	0	0	0	1	0	100
Salvia_verbenaca	0	0	1	0	forb	0	0	0	0	1	50
Sambucus_nigra	0	0	1	0	shrub	0	0	0	0	0	500
Sanguisorba_minor	0	0	1	0	forb	0	0	0	1	0	50
Scabiosa_columbaria	0	0	1	0	forb	0	0	0	0	0	40
Scabiosa_triandra	0	0	1	0	forb	0	0	0	0	0	100
Sedum_sexangulare	0	0	1	0	forb	0	0	0	0	0	10
Serapias_vomeracea	0	0	1	0	forb	0	0	0	1	0	60
Sherardia_arvensis	1	0	0	0	forb	0	0	0	0	0	25
Silene_latifolia	0	0.5	0.5	0	forb	0	0	0	0	1	80
Silene_viridiflora	0	0	1	0	forb	0	0	0	0	1	100
Silene_vulgaris	0	0	1	0	forb	0	0	0	0	1	30
Sisymbrium_officinale	1	0	0	0	forb	0	0	0	0	0	80
Sonchus_arvensis	0	0	1	1	forb	0	0	1	0	1	150
Sonchus_asper	1	0	0	1	forb	0	0	1	0	1	100
Sorbus_domestica	0	0	1	0	tree	0	0	0	0	0	500
Stachys_officinalis	0	0	1	0	forb	0	0	0	1	0	40
Stellaria_media	1	0	0	0	forb	0	0	0	0	0	30
Stellaria_pallida	1	0	0	0	forb	0	0	0	0	0	20
Symphytum_bulbosum	0	0	1	0	forb	0	0	0	1	0	50
Symphytum_officinale	0	0	1	0	forb	0	0	0	1	0	60
Tamarix_gallica	0	0	1	0	tree	0	0	0	0	0	500
Taraxacum_spec	0	0	1	0	forb	0	0	1	0	1	25
Teucrium_chamaedrys	0	0	1	0	forb	0	0	0	1	0	30
Teucrium_scordium	0	0	1	0	forb	0	0	0	1	0	60
Thlaspi_alliaceum	1	0	0	0	forb	0	0	0	0	0	30
Thymus_pulegioides	0	0	1	0	forb	0	0	0	0	0	30
Torilis_nodosa	1	0	0	0	forb	0	0	0	0	1	60
Trifolium_nigrescens	1	0	0	0	forb	1	0	0	0	0	30
Trifolium_repens	0	0	1	0	forb	1	0	0	0	1	20
Tripolium_pannonicum	0	1	0	0	forb	0	0	0	0	1	100
Ulmus_laevis	0	0	1	0	tree	0	0	0	0	1	1000
Valerianella_locusta	1	0	0	0	forb	0	0	0	0	0	30
Veronica_arvensis	1	0	0	0	forb	0	0	0	0	0	40
Veronica_hederifolia	1	0	0	0	forb	0	0	0	0	0	10
Veronica_officinalis	0	0	1	0	forb	0	0	0	0	1	50
Veronica_persica	1	0	0	0	forb	0	0	0	0	0	50
Viburnum_lantana	0	0	1	0	shrub	0	0	0	0	0	400
Viburnum_opulus	0	0	1	0	shrub	0	0	0	0	0	300
Vicia_sativa	1	0	0	0	forb	1	0	0	0	0	80
Vicia_villosa	0.5	0.5	0	0	forb	1	0	0	0	0	100
Vincetoxicum_hirundinaria	0	0	1	0	forb	0	0	1	1	0	120
Viola_hirta	0	0	1	0	forb	0	0	0	1	0	15
Viola_odorata	0	0	1	0	forb	0	0	0	1	0	15
Viola_reichenbachiana	0	0	1	0	forb	0	0	0	1	0	20

Appendix 6.2: Plant trait matrix (Part 4: Species A-E, Traits “Flowering time” - “Fruit type”)

	Flowering time (months)										
Species	(3-4)	(5-6)	(7-8)	(9-10)	leafcomposition	leaftype	phyllotaxy	pubescence	pollination	Seed dispersion	fleshy fruit (0/1)
Acer_campestre	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	wind	0
Achillea_millefolium_aggr	0	0.5	0.5	0	pinnately	scleromorphic	alternate	1	biotic	wind	0
Aegonychon_purpurocaeruleum	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	non-specialized	0
Agrimonia_eupatoria	0	0.5	0.5	0	pinnately	leaf	alternate	1	biotic	adhesive	0
Ailanthus_altissima	0	1	0	0	pinnately	leaf	alternate	1	biotic	wind	0
Ajuga_chamaepitys	0.25	0.25	0.25	0.25	Simple	leaf	opposite	2	biotic	non-specialized	0
Ajuga_reptans	0.5	0.5	0	0	Simple	leaf	opposite	1	biotic	non-specialized	0
Alliaria_petiolata	0	0.5	0.5	0	Simple	leaf	alternate	1	biotic	non-specialized	0
Alnus_glutinosa	1	0	0	0	Simple	leaf	alternate	1	abiotic	non-specialized	0
Anacamptis_coriophora	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	wind	0
Anacamptis_morio	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	wind	0
Anacamptis_pyramidalis	0	1	0	0	Simple	leaf	basal	1	biotic	wind	0
Anisantha_sterilis	0.5	0.5	0	0	Simple	scleromorphic	alternate	1	abiotic	wind	0
Anthemis_arvensis	0.5	0.5	0	0	pinnately	leaf	alternate	1	biotic	wind	0
Anthoxanthum_odoratum	0.33	0.33	0.33	0	Simple	leaf	alternate	1	abiotic	adhesive	0
Aphanes_arvensis	0	0.33	0.33	0.333	Simple	leaf	alternate	2	biotic	non-specialized	0
Arabidopsis_thaliana	1	0	0	0	Simple	leaf	alternate	1	biotic	adhesive	0
Arabis_sagittata	0	0.5	0.5	0	Simple	leaf	alternate	1	biotic	wind	0
Arenaria_serpyllifolia	0.25	0.25	0.25	0.25	Simple	leaf	opposite	1	biotic	adhesive	0
Aristolochia_clematitis	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	wind	0
Aristolochia_rotunda	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	non-specialized	
Arum_italicum	0.5	0.5	0	0	Simple	leaf	basal	1	biotic	myrmecochory	1
Asparagus_acutifolius	0	0	0.5	0.5	Simple	needle	whorled	1	biotic	ingested	1
Asparagus_officinalis	0	1	0	0	Simple	needle	whorled	1	biotic	ingested	1
Asperula_laevigata	0	0	0.5	0.5	Simple	leaf	whorled	1	biotic	non-specialized	0
Avena_fatua	0.5	0.5	0	0	Simple	leaf	alternate	1	abiotic	wind	0
Ballota_nigra	0	0.5	0.5	0	Simple	leaf	opposite	1	biotic	myrmecochory	0
Bellis_perennis	0.25	0.25	0.25	0.25	Simple	leaf	basal	1	biotic	wind	0
Berberis_vulgaris	0	1	0	0	Simple	leaf	alternate	1	biotic	ingested	1
Brachypodium_phoenicoides	0	0.5	0.5	0	Simple	scleromorphic	alternate	1	abiotic	wind	0
Brachypodium_sylvaticum	0	0.5	0.5	0	Simple	scleromorphic	alternate	1	abiotic	wind	0
Bromus_erecta	0	0.5	0.5	0	Simple	scleromorphic	alternate	1	abiotic	wind	0
Calystegia_sepium	0	0.33	0.33	0.333	Simple	leaf	alternate	1	biotic	wind	0
Campanula_rapunculus	0	0.33	0.33	0.333	Simple	leaf	alternate	2	biotic	wind	0
Cardamine_hirsuta	1	0	0	0	pinnately	leaf	alternate	1	biotic	ballistic	0
Carduus_pycnocephalus	0.33	0.33	0.33	0	Simple	leaf	basal	1	biotic	wind	0
Carex_acuta	0.5	0.5	0	0	Simple	scleromorphic	alternate	1	abiotic	wind	0
Carex_acutiformis	0.5	0.5	0	0	Simple	leaf	alternate	1	abiotic	wind	0
Carex_distans	0.5	0.5	0	0	Simple	leaf	alternate	1	abiotic	wind	0
Carex_flacca	0.5	0.5	0	0	Simple	leaf	alternate	1	abiotic	wind	0
Carex_liparocarpos	0.5	0.5	0	0	Simple	leaf	alternate	1	abiotic	wind	0
Carpinus_betulus	0	1	0	0	Simple	leaf	alternate	1	abiotic	wind	0
Celtis_australis	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	ingested	1
Centaurea_nigrescens	0	0.5	0.5	0	Simple	leaf	alternate	1	biotic	wind	0
Centaurium_erythraea	0	0.33	0.33	0.333	Simple	leaf	basal	1	biotic	wind	0
Cerastium_brachypetalum	0.25	0.25	0.25	0.25	Simple	leaf	opposite	2	biotic	wind	0
Cerastium_fontanum	0.5	0.5	0	0	Simple	leaf	opposite	1	biotic	wind	0
Cerastium_glomeratum	0.25	0.25	0.25	0.25	Simple	leaf	opposite	2	biotic	wind	0
Cerastium_semidecandrum	1	0	0	0	Simple	scleromorphic	opposite	1	biotic	wind	0
Chaerophyllum_temulum	0	0.5	0.5	0	palmately	leaf	alternate	1	biotic	ballistic	0
Cichorium_intybus	0	0	0.5	0.5	Simple	scleromorphic	alternate	1	biotic	wind	0
Cirsium_arvense	0	0.33	0.33	0.333	Simple	scleromorphic	alternate	1	biotic	wind	0
Clematis_flammula	0	0.5	0.5	0	palmately	leaf	alternate	1	biotic	wind	0
Clinopodium_vulgare	0	0.5	0.5	0	Simple	leaf	opposite	1	biotic	wind	0
Convolvulus_arvensis	0.25	0.25	0.25	0.25	Simple	leaf	opposite	1	biotic	non-specialized	0
Cornus_mas	1	0	0	0	Simple	leaf	opposite	1	biotic	ingested	1
Cornus_sanguinea	0	1	0	0	Simple	leaf	opposite	1	biotic	ingested	1
Cotinus_coggygria	0.33	0.33	0.33	0	Simple	leaf	alternate	1	biotic	wind	0
Crataegus_monogyna	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	ingested	1
Crepis_capillaris	0	1	0	0	Simple	leaf	basal	1	biotic	wind	0
Crepis_foetida	0	0.33	0.33	0.333	Simple	leaf	basal	2	biotic	wind	0
Cynoglossum_officinale	0.5	0.5	0	0	Simple	leaf	alternate	2	biotic	adhesive	0
Dactylis_glomerata	0	0.5	0.5	0	Simple	leaf	alternate	1	abiotic	adhesive	0
Daucus_carota	0.25	0.25	0.25	0.25	pinnately	leaf	alternate	1	biotic	adhesive	0
Dioscorea_communis	0	1	0	0	Simple	leaf	alternate	1	biotic	ingested	1
Diplotaxis_tenuifolia	0	0.33	0.33	0.333	Simple	leaf	basal	1	biotic	adhesive	0
Echium_vulgare	0.25	0.25	0.25	0.25	Simple	leaf	alternate	2	biotic	adhesive	0
Elaeagnus_angustifolia	0	1	0	0	Simple	scleromorphic	alternate	3	biotic	ingested	1
Equisetum_ramosissimum	0	0	0	0	Simple	scleromorphic	whorled	1	abiotic	wind	0
Erigeron_sumatrensis	0	0.33	0.33	0.333	Simple	leaf	alternate	1	biotic	wind	0
Erodium_cicutarium	0.25	0.25	0.25	0.25	palmately	leaf	basal	1	biotic	adhesive	0
Eryngium_campestre	0	0	0.5	0.5	Simple	scleromorphic	alternate	1	biotic	wind	0
Euonymus_europaeus	0.5	0.5	0	0	Simple	leaf	opposite	1	biotic	ingested	1
Eupatorium_cannabinum	0	0	0.5	0.5	Simple	leaf	alternate	1	biotic	wind	0
Euphorbia_cyparissias	0.5	0.5	0	0	Simple	leaf	whorled	1	biotic	myrmecochory	0
Euphorbia_helioscopia	0.33	0.33	0.33	0	Simple	leaf	whorled	1	biotic	ballistic	0

Appendix 6.2: Plant trait matrix (Part 5: Species F-Pr, Traits “Flowering time” - “Fruit type”)

	Flowering time (months)										
Species	(3-4)	(5-6)	(7-8)	(9-10)	leafcomposition	leaftype	phyllotaxy	pubescence	pollination	Seed dispersion	fleshy fruit (0/1)
Frangula_alnus	0	1	0	0	Simple	leaf	opposite	1	biotic	ingested	1
Fraxinus_angustifolia	1	0	0	0	pinnately	leaf	alternate	1	abiotic	wind	0
Fraxinus_excelsior	1	0	0	0	pinnately	leaf	alternate	1	abiotic	wind	0
Fraxinus_ornus	0.5	0.5	0	0	pinnately	leaf	alternate	1	abiotic	wind	0
Galium_aparine	0.25	0.25	0.25	0.25	Simple	leaf	whorled	3	biotic	adhesive	0
Galium_mollugo	0	0.5	0.5	0	Simple	leaf	whorled	1	biotic	adhesive	0
Genista_tinctoria	0	0.5	0.5	0	Simple	leaf	alternate	1	biotic	ballistic	0
Geranium_columbinum	0	0.33	0.33	0.333	Simple	leaf	basal	1	biotic	ballistic	0
Geranium_dissectum	0.33	0.33	0.33	0	Simple	leaf	basal	1	biotic	ballistic	0
Geranium_molle	0.5	0.5	0	0	Simple	leaf	basal	2	biotic	ballistic	0
Geranium_purpureum	0.33	0.33	0.33	0	Simple	leaf	basal	1	biotic	ballistic	0
Geranium_robertianum	0	0.5	0.5	0	Simple	leaf	basal	1	biotic	ballistic	0
Geum_urbanum	0	0.5	0.5	0	palmately	leaf	alternate	1	biotic	adhesive	0
Gladiolus_italicus	0.5	0.5	0	0	Simple	leaf	basal	1	biotic	wind	0
Glechoma_hederacea	0.5	0.5	0	0	Simple	leaf	opposite	2	biotic	adhesive	0
Hedera_helix	0	0	0	1	Simple	scleromorphic	alternate	1	biotic	ingested	1
Helianthemum_jonium	0.5	0.5	0	0	Simple	scleromorphic	opposite	3	biotic	non-specialized	0
Helianthemum_nummularium	0	0.5	0.5	0	Simple	scleromorphic	opposite	2	biotic	non-specialized	0
Helminthotheca_echioides	0	0.5	0.5	0	Simple	leaf	basal	2	biotic	wind	0
Hippocrepis_emerus	0.5	0.5	0	0	pinnately	leaf	alternate	1	biotic	non-specialized	0
Hordeum_murinum	0	0.33	0.33	0.333	Simple	leaf	alternate	2	abiotic	wind	0
Humulus_lupulus	0	0	1	0	Simple	leaf	opposite	1	abiotic	wind	0
Hypericum_perforatum	0	0.5	0.5	0	Simple	leaf	opposite	1	biotic	adhesive	0
Hypochaeris_radicata	0.33	0.33	0.33	0	Simple	leaf	basal	2	biotic	wind	0
Inula_salicina	0	0.33	0.33	0.333	Simple	leaf	alternate	1	biotic	wind	0
Iris_foetidissima	0	0.5	0.5	0	Simple	leaf	alternate	1	biotic	ingested	1
Jacobaea_erratica	0	0.33	0.33	0.333	Simple	leaf	alternate	1	biotic	wind	0
Juniperus_communis	1	0	0	0	Simple	needle	whorled	1	abiotic	ingested	1
Knautia_integrifolia	0.5	0.5	0	0	Simple	leaf	opposite	1	biotic	myrmecochory	0
Lamium_purpureum	0.25	0.25	0.25	0.25	Simple	leaf	opposite	1	biotic	myrmecochory	0
Lathyrus_sphaericus	0	1	0	0	pinnately	leaf	alternate	1	biotic	non-specialized	0
Lepidium_campestre	0	1	0	0	Simple	leaf	alternate	1	biotic	ballistic	0
Ligustrum_vulgare	0.5	0.5	0	0	Simple	scleromorphic	alternate	1	biotic	ingested	1
Linum_bienne	0	0.5	0.5	0	Simple	leaf	alternate	1	biotic	wind	0
Lonicera_caprifolium	0	0.5	0.5	0	Simple	leaf	opposite	1	biotic	ingested	1
Lonicera_japonica	0.5	0.5	0	0	Simple	leaf	opposite	1	biotic	ingested	1
Lotus_corniculatus	0.25	0.25	0.25	0.25	pinnately	leaf	alternate	1	biotic	ballistic	0
Luzula_campestris	0.33	0.33	0.33	0	Simple	scleromorphic	alternate	2	abiotic	myrmecochory	0
Lycopus_europaeus	0.33	0.33	0.33	0	Simple	leaf	opposite	1	biotic	water	0
Malus_pumila	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	ingested	1
Melilotus_indicus	0	0.5	0.5	0	pinnately	leaf	alternate	2	biotic	non-specialized	0
Mentha_aquatica	0	0.33	0.33	0.333	Simple	leaf	opposite	2	biotic	water	0
Myosotis_arvensis	0.33	0.33	0.33	0	Simple	leaf	alternate	2	biotic	non-specialized	0
Myosotis_ramosissima	0.5	0.5	0	0	Simple	leaf	alternate	2	biotic	non-specialized	0
Myosoton_aquaticum	0	0.5	0.5	0	Simple	leaf	opposite	1	biotic	non-specialized	0
Neotinea_tridentata	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	wind	0
Ochlopoa_annua	0.25	0.25	0.25	0.25	Simple	leaf	alternate	1	abiotic	adhesive	0
Onopordum_acanthium	0	0	1	0	Simple	scleromorphic	alternate	3	biotic	wind	0
Ornithogalum_orthophyllum	0	0.5	0.5	0	Simple	leaf	alternate	1	biotic	myrmecochory	0
Oxalis_corniculata	0.5	0.5	0	0	palmately	leaf	alternate	1	biotic	myrmecochory	0
Oxalis_dillenii	0	0	0.5	0.5	palmately	leaf	alternate	2	biotic	non-specialized	0
Phillyrea_angustifolia	0.5	0.5	0	0	Simple	scleromorphic	opposite	3	biotic	ingested	1
Phillyrea_latifolia	0.5	0.5	0	0	Simple	scleromorphic	opposite	1	biotic	ingested	1
Phragmites_australis	0	0.33	0.33	0.333	Simple	leaf	alternate	1	abiotic	wind	0
Pinus_halepensis	1	0	0	0	Simple	needle	whorled	1	abiotic	wind	0
Pinus_nigra	0.5	0.5	0	0	Simple	needle	whorled	1	abiotic	wind	0
Pinus_pinaster	0.5	0.5	0	0	Simple	needle	whorled	1	abiotic	wind	0
Pinus_pinea	0.5	0.5	0	0	Simple	needle	whorled	1	abiotic	non-specialized	0
Pinus_sylvestris	0.5	0.5	0	0	Simple	needle	whorled	1	abiotic	wind	0
Plantago_coronopus	0.33	0.33	0.33	0	Simple	succulent	basal	1	abiotic	water	0
Plantago_lanceolata	0	0.5	0.5	0	Simple	leaf	basal	1	abiotic	adhesive	0
Plantago_major	0.25	0.25	0.25	0.25	Simple	leaf	basal	1	abiotic	adhesive	0
Plantago_media	0	0.5	0.5	0	Simple	leaf	basal	1	abiotic	adhesive	0
Platanthera_chlorantha	0	0.5	0.5	0	Simple	leaf	alternate	1	biotic	wind	0
Poa_bulbosa	0.33	0.33	0.33	0	Simple	scleromorphic	alternate	1	abiotic	wind	0
Poa_pratensis	0	0.33	0.33	0.333	Simple	leaf	alternate	1	abiotic	adhesive	0
Polygala_comosa	0	0.5	0.5	0	Simple	scleromorphic	alternate	1	biotic	wind	0
Populus_alba	1	0	0	0	Simple	leaf	alternate	4	abiotic	wind	0
Populus_nigra	1	0	0	0	Simple	leaf	alternate	1	abiotic	wind	0
Potentilla_hirta	0	0.5	0.5	0	palmately	leaf	basal	4	biotic	wind	0
Potentilla_reptans	0	0.33	0.33	0.333	palmately	leaf	alternate	1	biotic	myrmecochory	0
Prunella_laciniata	0.33	0.33	0.33	0	Simple	leaf	opposite	2	biotic	ballistic	0
Prunella_vulgaris	0.25	0.25	0.25	0.25	Simple	leaf	opposite	2	biotic	ballistic	0
Prunus_avium	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	ingested	1
Prunus_spinosa	1	0	0	0	Simple	leaf	alternate	1	biotic	ingested	1

Appendix 6.2: Plant trait matrix (Part 6: Species Ps-Z, Traits “Flowering time” - “Fruit type”)

	Flowering time (months)										
Species	(3-4)	(5-6)	(7-8)	(9-10)	leafcomposition	leaftype	phyllotaxy	pubescence	pollination	Seed dispersion	fleshy fruit (0/1)
Pteridium_aquilinum	0	0	0	0	pinnately	scleromorphic	basal	1	abiotic	wind	0
Pyracantha_coccinea	0.5	0.5	0	0	Simple	scleromorphic	alternate	1	biotic	ingested	1
Pyrus_communis	0.5	0.5	0	0	Simple	scleromorphic	alternate	1	biotic	ingested	1
Quercus_ilex	0	1	0	0	Simple	scleromorphic	alternate	2	abiotic	non-specialized	0
Quercus_robur	0.5	0.5	0	0	Simple	leaf	alternate	2	abiotic	non-specialized	0
Ranunculus_bulbosus	1	0	0	0	palmately	leaf	alternate	1	biotic	non-specialized	0
Ranunculus_parviflorus	0	1	0	0	Simple	leaf	alternate	2	biotic	non-specialized	0
Ranunculus_polyanthemos	0	0.5	0.5	0	Simple	leaf	alternate	1	biotic	non-specialized	0
Ranunculus_sardous	0.25	0.25	0.25	0.25	palmately	leaf	alternate	1	biotic	non-specialized	0
Raphanus_raphanistrum	0	0	1	0	Simple	leaf	alternate	1	biotic	non-specialized	0
Reseda_alba	0.5	0.5	0	0	pinnately	leaf	alternate	1	biotic	non-specialized	0
Rhamnus_alaternus	1	0	0	0	Simple	scleromorphic	alternate	1	biotic	ingested	1
Rhamnus_cathartica	0.5	0.5	0	0	Simple	leaf	opposite	1	biotic	ingested	1
Robinia_pseudoacacia	0	1	0	0	pinnately	leaf	alternate	1	biotic	non-specialized	0
Rosa_canina	0	0.5	0.5	0	pinnately	leaf	alternate	1	biotic	ingested	1
Rubia_peregrina	0.5	0.5	0	0	Simple	leaf	whorled	1	biotic	ingested	1
Rubus_ulmifolius	0	0.5	0.5	0	palmately	leaf	alternate	1	biotic	ingested	1
Ruscus_aculeatus	1	0	0	0	Simple	scleromorphic	alternate	1	abiotic	ingested	1
Salvia_verbenaca	0.25	0.25	0.25	0.25	Simple	leaf	basal	2	biotic	adhesive	0
Sambucus_nigra	0.5	0.5	0	0	pinnately	leaf	opposite	1	biotic	ingested	1
Sanguisorba_minor	0	0	1	0	pinnately	scleromorphic	alternate	2	biotic	wind	0
Scabiosa_columbaria	0.25	0.25	0.25	0.25	pinnately	leaf	opposite	1	biotic	wind	0
Scabiosa_triandra	0	0.33	0.33	0.333	pinnately	leaf	opposite	1	biotic	wind	0
Sedum_sexangulare	0	0.5	0.5	0	Simple	succulent	alternate	1	biotic	wind	0
Serapias_vomeracea	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	wind	0
Sherardia_arvensis	0.33	0.33	0.33	0	Simple	leaf	whorled	1	biotic	wind	0
Silene_latifolia	0	0.33	0.33	0.333	Simple	leaf	opposite	2	biotic	wind	0
Silene_viridiflora	0	0.5	0.5	0	Simple	leaf	opposite	1	biotic	wind	0
Silene_vulgaris	0.33	0.33	0.33	0	Simple	scleromorphic	opposite	1	biotic	wind	0
Sisymbrium_officinale	0	0.5	0.5	0	Simple	leaf	alternate	1	biotic	wind	0
Sonchus_arvensis	0	0.33	0.33	0.333	Simple	leaf	alternate	1	biotic	wind	0
Sonchus_asper	0.25	0.25	0.25	0.25	Simple	leaf	alternate	1	biotic	wind	0
Sorbus_domestica	0.5	0.5	0	0	pinnately	leaf	alternate	1	biotic	ingested	1
Stachys_officinalis	0	0.33	0.33	0.333	Simple	leaf	opposite	1	biotic	non-specialized	0
Stellaria_media	0.25	0.25	0.25	0.25	Simple	leaf	opposite	1	biotic	non-specialized	0
Stellaria_pallida	0.5	0.5	0	0	Simple	leaf	opposite	1	biotic	non-specialized	0
Symphytum_bulbosum	0	1	0	0	Simple	leaf	opposite	2	biotic	myrmecochory	0
Symphytum_officinale	0	0.5	0.5	0	Simple	leaf	opposite	2	biotic	myrmecochory	0
Tamarix_gallica	0.5	0.5	0	0	Simple	needle	alternate	3	biotic	wind	0
Taraxacum_spec	0.25	0.25	0.25	0.25	Simple	leaf	basal	1	biotic	wind	0
Teucrium_chamaedrys	0	0.5	0.5	0	Simple	scleromorphic	opposite	2	biotic	wind	0
Teucrium_scordium	0	0.5	0.5	0	Simple	scleromorphic	opposite	1	biotic	wind	0
Thlaspi_alliaceum	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	wind	0
Thymus_pulegioides	0.33	0.33	0.33	0	Simple	scleromorphic	opposite	1	biotic	myrmecochory	0
Torilis_nodosa	0.33	0.33	0.33	0	pinnately	leaf	alternate	2	biotic	adhesive	0
Trifolium_nigrescens	0.5	0.5	0	0	palmately	leaf	basal	2	biotic	non-specialized	0
Trifolium_repens	0.25	0.25	0.25	0.25	palmately	leaf	basal	2	biotic	non-specialized	0
Tripolium_pannonicum	0	0	0.5	0.5	Simple	succulent	alternate	1	biotic	wind	0
Ulmus_laevis	1	0	0	0	Simple	leaf	alternate	1	abiotic	wind	0
Valerianella_locusta	0.5	0.5	0	0	Simple	leaf	alternate	1	biotic	wind	0
Veronica_arvensis	0.5	0.5	0	0	Simple	leaf	alternate	2	biotic	ballistic	0
Veronica_hederifolia	0.5	0.5	0	0	Simple	leaf	alternate	2	biotic	myrmecochory	0
Veronica_officinalis	0	0.5	0.5	0	Simple	leaf	alternate	2	biotic	ballistic	0
Veronica_persica	0.25	0.25	0.25	0.25	Simple	leaf	alternate	2	biotic	myrmecochory	0
Viburnum_lantana	0.5	0.5	0	0	Simple	leaf	opposite	2	biotic	ingested	1
Viburnum_opulus	0	1	0	0	Simple	leaf	opposite	2	biotic	ingested	1
Vicia_sativa	0.5	0.5	0	0	pinnately	leaf	alternate	1	biotic	non-specialized	0
Vicia_villosa	0.5	0.5	0	0	pinnately	leaf	alternate	2	biotic	non-specialized	0
Vincetoxicum_hirundinaria	0	0.5	0.5	0	Simple	scleromorphic	opposite	1	biotic	wind	0
Viola_hirta	1	0	0	0	Simple	leaf	basal	2	biotic	myrmecochory	0
Viola_odorata	1	0	0	0	Simple	leaf	basal	2	biotic	myrmecochory	0
Viola_reichenbachiana	0.33	0.33	0.33	0	Simple	leaf	basal	2	biotic	myrmecochory	0

Appendix 6.2: Plant trait matrix (Part 7: Species A-E, Traits “Family” - “Distributional range”)

Species	Family	Ruderal plant	Indicator values						Leaf phenology	Salt tolerance	Distributional range
			Light	Temperature	Continent	Humidity	Acidity	Nutrients			
Acer_campestre	Others	0	5	7	4	5	7	6	s	1	wide
Achillea_millefolium_aggr	Asteraceae	1	8			4		5	s	1	wide
Aegonychon_purpurocaeruleum	Others	0	5	7	6	4	8	4	w	0	wide
Agrimonia_eupatoria	Rosaceae	0	7	6	5	4	8	4	s	0	wide
Ailanthus_altissima	Others	0	6	7	5	5	5	5	s	1	neo
Ajuga_chamaepitys	Lamiaceae	0	7	8	5	4	9	2	w	0	mediterranean
Ajuga_reptans	Lamiaceae	0	6		4	6		6	w	0	wide
Alliaria_petiolata	Brassicaceae	1	5	6	5	5	7	9	s	0	wide
Alnus_glutinosa	Others	0	5	5	5	9	6	8	s	1	wide
Anacamptis_coriophora	Orchidaceae	0	7	8	5	3	5	3	w	0	submediterranean
Anacamptis_morio	Orchidaceae	0	7	5	4	4	7	3	s	0	wide
Anacamptis_pyramidalis	Orchidaceae	0	8	7	5	3	9	2	s	0	submediterranean
Anisantha_sterilis	Poaceae	1	7	7	5	4		5	s	0	submediterranean
Anthemis_arvensis	Asteraceae	1	7	6	4	4	3	6	w	0	wide
Anthoxanthum_odoratum	Poaceae	0			5		5	3	s	1	wide
Aphanes_arvensis	Rosaceae	0	6	5	5	6	4	5	w	0	wide
Arabidopsis_thaliana	Brassicaceae	1	6		5	4	5	4	w	0	wide
Arabis_sagittata	Brassicaceae	0	7	6	6	4	8	3	s	0	wide
Arenaria_serpyllifolia	Caryophyllaceae	1	9	5		4			w	0	wide
Aristolochia_clematitis	Others	0	6	7	5	4	8	8	s	0	mediterranean
Aristolochia_rotunda	Others	0	6	7	5	4	6	3	s	0	mediterranean
Arum_italicum	Others	0	6	8	4	4	5	5	s	0	submediterranean
Asparagus_acutifolius	Others	0	6	9	4	2	5	5	i	0	mediterranean
Asparagus_officinalis	Others	0	8	8	5	5	5	5	s	0	mediterranean
Asperula_laevigata	Others	0	6	6	4	4	7	3	s	0	mediterranean
Avena_fatua	Poaceae	1	6		6	6	7		v	0	wide
Ballota_nigra	Lamiaceae	1	8	6	5	5		8	w	0	mediterranean
Bellis_perennis	Asteraceae	1	9	5	4			5	w	0	wide
Berberis_vulgaris	Others	1	6	6	5	4	8	3	s	0	wide
Brachypodium_phoenicoides	Poaceae	0	6	5	5	4	7	4	s	0	mediterranean
Brachypodium_sylvaticum	Poaceae	0	4	5	5	5	6	6	s	0	wide
Bromus_erecta	Poaceae	0	8	5	7	3	8	3	s	0	wide
Calystegia_sepium	Others	1	8	6	5	6	7	9	s	0	wide
Campanula_rapunculus	Others	0	7	7	5	4	6	4	s	0	wide
Cardamine_hirsuta	Brassicaceae	1	7	8	5	3	5	4	w	0	wide
Carduus_pycnocephalus	Asteraceae	1	7	8	4	3		3	s	0	mediterranean
Carex_acuta	Cyperaceae	0	7	4	7	9	6	4	s	0	wide
Carex_acutiformis	Cyperaceae	0	7	5	5	9	7	5	s	0	wide
Carex_distans	Cyperaceae	0	9	6	5	7	8		w	1	wide
Carex_flacca	Cyperaceae	0	7	5	5	6	8		s	1	wide
Carex_liparocarpos	Cyperaceae	0	8	7	6	2	6	2	s	0	wide
Carpinus_betulus	Others	0	4	6	4				s	0	wide
Celtis_australis	Others	0	7	8	5	3	7	4	s	1	mediterranean
Centaurea_nigrescens	Asteraceae	0	7	6	5	4	5	4	s	0	wide
Centaurium_erythraea	Others	0	8	6	5	5	6		s	0	wide
Cerastium_brachypetalum	Caryophyllaceae	1	10	7	5	3	7	2	w	0	wide
Cerastium_fontanum	Caryophyllaceae	1	6			5		5	w	1	wide
Cerastium_glomeratum	Caryophyllaceae	1	7		5	5	5	5	w	0	submediterranean
Cerastium_semidecandrum	Caryophyllaceae	1	8	7	5	4			s	0	wide
Chaerophyllum_temulum	Others	0	5	6	5	5		8	s	0	wide
Cichorium_intybus	Asteraceae	1	9	6	5	3	8	5	s	0	wide
Cirsium_arvense	Asteraceae	1	8			4		7	s	1	wide
Clematis_flammula	Others	0	7	9	5	3	5	4	s	0	mediterranean
Clinopodium_vulgare	Lamiaceae	1	7	5	4	4	7	3	s	0	wide
Convolvulus_arvensis	Others	1	7	7	5	4	5	5	s	0	wide
Cornus_mas	Others	0	6	7	6	5	8	4	s	0	wide
Cornus_sanguinea	Others	0	7	5	5	7	8		s	0	wide
Cotinus_coggygria	Others	0	7	6	7	3	7	2	s	0	mediterranean
Crataegus_monogyna	Rosaceae	0	6	7	5	4	6	3	s	0	wide
Crepis_capillaris	Asteraceae	1	7	6	5	4	5	3	s	0	wide
Crepis_foetida	Asteraceae	1	11	9	5	2		2	s	0	submediterranean
Cynoglossum_officinale	Others	1	8	5	5	3	7	8	s	0	wide
Dactylis_glomerata	Poaceae	1	7	6	5	4	5	6	s	0	wide
Daucus_carota	Others	1	8	6	5	4	5	4	s	0	wide
Dioscorea_communis	Others	0	5	7	5	5	8	6	s	0	submediterranean
Diplotaxis_tenuifolia	Brassicaceae	1	8	7	5	4	6	5	w	0	submediterranean
Echium_vulgare	Others	1	9	7	5	4	5	4	w	0	wide
Elaeagnus_angustifolia	Others	0	9	7	5	3		2	s	1	neo
Equisetum_ramosissimum	Others	0	7	7	6	3	7	1	s	0	wide
Erigeron_sumatrensis	Asteraceae	1	8	8	5	3		7	s	0	neo
Erodium_cicutarium	Others	1	8	7	5	3	5	3	w	0	wide
Eryngium_campestre	Others	0	9	7	5	3	8	3	w	0	submediterranean
Euonymus_europaeus	Others	0	6	5	5	5	8	5	s	0	wide
Eupatorium_cannabinum	Asteraceae	0	7	7	5	7	5	7	s	0	wide
Euphorbia_cyparissias	Others	0	7	7	5	3	5	5	w	0	wide
Euphorbia_helioscopia	Others	0	9	7	5	3	5	6	w	0	wide

Appendix 6.2: Plant trait matrix (Part 8: Species F-Pr, Traits “Family” - “Distributional range”)

		Ruderal	Indicator values							Salt	Distributional
Species	Family	plant	Light	Temperature	Continent	Humidity	Acidity	Nutrients	Leaf phenology	tolerance	range
Frangula_alnus	Others	0	6	5	4	7	5	5	s	0	wide
Fraxinus_angustifolia	Oleaceae	0	4	8	6	7	7	8	s	0	submediterranean
Fraxinus_excelsior	Oleaceae	0	4	5	4	7	7	7	s	1	wide
Fraxinus_ornus	Oleaceae	0	5	8	6	3	8	3	s	0	submediterranean
Galium_aparine	Others	1	6		5	4	5	5	v	0	wide
Galium_mollugo	Others	1	6	5	5	5	5	4	s	0	wide
Genista_tinctoria	Fabaceae	0	5	6	5	5	3	3	w	0	wide
Geranium_columbinum	Others	1	7	9	6	2	5	2	s	0	submediterranean
Geranium_dissectum	Others	1	7	8	5	2	5	2	w	0	wide
Geranium_molle	Others	1	7	6	5	3	5	4	w	0	wide
Geranium_purpureum	Others	1	7	8	5	3	6	3	w	0	submediterranean
Geranium_robertianum	Others	1	4	6	5	4	5	5	w	0	wide
Geum_urbanum	Rosaceae	1	4	5	5	5	6	7	w	0	wide
Gladiolus_italicus	Others	0	9	9	5	3	5	3	s	0	mediterranean
Glechoma_hederacea	Lamiaceae	1	6	7	4	4	5	3	w	0	wide
Hedera_helix	Others	0	4	5	4	5			i	0	wide
Helianthemum_jonium	Others	0	11	10	4	2	7	1	i	0	mediterranean
Helianthemum_ nummularium	Others	0	9		6	4	7	2	i	0	wide
Helminthotheca_ echioides	Asteraceae	1	11	8	5	2		2	s	0	mediterranean
Hippocrepis_emerus	Fabaceae	0	7	6	4	3	9	2	i	0	submediterranean
Hordeum_murinum	Poaceae	1	8	8	4	5	5	3	s	0	wide
Humulus_lupulus	Others	0	7	6	4	8	6	8	s	0	wide
Hypericum_perforatum	Others	1	7	8	6				s	0	wide
Hypochaeris_radicata	Asteraceae	0	9	8	4	2		1	s	1	wide
Inula_salicina	Asteraceae	0	7	5	5	4	9	2	s	1	wide
Iris_foetidissima	Others	0	7	7	5	4	4	5	w	1	submediterranean
Jacobaea_erratica	Asteraceae	0	7	6	4	4	7	4	s	0	wide
Juniperus_communis	Others	0	8	0	0	4	0	4	i	0	wide
Knautia_integrifolia	Others	0	7	8	5	3	3	2	s	0	mediterranean
Lamium_purpureum	Lamiaceae	1	7	7	5	4	5	5	w	0	wide
Lathyrus_sphaericus	Fabaceae	1	10	9	5	2	5	2	s	0	mediterranean
Lepidium_campestre	Brassicaceae	1	7	7	4	4	5	4	s	0	wide
Ligustrum_vulgare	Oleaceae	0	7	6	4		8		s	0	wide
Linum_bienne	Others	0	7	7	5	3	7	2	s	0	submediterranean
Lonicera_caprifolium	Others	0	6	5	6	6		5	s	0	submediterranean
Lonicera_japonica	Others	0							s	0	neo
Lotus_corniculatus	Fabaceae	1	7		5	4	7	2	s	0	wide
Luzula_campestris	Others	0	7	4	4	4	3	2	s	0	wide
Lycopus_europaeus	Lamiaceae	0	7	6	5	9		7	w	0	wide
Malus_pumila	Rosaceae	0	7	7	5	5	5	5	s	0	wide
Melilotus_indicus	Fabaceae	1	7	7	4	4	5	5	s	1	mediterranean
Mentha_aquatica	Lamiaceae	0	7	5	5	9	7	4	s	0	wide
Myosotis_arvensis	Others	1	6	5	5	5		6	w	0	wide
Myosotis_ramosissima	Others	1	9	8	5	2	4	3	w	0	wide
Myosoton_aquaticum	Caryophyllaceae	0	7	5	4	8		8	w	0	wide
Neotinea_tridentata	Orchidaceae	0	8	6	5	3	6	3	w	0	wide
Ochlopoa_annua	Poaceae	1	7		5	6		8	w	1	wide
Onopordum_acanthium	Asteraceae	1	11	7	6	4	7	8	s	0	submediterranean
Ornithogalum_ orthophyllum	Others	0	7	5	4	3	6	2	s	0	submediterranean
Oxalis_corniculata	Others	0	7	7	0	4		6	s	0	mediterranean
Oxalis_dillenii	Others	1	7	7	5	5	5	7	s	0	neo
Phillyrea_angustifolia	Oleaceae	0	11	10	4	1		2	i	0	mediterranean
Phillyrea_latifolia	Oleaceae	0	5	8	4	4		5	i	0	mediterranean
Phragmites_australis	Poaceae	0	7	5		10	7	5	w	1	wide
Pinus_halepensis	Pinaceae	0	11	10	4	2	0	2	i	1	mediterranean
Pinus_nigra	Pinaceae	0	7	7	4	2	9	2	i	1	submediterranean
Pinus_pinaster	Pinaceae	0	10	8	4	2	4	3	i	1	mediterranean
Pinus_pinea	Pinaceae	0	11	8	5	2	4	3	i	0	mediterranean
Pinus_sylvestris	Pinaceae	0	7	0	7	0	0	0	i	0	wide
Plantago_coronopus	Plantaginaceae	0	8	7	5	7	7	4	s	1	wide
Plantago_lanceolata	Plantaginaceae	1	6	7	5				w	0	wide
Plantago_major	Plantaginaceae	1	8			5		7	s	0	wide
Plantago_media	Plantaginaceae	1	7		7	4	8	3	w	0	wide
Platanthera_chlorantha	Orchidaceae	0	6		4	7	7		s	0	wide
Poa_bulbosa	Poaceae	0	8	8	7	2	4	1	w	0	wide
Poa_pratensis	Poaceae	1	6			5			w	0	wide
Polygala_comosa	Others	0	8	6	6	3	8	2	s	0	wide
Populus_alba	Others	0	5	8	7	5	8	6	s	0	wide
Populus_nigra	Others	0	5	7	6	8	7	7	s	0	wide
Potentilla_hirta	Rosaceae	0	11	7	3	3	7	3	s	0	mediterranean
Potentilla_reptans	Rosaceae	1	6	6	5	6	7	5	w	0	wide
Prunella_laciniata	Lamiaceae	0	8	8	5	3	7	2	w	0	submediterranean
Prunella_vulgaris	Lamiaceae	0	7	6	4	6	4		w	0	wide
Prunus_avium	Rosaceae	0	4	5	6	5	7	5	s	0	wide
Prunus_spinosa	Rosaceae	0	7	5	5				s	0	wide

Appendix 6.2: Plant trait matrix (Part 9: Species Ps-Z, Traits “Family” - “Distributional range”)

		Ruderal	Indicator values							Salt	Distributional
Species	Family	plant	Light	Temperature	Continent	Humidity	Acidity	Nutrients	Leaf phenology	tolerance	range
Pteridium_aquilinum	Others	0	6	5	4	6	3	3	s	0	wide
Pyracantha_coccinea	Rosaceae	0	5	8	4	3	5	3	i	0	mediterranean
Pyrus_communis	Rosaceae	0	7	7	5	5	5	5	s	0	wide
Quercus_ilex	Others	0	2	9	4	3			i	0	mediterranean
Quercus_robur	Others	0	7	6	6	6	5	6	s	0	wide
Ranunculus_bulbosus	Others	0	8	6	5	3	7	3	s	0	wide
Ranunculus_parviflorus	Others	1	8	7	4	5	6	5	s	0	submediterranean
Ranunculus_polyanthemos	Others	0	6		6	5	6		s	0	wide
Ranunculus_sardous	Others	1	8	7	5	8		7	s	1	submediterranean
Raphanus_raphanistrum	Brassicaceae	1	11	5	5		4	5	s	0	mediterranean
Reseda_alba	Others	0	11	8	4	3	7	1	s	0	mediterranean
Rhamnus_alaternus	Others	0	4	9	5	2	4	4	i	0	mediterranean
Rhamnus_cathartica	Others	0	7	5	5	4	8		s	0	wide
Robinia_pseudoacacia	Fabaceae	0	5	7	5	4		8	s	1	neo
Rosa_canina	Rosaceae	0	8	5	5	4			s	0	wide
Rubia_peregrina	Others	1	5	9	4	4	5	3	i	0	mediterranean
Rubus_ulmifolius	Rosaceae	0	5	8	5	4	5	8	w	0	submediterranean
Ruscus_aculeatus	Others	0	4	8	5	4	5	5	i	0	submediterranean
Salvia_verbenaca	Lamiaceae	1	8	8	4	3	5	7	s	0	mediterranean
Sambucus_nigra	Others	0	7	5	4	5		9	s	0	wide
Sanguisorba_minor	Rosaceae	0	7	6	5	3	8	2	s	0	wide
Scabiosa_columbaria	Others	0	8	5	5	4	8	2	s	0	wide
Scabiosa_triandra	Others	0							s	0	submediterranean
Sedum_sexangulare	Others	0	7	5	4	7	8	1	w	0	wide
Serapias_vomeracea	Orchidaceae	0	10	8	5	3	4	2	s	0	mediterranean
Sherardia_arvensis	Others	1	8	6	5	5	8	5	w	0	mediterranean
Silene_latifolia	Caryophyllaceae	1	8			4		7	s	1	wide
Silene_viridiflora	Caryophyllaceae	0	5	7	6	4	5	5	s	0	wide
Silene_vulgaris	Caryophyllaceae	0	8			4	7	2	s	0	wide
Sisymbrium_officinale	Brassicaceae	1	8	6	5	4		7	s	0	wide
Sonchus_arvensis	Asteraceae	1	7	5		5	7		s	1	wide
Sonchus_asper	Asteraceae	1	7	5		4	7	7	s	1	wide
Sorbus_domestica	Rosaceae	0	4	7	5	3	8	3	s	0	submediterranean
Stachys_officinalis	Lamiaceae	0	6	5	4	6	4	3	s	0	wide
Stellaria_media	Caryophyllaceae	1	6			4	7	8	w	0	wide
Stellaria_pallida	Caryophyllaceae	1	8	8	5	3	5	4	s	0	wide
Symphytum_bulbosum	Others	0	4	7	6	4	5	3	s	0	wide
Symphytum_officinale	Others	0	7	6	4	8		8	s	0	wide
Tamarix_gallica	Others	0	11	7	4	6	5	3	i	1	mediterranean
Taraxacum_spec	Asteraceae	1	7			5		7	s	0	wide
Teucrium_chamaedrys	Lamiaceae	0	7	6	5	2	8	1	i	0	wide
Teucrium_scordium	Lamiaceae	0	7	7	5	8	8	2	w	1	wide
Thlaspi_alliaceum	Brassicaceae	1	6	6	5	4	6	5	s	0	mediterranean
Thymus_pulegioides	Lamiaceae	0	8		5	4		1	i	0	wide
Torilis_nodosa	Others	1	7	8	6	4	7	6	s	0	submediterranean
Trifolium_nigrescens	Fabaceae	1	8	6	5	5	5	6	s	0	mediterranean
Trifolium_repens	Fabaceae	1	8					7	w	1	wide
Tripolium_pannonicum	Asteraceae	0	8	7		9	7	7	w	1	wide
Ulmus_laevis	Others	0	4	6	5	8	7	7	s	0	wide
Valerianella_locusta	Others	0	7	5	5	5	7		w	0	submediterranean
Veronica_arvensis	Plantaginaceae	1	5	5	5	5	6		w	0	wide
Veronica_hederifolia	Plantaginaceae	1	6	6	5	5	3	7	s	0	wide
Veronica_officinalis	Plantaginaceae	0	5		5	4	2	3	w	0	wide
Veronica_persica	Plantaginaceae	1	8	7	5	5	5	6	w	0	neo
Viburnum_lantana	Others	0	7	5	5	4	8	5	w	0	wide
Viburnum_opulus	Others	0	6	5	5	7	7	6	s	0	wide
Vicia_sativa	Fabaceae	1	5	5	6				w	0	mediterranean
Vicia_villosa	Fabaceae	1	7	6	5	4	4	5	w	0	submediterranean
Vincetoxicum_hirundinaria	Others	0	6	5	5	3	7	3	s	0	wide
Viola_hirta	Others	0	6	5	5	3	8	2	s	0	wide
Viola_odorata	Others	0	5	6	5	5		8	w	0	wide
Viola_reichenbachiana	Others	0	4	5	4	5	7	6	w	0	wide

Appendix 7.1: Moth species abundance matrix (Part 1: Species A-Cha, Site V1-V20)

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14	V15	V16	V17	V18	V19	V20
Abrostola asclepiadis	4	0	4	2	0	0	0	0	0	0	0	0	2	1	2	0	1	0	0	0
Acentria ephemerella	6	2	3	4	22	0	14	29	3	2	0	1	0	0	0	0	0	1	0	0
Acleris kochiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Acleris rhombana	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Acleris variegana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acontia lucida	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Acontia trabealis	2	0	0	0	0	0	2	0	0	0	1	0	1	0	0	0	0	0	0	5
Acrobasis advenella	1	3	0	1	1	1	7	1	0	0	2	13	5	2	1	0	0	0	1	2
Acrobasis consociella	71	174	17	32	12	41	37	90	8	27	21	45	21	47	16	1	6	7	10	27
Acrobasis fallouella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acrobasis foroiuliensis	0	3	0	0	0	0	0	0	4	1	0	0	1	1	0	0	0	2	1	2
Acrobasis marmorea	0	0	0	0	0	1	0	2	1	0	0	0	0	1	0	0	0	1	0	10
Acrobasis suavella	1	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Acronicta aceris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acronicta cuspis	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Acronicta psi	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acronicta rumicis	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
Aedia leucomelas	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Agapeta hamana	0	0	1	0	1	0	1	0	0	0	0	1	0	0	1	0	0	1	0	0
Agapeta zoegana	0	3	0	4	0	4	1	1	0	1	0	1	1	1	0	0	1	1	2	10
Agdistis cf. tamaricis	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Agriphila brioniellus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agriphila geniculea	0	0	0	35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agrotera nemoralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agrotis bigramma	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agrotis exclamationis	1	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1
Agrotis ipsilon	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	0	0	1	0	0
Agrotis segetum	0	0	0	0	0	1	0	0	0	0	1	1	0	0	1	0	0	1	0	1
Alabonia geoffrella	0	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
Aleimma loeflingiana	2	1	3	24	3	1	3	0	0	0	0	0	0	15	0	0	1	0	3	0
Amphipyra pyramidea	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0
Anacampsis populella	0	0	0	0	0	0	0	0	1	0	0	3	10	1	0	0	0	0	0	2
Anania crocealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anarta trifolii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ancylis apicella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ancylis mitterbacheriana	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ancylis obtusana	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0
Ancylis selenana	41	28	0	1	0	0	0	6	5	7	0	0	0	0	0	0	0	0	12	3
Ancylis unculana	0	2	0	1	0	0	0	0	0	1	1	2	0	3	0	1	1	1	0	0
Apeira syringaria	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	1
Apoda limacodes	3	1	0	0	2	6	1	6	0	1	0	1	0	1	3	0	0	0	0	0
Araeopteron ecphaea	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Archips betulana	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Archips podana	17	20	16	52	29	3	9	61	24	22	26	8	7	19	19	3	10	1	16	7
Archips rosana	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0
Archips xylosteana	1	0	0	1	2	0	0	0	0	0	0	0	0	2	2	0	0	0	0	0
Arctia villica	6	1	16	4	1	1	3	6	0	2	1	0	0	11	10	1	0	9	1	0
Ascotis selenaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Athetis hospes	16	4	1	0	0	0	1	5	0	2	0	1	1	0	0	0	0	0	3	2
Autographa gamma	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bactra robustana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
Batia spec.	0	1	1	0	1	0	0	0	0	1	0	0	1	3	2	0	0	0	1	1
Blastobasis glandulella	0	0	0	0	0	0	0	2	0	0	5	6	4	10	1	1	1	1	3	5
Bucculatrix spec	13	0	1	0	3	2	9	10	2	0	5	2	10	7	0	0	0	0	0	8
Cacoecimorpha pronubana	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	1
Cadra figulilella	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Calamotropha paludella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Callopistria juventina	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Calophasia platyptera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Caloptilia alchimiella	13	6	1	0	0	3	0	9	0	0	2	1	6	4	2	1	1	1	0	1
Capperia cf. loranus	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	1
Caradrina aspersa	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Caradrina morpheus	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Carcina quercana	5	0	0	0	1	1	0	0	0	1	0	0	1	10	1	0	0	1	1	0
Carpatolechia aenigma	52	93	9	69	6	71	0	112	0	0	0	0	1	0	0	0	0	0	0	0
Cataclysta lemnata	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Catarhoe rubidata	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	1
Catephia alchymista	0	0	0	1	0	1	0	1	0	0	0	0	0	3	1	0	1	0	0	0
Catocala conversa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Catocala promissa	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Catoptria falsella	1	0	0	0	1	1	0	1	0	0	0	0	2	0	0	0	0	0	0	0
Catoptria pinella	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Celypha flavipalpana	3	0	0	0	0	0	6	0	2	0	0	0	0	6	0	0	2	2	3	0
Cerura erminea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Charanyca ferruginea	10	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Charanyca trigrammica	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 2: Species Chi-Ep, Site V1-V20)

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14	V15	V16	V17	V18	V19	V20
Chiasmia aestimaria	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0
Chiasmia clathrata	0	0	0	1	0	0	2	1	1	0	0	0	0	0	0	0	1	0	2	2
Chilo luteellus	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	8
Chilo phragmitella	1	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0
Chilodes maritima	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloantha hyperici	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroclystis v-ata	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Chrysocrambus linetella	0	0	1	0	0	0	0	0	4	2	0	1	0	1	0	0	0	1	0	3
Chrysoteuchia culmella	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Cilix glaucata/hispanica	0	1	1	0	1	0	0	4	1	2	10	7	4	1	2	0	2	1	0	2
Clepsis consimilana	4	1	0	6	1	3	1	1	4	5	0	4	0	11	6	0	0	2	2	7
Clepsis rurinana	0	0	0	0	0	0	0	0	0	0	1	0	2	11	0	0	0	0	1	1
Clostera pigra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cnaemidophorus rhododactyla	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Cnephasia pasiuana	2	0	0	0	0	0	0	0	0	0	0	0	0	5	2	2	0	0	0	0
Coleophora cf. colutella	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Colobochyla salicalis	0	0	0	0	1	0	2	0	0	2	1	0	0	4	0	0	1	0	0	0
Comibaena bajularia	3	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	0
Conisania luteago	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0
Cosmia affinis	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Cosmia trapezina	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Cosmopterix lienigiella	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Cosmopterix orichalcea	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cosmopterix scribaiella	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Cosmorhoe ocellata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
Cossus cossus	0	1	0	0	0	2	0	1	0	0	0	0	1	1	0	0	0	0	0	0
Costaconvexa polygrammata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Craniophora ligustri	0	0	3	16	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0	0
Crocallis elinguaria	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Crombrugghia distans/tristis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cryphia algae	0	0	0	0	0	1	0	0	0	1	0	1	0	0	0	0	1	0	0	6
Cryphia ochsi	0	0	0	0	0	2	0	2	1	0	1	0	0	1	0	0	0	0	0	3
Cyclophora annularia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyclophora punctaria	2	1	2	0	0	0	0	3	1	1	1	9	11	0	0	0	1	0	0	1
Cyclophora puppillaria	0	1	0	5	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Cydia amplana	1	11	0	2	0	1	0	0	0	2	5	21	6	2	0	1	7	1	5	7
Cydia fagiglandana	7	29	0	63	0	3	0	9	0	1	0	1	4	14	0	1	2	0	8	6
Cydia pomonella	0	0	0	0	0	0	0	0	0	0	0	3	0	1	0	0	1	0	0	2
Deltote bankiana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Deltote pygarga	11	8	10	21	13	3	17	6	2	8	12	2	0	10	4	2	16	0	13	2
Denticucullus pygmina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Diaphora mendica	4	0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Dichomeris alacella	22	11	0	11	4	1	18	13	0	0	6	13	14	2	3	0	41	0	7	10
Dichomeris derasella	3	5	0	0	0	0	0	9	0	0	1	1	2	1	1	0	0	0	1	1
Dichomeris marginella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Dioryctria abietella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dioryctria pinae	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dioryctria sylvestrella	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Ditula angustiorana	0	0	0	0	0	0	1	0	0	0	0	0	0	4	0	0	0	0	0	0
Dolicharthria punctalis	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Donacaula forficella	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Drymonia dodonaea	0	0	1	1	2	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0
Duponchelia fovealis	0	0	0	0	0	0	4	0	0	0	0	1	0	0	0	0	0	0	0	1
Dypterygia scabriuscula	1	0	0	0	2	0	1	0	0	1	1	0	0	1	0	0	3	2	0	0
Dysauxes ancilla	1	0	2	1	0	1	0	1	1	0	0	0	0	6	0	0	1	8	1	0
Dysauxes famula	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0
Dysauxes punctata	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Dysgonia algira	0	0	0	1	0	1	0	0	0	1	1	0	1	1	1	0	0	0	1	0
Dyspessa ulula	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Earias clorana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Earias vernana	1	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	3
Eilema caniola	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Eilema complana	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
Eilema depressa	9	2	19	3	0	3	3	14	2	18	5	4	5	111	18	0	0	7	1	7
Eilema sororcula	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Elaphria venustula	11	5	17	4	6	0	5	0	0	2	3	1	0	16	1	4	18	12	6	15
Elegia similella	1	6	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	1	0
Ematheudes punctella	0	3	1	0	0	0	0	0	1	0	2	1	2	2	0	1	10	4	0	19
Emmelina monodactyla	0	2	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Endotricha flammealis	0	1	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	1
Epagoge grotiana	0	0	0	0	0	2	0	0	1	2	0	0	0	0	0	0	0	0	0	0
Ephestia woodiella	19	18	30	12	0	59	67	25	2	4	0	54	78	20	12	1	0	11	1	43
Epiblema foenella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Epicallima formosella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Epinotia festivana	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
Epione repandaria	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Epirrhoe cf. alternata	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 3: Species Et-Lo, Site V1-V20)

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14	V15	V16	V17	V18	V19	V20
Ethmia bipunctella	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Ethmia quadrillella	0	1	0	2	0	0	0	1	2	0	0	1	0	2	0	0	0	0	1	0
Ethmia terminella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Etiella zinckenella	1	0	0	0	0	0	7	1	0	0	0	0	5	0	0	0	0	0	0	1
Eublemma parva	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euchromius superbellus	4	7	0	0	0	3	5	21	0	1	1	4	3	3	0	0	1	0	0	1
Eucosma cana	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2	0	0	0
Eucosma conterminana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	24
Eucosma metzneriana	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Eudonia delunella	2	0	2	14	6	2	6	1	0	9	0	0	0	6	0	0	0	0	0	0
Eudonia lacustrata	1	0	1	1	0	2	1	0	0	0	0	0	0	2	0	0	0	0	0	2
Eudonia mercurella	6	9	6	0	0	2	1	1	1	1	4	4	0	2	0	1	1	2	0	3
Eudonia pallida	0	0	0	0	0	0	0	0	0	1	0	1	0	3	2	1	1	0	0	2
Eupithecia centaureata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eupithecia haworthiata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eupithecia ultimaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Euplagia quadripunctaria	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euplexia lucipara	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euproctis chrysorrhoea	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Eutelia adulatrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euzophera fuliginosella	6	18	1	1	3	2	3	3	0	2	0	0	1	25	1	0	0	1	0	1
Evergestis extimalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Furcula bifida	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Galleria mellonella	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
Gastropacha quercifolia	0	0	0	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Glyptoteles leucacrinella	0	0	0	0	0	0	2	0	1	6	1	0	8	10	2	0	0	0	1	1
Gymnoscelis rufifasciata	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gypsonoma aceriana	10	10	0	1	2	0	3	21	3	0	0	5	0	4	0	0	0	0	0	2
Gypsonoma minutana	2	3	0	3	0	0	8	0	1	0	0	3	13	0	0	0	0	0	4	10
Habrosyne pyritoides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hadena bicruris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Harpyia milhauseri	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Hedya nubiferana	9	3	1	7	0	0	2	2	2	6	2	2	3	20	12	0	3	1	3	1
Hedya pruniana	0	2	0	0	1	0	1	0	0	0	1	3	0	2	1	0	1	0	6	0
Helicoverpa armigera	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Heliothis viriplaca	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Hellinsia cf. inulae	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Hemistola chrysoprasaria	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Hemithea aestivaria	0	2	0	0	0	0	0	0	1	0	0	0	0	4	2	1	1	2	2	1
Herminia tarsicrinalis	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Herminia tarsipennalis	0	0	0	0	0	0	1	0	0	0	0	0	1	4	1	0	0	0	0	0
Herminia tenuialis	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Heterogenea asella	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0
Homaloxestis briantiella	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Homoeosoma sinuella	23	6	3	0	5	5	2	2	0	1	0	0	0	1	1	0	1	0	2	12
Hoplodrina ambigua	0	0	0	1	0	0	2	0	1	0	1	0	0	3	2	0	0	0	0	0
Horisme tersata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Horisme vitalbata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Hypomecis punctinalis	4	3	0	0	0	0	0	2	1	1	6	0	1	2	0	0	3	0	0	0
Hypsopygia costalis	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Hypsopygia glaucinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Idaea aversata	4	0	2	1	4	1	9	1	0	1	6	1	3	9	9	0	5	0	1	2
Idaea degeneraria/rubraria	0	1	0	12	5	6	2	1	0	0	1	0	0	0	1	0	3	0	0	0
Idaea dimidiata	0	0	1	3	0	0	0	0	0	1	0	0	1	1	0	1	2	0	0	0
Idaea filicata	0	0	0	2	0	0	1	0	0	0	0	0	0	1	1	0	0	1	1	0
Idaea fuscovenosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea muricata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea politaria	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1
Idaea rusticata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Idaea seriata	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
Idaea subsericeata	1	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Ipimorpha subtusa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Isturgia arenacearia	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Lacanobia oleracea	0	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Lacanobia w-latinum	2	0	1	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	1	1
Laelia coenosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lamoria anella	0	0	0	0	0	0	0	2	2	4	0	1	6	0	1	0	0	0	0	1
Laothoe populi	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Lasiocampa quercus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Laspeyria flexula	2	0	1	0	0	0	1	1	0	0	0	0	0	4	0	0	0	0	0	0
Leucania loreyi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leucania obsoleta	4	5	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Ligdia adustata	6	7	3	5	4	4	4	4	3	13	3	3	13	3	2	0	1	2	2	30
Lithosia quadra	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Lomaspilis marginata	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Lomographa bimaculata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Loryma egregialis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Loxostege sticticalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 4: Species Ly-Pe, Site V1-V20)

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14	V15	V16	V17	V18	V19	V20
Lygephila craccae	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Lymantria dispar	2	8	0	0	0	5	1	6	1	1	5	1	3	1	1	1	0	2	2	5
Macaria alternata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Macaria liturata	5	2	2	1	3	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0
Macaria notata	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
Malacosoma castrensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Mecyna asinalis	1	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	1	1	1
Meganola albula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Meganola togatulalis	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menophra abruptaria	0	0	2	1	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	1
Mesapamea secalis	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Metachrostis velox	0	0	0	1	0	2	1	0	0	0	0	0	1	0	0	1	0	0	0	0
Metasia ophialis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Metendothenia atropunctana	0	0	0	1	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
Miltochrista miniata	4	0	6	14	0	0	0	0	0	0	0	3	1	6	2	0	1	0	1	2
Mimas tiliae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Minoa murinata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Minucia lunaris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Moma alpium	0	0	0	6	1	0	0	1	1	1	3	0	0	3	0	0	0	0	0	0
Monopis monachella	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Monopis obviella	2	8	0	0	0	0	1	3	0	0	0	1	0	0	0	0	0	0	0	0
Mormo maura	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Morophaga choragella	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Morophaga morella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Myelois circumvoluta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Mythimna albipuncta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna congrua	1	0	0	0	0	0	0	1	0	1	0	0	0	1	2	1	0	0	0	3
Mythimna pallens	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0
Mythimna riparia	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna sicula	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna straminea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna turca	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna vitellina	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nephopterix angustella	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0
Neurothaumasia ankerella	0	10	0	1	3	3	2	3	2	8	6	4	2	4	0	2	5	1	0	3
Noctua fimbriata	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Noctua janthina/janthe	0	0	1	3	1	1	1	0	1	0	0	1	0	0	0	1	0	0	0	1
Noctua pronuba	0	2	2	3	1	0	0	0	0	1	1	1	0	3	2	1	3	1	0	0
Noctua tirrenica	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nola aerugula	0	0	0	0	0	1	2	0	0	3	0	0	0	2	1	2	9	0	5	7
Nola chlamitulalis	2	2	1	0	1	0	2	8	0	2	2	1	1	1	6	0	4	3	0	0
Nomophila noctuella	23	6	1	8	5	1	3	4	2	0	2	7	23	3	3	1	7	0	1	14
Notocelia cynosbatella	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Notocelia roborana	2	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	2	0	1
Notocelia rosaecolana/trimaculana	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Notocelia uddmanniana	7	6	0	0	0	0	2	2	0	3	4	0	1	9	4	0	1	6	1	4
Notodonta tritophus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Nyctegretis lineana	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Nycterosea obstipata	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
Nyctobrya muralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ochropleura plecta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ocneria rubea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oligia latruncula	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0
Oncocera semirubella	1	3	1	0	2	3	5	0	6	4	2	1	3	3	0	2	0	3	22	12
Opisthograptis luteolata	3	1	0	1	1	0	0	0	0	0	0	1	0	1	3	0	0	0	0	0
Orgyia antiqua	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ostrinia nubilalis	0	0	0	1	1	0	1	2	0	0	0	0	1	2	0	0	1	0	0	4
Palpita vitrealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Pammene fasciana	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
Pandemis cerasana	0	0	1	0	2	6	0	29	4	6	0	1	0	7	2	1	2	0	2	3
Pandemis heparana	0	0	2	1	3	0	1	7	9	8	5	2	0	2	3	0	2	0	12	1
Paradoxus osyridellus	32	0	1	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Parahypopta caestrum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
Parapoynx stratiotata	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Parascotia fuliginaria	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Paraswammerdamia albicapitella	0	2	0	0	0	0	0	6	0	0	0	6	1	0	1	0	2	0	0	3
Paraswammerdamia nebulella	16	17	8	9	13	9	11	12	4	8	21	23	32	14	19	8	10	7	7	21
Paratalanta pandalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Parectopa robiniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Pasiphila chloerata	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Pasiphila rectangulata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Pechipogo plumigeralis	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Pediasia contaminella	0	0	2	8	0	1	0	0	0	2	0	0	0	3	0	0	0	1	0	3
Pelochrista mollitana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pelosia muscerda	0	0	0	1	0	0	0	0	0	0	0	1	1	1	1	0	5	0	0	1
Pempelia palumbella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Penestoglossa dardoinella	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Peribatodes rhomboidaria	28	11	54	35	40	30	25	9	11	31	34	5	42	75	31	7	9	39	5	29
Peridea anceps	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Petrophora chlorosata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 5: Species Ph-Z, Site V1-V20)

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14	V15	V16	V17	V18	V19	V20
Phalera bucephala	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	1
Phalonidia albipalpana	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pheosia tremula	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Philereme transversata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Philereme vetulata	0	0	1	0	0	0	0	0	0	0	2	0	0	7	0	0	1	3	0	0
Photedes morrisii	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Phragmataecia castaneae	0	0	1	1	2	2	0	2	0	3	0	0	0	0	0	0	0	2	0	5
Phragmatobia fuliginosa	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0
Phtheochroa pulvillana	2	2	0	5	3	0	2	2	0	0	0	0	0	4	4	0	0	0	2	0
Phycitodes binaevella	1	0	2	1	0	1	0	0	1	0	0	0	0	1	0	0	0	1	0	7
Phyllophila obliterata	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Phytometra viridaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Piniphila bifasciana	46	0	41	6	3	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Platyptilia cf. farfarellus	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Platytes alpinella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pleuropyta ruralis	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Plodia interpunctella	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Plutella xylostella	0	0	0	6	2	0	0	0	0	0	0	0	0	1	0	3	0	0	0	5
Polyphaenis sericata	0	0	0	0	0	1	0	0	3	0	0	0	1	0	0	0	0	1	0	0
Propiromorpha rhodophana	3	2	0	0	2	0	0	2	1	5	0	1	8	2	0	0	1	0	2	9
Pseudargyrotoza conwagana	0	1	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	2
Pseudoips prasinana	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pseudotelphusa scalella	23	54	19	12	4	13	0	42	0	4	4	41	34	15	2	0	19	1	0	14
Pterostoma palpina	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1
Pyralis farinalis	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pyrausta aurata	0	0	0	0	0	0	1	1	1	2	0	0	0	0	0	1	0	0	0	3
Pyrausta despicata	3	0	0	4	0	2	0	0	0	0	0	0	0	1	0	0	1	0	0	1
Pyrausta purpuralis	0	0	0	2	0	0	0	1	0	1	0	0	0	0	0	0	2	0	0	0
Pyroderces argyrogrammos	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1
Rhigognostis hufnagelii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhodometra sacraria	0	0	0	2	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0
Rhodophaea formosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0
Rhyacionia buoliana/pinicolana	2	0	4	1	7	1	0	0	1	0	1	0	0	2	1	0	0	0	1	0
Rivula sericealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Schoenobius gigantella	1	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0
Schrankia costaestrigalis	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1
Sciota rhenella	7	6	1	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0
Sclerocona acutella	4	2	0	0	0	0	0	5	0	0	0	2	0	0	0	0	0	0	0	6
Scoparia basistrigalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scopula emutaria	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scopula imitaria	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0
Scopula nigropunctata	2	3	0	0	1	0	0	1	1	0	0	0	1	3	0	0	2	1	2	2
Scopula rubiginata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scythropia crataegella	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Senta flammea	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sideridis rivularis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sitochroa palealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Spatalia argentina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spilonota ocellana	0	0	0	1	2	0	0	0	0	0	0	0	0	4	0	0	3	0	1	0
Spilosoma lubricipeda	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
Spilosoma lutea	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spodoptera exigua	386	96	0	1	0	0	3	111	22	15	0	0	0	1	0	0	0	0	18	1
Stauropus fagi	0	1	1	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stegania trimaculata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stemmatophora brunnealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Subacronicta megacephala	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	0	0	0	0	0
Symmoca signatella	1	0	0	2	0	1	0	16	2	3	0	0	3	4	4	0	1	3	0	5
Synaphe punctalis	2	0	0	0	2	1	0	1	6	0	3	0	0	0	0	0	0	0	2	4
Tegostoma comparalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Teleiodes luculella	52	54	7	3	4	9	5	22	0	4	3	41	54	30	1	2	12	5	18	24
Tethea ocularis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thalera fimbrialis	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Thaumetopoea pityocampa	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0
Thetidia smaragdaria	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Thumatha senex	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Timandra comae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trachea atriplicis	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Trachonitis cristella	10	3	1	6	2	0	6	4	2	6	2	4	7	8	3	0	4	2	3	8
Trichoplusia ni	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Tyta luctuosa	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	2
Udea ferrugalis	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Watsonalla binaria	5	0	0	0	0	1	0	1	1	0	0	0	1	0	0	0	0	0	0	0
Xestia c-nigrum	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Yponomeuta cf. cagnagella	6	9	1	0	0	7	1	1	9	9	8	7	12	12	6	1	0	1	7	20
Yponomeuta evonymella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Yponomeuta irrorella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Yponomeuta plumbella	0	0	0	0	0	6	1	10	10	17	11	1	7	5	2	2	11	4	7	35
Ypsolopha nemorella	23	4	1	2	0	4	0	1	3	1	4	0	11	4	5	1	2	3	0	4
Zebeeba falsalis	0	2	3	24	1	1	0	0	0	0	0	2	1	0	0	0	0	0	0	0
Zeiraphera griseana	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Zeuzera pyrina	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 6: Species A-Cha, Site V21-C10)

	V21	V22	V23	V24	V25	V26	V27	V28	V29	V30	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10
Abrostola asclepiadis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acentria ephemerella	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	0	12	13	0	2
Acleris kochiella	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
Acleris rhombana	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acleris variegana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acontia lucida	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Acontia trabealis	0	0	4	1	0	2	1	4	1	1	1	0	9	0	0	0	1	0	0	0
Acrobasis advenella	0	2	0	0	1	1	0	12	1	3	5	10	2	13	1	2	1	2	2	11
Acrobasis consociella	16	39	5	11	49	33	17	144	31	26	11	1	3	35	4	2	0	1	18	2
Acrobasis fallouella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acrobasis foroiuliensis	1	0	0	0	0	0	2	0	1	2	0	0	0	0	0	0	0	0	0	0
Acrobasis marmorea	1	0	0	0	0	0	0	1	3	3	0	0	0	0	0	0	0	0	0	0
Acrobasis suavella	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acronicta aceris	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
Acronicta cuspis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acronicta psi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acronicta rumicis	0	0	0	0	0	2	0	2	0	0	0	0	0	1	0	1	0	0	1	0
Aedia leucomelas	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
Agapeta hamana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Agapeta zoegana	8	2	2	2	0	4	2	3	0	9	0	2	0	0	0	3	0	0	1	0
Agdistis cf. tamaricis	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agriphila brioniellus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agriphila geniculea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agrotera nemoralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agrotis bigramma	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agrotis exclamationis	0	3	0	1	0	0	0	2	0	0	0	0	0	0	0	1	0	0	1	0
Agrotis ipsilon	0	0	0	0	0	0	0	0	0	1	1	1	0	1	0	1	0	0	1	1
Agrotis segetum	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0
Alabonia geoffrella	0	0	0	1	1	0	0	0	1	1	1	0	0	1	0	0	2	2	0	0
Aleimma loeflingiana	0	8	3	13	4	22	2	6	12	12	0	0	0	0	0	0	0	0	0	0
Amphipyra pyramidea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anacampsis populella	0	6	1	0	9	2	2	0	0	0	0	0	0	0	0	1	0	0	0	0
Anania crocealis	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0
Anarta trifolii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ancylis apicella	0	0	1	0	1	0	0	0	0	0	0	0	0	4	0	1	0	1	0	0
Ancylis mitterbacheriana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ancylis obtusana	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Ancylis selenana	3	0	28	0	13	3	6	1	0	2	4	2	1	102	1	2	5	3	24	0
Ancylis unculana	0	1	0	0	1	0	0	1	0	0	0	1	0	0	0	0	1	1	1	0
Apeira syringaria	0	0	0	0	0	0	0	2	0	1	1	0	2	0	0	4	0	0	1	0
Apoda limacodes	0	3	0	0	1	1	1	0	1	0	0	1	2	2	1	2	0	0	6	6
Araeopteron ecphaea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Archips betulana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Archips podana	31	17	13	10	28	10	23	20	9	13	17	25	19	23	11	21	13	11	46	5
Archips rosana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Archips xylosteana	0	2	2	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Arctia villica	0	13	0	6	0	7	3	11	7	4	2	5	9	6	2	5	4	11	8	7
Ascotis selenaria	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0
Athetis hospes	1	0	7	0	3	0	2	1	0	0	23	0	11	8	1	0	5	6	5	0
Autographa gamma	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bactra robustana	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Batia spec.	0	3	0	2	0	0	0	2	0	0	0	0	0	0	0	0	2	0	0	0
Blastobasis glandulella	0	0	0	0	1	0	0	6	4	1	2	0	0	3	0	1	2	1	1	0
Bucculatrix spec	0	32	3	0	4	2	3	22	0	0	0	0	0	127	0	0	0	0	0	9
Cacoecimorpha pronubana	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	0
Cadra figulilella	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Calamotropha paludella	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Callopistria juventina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Calophasia platyptera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Caloptilia alchimiella	0	2	0	3	2	3	0	0	2	0	0	0	1	0	0	0	4	0	3	1
Capperia cf. loranus	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Caradrina aspersa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Caradrina morpheus	0	2	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	0	0	0
Carcina quercana	0	14	0	1	3	0	0	0	2	1	0	0	0	4	0	0	1	1	1	0
Carpatolechia aenigma	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cataclysta lemnata	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Catarhoe rubidata	0	1	0	0	0	2	0	2	2	2	0	1	0	0	0	1	0	0	0	0
Catephia alchymista	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0
Catocala conversa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Catocala promissa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Catoptria falsella	0	0	1	0	0	1	0	0	0	0	2	5	0	11	2	0	1	1	1	4
Catoptria pinella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Celypha flavipalpana	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Cerura erminea	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Charanyca ferruginea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	6	1	0
Charanyca trigrammica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 7: Species Chi-Ep, Site V21-C10)

	V21	V22	V23	V24	V25	V26	V27	V28	V29	V30	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10
Chiasmia aestimaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chiasmia clathrata	0	1	5	1	3	0	1	0	1	0	8	0	5	0	16	1	0	2	1	2
Chilo luteellus	1	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
Chilo phragmitella	0	0	2	0	0	0	0	3	3	0	0	0	1	0	0	0	1	0	0	0
Chilodes maritima	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
Chloantha hyperici	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroclystis v-ata	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	1	0	1	0	2
Chrysocrambus linetella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chrysoteuchia culmella	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Cilix glaucata/hispanica	2	5	0	0	0	3	0	0	0	0	2	2	4	6	3	0	7	2	4	2
Clepsis consimilana	0	7	0	0	4	1	1	3	0	5	0	0	0	0	0	0	0	0	0	0
Clepsis rurinana	0	5	0	0	0	1	0	0	0	0	4	4	0	2	1	0	3	3	0	0
Clostera pigra	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Cnaemidophorus rhododactyla	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Cnephasia pasiuana	0	5	0	0	1	0	0	3	5	0	0	1	8	0	1	4	1	0	2	1
Coleophora cf. colutella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Colobochyla salicalis	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Comibaena bajularia	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	1
Conisania luteago	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Cosmia affinis	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Cosmia trapezina	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Cosmopterix lienigiella	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0
Cosmopterix orichalcea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cosmopterix scribaiella	0	1	0	1	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0
Cosmorhoe ocellata	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cossus cossus	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Costaconvexa polygrammata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Craniophora ligustri	0	0	0	0	0	0	1	0	0	0	0	0	1	1	0	2	1	4	4	2
Crocallis elinguaria	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
Crombrugghia distans/tristis	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0
Cryphia algae	0	0	0	0	0	0	1	5	0	0	0	0	0	0	0	0	1	0	0	0
Cryphia ochsi	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Cyclophora annularia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2
Cyclophora punctaria	0	0	0	0	2	1	0	6	0	0	0	0	0	0	0	0	0	0	0	0
Cyclophora puppillaria	0	1	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	3
Cydia amplana	5	0	5	2	3	6	5	0	1	4	8	0	2	0	2	1	0	1	0	0
Cydia fagiglandana	3	0	5	1	4	14	2	1	0	2	17	0	10	0	7	3	9	1	16	4
Cydia pomonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Deltote bankiana	0	0	1	0	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0
Deltote pygarga	24	10	9	3	8	3	5	11	16	5	7	7	4	26	10	15	18	23	49	2
Denticucullus pygmina	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0
Diaphora mendica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dichomeris alacella	7	0	4	0	44	6	14	30	0	17	3	0	4	17	4	0	1	4	43	5
Dichomeris derasella	0	1	8	0	3	1	4	2	0	0	0	0	2	4	0	0	1	0	9	0
Dichomeris marginella	0	0	0	0	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
Dioryctria abietella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dioryctria pinae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dioryctria sylvestrella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Ditula angustiorana	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Dolicharthria punctalis	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0	0	1	0
Donacaula forficella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Drymonia dodonaea	0	1	0	1	1	0	0	2	4	2	1	0	0	0	0	0	0	0	0	1
Duponchelia fovealis	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Dypterygia scabriuscula	0	1	0	0	0	0	0	2	1	0	0	5	2	4	0	0	1	0	3	0
Dysauxes ancilla	0	7	0	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0
Dysauxes famula	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Dysauxes punctata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dysgonia algira	0	0	1	0	0	0	1	1	0	0	0	0	0	1	1	0	1	0	0	0
Dyspessa ulula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Earias clorana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Earias vernana	0	1	1	2	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0
Eilema caniola	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0
Eilema complana	2	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0
Eilema depressa	2	12	0	0	1	0	0	9	3	0	0	0	11	5	0	7	12	16	3	2
Eilema sororcula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
Elaphria venustula	4	1	43	50	7	27	25	1	4	8	2	1	20	18	1	1	14	43	5	1
Elegia similella	0	0	2	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Ematheudes punctella	0	0	2	2	2	0	3	11	1	2	2	3	4	1	2	0	2	3	1	6
Emmelina monodactyla	0	0	1	0	0	0	0	0	0	0	0	3	0	2	0	1	0	2	0	0
Endotricha flammealis	0	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Epagoge grotiana	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Ephestia woodiella	0	60	2	3	2	28	6	117	5	1	34	13	308	9	8	11	24	9	17	91
Epiblema foenella	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Epicallima formosella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Epinotia festivana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Epione repandaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Epirrhoe cf. alternata	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 8: Species Et-Lo, Site V21-C10)

	V21	V22	V23	V24	V25	V26	V27	V28	V29	V30	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10
Ethmia bipunctella	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ethmia quadrillella	0	0	0	0	0	0	1	0	0	0	6	1	0	0	19	2	2	3	4	1
Ethmia terminella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Etiella zinckenella	0	0	0	1	0	0	0	1	0	0	0	0	5	0	0	0	0	3	2	33
Eublemma parva	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euchromius superbellus	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Eucosma cana	0	1	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0
Eucosma conterminana	7	2	2	2	3	9	16	0	1	4	0	0	0	2	1	0	0	0	2	0
Eucosma metzneriana	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eudonia delunella	1	0	0	3	0	0	0	2	0	0	0	0	1	0	0	0	4	1	0	1
Eudonia lacustrata	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Eudonia mercurella	0	3	0	2	2	7	0	5	0	2	4	6	3	14	13	1	11	2	4	5
Eudonia pallida	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	1
Eupithecia centaureata	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
Eupithecia haworthiata	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0
Eupithecia ultimaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euplagia quadripunctaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Euplexia lucipara	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euproctis chrysorrhoea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eutelia adulatrix	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0
Euzophera fuliginosella	0	2	1	0	1	0	0	0	3	1	1	0	0	6	0	1	3	0	7	2
Evergestis extimalis	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
Furcula bifida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Galleria mellonella	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Gastropacha quercifolia	3	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Glyptoteles leucacrinella	1	3	0	1	1	0	1	1	0	0	0	0	1	0	0	3	0	2	0	1
Gymnoscelis rufifasciata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gypsonoma aceriana	1	18	5	1	5	3	6	1	2	3	0	0	0	3	1	0	0	0	0	0
Gypsonoma minutana	0	22	2	1	22	2	0	11	0	2	0	0	0	0	2	3	0	1	0	0
Habrosyne pyritoides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Hadena bicruris	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Harpyia milhauseri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Hedya nubiferana	0	10	4	0	4	2	2	7	2	3	1	0	0	5	0	2	5	3	4	2
Hedya pruniana	0	1	1	0	5	3	0	3	4	1	0	0	0	0	0	0	0	1	0	0
Helicoverpa armigera	0	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0
Heliothis viriplaca	0	0	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0
Hellinsia cf. inulae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Hemistola chrysoprasaria	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Hemithea aestivaria	1	1	0	0	0	0	2	1	2	0	0	1	0	1	0	1	0	0	0	0
Herminia tarsicrinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Herminia tarsipennalis	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Herminia tenuialis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Heterogenea asella	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Homaloxestis briantiella	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
Homoeosoma sinuella	0	0	4	2	6	0	5	7	0	0	4	0	6	1	1	0	1	3	4	0
Hoplodrina ambigua	0	3	0	0	0	0	0	1	0	0	2	0	0	0	0	2	0	0	0	0
Horisme tersata	0	0	0	0	0	0	0	0	0	0	3	0	0	1	0	0	3	1	2	0
Horisme vitalbata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hypomecis punctinalis	1	0	0	2	2	0	0	5	0	1	6	7	13	20	5	7	5	5	0	1
Hypsopygia costalis	0	0	0	1	0	0	0	6	0	0	0	0	4	0	0	0	0	0	1	0
Hypsopygia glaucinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea aversata	0	9	0	2	0	3	0	5	3	4	1	2	8	0	0	5	1	1	0	1
Idaea degeneraria/rubraria	1	4	0	2	0	1	1	0	0	0	0	0	2	0	0	1	1	0	0	0
Idaea dimidiata	0	3	0	0	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	0
Idaea filicata	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
Idaea fuscovenosa	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea muricata	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Idaea politaria	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea rusticata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea seriata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea subsericeata	0	0	0	2	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0
Ipimorpha subtusa	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Isturgia arenacearia	0	0	2	0	1	0	1	0	0	0	0	0	28	0	0	0	4	10	0	0
Lacanobia oleracea	0	0	0	0	0	0	0	2	1	1	0	0	0	0	0	1	0	0	0	0
Lacanobia w-latinum	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0
Laelia coenosa	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Lamoria anella	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Laothoe populi	0	4	0	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0
Lasiocampa quercus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Laspeyria flexula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Leucania loreyi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leucania obsoleta	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0	2	0
Ligdia adustata	5	9	12	0	9	9	14	8	1	9	9	5	1	22	10	0	8	13	7	0
Lithosia quadra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lomaspilis marginata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
Lomographa bimaculata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
Loryma egregialis	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Loxostege sticticalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 9: Species Ly-Pe, Site V21-C10)

	V21	V22	V23	V24	V25	V26	V27	V28	V29	V30	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10
Lygephila craccae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lymantria dispar	2	1	2	5	4	3	4	0	1	3	3	0	0	0	3	0	2	0	0	4
Macaria alternata	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Macaria liturata	0	0	0	0	0	0	0	0	0	0	1	1	0	2	1	2	1	0	0	0
Macaria notata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Malacosoma castrensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mecyna asinalis	0	1	0	0	0	1	0	2	0	3	1	1	1	0	0	0	0	1	1	0
Meganola albula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Meganola togatulalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menophra abruptaria	0	1	0	1	0	2	0	0	0	0	1	0	0	0	1	2	1	0	0	1
Mesapamea secalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Metachrostis velox	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0
Metasia ophialis	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Metendothenia atropunctana	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Miltochrista miniata	0	5	1	1	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0
Mimas tiliae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Minoa murinata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Minucia lunaris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Moma alpium	0	0	0	0	1	0	0	1	0	0	0	1	0	1	0	1	1	0	1	0
Monopis monachella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Monopis obviella	0	0	1	0	4	0	0	0	0	0	0	3	4	1	0	0	0	1	5	2
Mormo maura	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Morophaga choragella	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Morophaga morella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Myelois circumvoluta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna albipuncta	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna congrua	0	0	0	0	0	0	0	2	0	0	1	0	1	0	0	0	0	0	1	0
Mythimna pallens	0	0	0	0	0	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0
Mythimna riparia	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Mythimna sicula	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Mythimna straminea	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
Mythimna turca	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	2	0
Mythimna vitellina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nephopterix angustella	0	0	0	1	0	0	0	2	0	0	2	0	0	1	0	1	0	0	1	0
Neurothaumasia ankerella	0	2	0	0	6	0	1	3	0	0	0	5	1	2	8	1	11	2	8	10
Noctua fimbriata	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Noctua janthina/janthe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Noctua pronuba	1	0	0	1	0	1	0	0	2	0	1	1	4	0	0	1	0	1	0	2
Noctua tirrenica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Nola aerugula	3	4	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	1	0
Nola chlamitulalis	2	0	0	0	2	6	0	8	12	3	0	0	0	0	0	0	1	0	0	0
Nomophila noctuella	1	0	2	7	2	1	0	8	0	4	5	1	8	0	18	1	0	3	5	3
Notocelia cynosbatella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Notocelia roborana	0	2	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
Notocelia rosaecolana/trimaculana	0	0	0	0	0	0	0	0	0	0	2	2	0	14	1	1	8	0	1	4
Notocelia uddmanniana	0	8	2	4	1	4	4	1	7	6	1	1	2	2	0	3	1	0	2	0
Notodonta tritophus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nyctegretis lineana	0	1	1	0	4	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0
Nycterosea obstipata	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0
Nyctobrya muralis	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Ochropleura plecta	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0
Ocneria rubea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oligia latruncula	0	1	0	0	0	0	0	1	2	0	0	0	0	0	0	0	2	1	0	0
Oncocera semirubella	1	5	3	2	20	2	3	15	0	0	18	3	59	2	9	0	5	7	13	3
Opisthograptis luteolata	0	3	1	1	0	0	0	0	0	0	0	1	1	0	0	4	13	6	1	1
Orgyia antiqua	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
Ostrinia nubilalis	0	0	0	1	0	2	0	40	1	0	0	12	11	5	3	1	2	2	7	0
Palpita vitrealis	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Pammene fasciana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pandemis cerasana	3	0	0	1	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
Pandemis heparana	5	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Paradoxus osyridellus	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Parahypopta caestrum	0	1	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Parapoynx stratiotata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Parascotia fuliginaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Paraswammerdamia albicapitella	2	0	1	0	8	3	4	2	0	1	0	0	0	0	0	0	4	0	2	0
Paraswammerdamia nebulella	5	17	20	10	22	25	8	13	0	10	0	14	6	38	4	16	14	11	19	7
Paratalanta pandalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Parectopa robiniella	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pasiphila chloerata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pasiphila rectangulata	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Pechipogo plumigeralis	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pediasia contaminella	1	1	0	1	0	1	0	0	5	0	0	0	1	0	0	2	0	0	0	1
Pelochrista mollitana	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Pelosia muscerda	2	1	0	0	0	1	0	1	1	0	0	0	1	1	0	0	0	0	1	0
Pempelia palumbella	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	3	0
Penestoglossa dardoinella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Peribatodes rhomboidaria	13	91	1	15	6	21	5	47	20	35	8	30	17	7	3	27	47	34	5	14
Peridea anceps	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Petrophora chlorosata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 10: Species Ph-Z, Site V21-C10)

	V21	V22	V23	V24	V25	V26	V27	V28	V29	V30	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10
Phalera bucephala	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
Phalonidia albipalpana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pheosia tremula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Philereme transversata	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Philereme vetulata	0	4	1	0	0	1	0	2	1	2	0	0	0	0	0	1	1	0	0	0
Photedes morrisii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phragmataecia castaneae	1	0	2	1	0	1	1	4	28	3	0	0	1	0	0	1	0	1	4	0
Phragmatobia fuliginosa	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	0
Phtheochroa pulvillana	0	3	2	5	9	3	4	1	2	3	2	1	1	2	3	0	12	5	3	7
Phycitodes binaevella	0	0	0	0	0	0	0	14	0	0	4	8	12	2	4	2	2	4	3	1
Phyllophila obliterata	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0
Phytometra viridaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Piniphila bifasciana	0	6	0	1	0	1	0	0	0	0	0	0	5	0	0	0	2	8	0	0
Platyptilia cf. farfarellus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Platytes alpinella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pleuropyta ruralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Plodia interpunctella	0	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0	0
Plutella xylostella	0	2	0	7	0	8	1	0	0	0	3	0	7	0	7	1	2	6	0	1
Polyphaenis sericata	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Propiromorpha rhodophana	4	4	18	0	2	5	4	1	1	2	3	6	1	2	2	0	0	5	2	1
Pseudargyrotoza conwagana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Pseudoips prasinana	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Pseudotelphusa scalella	4	1	3	3	5	9	14	137	1	8	0	2	4	3	3	0	4	0	8	4
Pterostoma palpina	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Pyralis farinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pyrausta aurata	1	1	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	1	0	1
Pyrausta despicata	0	0	0	0	0	1	0	3	0	0	0	0	1	0	0	1	0	0	0	1
Pyrausta purpuralis	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Pyroderces argyrogrammos	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0
Rhigognostis hufnagelii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Rhodometra sacraria	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0
Rhodophaea formosa	0	0	0	0	0	0	0	0	0	0	3	2	1	4	0	0	1	0	0	0
Rhyacionia buoliana/pinicolana	1	0	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	2	0	0
Rivula sericealis	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Schoenobius gigantella	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
Schrankia costaestrigalis	0	0	1	0	0	0	0	2	1	0	1	4	0	5	0	1	0	1	12	5
Sciota rhenella	1	1	0	0	14	1	0	1	0	0	0	0	0	1	0	0	0	0	2	0
Sclerocona acutella	2	0	2	6	1	0	3	1	1	3	0	0	2	0	0	4	0	0	0	0
Scoparia basistrigalis	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	3	1	1	1
Scopula emutaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scopula imitaria	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0	0	1	0	0	0
Scopula nigropunctata	0	4	1	0	0	0	3	0	0	0	2	6	9	3	1	3	2	2	27	0
Scopula rubiginata	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Scythropia crataegella	0	0	0	5	0	0	2	0	0	0	0	0	0	0	1	1	1	3	8	0
Senta flammea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sideridis rivularis	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Sitochroa palealis	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Spatalia argentina	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	1	0	0	0
Spilonota ocellana	0	0	0	2	1	0	1	0	3	0	0	0	0	1	2	1	0	0	1	0
Spilosoma lubricipeda	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spilosoma lutea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spodoptera exigua	10	1	89	0	133	1	21	8	0	0	0	0	5	28	0	1	0	0	87	0
Stauropus fagi	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0
Stegania trimaculata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Stemmatophora brunnealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Subacronicta megacephala	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Symmoca signatella	4	3	0	0	0	1	1	1	0	0	1	2	2	10	0	1	7	0	4	0
Synaphe punctalis	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tegostoma comparalis	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Teleiodes luculella	2	5	15	5	80	68	52	45	1	15	3	0	6	0	2	0	1	1	23	0
Tethea ocularis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Thalera fimbrialis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thaumetopoea pityocampa	1	0	0	0	0	0	0	0	0	0	25	1	1	0	2	0	0	0	0	0
Thetidia smaragdaria	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Thumatha senex	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Timandra comae	0	0	0	0	1	0	0	5	0	0	2	5	6	0	0	0	0	0	0	0
Trachea atriplicis	0	0	0	0	0	0	0	1	0	0	0	0	1	2	0	0	0	0	0	0
Trachonitis cristella	0	6	5	3	10	4	6	10	3	5	13	7	21	16	20	0	6	14	1	4
Trichoplusia ni	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tyta luctuosa	0	0	0	0	0	0	0	1	0	1	0	0	4	0	0	0	0	1	0	1
Udea ferrugalis	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0
Watsonalla binaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2
Xestia c-nigrum	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	1
Yponomeuta cf. cagnagella	2	9	0	6	8	4	2	76	13	4	1	0	1	1	0	0	2	4	1	0
Yponomeuta evonymella	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Yponomeuta irrorella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
Yponomeuta plumbella	5	8	6	1	12	0	2	2	0	3	1	4	2	9	2	4	0	0	0	0
Ypsolopha nemorella	1	7	1	0	3	0	2	1	0	4	0	3	0	0	3	0	2	0	0	1
Zebeeba falsalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Zeiraphera griseana	0	0	0	0	0	1	0	0	0	0	4	0	0	0	0	0	0	0	0	0
Zeuzera pyrina	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 11: Species A-Cha, Site C11-C30)

	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30
Abrostola asclepiadis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acentria ephemerella	5	0	0	0	0	3	11	0	0	1	0	1	7	3	3	0	43	0	0	0
Acleris kochiella	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Acleris rhombana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acleris variegana	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Acontia lucida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acontia trabealis	0	1	0	4	4	0	0	0	0	0	0	0	1	0	0	1	3	0	1	0
Acrobasis advenella	0	11	0	9	1	0	4	2	5	0	0	1	3	4	2	0	0	1	2	4
Acrobasis consociella	0	8	2	2	1	4	4	1	30	2	3	0	7	6	2	1	2	1	1	2
Acrobasis fallouella	0	0	0	0	0	0	0	4	0	0	0	1	0	0	2	33	2	0	0	0
Acrobasis foroiuliensis	0	1	0	1	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0
Acrobasis marmorea	0	1	0	2	0	0	0	0	1	0	7	0	1	0	1	0	0	0	0	0
Acrobasis suavella	0	0	0	1	0	0	0	0	0	2	0	0	3	0	2	0	0	0	0	0
Acronicta aceris	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	2	0	0	0
Acronicta cuspis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acronicta psi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0
Acronicta rumicis	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Aedia leucomelas	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agapeta hamana	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Agapeta zoegana	0	2	0	0	3	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Agdistis cf. tamaricis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agriphila brioniellus	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Agriphila geniculea	0	0	0	0	0	0	1	0	0	0	0	0	0	0	3	0	0	0	0	0
Agrotera nemoralis	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
Agrotis bigramma	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Agrotis exclamationis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agrotis ipsilon	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0
Agrotis segetum	0	5	0	3	0	0	0	0	3	0	0	0	0	0	0	1	0	3	1	1
Alabonia geoffrella	0	0	0	0	0	3	0	0	0	0	2	0	0	0	1	0	0	1	2	0
Aleimma loeflingiana	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Amphipyra pyramidea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anacampsis populella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anania crocealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anarta trifolii	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ancylis apicella	1	0	0	0	0	1	0	1	0	8	0	1	2	0	0	1	4	0	0	0
Ancylis mitterbacheriana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ancylis obtusana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ancylis selenana	7	0	0	0	6	82	0	14	4	3	0	7	2	1	1	7	3	0	0	1
Ancylis unculana	1	1	0	0	1	0	0	1	0	0	0	0	3	0	0	1	0	0	0	0
Apeira syringaria	0	2	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1
Apoda limacodes	1	0	0	0	0	0	0	0	1	0	4	1	3	1	8	0	0	3	1	1
Araeopteron ecphaea	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Archips betulana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Archips podana	10	16	7	1	4	27	3	27	6	10	10	10	10	0	5	41	27	6	0	7
Archips rosana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Archips xylosteana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Arctia villica	3	0	6	0	6	1	1	0	3	1	16	0	74	1	10	0	1	3	1	4
Ascotis selenaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Athetis hospes	0	1	1	0	3	0	0	0	0	0	0	1	0	0	0	0	4	0	0	0
Autographa gamma	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Bactra robustana	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Batia spec.	0	1	0	2	0	3	0	0	2	0	0	0	0	0	1	0	1	0	0	0
Blastobasis glandulella	0	11	0	10	0	8	2	0	1	0	0	0	0	1	0	0	0	49	9	19
Bucculatrix spec	0	0	0	0	0	0	0	0	11	0	0	0	3	0	1	0	0	8	0	0
Cacoecimorpha pronubana	0	0	0	0	0	0	3	0	0	0	0	0	0	1	0	0	1	0	0	0
Cadra figulilella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Calamotropha paludella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Callopistria juventina	0	0	0	0	0	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Calophasia platyptera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Caloptilia alchimiella	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	2	0	0
Capperia cf. loranus	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Caradrina aspersa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Caradrina morpheus	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Carcina quercana	1	0	0	1	0	0	1	0	5	0	0	0	7	0	1	2	0	1	0	1
Carpatolechia aenigma	0	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cataclysta lemnata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Catarhoe rubidata	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
Catephia alchymista	0	0	0	2	0	0	0	0	0	0	4	1	0	0	0	1	0	1	0	0
Catocala conversa	0	2	0	0	0	0	0	0	1	0	1	0	2	0	0	0	0	0	2	2
Catocala promissa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Catoptria falsella	0	1	0	0	1	0	3	1	1	0	0	0	3	0	0	0	2	2	1	0
Catoptria pinella	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Celypha flavipalpana	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cerura erminea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Charanyca ferruginea	1	0	0	0	0	0	1	0	0	0	1	0	3	0	0	0	0	1	0	0
Charanyca trigrammica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0

Appendix 7.1: Moth species abundance matrix (Part 12: Species Chi-Ep, Site C11-C30)

	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30
Chiasmia aestimaria	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chiasmia clathrata	0	0	6	0	11	0	0	0	3	0	0	0	1	2	0	0	0	0	0	0
Chilo luteellus	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Chilo phragmitella	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chilodes maritima	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloantha hyperici	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroclystis v-ata	0	1	0	0	0	1	0	0	2	0	2	0	4	0	0	1	1	0	0	1
Chrysocrambus linetella	1	1	0	1	0	0	0	0	5	0	2	0	0	0	1	1	1	0	0	0
Chrysoteuchia culmella	1	3	0	6	0	4	0	0	35	0	67	0	36	1	13	39	0	1	1	11
Cilix glaucata/hispanica	0	14	5	3	1	1	0	0	2	2	1	1	2	0	0	0	0	1	0	2
Clepsis consimilana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Clepsis rurinana	0	1	0	1	0	0	1	0	0	3	0	0	0	0	0	1	0	0	0	0
Clostera pigra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Cnaemidophorus rhododactyla	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cnephasia pasiuana	0	0	1	0	0	1	0	0	0	0	2	0	6	0	5	0	3	3	3	0
Coleophora cf. colutella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Colobochyla salicalis	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Comibaena bajularia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Conisania luteago	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cosmia affinis	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Cosmia trapezina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
Cosmopterix lienigiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cosmopterix orichalcea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cosmopterix scribaiella	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0
Cosmorhoe ocellata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cossus cossus	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
Costaconvexa polygrammata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Craniophora ligustri	0	1	0	0	2	0	1	1	2	0	2	0	3	0	3	0	3	1	0	1
Crocallis elinguaria	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
Crombrugghia distans/tristis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Cryphia algae	0	0	0	0	3	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0
Cryphia ochsi	0	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyclophora annularia	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0	1	0	1	0	2
Cyclophora punctaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyclophora puppillaria	0	3	0	3	0	0	1	1	8	0	1	0	3	1	2	2	0	1	0	3
Cydia amplana	0	0	0	1	18	7	12	1	0	2	0	0	0	0	1	6	3	1	0	0
Cydia fagiglandana	1	3	0	1	19	2	35	0	3	0	0	0	4	0	5	3	2	4	0	2
Cydia pomonella	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Deltote bankiana	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Deltote pygarga	29	8	8	0	0	49	10	11	1	28	3	40	8	1	2	7	59	0	0	0
Denticucullus pygmina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Diaphora mendica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dichomeris alacella	6	11	0	7	0	0	0	0	3	0	0	0	2	0	0	2	1	2	0	0
Dichomeris derasella	0	4	0	0	0	0	0	0	2	0	0	0	1	0	2	0	1	0	0	0
Dichomeris marginella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dioryctria abietella	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Dioryctria pinae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dioryctria sylvestrella	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ditula angustiorana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dolicharthria punctalis	0	4	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0
Donacaula forficella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Drymonia dodonaea	1	0	0	0	0	0	0	0	0	1	0	0	1	0	4	0	0	6	2	1
Duponchelia fovealis	0	0	1	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
Dypterygia scabriuscula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Dysauxes ancilla	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dysauxes famula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dysauxes punctata	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Dysgonia algira	1	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Dyspessa ulula	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Earias clorana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Earias vernana	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Eilema caniola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eilema complana	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Eilema depressa	1	8	1	8	0	7	0	0	33	0	9	0	53	0	7	9	7	0	0	2
Eilema sororcula	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	1	0	0
Elaphria venustula	0	1	3	1	0	11	6	0	6	2	1	0	3	1	0	2	4	0	0	0
Elegia similella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ematheudes punctella	0	7	4	10	2	0	0	0	9	0	0	1	5	5	0	1	0	0	1	1
Emmelina monodactyla	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Endotricha flammealis	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	4	1	2	0	0
Epagoge grotiana	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ephestia woodiella	1	166	5	33	14	0	0	0	49	0	33	2	23	24	4	6	3	49	24	33
Epiblema foenella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Epicallima formosella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Epinotia festivana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
Epione repandaria	1	0	0	2	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0	2
Epirrhoe cf. alternata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 13: Species Et-Lo, Site C11-C30)

	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30
Ethmia bipunctella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ethmia quadrillella	0	0	1	1	0	4	8	1	1	0	2	0	2	0	9	1	3	0	0	1
Ethmia terminella	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
Etiella zinckenella	0	15	6	12	0	0	0	0	2	0	0	0	1	3	0	0	0	6	2	1
Eublemma parva	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euchromius superbellus	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Eucosma cana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eucosma conterminana	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Eucosma metzneriana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eudonia delunella	0	1	0	0	0	4	0	1	8	0	4	1	3	0	0	0	0	0	0	0
Eudonia lacustrata	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Eudonia mercurella	3	21	1	26	9	1	5	1	23	0	87	1	87	11	22	1	1	31	18	56
Eudonia pallida	0	0	0	0	1	4	0	0	3	0	0	0	1	0	0	0	0	0	1	0
Eupithecia centaureata	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Eupithecia haworthiata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eupithecia ultimaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euplagia quadripunctaria	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	1	0
Euplexia lucipara	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euproctis chrysorrhoea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eutelia adulatrix	0	0	0	0	0	0	0	0	2	0	0	0	3	1	0	0	0	0	0	1
Euzophera fuliginosella	0	1	0	0	0	2	0	1	1	0	2	0	0	0	3	0	5	0	0	0
Evergestis extimalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Furcula bifida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Galleria mellonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gastropacha quercifolia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Glyptoteles leucacrinella	0	0	0	2	0	1	0	0	1	0	7	0	11	0	0	2	0	3	0	0
Gymnoscelis rufifasciata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Gypsonoma aceriana	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	3	0	0	0
Gypsonoma minutana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
Habrosyne pyritoides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hadena bicruris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Harpyia milhauseri	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hedya nubiferana	2	4	1	0	0	0	2	0	3	1	13	0	12	0	3	3	0	12	2	0
Hedya pruniana	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Helicoverpa armigera	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Heliothis viriplaca	0	0	0	1	3	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0
Hellinsia cf. inulae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hemistola chrysoprasaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hemithea aestivaria	2	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	1	0	0	0
Herminia tarsicrinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Herminia tarsipennalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Herminia tenuialis	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Heterogenea asella	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Homaloxestis briantiella	0	0	0	8	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	2
Homoeosoma sinuella	0	3	0	3	2	0	0	0	3	0	0	0	2	1	1	0	1	1	0	2
Hoplodrina ambigua	0	2	1	0	0	0	0	0	1	0	1	0	1	0	0	0	0	0	0	0
Horisme tersata	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Horisme vitalbata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hypomecis punctinalis	0	8	2	4	0	1	0	4	6	3	1	2	3	1	1	4	4	11	0	8
Hypsopygia costalis	0	1	0	0	0	0	0	0	4	0	0	0	0	0	0	1	0	0	0	0
Hypsopygia glaucinalis	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Idaea aversata	1	2	1	3	2	4	3	0	6	0	5	0	11	0	9	4	3	5	1	2
Idaea degeneraria/rubraria	1	0	0	1	0	0	5	0	0	0	5	0	3	0	4	0	1	2	0	0
Idaea dimidiata	0	10	0	1	1	0	0	1	0	0	0	0	2	0	0	0	0	2	0	2
Idaea filicata	0	0	1	0	1	0	4	0	0	0	0	0	0	0	1	0	0	1	0	0
Idaea fuscovenosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea muricata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea politaria	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea rusticata	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	1
Idaea seriata	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea subsericeata	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Ipimorpha subtusa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Isturgia arenacearia	0	0	1	0	0	1	4	1	1	0	0	0	1	0	0	1	1	0	0	1
Lacanobia oleracea	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lacanobia w-latinum	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	1	0	0	0
Laelia coenosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lamoria anella	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Laothoe populi	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lasiocampa quercus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Laspeyria flexula	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Leucania loreyi	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leucania obsoleta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ligdia adustata	2	6	6	4	3	3	2	1	0	4	2	0	0	3	0	0	0	4	0	0
Lithosia quadra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lomaspilis marginata	0	0	0	1	0	0	0	1	0	0	2	0	0	0	1	0	1	0	0	0
Lomographa bimaculata	0	0	1	2	0	1	2	0	1	0	3	0	3	0	0	0	0	6	3	1
Loryma egregialis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Loxostege sticticalis	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 14: Species Ly-Pe, Site C11-C30)

	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30
Lygephila craccae	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lymantria dispar	11	0	6	1	1	1	6	10	2	2	7	5	1	3	3	6	1	0	1	1
Macaria alternata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Macaria liturata	3	0	0	1	0	0	4	8	3	3	3	3	4	1	3	2	15	1	0	4
Macaria notata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Malacosoma castrensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mecyna asinalis	0	1	1	0	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0
Meganola albula	0	0	0	0	0	0	0	0	0	2	2	0	0	0	0	0	2	0	0	0
Meganola togatulalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menophra abruptaria	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0
Mesapamea secalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Metachrostis velox	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Metasia ophialis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Metendothenia atropunctana	0	0	0	0	0	4	0	1	0	1	0	1	0	1	0	5	1	0	0	0
Miltochrista miniata	0	5	0	2	0	3	0	0	2	0	1	0	7	0	1	4	3	0	0	0
Mimas tiliae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Minoa murinata	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Minucia lunaris	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
Moma alpium	0	1	0	0	0	1	0	0	4	0	3	0	1	0	1	3	1	0	0	0
Monopis monachella	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Monopis obviella	0	2	0	0	1	0	1	0	4	0	2	1	1	0	4	0	0	0	0	0
Mormo maura	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Morophaga choragella	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Morophaga morella	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Myelois circumvoluta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna albipuncta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna congrua	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna pallens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna riparia	0	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0	0	0	0
Mythimna sicula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna straminea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna turca	0	0	1	0	0	0	0	0	0	0	3	0	1	0	0	0	0	0	0	1
Mythimna vitellina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nephopterix angustella	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Neurothaumasia ankerella	0	1	0	6	2	1	2	0	3	0	0	0	2	0	0	0	2	0	2	0
Noctua fimbriata	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Noctua janthina/janthe	0	4	0	1	0	0	1	0	0	0	0	0	0	2	0	1	0	0	0	0
Noctua pronuba	0	1	2	0	0	0	1	0	0	0	1	0	0	0	0	0	0	3	0	0
Noctua tirrenica	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nola aerugula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nola chlamitulalis	1	23	0	0	5	2	0	0	3	0	0	0	0	0	0	2	4	3	1	0
Nomophila noctuella	0	0	15	13	0	0	1	1	2	1	0	1	4	9	0	0	1	0	0	0
Notocelia cynosbatella	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Notocelia roborana	0	1	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1	2	0	0
Notocelia rosaecolana/trimaculana	3	0	1	5	0	14	0	0	7	0	8	1	7	1	2	0	0	2	1	0
Notocelia uddmanniana	3	3	1	0	1	0	0	0	5	0	3	0	5	0	0	0	2	4	0	1
Notodonta tritophus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nyctegretis lineana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nycterosea obstipata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nyctobrya muralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ochropleura plecta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ocneria rubea	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Oligia latruncula	1	0	1	0	0	0	2	1	0	0	0	0	2	0	0	0	0	2	0	0
Oncocera semirubella	4	30	6	1	50	2	1	0	2	0	0	0	1	2	5	4	4	5	1	4
Opisthograptis luteolata	3	4	0	0	1	2	1	0	2	0	3	0	13	0	2	3	0	2	2	0
Orgyia antiqua	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ostrinia nubilalis	0	7	0	1	0	0	3	0	1	0	0	0	1	0	1	0	0	0	0	0
Palpita vitrealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pammene fasciana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pandemis cerasana	2	0	0	0	0	1	0	1	0	0	4	0	0	0	0	0	0	0	0	0
Pandemis heparana	3	0	1	0	0	8	0	0	0	2	1	0	0	0	0	0	0	0	0	0
Paradoxus osyridellus	0	0	0	0	0	0	2	2	0	0	0	1	0	0	1	1	2	0	0	0
Parahypopta caestrum	0	0	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Parapoynx stratiotata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Parascotia fuliginaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Paraswammerdamia albicapitella	0	0	3	0	0	2	0	2	0	1	0	0	0	0	0	0	0	0	0	0
Paraswammerdamia nebulella	6	0	9	7	3	8	0	2	8	0	0	0	6	2	2	0	3	0	1	0
Paratalanta pandalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Parectopa robiniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pasiphila chloerata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pasiphila rectangulata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pechipogo plumigeralis	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pediasia contaminella	0	1	0	2	0	0	0	0	3	1	1	1	1	0	0	0	0	1	0	1
Pelochrista mollitana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Pelosia muscerda	0	1	0	0	0	0	0	0	1	0	1	0	5	0	0	3	7	0	0	0
Pempelia palumbella	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Penestoglossa dardoinella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Peribatodes rhomboidaria	33	24	25	60	9	29	28	18	64	0	97	0	105	5	28	66	7	22	5	21
Peridea anceps	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Petrophora chlorosata	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0

Appendix 7.1: Moth species abundance matrix (Part 15: Species Ph-Z, Site C11-C30)

	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30
Phalera bucephala	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phalonidia albipalpana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pheosia tremula	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Philereme transversata	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Philereme vetulata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Photedes morrisii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phragmataecia castaneae	0	1	2	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
Phragmatobia fuliginosa	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0	0	0
Phtheochroa pulvillana	3	1	2	2	1	0	0	0	0	1	0	0	2	0	0	0	0	2	0	1
Phycitodes binaevella	1	0	0	1	2	0	4	0	0	1	1	0	2	4	1	0	0	6	0	0
Phyllophila obliterata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phytometra viridaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Piniphila bifasciana	0	2	1	0	0	3	0	0	2	0	0	0	0	0	0	0	1	0	0	0
Platyptilia cf. farfarellus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Platytes alpinella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
Pleuropyta ruralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Plodia interpunctella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Plutella xylostella	0	1	3	0	2	3	1	0	3	1	0	0	1	0	0	4	7	0	0	0
Polyphaenis sericata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	0	0	0	0
Propiromorpha rhodophana	1	1	3	0	0	0	0	0	0	1	0	1	0	1	0	1	0	1	1	1
Pseudargyrotoza conwagana	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pseudoips prasinana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pseudotelphusa scalella	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	3	0	1
Pterostoma palpina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pyralis farinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pyrausta aurata	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0
Pyrausta despicata	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Pyrausta purpuralis	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0
Pyroderces argyrogrammos	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
Rhigognostis hufnagelii	0	0	1	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Rhodometra sacraria	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	3	1	0	0	0
Rhodophaea formosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Rhyacionia buoliana/pinicolana	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	4	0	0	0
Rivula sericealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0
Schoenobius gigantella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Schrankia costaestrigalis	0	6	0	3	0	0	0	1	0	0	0	0	0	0	0	2	0	1	0	1
Sciota rhenella	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Sclerocona acutella	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
Scoparia basistrigalis	8	0	0	3	0	8	2	4	5	0	19	0	23	2	3	3	1	7	1	0
Scopula emutaria	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scopula imitaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scopula nigropunctata	0	5	1	4	0	4	3	1	0	0	3	0	2	0	1	1	2	1	0	1
Scopula rubiginata	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Scythropia crataegella	1	1	9	2	4	45	3	8	7	4	0	0	0	1	0	4	4	0	0	0
Senta flammea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sideridis rivularis	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sitochroa palealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spatalia argentina	0	0	0	3	0	0	2	0	0	0	4	1	2	1	4	0	1	10	4	8
Spilonota ocellana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spilosoma lubricipeda	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spilosoma lutea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spodoptera exigua	8	1	0	0	0	10	1	3	0	11	0	3	0	0	0	31	44	4	0	0
Stauropus fagi	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0	0	0	2
Stegania trimaculata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stemmatophora brunnealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Subacronicta megacephala	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Symmoca signatella	5	1	0	0	0	7	1	0	3	0	12	1	16	0	4	29	1	0	1	2
Synaphe punctalis	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tegostoma comparalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Teleiodes luculella	1	0	0	2	1	13	0	0	0	0	0	0	0	0	0	3	0	1	0	0
Tethea ocularis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Thalera fimbrialis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thaumetopoea pityocampa	2	0	8	0	1	2	0	0	0	0	0	0	0	0	0	0	4	0	0	0
Thetidia smaragdaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thumatha senex	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Timandra comae	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1
Trachea atriplicis	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
Trachonitis cristella	0	1	1	7	1	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0
Trichoplusia ni	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tyta luctuosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	1
Udea ferrugalis	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Watsonalla binaria	4	5	0	1	3	1	1	2	3	4	4	4	5	0	1	18	3	1	0	8
Xestia c-nigrum	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	1
Yponomeuta cf. cagnagella	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Yponomeuta evonymella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Yponomeuta irrorella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Yponomeuta plumbella	0	0	2	2	0	0	0	0	0	1	0	0	0	0	0	3	1	0	0	1
Ypsolopha nemorella	1	12	1	1	0	0	0	0	2	0	0	0	2	2	2	0	0	1	0	0
Zebeeba falsalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Zeiraphera griseana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Zeuzera pyrina	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 7.2: Factor loadings of the two PCA-analyses of local and landscape factors. Loadings <-0.5 and >0.5 are marked in bold.

Local factors	SHN	Old, open forest	Plant diversity	Conifer sites/ Herb beta diversity	Tree health
Plant species richness	0.25	0.23	**0.64**	-0.06	0.20
Functional dispersion of plants	-0.17	0.00	**0.81**	0.14	-0.14
Herb layer heterogeneity	-0.14	-0.17	-0.05	**0.65**	0.43
Shrub layer heterogeneity	-0.24	-0.24	**0.60**	-0.05	0.21
Ellenberg indicator "Nutrients"	**0.86**	0.13	-0.05	-0.08	0.11
Ellenberg indicator "Humidity"	**0.87**	0.14	-0.20	-0.06	0.04
Ellenberg indicator "Temperature"	**-0.51**	-0.32	0.09	0.12	0.38
Forest density	0.12	**-0.87**	-0.11	0.26	0.07
Crown density	**0.77**	-0.25	-0.04	0.22	-0.04
Cover of deciduous trees	0.42	-0.08	**-0.56**	-0.20	0.12
Cover of conifer trees	-0.01	0.09	0.37	**0.81**	-0.23
Mean basal area	0.21	**0.82**	0.02	0.34	-0.20
Standard deviation of basal areas	0.13	**0.58**	-0.15	**0.59**	0.04
Proportion of dead trees	-0.09	0.08	-0.05	0.01	**-0.83**
Landscape factors	Habitat diversity	Edges/ modified areas	Landscape diversity	Landscape heterogeneity	Open habitats
Distance to edges	-0.17	**-0.9**	-0.14	0.07	0.10
Distance to canals	**-0.66**	-0.11	-0.09	**-0.56**	0.12
Distance to industry	**-0.75**	0.05	-0.18	-0.08	-0.23
Diversity of natural habitats (200m)	**0.76**	0.25	0.21	0.18	0.39
Proportion of open habitats (200m)	0.14	-0.05	-0.02	0.13	**0.96**
Proportion of reed habitats (200m)	**0.75**	0.20	0.31	0.13	-0.14
Edge density (500m)	0.27	0.32	0.27	**0.76**	0.20
Diversity of natural habitats (500m)	0.47	0.51	**0.59**	0.26	0.09
Edge density (1000m)	0.13	0.03	0.15	**0.92**	0.09
Diversity of natural habitats (1000m)	0.36	0.36	**0.80**	0.21	0.00
Proportion of forest areas (1000m)	-0.31	**-0.76**	-0.48	-0.16	0.07
Proportion of open areas (1000m)	0.09	0.13	**0.64**	0.33	0.20
Proportion of reed areas (1000m)	0.21	-0.12	**0.87**	0.00	-0.14
Proportion of modified areas (1000m)	-0.08	**0.85**	-0.13	0.29	0.10

Appendix 7.3: Main results of linear mixed effects models, relating moth species diversity (upper part) or residual moth numbers caught in light-traps (lower part) at 60 sites in two nature reserves in NE Italy to descriptors of local habitat quality or landscape context of light-trap sites. Landscape predictors have white background, while local predictors have light-grey background. Models were constructed either using individual predictors separately, or in a multivariate regression approach. In the latter case, best model selection was done via AIC. Statistically significant effects ($p<0.05$) printed in bold face.

Model type	**Predictor**	**t-value**	**p-value**	**Regression coefficient (β)**	**Marginal R^2**	**Conditional R^2**
Moth diversity (Shannon index) related to individual predictors	**Habitat diversity**	**2.22**	**0.03**	**0.27**	**0.07**	**0.19**
	Landscape diversity	-1.81	0.08	-0.23	0.05	0.23
	Forest edges/ modified areas	0.44	0.66	0.05	0.003	0.17
	Landscape heterogeneity	1.69	0.1	0.21	0.04	0.21
	Open sites	1.44	0.16	0.18	0.03	0.18
	SHN	**3.10**	**0.003**	**0.36**	**0.13**	**0.22**
	Old, open forest	0.47	0.64	0.06	0.003	0.17
	Plant diversity	**2.02**	**0.05**	**0.24**	**0.06**	**0.21**
	Conifer sites	-1.39	0.17	-0.17	0.03	0.22
	Tree health	-1.26	0.21	-0.16	0.02	0.19
Best model						
	+SHN	**3.31**	**0.002**	**0.38**		
	+Plant diversity	**2.35**	**0.02**	**0.26**	**0.21**	**0.27**
Model type	**Predictor**	**t-value**	**p-value**	**Regression coefficient (β)**	**Marginal R^2**	**Conditional R^2**
Moth numbers (residuals) related to individual predictors	Habitat diversity	-0.04	0.97	-0.03	0.00001	0.00001
	Landscape diversity	**3.25**	**0.002**	**0.29**	**0.08**	**0.08**
	Forest edges/ modified areas	0.45	0.66	0.04	0.002	0.002
	Landscape heterogeneity	-0.5	0.62	-0.05	0.002	0.002
	Open habitats	-0.58	0.56	-0.05	0.003	0.003
	SHN	1.16	0.25	0.11	0.01	0.01
	Old, open forest	0.09	0.93	0.008	0.00006	0.00006
	Plant diversity	1.17	0.25	0.11	0.01	0.01
	Conifer sites	0.44	0.66	0.04	0.002	0.002
	Tree health	-0.49	0.62	-0.05	0.002	0.002
Best model						
	+Landscape diversity	**3.66**	**0.0004**	**0.33**		
	+SHN	**2.02**	**0.05**	**0.18**	**0.11**	**0.11**

Appendix 8.1: Indicator moth species for the two forest reserve fragments. The value behind each species' name is the indicator value, given by the indval-function in the labdsv package (Roberts 2016). Listed species all had a probability >0.05 to appear preferentially in one reserve. Species that were exclusively found in only one reserve are marked in bold face.

PsV indicator species		PdC indicator species	
Teleiodes luculella	0.89	***Eudonia mercurella***	0.85
Acrobasis consociella	0.87	*Hypomecis punctinalis*	0.66
Yponomeuta cf. *cagnagella*	0.82	*Notocelia rosaecolana/trimaculana*	0.65
Pseudotelphusa scalella	0.81	***Scoparia basistrigalis***	0.63
Clepsis consimilana	0.70	*Ethmia quadrillella*	0.58
Paraswammerdamia nebulella	0.66	*Macaria liturata*	0.56
Yponomeuta plumbella	0.64	*Watsonalla binaria*	0.56
Aleimma loeflingiana	0.63	*Scopula nigropunctata*	0.56
Gypsonoma aceriana	0.62	*Scythropia crataegella*	0.54
Agapeta zoegana	0.58	*Opisthograptis luteolata*	0.51
Ligdia adustata	0.58	*Catoptria falsella*	0.48
Ypsolopha nemorella	0.56	***Spatalia argentina***	0.47
Dichomeris alacella	0.53	*Chrysoteucha culmella*	0.46
Caloptilia alchimiella	0.53	*Phycitodes binaevella*	0.46
Pandemis cerasana	0.51	*Lomographa bimaculata*	0.40
Notocelia uddmanniana	0.50	*Chloroclystis v-ata*	0.39
Dysauxes ancilla	0.50	*Schrankia costaestrigalis*	0.37
Gypsonoma minutana	0.50	*Etiella zinckenella*	0.37
Hedya pruniana	0.49	*Cyclophora puppillaria*	0.36
Cyclophora punctaria	0.47	*Isturgia arenacearia*	0.36
Pandemis heparana	0.46	*Ancylis apicella*	0.34
Phragmataecia castaneae	0.44	*Thaumetopoea pityocampa*	0.28
Nola aerugula	0.42	***Cyclophora annularia***	0.23
Euchromius superbellus	0.37	***Eutelia adulatrix***	0.23
Paraswammerdamia albicapitella	0.35	***Horisme tersata***	0.23
Phileremevetulata	0.34	***Catocala conversa***	0.20
Eucosma conterminana	0.34	***Pempelia palumbella***	0.20
Sclerocona acutella	0.33	*Mythimna turca*	0.19
Anacampsis populella	0.32	*Epione repandaria*	0.19
Acrobasis foroiuliensis	0.31	***Acronicta aceris***	0.17
Archips xylosteana	0.30		
Celypha flavipalpana	0.29		
Sciota rhenella	0.29		
Earias vernana	0.28		
Lamoria anella	0.27		
Synaphe punctalis	0.26		
Carpatolechia aenigma	0.26		
Elegia similella	0.25		
Eudonia lacustrata	0.24		
Metachrostis velox	0.24		
Abrostola asclepiadis	0.23		
Zebeeba falsalis	0.23		
Agrotis exclamationis	0.23		
Nyctegretis lineana	0.20		
Herminia tarsipennalis	0.17		
Schoenobius gigantella	0.17		

Appendix 8.2: Overview over the factor loadings obtained in the three local factor PCAs. Values of <-0.5 or >0.5 are marked in bold. λ: eigenvalues of the respective PC-axes.

Local factors (PsV)	Old, open forest λ=2.84	Plant species diversity λ=2.46	Humidity-nutrient-gradient λ=2.45	Herb-layer heterogeneity λ=1.69	Tree health λ=1.16
Plant species richness	0.03	0.47	0.41	0.09	-0.35
Functional dispersion of plant species	-0.03	**0.87**	-0.12	-0.03	0.03
Herb layer heterogeneity	0.04	-0.01	0.16	**0.87**	-0.07
Shrub layer heterogeneity	-0.45	**0.61**	-0.14	0.27	0.00
Ellenberg indicator “Humidity”	0.14	-0.29	**0.89**	0.05	0.05
Ellenberg indicator “Nutrients”	0.07	-0.02	**0.89**	-0.04	0.00
Ellenberg indicator “Temperature”	**-0.53**	**0.50**	-0.42	0.04	-0.20
Forest density	**-0.84**	-0.20	0.02	0.28	0.16
Canopy density	-0.16	-0.06	**0.66**	0.45	-0.01
Cover of deciduous trees	-0.26	**-0.76**	0.12	-0.02	-0.10
Cover of conifer trees	0.42	0.37	-0.08	**0.66**	0.18
Mean basal area	**0.89**	-0.09	0.08	0.22	0.03
Standard deviation of basal area	**0.75**	0.04	0.00	0.28	0.22
% dead standing trees	0.08	0.06	0.04	0.01	**0.93**
Local factors (only PdC)	Humidity-nutrient-gradient λ=3.44	Dense, young forest λ=2.27	Conifer cover λ=2.03	Heterogeneous, warm forest λ=1.63	Plant diversity λ=1.39
Plant species richness	0.05	-0.17	0.34	-0.07	**0.70**
Functional dispersion of plants	-0.31	-0.09	**0.75**	-0.22	0.13
Herb layer heterogeneity	-0.45	**0.66**	-0.03	0.26	-0.02
Shrub layer heterogeneity	-0.33	0.14	-0.09	-0.12	**0.78**
Ellenberg indicator “Humidity”	**0.87**	-0.03	-0.18	0.05	-0.05
Ellenberg indicator “Nutrients”	**0.88**	-0.01	-0.11	0.03	-0.08
Ellenberg indicator “Temperature”	-0.46	0.32	-0.18	**0.58**	-0.19
Forest density	0.11	**0.80**	0.27	0.04	-0.22
Canopy density	**0.79**	0.15	0.23	-0.11	-0.34
Cover of deciduous trees	**0.70**	-0.04	-0.30	0.30	0.01
Cover of conifer trees	-0.08	0.14	**0.88**	0.26	0.04
Mean basal area	0.28	**-0.64**	**0.50**	0.38	0.16
Standard deviation of basal area	0.23	-0.01	0.16	**0.92**	-0.10
% dead standing trees	-0.16	**-0.76**	0.08	-0.02	-0.19

Appendix 8.3: Overview over the factor loadings of the three landscape-scale PCAs. Values of <-0.5 or >0.5 are marked in bold. λ: eigenvalues of the respective PC-axes.

Landscape factors (only for PsV)	Habitat diversity $\lambda=2.07$	Modified areas $\lambda=1.95$	Open habitats $\lambda=1.42$	Distance to industry $\lambda=1.25$
Distance to reserve edge	**-0.48**	-0.34	0.28	0.40
Distance to canal	-0.19	**-0.60**	0.30	0.32
Distance to industry	-0.02	0.01	-0.07	**0.96**
Diversity of natural habitats (200m)	**0.92**	0.14	0.32	-0.07
Edge density (500m)	0.39	**0.79**	-0.21	0.25
Proportion of reed (200m)	**0.90**	0.04	-0.36	0.02
Proportion of grassland (200m)	-0.03	0.01	**0.98**	-0.04
Proportion of modified areas (500m)	-0.07	**0.91**	-0.02	-0.06
Landscape factors (only for PdC)	Habitat diversity $\lambda=3.31$	Distance to edges $\lambda=2.27$		
Distance to reserve edge	-0.26	**0.85**		
Distance to canal	**-0.53**	0.40		
Distance to industry	0.23	**0.72**		
Diversity of natural habitats (200m)	**0.93**	-0.15		
Edge density (500m)	**0.78**	-0.26		
Proportion of reed (200m)	**0.86**	-0.06		
Proportion of grassland (200m)	**0.75**	0.06		
Proportion of modified areas (500m)	0.36	**-0.88**		

Appendix 9.2: Moth trait matrix (Part 1: Species A-Chi, Trait „Hostplants”)

Species	Salicaceae	Fagaceae	Betulaceae	Oleaceae	Rosaceae	Ericaceae	Apiaceae	Asteraceae	Fabaceae	Lamiaceae	Ranunculaceae	Rubiaceae	Scrophulariaceae	Brassicaceae	Boraginaceae	Plantaginaceae
Abrostola_asclepiadis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acentria_ephemerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acleris_kochiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acleris_rhombana	0	0.5	0	0	0.5	0	0	0	0	0	0	0	0	0	0	0
Acleris_variegana	0	0	0.5	0	0.5	0	0	0	0	0	0	0	0	0	0	0
Acontia_lucida	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Acontia_trabealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acrobasis_advenella	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Acrobasis_consociella	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acrobasis_fallouella	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acrobasis_marmorea	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Acrobasis_suavella	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Acronicta_aceris	0.5	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acronicta_cuspis	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Acronicta_psi	0.25	0.25	0.25	0	0.25	0	0	0	0	0	0	0	0	0	0	0
Acronicta_rumicis	0.14	0.14	0.14	0	0.14	0	0	0.14	0	0	0	0	0	0.14	0	0.14
Aedia_leucomelas	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Agapeta_hamana	0	0	0	0	0	0	0	0.5	0.5	0	0	0	0	0	0	0
Agapeta_zoegana	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Agdistis_tamaricis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agriphila_brioniellus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agriphila_geniculea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Agrotera_nemoralis	0	0.33	0.33	0	0.33	0	0	0	0	0	0	0	0	0	0	0
Agrotis_bigramma	0	0	0	0	0	0	0	0.5	0	0	0	0	0	0.5	0	0
Agrotis_exclamationis	0	0.2	0	0	0.2	0	0.2	0.2	0	0	0	0	0	0	0	0.2
Agrotis_ipsilon	0	0	0	0	0.33	0	0	0.33	0	0	0	0	0	0.33	0	0
Agrotis_segetum	0	0	0	0	0.17	0	0.17	0.17	0.17	0	0	0.17	0	0.17	0	0
Alabonia_geoffrella	0	0.5	0	0	0.5	0	0	0	0	0	0	0	0	0	0	0
Aleimma_loeflingiana	0.33	0.33	0	0	0.33	0	0	0	0	0	0	0	0	0	0	0
Amphipyra_pyramidea	0.2	0.2	0.2	0.2	0.2	0	0	0	0	0	0	0	0	0	0	0
Anacampsis_populella	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anania_crocealis	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Anarta_trifolii	0	0	0	0	0	0	0	0.33	0	0	0	0	0.33	0.33	0	0
Ancylis_apicella	0	0	0	0.5	0.5	0	0	0	0	0	0	0	0	0	0	0
Ancylis_mitterbacheriana	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ancylis_obtusana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ancylis_selenana	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ancylis_unculana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Apeira_syringaria	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Apoda_limacodes	0	0.33	0.33	0	0.33	0	0	0	0	0	0	0	0	0	0	0
Araeopteron_ecphaea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Archips_betulana	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Archips_podana	0	0.25	0.25	0	0.25	0	0	0	0.25	0	0	0	0	0	0	0
Archips_rosana	0	0	0	0.5	0.5	0	0	0	0	0	0	0	0	0	0	0
Archips_xylosteana	0	0.33	0.33	0	0.33	0	0	0	0	0	0	0	0	0	0	0
Arctia_villica	0	0	0	0	0.2	0	0	0.2	0.2	0.2	0	0	0	0	0	0.2
Ascotis_selenaria	0	0	0.2	0	0.2	0	0	0.2	0.2	0.2	0	0	0	0	0	0
Athetis_hospes	0	0	0	0	0	0	0	0.33	0.33	0	0	0	0	0	0	0.33
Autographa_gamma	0.13	0	0	0	0	0	0.13	0.13	0.13	0.13	0	0	0.13	0.13	0	0.13
Bactra_robustana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Blastobasis_glandulella	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cacoecimorpha_pronubana	0	0	0	0.25	0.25	0	0	0	0.25	0.25	0	0	0	0	0	0
Cadra_figulilella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Calamotropha_paludella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Callopistria_juventina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Calophasia_platyptera	0	0	0	0	0	0	0	0	0	0	0	0	0.5	0	0	0.5
Caloptilia_alchimiella	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Capperia_loranus	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Caradrina_aspersa	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Caradrina_morpheus	0.2	0	0	0	0	0	0	0.2	0	0.2	0.2	0	0	0	0	0.2
Carcina_quercana	0	0.25	0.25	0	0.25	0.25	0	0	0	0	0	0	0	0	0	0
Carpatolechia_aenigma	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cataclysta_lemnata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Catarhoe_rubidata	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Catephia_alchymista	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Catocala_conversa	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Catocala_promissa	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Catoptria_falsella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Catoptria_pinella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Celypha_flavipalpana	0	0	0	0	0	0.33	0	0	0.33	0.33	0	0	0	0	0	0
Cerura_erminea	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Charanyca_ferruginea	0	0	0	0	0.25	0	0	0.25	0.25	0	0	0	0	0	0	0.25
Charanyca_trigrammica	0	0	0	0	0	0	0	0.25	0.25	0.25	0	0	0	0	0	0.25
Chiasmia_aestimaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chiasmia_clathrata	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Chilo_luteellus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chilo_phragmitella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chilodes_maritima	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 9.2: Moth trait matrix (Part 2: Species Chl-Et, Trait „Hostplants”)

Species	Salicaceae	Fagaceae	Betulaceae	Oleaceae	Rosaceae	Ericaceae	Apiaceae	Asteraceae	Fabaceae	Lamiaceae	Ranunculaceae	Rubiaceae	Scrophulariaceae	Brassicaceae	Boranginaceae	Plantaginaceae
Chloantha_hyperici	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroclystis_vata	0	0	0	0	0	0	0.25	0.25	0	0.25	0.25	0	0	0	0	0
Chrysocrambus_linetella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chrysoteuchia_culmella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cilix_glaucata	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Clepsis_consimilana	0	0	0.33	0.33	0.33	0	0	0	0	0	0	0	0	0	0	0
Clepsis_rurinana	0	0.2	0	0	0.2	0	0.2	0.2	0	0	0.2	0	0	0	0	0
Clostera_pigra	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cnaemidophorus_rhododactyla	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Cnephasia_pasiuana	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Coleophora_colutella	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Colobochyla_salicalis	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Comibaena_bajularia	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Conisania_luteago	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cosmia_affinis	0	0.5	0	0	0.5	0	0	0	0	0	0	0	0	0	0	0
Cosmia_trapezina	0.2	0.2	0.2	0.2	0.2	0	0	0	0	0	0	0	0	0	0	0
Cosmopterix_lienigiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cosmopterix_orichalcea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cosmopterix_scribaiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cosmorhoe_ocellata	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Cossus_cossus	0.33	0	0.33	0	0.33	0	0	0	0	0	0	0	0	0	0	0
Costaconvexa_polygrammata	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Craniophora_ligustri	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Crocallis_elinguaria	0.33	0.33	0	0	0.33	0	0	0	0	0	0	0	0	0	0	0
Crombrugghia_distans	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Cryphia_algae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cryphia_ochsi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyclophora_annularia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyclophora_punctaria	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyclophora_puppillaria	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cydia_amplana	0	0.5	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0
Cydia_fagiglandana	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cydia_pomonella	0	0.5	0	0	0.5	0	0	0	0	0	0	0	0	0	0	0
Deltote_bankiana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Deltote_pygarga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Denticucullus_pygmina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Diaphora_mendica	0.14	0	0	0	0.14	0	0	0.14	0.14	0.14	0	0.14	0	0	0	0.14
Dichomeris_alacella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dichomeris_derasella	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Dichomeris_marginella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dioryctria_abietella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dioryctria_pineae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dioryctria_sylvestrella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ditula_angustiorana	0	0	0	0	0.5	0.5	0	0	0	0	0	0	0	0	0	0
Dolicharthria_punctalis	0	0	0	0	0	0	0	0.5	0	0	0	0	0	0	0	0.5
Donacaula_forficella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Drymonia_dodonaea	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Duponchelia_fovealis	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Dypterygia_scabriuscula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dysauxes_ancilla	0	0	0	0	0	0	0	0.33	0	0	0	0	0	0	0.33	0.33
Dysauxes_famula	0	0	0	0	0	0	0	0.5	0	0	0	0	0	0	0	0.5
Dysauxes_punctata	0	0	0	0	0	0	0	0.5	0	0	0	0	0	0	0	0.5
Dysgonia_algira	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Dyspessa_ulula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Earias_clorana	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Earias_vernana	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eilema_caniola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eilema_complana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eilema_depressa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eilema_sororcula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Elaphria_venustula	0	0	0	0	0.5	0	0	0	0.5	0	0	0	0	0	0	0
Elegia_similella	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Emmelina_monodactyla	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Endotricha_flammealis	0.25	0.25	0	0	0.25	0	0	0	0.25	0	0	0	0	0	0	0
Epagoge_grotiana	0	0.5	0	0	0.5	0	0	0	0	0	0	0	0	0	0	0
Ephestia_woodiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Epiblema_foenella	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Epicallima_formosella	0.33	0	0	0	0.33	0	0	0	0.33	0	0	0	0	0	0	0
Epinotia_festivana	0	0.5	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0
Epione_repandaria	0.5	0	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0
Epirrhoe_alternata	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Ethmia_bipunctella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Ethmia_quadrillella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Ethmia_terminella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Etiella_zinckenella	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0

Appendix 9.2: Moth trait matrix (Part 3: Species Eu-Mac, Trait „Hostplants")

Species	Salicaceae	Fagaceae	Betulaceae	Oleaceae	Rosaceae	Ericaceae	Apiaceae	Asteraceae	Fabaceae	Lamiaceae	Ranunculaceae	Rubiaceae	Scrophulariaceae	Brassicaceae	Boranginaceae	Plantaginaceae
Eublemma_parva	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Euchromius_superbellus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eucosma_cana	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Eucosma_conterminana	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Eucosma_metzneriana	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Eudonia_delunella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eudonia_lacustrata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eudonia_mercurella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eudonia_pallida	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eupithecia_centaureata	0	0	0	0	0	0	0.33	0.33	0	0	0	0	0	0	0	0.33
Eupithecia_haworthiata	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Eupithecia_ultimaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euplagia_quadripunctaria	0.14	0.14	0	0	0.14	0	0	0.14	0.14	0.14	0	0	0	0	0.14	0
Euplexia_lucipara	0	0	0.13	0	0.13	0	0.13	0.13	0.13	0.13	0.13	0	0	0	0.13	0
Euproctis_chrysorrhoea	0.17	0.17	0.17	0.17	0.17	0	0	0	0.17	0	0	0	0	0	0	0
Eutelia_adulatrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euzophera_fuliginosella	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Evergestis_extimalis	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Furcula_bifida	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Galleria_mellonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gastropacha_quercifolia	0.33	0	0	0	0.33	0.33	0	0	0	0	0	0	0	0	0	0
Glyptoteles_leucacrinella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gymnoscelis_rufifasciata	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Gypsonoma_aceriana	0.33	0	0.33	0	0	0.33	0	0	0	0	0	0	0	0	0	0
Gypsonoma_minutana	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Habrosyne_pyritoides	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Hadena_bicruris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Harpyia_milhauseri	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hedya_nubiferana	0.25	0.25	0.25	0	0.25	0	0	0	0	0	0	0	0	0	0	0
Hedya_pruniana	0	0	0.5	0	0.5	0	0	0	0	0	0	0	0	0	0	0
Helicoverpa_armigera	0	0	0	0	0.5	0	0	0.5	0	0	0	0	0	0	0	0
Heliothis_viriplaca	0	0	0	0	0.2	0	0	0.2	0.2	0.2	0	0	0.2	0	0	0
Hellinsia_inulae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Hemistola_chrysoprasaria	0	0.33	0	0	0.33	0	0	0	0	0	0.33	0	0	0	0	0
Hemithea_aestivaria	0.17	0.17	0.17	0	0.17	0.17	0	0	0	0	0.17	0	0	0	0	0
Herminia_tarsicrinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Herminia_tarsipennalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Herminia_tenuialis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Heterogenea_asella	0	0.33	0.33	0	0.33	0	0	0	0	0	0	0	0	0	0	0
Homaloxestis_briantiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Homoeosoma_sinuella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Hoplodrina_ambigua	0	0	0	0	0	0	0	0.33	0	0	0	0	0.33	0	0	0.33
Horisme_tersata	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Horisme_vitalbata	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Hypomecis_punctinalis	0.2	0.2	0.2	0	0.2	0	0	0	0	0	0.2	0	0	0	0	0
Hypsopygia_costalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hypsopygia_glaucinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea_aversata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea_degeneraria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea_dimidiata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea_filicata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea_fuscovenosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea_muricata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea_politaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea_rusticata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea_seriata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idaea_subsericeata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ipimorpha_subtusa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Isturgia_arenacearia	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Lacanobia_oleracea	0	0	0	0	0.14	0	0	0.14	0.14	0.14	0.14	0	0	0.14	0	0.14
Lacanobia_wlatinum	0	0	0.17	0	0.17	0	0	0.17	0.17	0.17	0	0	0	0	0	0.17
Laelia_coenosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lamoria_anella	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Laothoe_populi	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lasiocampa_quercus	0.14	0.14	0.14	0.14	0.14	0.14	0	0	0.14	0	0	0	0	0	0	0
Laspeyria_flexula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leucania_loreyi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leucania_obsoleta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ligdia_adustata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lithosia_quadra	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lomaspilis_marginata	0.5	0	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0
Lomographa_bimaculata	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Loxostege_sticticalis	0	0	0	0	0	0	0	0.5	0.5	0	0	0	0	0	0	0
Lygephila_craccae	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Lymantria_dispar	0	0.5	0	0	0.5	0	0	0	0	0	0	0	0	0	0	0
Macaria_alternata	0.25	0.25	0.25	0	0.25	0	0	0	0	0	0	0	0	0	0	0
Macaria_liturata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Macaria_notata	0.5	0	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 9.2: Moth trait matrix (Part 4: Species Mal-Phe, Trait „Hostplants”)

Species	Salicaceae	Fagaceae	Betulaceae	Oleaceae	Rosaceae	Ericaceae	Apiaceae	Asteraceae	Fabaceae	Lamiaceae	Ranunculaceae	Rubiaceae	Scrophulariaceae	Brassicaceae	Boranginaceae	Plantaginaceae
Malacosoma_castrensis	0	0	0	0	0.33	0	0	0.33	0.33	0	0	0	0	0	0	0
Mecyna_asinalis	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Meganola_albula	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Meganola_togatulalis	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Menophra_abruptaria	0	0.25	0	0.25	0.25	0	0	0	0	0	0.25	0	0	0	0	0
Mesapamea_secalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Metachrostis_velox	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Metasia_ophialis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Metendothenia_atropunctana	0.25	0.25	0.25	0	0.25	0	0	0	0	0	0	0	0	0	0	0
Miltochrista_miniata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mimas_tiliae	0	0	0.5	0	0.5	0	0	0	0	0	0	0	0	0	0	0
Minoa_murinata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Minucia_lunaris	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Moma_alpium	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Monopis_monachella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Monopis_obviella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mormo_maura	0.5	0	0	0.5	0	0	0	0	0	0	0	0	0	0	0	0
Morophaga_choragella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Morophaga_morella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Myelois_circumvoluta	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Mythimna_albipuncta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna_congrua	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna_pallens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna_riparia	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Mythimna_sicula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna_straminea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna_turca	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mythimna_vitellina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nephopterix_angustella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Neurothaumasia_ankerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Noctua_fimbriata	0.13	0	0	0.13	0.13	0.13	0	0.13	0.13	0.13	0	0.13	0	0	0	0
Noctua_janthina	0.33	0	0	0	0.33	0	0	0.33	0	0	0	0	0	0	0	0
Noctua_pronuba	0.14	0	0	0	0.14	0	0	0.14	0.14	0	0	0	0.14	0.14	0	0.14
Noctua_tirrenica	0	0	0	0	0.2	0	0	0.2	0.2	0	0	0	0	0.2	0	0.2
Nola_aerugula	0.25	0	0.25	0	0.25	0	0	0	0.25	0	0	0	0	0	0	0
Nola_chlamitulalis	0	0	0	0	0	0	0	0	0	0.5	0	0	0.5	0	0	0
Nomophila_noctuella	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Notocelia_cynosbatella	0	0.33	0.33	0	0.33	0	0	0	0	0	0	0	0	0	0	0
Notocelia_roborana	0	0.5	0	0	0.5	0	0	0	0	0	0	0	0	0	0	0
Notocelia_rosaecolana	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Notocelia_uddmanniana	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Notodonta_tritophus	0.5	0	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0
Nyctegretis_lineana	0	0	0	0	0	0	0	0.5	0.5	0	0	0	0	0	0	0
Nycterosea_obstipata	0	0	0	0	0	0	0	0.25	0	0.25	0	0.25	0	0.25	0	0
Nyctobrya_muralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ochropleura_plecta	0	0	0	0	0.13	0	0.13	0.13	0.13	0	0	0.13	0	0.13	0.13	0.13
Ocneria_rubea	0	0.5	0	0	0	0.5	0	0	0	0	0	0	0	0	0	0
Oligia_latruncula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oncocera_semirubella	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Opisthograptis_luteolata	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Orgyia_antiqua	0.11	0.11	0.11	0.11	0.11	0.11	0	0.11	0.11	0.11	0	0	0	0	0	0
Ostrinia_nubilalis	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Palpita_vitrealis	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Pammene_fasciana	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pandemis_cerasana	0.25	0.25	0.25	0	0.25	0	0	0	0	0	0	0	0	0	0	0
Pandemis_heparana	0.25	0.25	0.25	0	0.25	0	0	0	0	0	0	0	0	0	0	0
Paradoxus_osyridellus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Parahypopta_caestrum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Parapoynx_stratiotata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Parascotia_fuliginaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Paraswammerdamia_albicapitella	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Paraswammerdamia_nebulella	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Paratalanta_pandalis	0	0	0	0	0	0	0	0.5	0	0.5	0	0	0	0	0	0
Parectopa_robiniella	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Pasiphila_chloerata	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Pasiphila_rectangulata	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Pechipogo_plumigeralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pediasia_contaminella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pelochrista_mollitana	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Pelosia_muscerda	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pempelia_palumbella	0	0	0	0	0	0.5	0	0	0	0.5	0	0	0	0	0	0
Penestoglossa_dardoinella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Peribatodes_rhomboidaria	0	0.25	0	0.25	0.25	0	0	0	0	0	0.25	0	0	0	0	0
Peridea_anceps	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Petrophora_chlorosata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phalera_bucephala	0.2	0.2	0.2	0.2	0.2	0	0	0	0	0	0	0	0	0	0	0
Phalonidia_albipalpana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pheosia_tremula	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix 9.2: Moth trait matrix (Part 5: Species Phi-Z, Trait „Hostplants”)

Species	Salicaceae	Fagaceae	Betulaceae	Oleaceae	Rosaceae	Ericaceae	Apiaceae	Asteraceae	Fabaceae	Lamiaceae	Ranunculaceae	Rubiaceae	Scrophulariaceae	Brassicaceae	Boraginaceae	Plantaginaceae
Philereme_transversata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Philereme_vetulata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Photedes_morrisii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phragmataecia_castaneae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phragmatobia_fuliginosa	0	0	0	0	0.25	0	0	0.25	0	0	0	0	0	0	0.25	0.25
Phtheochroa_pulvillana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phycitodes_binaevella	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Phyllophila_obliterata	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Phytometra_viridaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Piniphila_bifasciana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Platyptilia_farfarellus	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Platytes_alpinella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pleuropyta_ruralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Plodia_interpunctella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Plutella_xylostella	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Polyphaenis_sericata	0	0	0	0.5	0.5	0	0	0	0	0	0	0	0	0	0	0
Propiromorpha_rhodophana	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Pseudargyrotoza_conwagana	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Pseudoips_prasinana	0	0.5	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0
Pseudotelphusa_scalella	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pterostoma_palpina	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pyralis_farinalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pyrausta_aurata	0	0	0	0	0	0	0	0	0	0.5	0	0	0	0	0	0.5
Pyrausta_despicata	0	0	0	0	0	0	0	0	0	0.5	0	0	0	0	0	0.5
Pyrausta_purpuralis	0	0	0	0	0.33	0	0	0	0	0.33	0	0	0	0	0	0.33
Pyroderces_argyrogrammos	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Rhigognostis_hufnagelii	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Rhodometra_sacraria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhodophaea_formosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhyacionia_buoliana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rivula_sericealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Schoenobius_gigantella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Schrankia_costaestrigalis	0	0	0	0	0	0.5	0	0	0	0.5	0	0	0	0	0	0
Sciota_rhenella	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sclerocona_acutella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scoparia_basistrigalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scopula_emutaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scopula_imitaria	0	0	0	0.25	0.25	0	0	0	0.25	0	0.25	0	0	0	0	0
Scopula_nigropunctata	0	0	0	0	0	0	0	0.33	0	0.33	0.33	0	0	0	0	0
Scopula_rubiginata	0	0	0	0	0	0	0	0.33	0.33	0.33	0	0	0	0	0	0
Scythropia_crataegella	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Senta_flammea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sideridis_rivularis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sitochroa_palealis	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Spatalia_argentina	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spilonota_ocellana	0	0.33	0.33	0	0.33	0	0	0	0	0	0	0	0	0	0	0
Spilosoma_lubricipeda	0.13	0	0	0	0.13	0	0	0.13	0.13	0.13	0	0.13	0	0	0.13	0.13
Spilosoma_lutea	0	0	0	0	0	0	0	0.5	0	0	0	0	0	0.5	0	0
Spodoptera_exigua	0	0	0	0	0	0	0.2	0.2	0.2	0.2	0	0	0	0.2	0	0
Stauropus_fagi	0	0.33	0.33	0	0.33	0	0	0	0	0	0	0	0	0	0	0
Stegania_trimaculata	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stemmatophora_brunnealis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Subacronicta_megacephala	0.5	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Symmoca_signatella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Synaphe_punctalis	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Tegostoma_comparalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Teleiodes_luculella	0.33	0.33	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0
Tethea_ocularis	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thalera_fimbrialis	0	0	0	0	0	0	0.33	0.33	0.33	0	0	0	0	0	0	0
Thaumetopoea_pityocampa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thetidia_smaragdaria	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Thumatha_senex	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Timandra_comae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trachea_atriplicis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trachonitis_cristella	0	0	0.5	0	0.5	0	0	0	0	0	0	0	0	0	0	0
Trichoplusia_ni	0	0	0	0	0	0	0	0.5	0	0	0	0	0	0.5	0	0
Tyta_luctuosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Udea_ferrugalis	0	0	0	0	0	0	0	0.5	0	0.5	0	0	0	0	0	0
Watsonalla_binaria	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Xestia_cnigrum	0	0	0	0	0.14	0	0	0.14	0.14	0	0.14	0.14	0.14	0	0	0.14
Yponomeuta_cagnagella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Yponomeuta_evonymella	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Yponomeuta_irrorella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Yponomeuta_plumbella	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Ypsolopha_nemorella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Zebeeba_falsalis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Zeiraphera_griseana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Zeuzera_pyrina	0	0.25	0.25	0.25	0.25	0	0	0	0	0	0	0	0	0	0	0

Appendix 9.2: Moth trait matrix (Part 6: Species A-Chi, Traits „Specialization” and „Foodtype”)

Species	Degree of Specialization	in beehives	on deciduous trees	on conifers	Herbs	Grass feeding	In fruits	Lichen Algae	Fungi	Moss	Detritus	Water-plants	In Wood	Roots
Abrostola_asclepiadis	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Acentria_ephemerella	4	0	0	0	0	0	0	0	0	0	0	1	0	0
Acleris_kochiella	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Acleris_rhombana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Acleris_variegana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Acontia_lucida	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Acontia_trabealis	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Acrobasis_advenella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Acrobasis_consociella	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Acrobasis_fallouella	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Acrobasis_marmorea	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Acrobasis_suavella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Acronicta_aceris	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Acronicta_cuspis	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Acronicta_psi	4	0	1	0	0	0	0	0	0	0	0	0	0	0
Acronicta_rumicis	4	0	1	1	1	1	0	0	0	0	0	0	0	0
Aedia_leucomelas	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Agapeta_hamana	3	0	0	0	1	0	0	0	0	0	0	0	0	1
Agapeta_zoegana	3	0	0	0	1	0	0	0	0	0	0	0	0	1
Agdistis_tamaricis	2	0	0	1	0	0	0	0	0	0	0	0	0	0
Agriphila_brioniellus	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Agriphila_geniculea	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Agrotera_nemoralis	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Agrotis_bigramma	4	0	0	0	1	1	0	0	0	0	0	0	0	1
Agrotis_exclamationis	4	0	0	0	1	1	0	0	0	0	0	0	0	1
Agrotis_ipsilon	4	0	0	0	1	1	0	0	0	0	0	0	0	1
Agrotis_segetum	4	0	0	1	1	1	0	0	0	0	0	0	0	1
Alabonia_geoffrella	3	0	1	0	0	0	0	0	0	0	1	0	1	0
Aleimma_loeflingiana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Amphipyra_pyramidea	4	0	1	0	0	0	0	0	0	0	0	0	0	0
Anacampsis_populella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Anania_crocealis	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Anarta_trifolii	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Ancylis_apicella	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Ancylis_mitterbacheriana	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Ancylis_obtusana	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Ancylis_selenana	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Ancylis_unculana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Apeira_syringaria	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Apoda_limacodes	4	0	1	0	0	0	0	0	0	0	0	0	0	0
Araeopteron_ecphaea	1	0	0	0	0	1	0	0	0	0	0	0	0	0
Archips_betulana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Archips_podana	4	0	1	1	1	0	0	0	0	0	0	0	0	0
Archips_rosana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Archips_xylosteana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Arctia_villica	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Ascotis_selenaria	5	0	1	0	1	0	0	0	0	0	0	0	0	0
Athetis_hospes	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Autographa_gamma	4	0	1	0	1	1	0	0	0	0	0	0	0	0
Bactra_robustana	2	0	0	0	0	1	0	0	0	0	0	0	0	1
Blastobasis_glandulella	2	0	1	0	0	0	1	0	0	0	0	0	0	0
Cacoecimorpha_pronubana	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Cadra_figulilella	4	0	0	0	0	0	1	0	0	0	1	0	0	0
Calamotropha_paludella	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Callopistria_juventina	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Calophasia_platyptera	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Caloptilia_alchimiella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Capperia_loranus	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Caradrina_aspersa	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Caradrina_morpheus	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Carcina_quercana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Carpatolechia_aenigma	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Cataclysta_lemnata	4	0	0	0	0	0	0	0	0	0	0	1	0	0
Catarhoe_rubidata	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Catephia_alchymista	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Catocala_conversa	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Catocala_promissa	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Catoptria_falsella	1	0	0	0	0	0	0	0	0	1	0	0	0	0
Catoptria_pinella	3	0	0	0	0	1	0	0	0	1	0	0	0	1
Celypha_flavipalpana	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Cerura_erminea	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Charanyca_ferruginea	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Charanyca_trigrammica	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Chiasmia_aestimaria	3	0	0	1	0	0	0	0	0	0	0	0	0	0
Chiasmia_clathrata	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Chilo_luteellus	1	0	0	0	0	1	0	0	0	0	0	0	0	0
Chilo_phragmitella	2	0	0	0	0	1	0	0	0	0	0	0	0	1
Chilodes_maritima	1	0	0	0	0	1	0	0	0	0	0	0	0	0

Appendix 9.2: Moth trait matrix (Part 7: Species Chl-Et, Traits „Specialization” and „Foodtype”)

Species	Degree of Specialization	In beehives	on deciduous trees	on conifers	Herbs	Grass feeding	In fruits	Lichen Algae	Fungi	Moss	Detritus	Water-plants	In Wood	Roots
Chloantha_hyperici	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Chloroclystis_vata	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Chrysocrambus_linetella	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Chrysoteuchia_culmella	3	0	0	0	0	1	0	0	0	1	0	0	0	1
Cilix_glaucata	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Clepsis_consimilana	3	0	1	0	0	0	0	0	0	0	1	0	0	0
Clepsis_rurinana	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Clostera_pigra	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Cnaemidophorus_rhododactyla	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Cnephasia_pasiuana	3	0	0	0	1	1	0	0	0	0	0	0	0	0
Coleophora_colutella	2	0	1	0	1	0	0	0	0	0	0	0	0	0
Colobochyla_salicalis	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Comibaena_bajularia	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Conisania_luteago	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Cosmia_affinis	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Cosmia_trapezina	4	0	1	0	0	0	0	0	0	0	0	0	0	0
Cosmopterix_lienigiella	1	0	0	0	0	1	0	0	0	0	0	0	0	0
Cosmopterix_orichalcea	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Cosmopterix_scribaiella	1	0	0	0	0	1	0	0	0	0	0	0	0	0
Cosmorhoe_ocellata	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Cossus_cossus	3	0	1	0	0	0	0	0	0	0	0	0	1	0
Costaconvexa_polygrammata	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Craniophora_ligustri	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Crocallis_elinguaria	4	0	1	0	0	0	0	0	0	0	0	0	0	0
Crombrugghia_distans	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Cryphia_algae	2	0	0	0	0	0	0	1	0	0	0	0	0	0
Cryphia_ochsi	2	0	0	0	0	0	0	1	0	0	0	0	0	0
Cyclophora_annularia	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Cyclophora_punctaria	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Cyclophora_puppillaria	3	0	1	0	1	0	0	0	0	0	0	0	0	0
Cydia_amplana	3	0	1	0	0	0	1	0	0	0	0	0	0	0
Cydia_fagiglandana	2	0	1	0	0	0	1	0	0	0	0	0	0	0
Cydia_pomonella	3	0	1	0	0	0	1	0	0	0	0	0	0	0
Deltote_bankiana	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Deltote_pygarga	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Denticucullus_pygmina	3	0	0	0	1	1	0	0	0	0	0	0	0	0
Diaphora_mendica	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Dichomeris_alacella	4	0	0	0	0	0	0	1	0	1	0	0	0	0
Dichomeris_derasella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Dichomeris_marginella	1	0	0	1	0	0	0	0	0	0	0	0	0	0
Dioryctria_abietella	2	0	0	1	0	0	1	0	0	0	0	0	1	0
Dioryctria_pineae	2	0	0	1	0	0	1	0	0	0	0	0	1	0
Dioryctria_sylvestrella	2	0	0	1	0	0	0	0	0	0	0	0	1	0
Ditula_angustiorana	4	0	1	1	0	0	0	0	0	0	0	0	0	0
Dolicharthria_punctalis	4	0	0	0	1	0	0	0	0	0	1	0	0	0
Donacaula_forficella	3	0	0	0	0	1	0	0	0	0	0	0	0	0
Drymonia_dodonaea	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Duponchelia_fovealis	4	0	0	0	1	0	0	0	0	0	0	1	0	0
Dypterygia_scabriuscula	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Dysauxes_ancilla	3	0	0	0	1	0	0	1	0	1	1	0	0	0
Dysauxes_famula	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Dysauxes_punctata	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Dysgonia_algira	3	0	1	0	1	0	0	0	0	0	0	0	0	0
Dyspessa_ulula	2	0	0	0	1	0	0	0	0	0	0	0	0	1
Earias_clorana	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Earias_vernana	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Eilema_caniola	2	0	0	0	0	0	0	1	0	1	0	0	0	0
Eilema_complana	2	0	0	0	0	0	0	1	0	0	0	0	0	0
Eilema_depressa	1	0	0	0	0	0	0	1	0	0	0	0	0	0
Eilema_sororcula	2	0	0	0	0	0	0	1	0	0	0	0	0	0
Elaphria_venustula	3	0	1	0	1	0	0	0	0	0	0	0	0	0
Elegia_similella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Emmelina_monodactyla	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Endotricha_flammealis	4	0	0.5	0	0	0	0	0	0	0	1	0	0	0
Epagoge_grotiana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Ephestia_woodiella	4	0	0	0	0.5	0	0	0	0	0	1	0	0	0
Epiblema_foenella	1	0	0	0	1	0	0	0	0	0	0	0	0	1
Epicallima_formosella	4	0	1	0	0	0	0	0	0	0	1	0	1	0
Epinotia_festivana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Epione_repandaria	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Epirrhoe_alternata	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Ethmia_bipunctella	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Ethmia_quadrillella	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Ethmia_terminella	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Etiella_zinckenella	2	0	0	0	1	0	1	0	0	0	0	0	0	0

Appendix 9.2: Moth trait matrix (Part 8: Species Eu-Mac, Traits „Specialization” and „Foodtype”)

Species	Degree of Specialization	In beehives	on deciduous trees	on conifers	Herbs	Grass feeding	In fruits	Lichen Algae	Fungi	Moss	Detritus	Water-plants	In Wood	Roots
Eublemma_parva	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Euchromius_superbellus	4	0	0	0	0	0	0	0	0	0	1	0	0	0
Eucosma_cana	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Eucosma_conterminana	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Eucosma_metzneriana	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Eudonia_delunella	1	0	0	0	0	0	0	1	0	1	0	0	0	0
Eudonia_lacustrata	2	0	0	0	0	0	0	0	0	1	0	0	0	0
Eudonia_mercurella	2	0	0	0	0	0	0	1	0	1	0	0	0	0
Eudonia_pallida	2	0	0	0	0	0	0	0	0	1	0	0	0	0
Eupithecia_centaureata	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Eupithecia_haworthiata	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Eupithecia_ultimaria	3	0	1	1	0	0	0	0	0	0	0	0	0	0
Euplagia_quadripunctaria	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Euplexia_lucipara	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Euproctis_chrysorrhoea	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Eutelia_adulatrix	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Euzophera_fuliginosella	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Evergestis_extimalis	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Furcula_bifida	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Galleria_mellonella	1	1	0	0	0	0	0	0	0	0	0	0	0	0
Gastropacha_quercifolia	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Glyptoteles_leucacrinella	4	0	0	0	0.5	0	0	0	0	0	1	0	0	0
Gymnoscelis_rufifasciata	3	0	1	0	0	1	0	0	0	0	0	0	0	0
Gypsonoma_aceriana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Gypsonoma_minutana	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Habrosyne_pyritoides	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Hadena_bicruris	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Harpyia_milhauseri	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Hedya_nubiferana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Hedya_pruniana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Helicoverpa_armigera	4	0	0	0	1	1	0	0	0	0	0	0	0	0
Heliothis_viriplaca	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Hellinsia_inulae	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Hemistola_chrysoprasaria	3	0	1	0	1	0	0	0	0	0	0	0	0	0
Hemithea_aestivaria	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Herminia_tarsicrinalis	3	0	0	0	0.5	0	0	0	0	0	1	0	0	0
Herminia_tarsipennalis	4	0	0.5	0	0	0	0	0	0	0	1	0	0	0
Herminia_tenuialis	4	0	0	0	0	0	0	0	0	0	1	0	0	0
Heterogenea_asella	4	0	1	0	0	0	0	0	0	0	0	0	0	0
Homaloxestis_briantiella	4	0	0	0	0	0	0	0	0	0	1	0	0	0
Homoeosoma_sinuella	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Hoplodrina_ambigua	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Horisme_tersata	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Horisme_vitalbata	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Hypomecis_punctinalis	4	0	1	0	0	0	0	0	0	0	0	0	0	0
Hypsopygia_costalis	4	0	0	0	0.5	0	0	0	0	0	1	0	0	0
Hypsopygia_glaucinalis	4	0	0	0	0.5	0	0	0	0	0	1	0	0	0
Idaea_aversata	4	0	0	0	1	0	0	0	0	0	1	0	0	0
Idaea_degeneraria	4	0	0	0	1	0	0	0	0	0	1	0	0	0
Idaea_dimidiata	4	0	0	0	1	0	0	0	0	0	1	0	0	0
Idaea_filicata	4	0	0	0	1	0	0	0	0	0	1	0	0	0
Idaea_fuscovenosa	4	0	0	0	1	0	0	0	0	0	1	0	0	0
Idaea_muricata	4	0	0	0	1	0	0	0	0	0	1	0	0	0
Idaea_politaria	4	0	0	0	1	0	0	0	0	0	1	0	0	0
Idaea_rusticata	4	0	0	0	1	0	0	0	0	0	1	0	0	0
Idaea_seriata	4	0	0	0	1	0	0	0	0	0	1	0	0	0
Idaea_subsericeata	4	0	0	0	1	0	0	0	0	0	1	0	0	0
Ipimorpha_subtusa	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Isturgia_arenacearia	2	0	1	0	1	0	0	0	0	0	0	0	0	0
Lacanobia_oleracea	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Lacanobia_wlatinum	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Laelia_coenosa	3	0	0	0	0	1	0	0	0	0	0	0	0	0
Lamoria_anella	1	1	0	0	1	0	0	0	0	1	0	0	0	0
Laothoe_populi	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Lasiocampa_quercus	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Laspeyria_flexula	2	0	0	0	0	0	0	1	0	0	0	0	0	0
Leucania_loreyi	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Leucania_obsoleta	1	0	0	0	0	1	0	0	0	0	0	0	0	0
Ligdia_adustata	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Lithosia_quadra	2	0	0	0	0	0	0	1	0	0	0	0	0	0
Lomaspilis_marginata	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Lomographa_bimaculata	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Loxostege_sticticalis	4	0	0	0	1	0	0	0	0	0	0	0	0	1
Lygephila_craccae	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Lymantria_dispar	4	0	1	0	0	0	0	0	0	0	0	0	0	0
Macaria_alternata	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Macaria_liturata	2	0	0	1	0	0	0	0	0	0	0	0	0	0
Macaria_notata	3	0	1	0	0	0	0	0	0	0	0	0	0	0

Appendix 9.2: Moth trait matrix (Part 9: Species Mal-Phe, Traits „Specialization” and „Foodtype”)

Species	Degree of Specialization	In beehives	on deciduous trees	on conifers	Herbs	Grass feeding	In fruits	Lichen Algae	Fungi	Moss	Detritus	Water-plants	In Wood	Roots
Malacosoma_castrensis	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Mecyna_asinalis	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Meganola_albula	3	0	1	0	1	0	0	0	0	0	0	0	0	0
Meganola_togatulalis	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Menophra_abruptaria	4	0	1	0	0	0	0	0	0	0	0	0	0	0
Mesapamea_secalis	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Metachrostis_velox	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Metasia_ophialis	2	0	0	0	0	1	0	0	0	0	1	0	0	0
Metendothenia_atropunctana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Miltochrista_miniata	2	0	0	0	0	0	0	1	0	0	0	0	0	0
Mimas_tiliae	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Minoa_murinata	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Minucia_lunaris	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Moma_alpium	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Monopis_monachella	4	0	0	0	0	0	0	0	0	0	1	0	0	0
Monopis_obviella	4	0	0	0	0	0	0	0	0	0	1	0	0	0
Mormo_maura	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Morophaga_choragella	4	0	0	0	0	0	0	0	1	0	0	0	1	0
Morophaga_morella	4	0	0	0	0	0	0	0	1	0	0	0	1	0
Myelois_circumvoluta	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Mythimna_albipuncta	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Mythimna_congrua	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Mythimna_pallens	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Mythimna_riparia	3	0	0	0	1	1	0	0	0	0	0	0	0	0
Mythimna_sicula	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Mythimna_straminea	3	0	0	0	0	1	0	0	0	0	0	0	0	0
Mythimna_turca	3	0	0	0	0	1	0	0	0	0	0	0	0	0
Mythimna_vitellina	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Nephopterix_angustella	1	0	1	0	0	0	1	0	0	0	0	0	0	0
Neurothaumasia_ankerella	4	0	0	0	0	0	0	0	1	0	1	0	1	0
Noctua_fimbriata	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Noctua_janthina	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Noctua_pronuba	4	0	1	0	1	1	0	0	0	0	0	0	0	0
Noctua_tirrenica	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Nola_aerugula	3	0	1	0	1	0	0	0	0	0	0	0	0	0
Nola_chlamitulalis	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Nomophila_noctuella	4	0	0	0	1	1	0	0	0	0	0	0	0	0
Notocelia_cynosbatella	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Notocelia_roborana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Notocelia_rosaecolana	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Notocelia_uddmanniana	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Notodonta_tritophus	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Nyctegretis_lineana	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Nycterosea_obstipata	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Nyctobrya_muralis	2	0	0	0	0	0	0	1	0	0	0	0	0	0
Ochropleura_plecta	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Ocneria_rubea	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Oligia_latruncula	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Oncocera_semirubella	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Opisthograptis_luteolata	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Orgyia_antiqua	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Ostrinia_nubilalis	4	0	0	0	1	1	0	0	0	0	0	0	0	0
Palpita_vitrealis	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Pammene_fasciana	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Pandemis_cerasana	4	0	1	1	0	0	0	0	0	0	0	0	0	0
Pandemis_heparana	4	0	1	1	0	0	0	0	0	0	0	0	0	0
Paradoxus_osyridellus	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Parahypopta_caestrum	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Parapoynx_stratiotata	4	0	0	0	0	0	0	0	0	0	0	1	0	0
Parascotia_fuliginaria	2	0	0	0	0	0	0	1	1	0	0	0	0	0
Paraswammerdamia_albicapitella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Paraswammerdamia_nebulella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Paratalanta_pandalis	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Parectopa_robiniella	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Pasiphila_chloerata	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Pasiphila_rectangulata	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Pechipogo_plumigeralis	4	0	0	0	0.5	0	0	0	0	0	1	0	0	0
Pediasia_contaminella	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Pelochrista_mollitana	1	0	0	0	1	0	0	0	0	0	0	0	0	1
Pelosia_muscerda	2	0	0	0	0	0	0	1	0	0	0	0	0	0
Pempelia_palumbella	3	0	1	0	1	0	0	0	0	0	0	0	0	0
Penestoglossa_dardoinella	4	0	0	0	1	1	0	0	0	0	0	0	0	0
Peribatodes_rhomboidaria	4	0	1	0	0	0	0	0	0	0	0	0	0	0
Peridea_anceps	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Petrophora_chlorosata	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Phalera_bucephala	4	0	1	0	0	0	0	0	0	0	0	0	0	0
Phalonidia_albipalpana	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Pheosia_tremula	2	0	1	0	0	0	0	0	0	0	0	0	0	0

Appendix 9.2: Moth trait matrix (Part 10: Species Phi-Z, Traits „Specialization” and „Foodtype”)

Species	Degree of Specialization	In beehives	on deciduous trees	on conifers	Herbs	Grass feeding	In fruits	Lichen Algae	Fungi	Moss	Detritus	Water-plants	In Wood	Roots
Philereme_transversata	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Philereme_vetulata	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Photedes_morrisii	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Phragmataecia_castaneae	1	0	0	0	0	1	0	0	0	0	0	0	0	0
Phragmatobia_fuliginosa	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Phtheochroa_pulvillana	1	0	0	0	1	0	0	0	0	0	0	0	0	1
Phycitodes_binaevella	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Phyllophila_obliterata	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Phytometra_viridaria	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Piniphila_bifasciana	1	0	0	1	0	0	0	0	0	0	0	0	0	0
Platyptilia_farfarellus	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Platytes_alpinella	3	0	0	0	0	0	0	0	0	1	0	0	0	0
Pleuropyta_ruralis	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Plodia_interpunctella	4	0	0	0	0.5	0	0	0	0	0	1	0	0	0
Plutella_xylostella	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Polyphaenis_sericata	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Propiromorpha_rhodophana	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Pseudargyrotoza_conwagana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Pseudoips_prasinana	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Pseudotelphusa_scalella	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Pterostoma_palpina	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Pyralis_farinalis	4	0	0	0	0.5	0	0	0	0	0	1	0	0	0
Pyrausta_aurata	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Pyrausta_despicata	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Pyrausta_purpuralis	3	0	1	0	1	0	0	0	0	0	0	0	0	0
Pyroderces_argyrogrammos	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Rhigognostis_hufnagelii	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Rhodometra_sacraria	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Rhodophaea_formosa	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Rhyacionia_buoliana	1	0	0	1	0	0	0	0	0	0	0	0	0	0
Rivula_sericealis	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Schoenobius_gigantella	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Schrankia_costaestrigalis	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Sciota_rhenella	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Sclerocona_acutella	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Scoparia_basistrigalis	2	0	0	0	0	0	0	1	0	1	1	0	0	0
Scopula_emutaria	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Scopula_imitaria	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Scopula_nigropunctata	3	0	0.5	0	1	0	0	0	0	0	1	0	0	0
Scopula_rubiginata	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Scythropia_crataegella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Senta_flammea	1	0	0	0	0	1	0	0	0	0	0	0	0	0
Sideridis_rivularis	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Sitochroa_palealis	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Spatalia_argentina	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Spilonota_ocellana	4	0	1	0	0	0	0	0	0	0	0	0	0	0
Spilosoma_lubricipeda	4	0	1	0	1	1	0	0	0	0	0	0	0	0
Spilosoma_lutea	4	0	0	0	1	0	0	0	0	0	0	0	0	0
Spodoptera_exigua	4	0	1	0	1	1	0	0	0	0	0	0	0	0
Stauropus_fagi	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Stegania_trimaculata	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Stemmatophora_brunnealis	3	0	0	0	1	0	0	0	0	0	0	0	0	1
Subacronicta_megacephala	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Symmoca_signatella	4	0	1	0	0.5	0	0	0	0	0	1	0	0	0
Synaphe_punctalis	3	0	0	0	1	0	0	0	0	1	0	0	0	1
Tegostoma_comparalis	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Teleiodes_luculella	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Tethea_ocularis	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Thalera_fimbrialis	3	0	1	0	1	0	0	0	0	0	0	0	0	0
Thaumetopoea_pityocampa	1	0	0	1	0	0	0	0	0	0	0	0	0	0
Thetidia_smaragdaria	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Thumatha_senex	2	0	0	0	0	0	0	1	0	1	0	0	0	0
Timandra_comae	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Trachea_atriplicis	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Trachonitis_cristella	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Trichoplusia_ni	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Tyta_luctuosa	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Udea_ferrugalis	3	0	0	0	1	0	0	0	0	0	0	0	0	0
Watsonalla_binaria	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Xestia_cnigrum	4	0	1	0	1	0	0	0	0	0	0	0	0	0
Yponomeuta_cagnagella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Yponomeuta_evonymella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Yponomeuta_irrorella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Yponomeuta_plumbella	3	0	1	0	0	0	0	0	0	0	0	0	0	0
Ypsolopha_nemorella	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Zebeeba_falsalis	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Zeiraphera_griseana	2	0	0	1	0	0	0	0	0	0	0	0	0	0
Zeuzera_pyrina	4	0	1	0	0	0	0	0	0	0	0	0	1	0

Appendix 9.2: Moth trait matrix (Part 11: Species A-Chi, Traits „Wingsize" - „Time of activity")

Species	Wingsize	Endophagous	Ectophagous	Concealed	Voltinism	Overwintering stage	Gregariously caterpillars	proboscis	Time of activity	
									day	night
Abrostola_asclepiadis	33.5	0	1	0	2	Pupae	0	1	0	1
Acentria_ephemerella	14.5	0.5	0.5	0	2	Larva	0	0	0	1
Acleris_kochiella	16.5	0	0	1	3	Adult	0	0.5	0	1
Acleris_rhombana	20.5	0	0	1	3	Egg	0	1	0	1
Acleris_variegana	18	0	0	1	3	Egg	0	1	0	1
Acontia_lucida	28	0	1	0	3	Pupae	0	1	1	1
Acontia_trabealis	19	0	1	0	3	Pupae	0	1	1	1
Acrobasis_advenella	21	0	0	1	3	Larva	0	1	0	1
Acrobasis_consociella	20.5	0	0	1	2	Larva	0	1	0	1
Acrobasis_fallouella	18	0	0	1	3	Larva	0	1	0	1
Acrobasis_marmorea	20.5	0	0	1	2	Larva	0	1	0	1
Acrobasis_suavella	23	0	0	1	3	Larva	0	1	0	1
Acronicta_aceris	40	0	1	0	3	Pupae	0	1	0	1
Acronicta_cuspis	41	0	1	0	2	Pupae	0	1	0	1
Acronicta_psi	35	0	1	0	3	Pupae	0	1	0	1
Acronicta_rumicis	32.5	0	1	0	3	Pupae	0	1	0	1
Aedia_leucomelas	34	0	1	0	3	Pupae	0	1	0	1
Agapeta_hamana	21	0	0	1	3	Pupae	0	0.5	0	1
Agapeta_zoegana	23	0	0	1	2	Larva	0	1	0	1
Agdistis_tamaricis	22.5	0	1	0	3	Larva	0	1	0	1
Agriphila_brioniellus	24	0	0	1	2	Larva	0	1	0	1
Agriphila_geniculea	22.5	0	0	1	2	Larva	0	1	0	1
Agrotera_nemoralis	22	0	0	1	2	Larva	0	1	0	1
Agrotis_bigramma	44	0	1	0	3	Larva	0	1	0	1
Agrotis_exclamationis	35	0	1	0	3	Larva	0	1	0	1
Agrotis_ipsilon	42.5	0	1	0	3	Larva	0	1	0	1
Agrotis_segetum	33.5	0	1	0	3	Larva	0	1	0	1
Alabonia_geoffrella	19	1	0	0	2	Larva	0	1	1	1
Aleimma_loeflingiana	18.5	0	0	1	2	Egg	0	1	0	1
Amphipyra_pyramidea	46	0	1	0	2	Egg	0	1	0	1
Anacampsis_populella	17.5	0	0	1	2	Egg	0	1	0	1
Anania_crocealis	23.5	0.5	0	0.5	3	Larva	0	1	0	1
Anarta_trifolii	32.5	0	1	0	3	Pupae	0	1	0.5	1
Ancylis_apicella	15.5	0	0	1	3	Larva	0	0	0	1
Ancylis_mitterbacheriana	14.5	0	0	1	2	Larva	0	0	0	1
Ancylis_obtusana	12.5	0	0	1	2	Larva	0	0	0	1
Ancylis_selenana	12.5	0	0	1	3	Larva	0	0	0	1
Ancylis_unculana	16	0	0	1	3	Larva	0	0	0	1
Apeira_syringaria	40	0	1	0	3	Larva	0	1	0	1
Apoda_limacodes	26	0	1	0	2	Pupae	0	0	0	1
Araeopteron_ecphaea	10.5	0	1	0	3	n/a	0	0.5	0	1
Archips_betulana	19	0	0	1	2	Larva	0	0.5	0	1
Archips_podana	22	0	0	1	3	Larva	0	0.5	0	1
Archips_rosana	17.5	0	0	1	3	Larva	0	0.5	0	1
Archips_xylosteana	18	0	0	1	2	Larva	0	0.5	0	1
Arctia_villica	52.5	0	1	0	2	Larva	0	0	0.5	1
Ascotis_selenaria	40.5	0	1	0	3	Pupae	0	1	0	1
Athetis_hospes	28	0	1	0	3	Larva	0	1	0	1
Autographa_gamma	37.5	0	1	0	3	Larva	0	1	0.5	0.5
Bactra_robustana	17	1	0	0	2	Larva	0	0	0	1
Blastobasis_glandulella	17.5	1	0	0	2	Pupae	0	1	0	1
Cacoecimorpha_pronubana	18.5	0	0	1	3	Larva	0	0.5	0	1
Cadra_figulilella	14	0	0	1	3	Larva	0	0.5	0	1
Calamotropha_paludella	27.5	1	0	0	3	Larva	0	0.5	0	1
Callopistria_juventina	36	0	1	0	2	Larva	0	1	0	1
Calophasia_platyptera	28	0	1	0	3	Pupae	0	1	0	1
Caloptilia_alchimiella	11.5	1	0	0	2	Pupae	0	1	0	1
Capperia_loranus	16	0	1	0	3	Larva	0	1	0	1
Caradrina_aspersa	29.5	0	1	0	3	Larva	0	1	0	1
Caradrina_morpheus	35	0.5	0.5	0	3	Larva	0	1	0	1
Carcina_quercana	19	0	0	1	2	Larva	0	0	0	1
Carpatolechia_aenigma	11.5	0	0	1	2	Egg	0	1	0	1
Cataclysta_lemnata	20	0	1	0	3	Larva	0	0.5	0	1
Catarhoe_rubidata	28.5	0	1	0	3	Pupae	0	1	0	1
Catephia_alchymista	45	0	1	0	3	Pupae	0	1	0	1
Catocala_conversa	52	0	1	0	2	Egg	0	1	0	1
Catocala_promissa	62.5	0	1	0	2	Egg	0	1	0	1
Catoptria_falsella	20	0	0	1	3	Larva	0	1	0	1
Catoptria_pinella	21	0	0	1	2	Larva	0	1	0	1
Celypha_flavipalpana	15	1	0	0	3	Larva	0	0	0	1
Cerura_erminea	60.5	0	1	0	2	Pupae	0	0	0	1
Charanyca_ferruginea	36	0	1	0	2	Larva	0	1	0	1
Charanyca_trigrammica	37.5	0	1	0	2	Larva	0	1	0	1
Chiasmia_aestimaria	23	0	0	1	3	Pupae	0	1	0	1
Chiasmia_clathrata	22.5	0	1	0	3	Pupae	0	1	1	1
Chilo_luteellus	31.5	1	0	0	1	Larva	0	0.5	0	1
Chilo_phragmitella	32	1	0	0	1	Larva	0	0.5	0	1
Chilodes_maritima	32.5	1	0	0	2	Larva	0	1	0	1

Appendix 9.2: Moth trait matrix (Part 12: Species Chl-Et, Traits „Wingsize” - „Time of activity”)

Species	Wingsize	Endophagous	Ectophagous	Concealed	Voltinism	Overwintering stage	Gregariously caterpillars	proboscis	Time of activity	
									day	night
Chloantha_hyperici	35	0	1	0	3	Pupae	0	1	0	1
Chloroclystis_vata	16.5	0	1	0	3	Pupae	0	1	0	1
Chrysocrambus_linetella	23.5	0	0	1	2	Larva	0	1	0.5	1
Chrysoteuchia_culmella	20	1	0	0	2	Larva	0	1	0.5	1
Cilix_glaucata	20	0	1	0	3	Pupae	0	0	0	1
Clepsis_consimilana	16	0	1	0	3	Larva	0	0	0	1
Clepsis_rurinana	18.5	0	0	1	3	Larva	0	1	0	1
Clostera_pigra	24.5	0	1	0	3	Pupae	0	0	0	1
Cnaemidophorus_rhododactyla	22	0	0.5	0.5	2	Larva	0	1	0	1
Cnephasia_pasiuana	17.5	0.5	0	0.5	2	Larva	0	0	0	1
Coleophora_colutella	13	0	0	1	2	Larva	0	1	0	1
Colobochyla_salicalis	28	0	1	0	3	Pupae	0	1	0	1
Comibaena_bajularia	25	0	1	0	2	Larva	0	1	0	1
Conisania_luteago	38.5	0	1	0	2	Pupae	0	1	0	1
Cosmia_affinis	31.5	0	0	1	3	Egg	0	1	0	1
Cosmia_trapezina	29	0	0.5	0.5	3	Egg	0	1	0	1
Cosmopterix_lienigiella	11.5	1	0	0	2	Larva	0	1	0	1
Cosmopterix_orichalcea	9	1	0	0	3	Larva	0	1	0	1
Cosmopterix_scribaiella	10.5	1	0	0	2	Larva	0	1	0	1
Cosmorhoe_ocellata	22.5	0	1	0	3	Larva	0	1	0	1
Cossus_cossus	82	1	0	0	1	Larva	0	0	0	1
Costaconvexa_polygrammata	26	0	1	0	3	Pupae	0	1	0	1
Craniophora_ligustri	32.5	0	1	0	3	Pupae	0	1	0	1
Crocallis_elinguaria	36.5	0	1	0	2	Larva	0	0	0	1
Crombrugghia_distans	18.5	0	1	0	3	Larva	0	1	0	1
Cryphia_algae	27	0	0	1	2	Larva	0	1	0	1
Cryphia_ochsi	21	0	0	1	2	Larva	0	1	0	1
Cyclophora_annularia	22.5	0	1	0	3	Pupae	0	1	0	1
Cyclophora_punctaria	25	0	1	0	3	Pupae	0	1	0	1
Cyclophora_puppillaria	23	0	1	0	3	Pupae	0	1	0	1
Cydia_amplana	18	1	0	0	2	Larva	0	0	0	1
Cydia_fagiglandana	15	1	0	0	3	Larva	0	0	0	1
Cydia_pomonella	18	1	0	0	3	Larva	0	0	0	1
Deltote_bankiana	26	0	1	0	3	Pupae	0	1	0.5	0.5
Deltote_pygarga	21	0	1	0	3	Pupae	0	1	0	1
Denticucullus_pygmina	26	0	1	0	2	Larva	0	1	0	1
Diaphora_mendica	33	0	1	0	2	Larva	0	0	0	1
Dichomeris_alacella	13.5	0	0	1	2	Larva	0	1	0	1
Dichomeris_derasella	22	0	0	1	2	Pupae	0	1	0	1
Dichomeris_marginella	15	0	0	1	2	Larva	0	1	0	1
Dioryctria_abietella	29	1	0	0	3	Larva	0	1	0	1
Dioryctria_pineae	32	1	0	0	2	Larva	0	1	0	1
Dioryctria_sylvestrella	31.5	1	0	0	3	Larva	0	1	0	1
Ditula_angustiorana	15	0.5	0	0.5	2	Larva	0	1	0	1
Dolicharthria_punctalis	24.5	0	0	1	3	Larva	0	1	0	1
Donacaula_forficella	28.5	1	0	0	3	Larva	0	0	0	1
Drymonia_dodonaea	35.5	0	1	0	3	Pupae	0	0	0	1
Duponchelia_fovealis	20	0.5	0	0.5	3	Larva	0	1	0	1
Dypterygia_scabriuscula	34.5	0	1	0	3	Pupae	0	1	0	1
Dysauxes_ancilla	23.5	0	1	0	2	Larva	0	1	0.5	1
Dysauxes_famula	22.5	0	1	0	2	Larva	0	1	0.5	1
Dysauxes_punctata	19.5	0	1	0	2	Larva	0	1	0.5	1
Dysgonia_algira	43	0	1	0	3	Larva	0	1	1	1
Dyspessa_ulula	22.5	1	0	0	1	Larva	0	0	1	1
Earias_clorana	18	0	0	1	3	Pupae	0	1	0	1
Earias_vernana	19.5	0	0	1	3	Pupae	0	1	0	1
Eilema_caniola	31.5	0	1	0	2	Larva	0	1	0	1
Eilema_complana	34	0	1	0	2	Larva	0	1	0	1
Eilema_depressa	32	0	1	0	2	Larva	0	1	0	1
Eilema_sororcula	28.5	0	1	0	2	Larva	0	1	0	1
Elaphria_venustula	21	0	1	0	3	Pupae	0	1	0	1
Elegia_similella	20.5	0	0	1	3	Pupae	0	1	0	1
Emmelina_monodactyla	22.5	0	1	0	3	Adult	0	1	0	1
Endotricha_flammealis	20.5	0	0	1	2	Pupae	0	1	0	1
Epagoge_grotiana	15.5	0	0	1	2	Larva	0	0.5	0	1
Ephestia_woodiella	17	0	0	1	3	Larva	0	0.5	0	1
Epiblema_foenella	21	1	0	0	2	Larva	0	0	0	1
Epicallima_formosella	12.5	1	0	0	2	Larva	0	1	0	1
Epinotia_festivana	15	1	0	0	2	Larva	0	0	0	1
Epione_repandaria	27.5	0	1	0	3	Egg	0	1	0	1
Epirrhoe_alternata	22.5	0	1	0	3	Pupae	0	1	1	1
Ethmia_bipunctella	23.5	0	0	1	3	Pupae	0	1	0	1
Ethmia_quadrillella	17	0	0	1	3	Pupae	0	1	0	1
Ethmia_terminella	19	0	0	1	3	Pupae	0	1	0	1
Etiella_zinckenella	21.5	1	0	0	3	Larva	0	1	0	1

Appendix 9.2: Moth trait matrix (Part 13: Species Eu-Mac, Traits „Wingsize" - „Time of activity")

Species	Wingsize	Endophagous	Ectophagous	Concealed	Voltinism	Overwintering stage	Gregariously caterpillars	proboscis	Time of activity	
									day	night
Eublemma_parva	12	0.5	0.5	0	3	Pupae	0	1	1	1
Euchromius_superbellus	14.75	0	0	1	2	Larva	0	1	0	1
Eucosma_cana	19.5	1	0	0	2	Larva	0	0	0	1
Eucosma_conterminana	17	0	0	1	2	Larva	0	1	0	1
Eucosma_metzneriana	20	1	0	0	2	Larva	0	0	0	1
Eudonia_delunella	17.5	0	0	1	2	Larva	0	1	0	1
Eudonia_lacustrata	18.5	0	0	1	2	Larva	0	1	0	1
Eudonia_mercurella	17.5	0	0	1	2	Larva	0	1	0	1
Eudonia_pallida	16.5	0	0	1	2	Larva	0	1	0	1
Eupithecia_centaureata	18	0	1	0	3	Pupae	0	1	0	1
Eupithecia_haworthiata	13	1	0	0	2	Pupae	0	1	0	1
Eupithecia_ultimaria	16	0	1	0	3	Pupae	0	1	0	1
Euplagia_quadripunctaria	47	0	1	0	2	Larva	0	1	0.5	0.5
Euplexia_lucipara	29.5	0	1	0	3	Pupae	0	1	0	1
Euproctis_chrysorrhoea	39	0	1	0	2	Larva	1	0	0	1
Eutelia_adulatrix	27	0	1	0	3	Pupae	0	1	0	1
Euzophera_fuliginosella	14.5	0	0	1	3	Larva	0	1	0	1
Evergestis_extimalis	26.5	0	0	1	3	Larva	0	1	0	1
Furcula_bifida	40	0	1	0	3	Pupae	0	0	0	1
Galleria_mellonella	34.5	0	0	1	3	Larva	0	0	0	1
Gastropacha_quercifolia	70	0	1	0	2	Larva	0	0	0	1
Glyptoteles_leucacrinella	15.5	0	0	1	3	Larva	0	1	0	1
Gymnoscelis_rufifasciata	17	0	1	0	3	Pupae	0	1	0	1
Gypsonoma_aceriana	14	1	0	0	2	Larva	0	0	0	1
Gypsonoma_minutana	12.5	0	0	1	2	Larva	0	0	0	1
Habrosyne_pyritoides	37.5	0	1	0	3	Pupae	0	1	0	1
Hadena_bicruris	35	0.5	0.5	0	3	Pupae	0	1	0	1
Harpyia_milhauseri	55	0	1	0	3	Pupae	0	0	0	1
Hedya_nubiferana	18	0	0	1	2	Larva	0	1	0	1
Hedya_pruniana	17	0	0	1	2	Larva	0	1	0	1
Helicoverpa_armigera	35	0.5	0.5	0	3	Pupae	0	1	1	1
Heliothis_viriplaca	33	0	1	0	3	Pupae	0	1	1	1
Hellinsia_inulae	18	0.5	0.5	0	3	Larva	0	1	0	1
Hemistola_chrysoprasaria	30	0	1	0	3	Larva	0	1	0	1
Hemithea_aestivaria	25.5	0	1	0	3	Larva	0	1	0	1
Herminia_tarsicrinalis	30	0	1	0	3	Larva	0	1	0	1
Herminia_tarsipennalis	32.5	0	1	0	3	Larva	0	1	0	1
Herminia_tenuialis	22.5	0	1	0	3	Larva	0	1	0	1
Heterogenea_asella	17.5	0	1	0	2	Pupae	0	0	1	1
Homaloxestis_briantiella	19	0	0	1	3	Pupae	0	1	0	1
Homoeosoma_sinuella	20.5	0	0	1	3	Larva	0	0	1	1
Hoplodrina_ambigua	33	0	1	0	3	Larva	0	1	0	1
Horisme_tersata	33.5	0	1	0	3	Pupae	0	1	0	1
Horisme_vitalbata	32.5	0	1	0	3	Pupae	0	1	0	1
Hypomecis_punctinalis	50.5	0	1	0	3	Pupae	0	1	0	1
Hypsopygia_costalis	19.5	0	0	1	3	Larva	0	1	0	1
Hypsopygia_glaucinalis	26.5	0	0	1	2	Larva	0	1	0	1
Idaea_aversata	27.5	0	1	0	3	Larva	0	1	0	1
Idaea_degeneraria	21.5	0	1	0	3	Larva	0	1	0	1
Idaea_dimidiata	17.5	0	1	0	3	Larva	0	1	0	1
Idaea_filicata	17.5	0	1	0	3	Larva	0	1	0	1
Idaea_fuscovenosa	17.5	0	1	0	2	Larva	0	1	0	1
Idaea_muricata	16.5	0	1	0	2	Larva	0	1	1	1
Idaea_politaria	16.5	0	1	0	2	Larva	0	1	0	1
Idaea_rusticata	16	0	1	0	3	Larva	0	1	0	1
Idaea_seriata	17.5	0	1	0	3	Larva	0	1	0	1
Idaea_subsericeata	19.5	0	1	0	3	Larva	0	1	0	1
Ipimorpha_subtusa	28.5	0	0	1	2	Egg	0	1	0	1
Isturgia_arenacearia	24.5	0	1	0	3	Pupae	0	1	0.5	1
Lacanobia_oleracea	34.5	0	1	0	3	Pupae	0	1	0	1
Lacanobia_wlatinum	39.5	0	1	0	3	Pupae	0	1	0	1
Laelia_coenosa	48	0	1	0	2	Larva	0	0	0	1
Lamoria_anella	33	0	0	1	3	Larva	0	0	0	1
Laothoe_populi	77.5	0	1	0	2	Pupae	0	0	0	1
Lasiocampa_quercus	60	0	1	0	2	Larva	0	0	0	1
Laspeyria_flexula	25	0	1	0	3	Larva	0	1	0	1
Leucania_loreyi	39	0	1	0	3	Larva	0	1	0	1
Leucania_obsoleta	38	0	1	0	3	Larva	0	1	0	1
Ligdia_adustata	22.5	0	1	0	3	Pupae	0	1	0	1
Lithosia_quadra	45	0	1	0	2	Larva	0	1	0	1
Lomaspilis_marginata	34	0	1	0	3	Pupae	0	1	1	1
Lomographa_bimaculata	24	0	1	0	2	Pupae	0	1	0	1
Loxostege_sticticalis	26.5	0	0	1	3	Larva	0	1	0.5	0.5
Lygephila_craccae	43	0	1	0	3	Egg	0	1	0	1
Lymantria_dispar	43.5	0	1	0	2	Egg	1	0	1	1
Macaria_alternata	24.5	0	1	0	2	Pupae	0	1	0	1
Macaria_liturata	24.5	0	1	0	2	Pupae	0	1	0	1
Macaria_notata	30	0	1	0	2	Pupae	0	1	0	1

Appendix 9.2: Moth trait matrix (Part 14: Species Mal-Phe, Traits „Wingsize” - „Time of activity”)

Species	Wingsize	Endophagous	Ectophagous	Concealed	Voltinism	Overwintering stage	Gregariously caterpillars	proboscis	Time of activity day	night
Malacosoma_castrensis	36	0	1	0	2	Egg	1	0	0	1
Mecyna_asinalis	29	0	0	1	3	Larva	0	1	0	1
Meganola_albula	21	0	1	0	2	Larva	0	1	0	1
Meganola_togatulalis	21	0	1	0	2	Larva	0	0.5	0	1
Menophra_abruptaria	39	0	1	0	3	Pupae	0	1	0	1
Mesapamea_secalis	28.5	0.5	0.5	0	2	Larva	0	1	0	1
Metachrostis_velox	18	1	0	0	3	Pupae	0	0.5	0	1
Metasia_ophialis	16	0	0	1	2	Larva	0	1	0	1
Metendothenia_atropunctana	16	0	0	1	3	Larva	0	1	0	1
Miltochrista_miniata	25	0	1	0	2	Larva	0	1	0	1
Mimas_tiliae	62.5	0	1	0	2	Pupae	0	0	0	1
Minoa_murinata	16	0	1	0	3	Pupae	0	1	1	1
Minucia_lunaris	57	0	1	0	2	Pupae	0	1	0	1
Moma_alpium	32.5	0	1	0	2	Pupae	0	1	0	1
Monopis_monachella	16	0	0	1	2	Larva	0	0	0	1
Monopis_obviella	11.5	0	0	1	3	Larva	0	0	0	1
Mormo_maura	60	0	1	0	2	Larva	0	1	0	1
Morophaga_choragella	25.5	1	0	0	2	Larva	0	0	0	1
Morophaga_morella	24.5	1	0	0	2	Larva	0	0	0	1
Myelois_circumvoluta	26.5	1	0	0	3	Larva	0	0	1	1
Mythimna_albipuncta	32.5	0	1	0	3	Larva	0	1	0	1
Mythimna_congrua	33.5	0	1	0	3	Larva	0	1	0	1
Mythimna_pallens	32.5	0	1	0	3	Larva	0	1	0	1
Mythimna_riparia	32.5	0	1	0	3	Larva	0	1	0	1
Mythimna_sicula	29	0	1	0	3	Larva	0	1	0	1
Mythimna_straminea	36	0	1	0	3	Larva	0	1	0	1
Mythimna_turca	41	0	1	0	3	Larva	0	1	0	1
Mythimna_vitellina	39.5	0	1	0	3	Larva	0	1	0	1
Nephopterix_angustella	22.5	0.5	0	0.5	3	Pupae	0	1	0	1
Neurothaumasia_ankerella	14	1	0	0	2	Larva	0	0	0	1
Noctua_fimbriata	50	0	1	0	2	Larva	0	1	0	1
Noctua_janthina	35	0	1	0	2	Larva	0	1	0	1
Noctua_pronuba	50	0	1	0	2	Larva	0	1	0	1
Noctua_tirrenica	49	0	1	0	3	Larva	0	1	0	1
Nola_aerugula	17.5	0	1	0	2	Larva	0	1	0	1
Nola_chlamitulalis	18	0	1	0	2	Pupae	0	0.5	0	1
Nomophila_noctuella	29	0	0	1	2	Larva	0	1	0.5	0.5
Notocelia_cynosbatella	19	0	0	1	2	Larva	0	1	0	1
Notocelia_roborana	19.5	0	0	1	2	Larva	0	1	0	1
Notocelia_rosaecolana	18	0	0	1	2	Larva	0	0.5	0	1
Notocelia_uddmanniana	17.5	0	0	1	2	Larva	0	0.5	0	1
Notodonta_tritophus	50	0	1	0	3	Pupae	0	0	0	1
Nyctegretis_lineana	17.5	0	0	1	3	Larva	0	1	1	1
Nycterosea_obstipata	19.5	0	1	0	3	Pupae	0	1	0	1
Nyctobrya_muralis	30.5	0	0	1	3	Larva	0	1	0	1
Ochropleura_plecta	27.5	0	1	0	3	Larva	0	1	0	1
Ocneria_rubea	28.5	0	1	0	3	Larva	0	0	0	1
Oligia_latruncula	25.5	0.5	0.5	0	3	Larva	0	1	0	1
Oncocera_semirubella	23	0	0	1	2	Larva	0	1	1	1
Opisthograptis_luteolata	34.5	0	1	0	3	Pupae	0	1	0	1
Orgyia_antiqua	27.5	0	1	0	3	Egg	0	0	0	1
Ostrinia_nubilalis	28	1	0	0	3	Larva	0	1	0.5	1
Palpita_vitrealis	29	0	0	1	2	Larva	0	1	0	1
Pammene_fasciana	15.5	1	0	0	2	Larva	0	0.5	0	1
Pandemis_cerasana	20	0	0	1	2	Larva	0	1	0	1
Pandemis_heparana	20	0	0	1	3	Larva	0	1	0	1
Paradoxus_osyridellus	18	0	0	1	2	Egg	0	0	0	1
Parahypopta_caestrum	30	1	0	0	2	Larva	0	0	0	1
Parapoynx_stratiotata	21.5	0	0	1	3	Larva	0	0.5	0	1
Parascotia_fuliginaria	23	0	1	0	2	Larva	0	0	0	1
Paraswammerdamia_albicapitella	11.5	0.5	0	0.5	3	Larva	1	1	0	1
Paraswammerdamia_nebulella	12.5	0.5	0	0.5	3	Larva	1	0	0	1
Paratalanta_pandalis	27	0	0.5	0.5	3	Larva	0	1	0	1
Parectopa_robiniella	6.5	1	0	0	3	Pupae	0	1	0.5	0.5
Pasiphila_chloerata	18	0	1	0	2	Egg	0	1	0	1
Pasiphila_rectangulata	17.5	0	1	0	2	Egg	0	1	0	1
Pechipogo_plumigeralis	24	0	1	0	3	Larva	0	1	0	1
Pediasia_contaminella	25	1	0	0	3	Larva	0	1	0	1
Pelochrista_mollitana	16.5	1	0	0	2	Larva	0	0.5	0	1
Pelosia_muscerda	26	0	1	0	2	Larva	0	1	0	1
Pempelia_palumbella	24	0	0	1	3	Larva	0	0	1	1
Penestoglossa_dardoinella	20.5	0	1	0	2	Larva	0	0	0	1
Peribatodes_rhomboidaria	34	0	1	0	3	Pupae	0	1	0	1
Peridea_anceps	57.5	0	1	0	2	Pupae	0	0	0	1
Petrophora_chlorosata	34	0	1	0	2	Pupae	0	1	0	1
Phalera_bucephala	48.5	0	1	0	2	Pupae	1	0	0	1
Phalonidia_albipalpana	13	0	0	1	3	Larva	0	0.5	0	1
Pheosia_tremula	50	0	1	0	3	Pupae	0	0	0	1

Appendix 9.2: Moth trait matrix (Part 15: Species Phi-Z, Traits „Wingsize” - „Time of activity”)

Species	Wingsize	Endophagous	Ectophagous	Concealed	Voltinism	Overwintering stage	Gregariously caterpillars	proboscis	Time of activity	
									day	night
Philereme_transversata	33	0	1	0	2	Egg	0	1	0	1
Philereme_vetulata	27	0	1	0	2	Egg	0	1	0	1
Photedes_morrisii	30	0	1	0	2	Larva	0	1	0	1
Phragmataecia_castaneae	38.5	1	0	0	1	Larva	0	0	0	1
Phragmatobia_fuliginosa	32.5	0	1	0	3	Larva	0	0	0.5	1
Phtheochroa_pulvillana	18.5	1	0	0	2	Larva	0	0.5	0	1
Phycitodes_binaevella	24.5	1	0	0	3	Larva	0	1	0	1
Phyllophila_obliterata	22.5	0	1	0	3	Pupae	0	1	0	1
Phytometra_viridaria	19.5	0	1	0	3	Pupae	0	1	0	1
Piniphila_bifasciana	13.5	0	0	1	2	Larva	0	0.5	0	1
Platyptilia_farfarellus	18.5	0.5	0	0.5	3	Larva	0	1	0	1
Platytes_alpinella	19.5	0	0	1	2	Larva	0	1	0	1
Pleuropyta_ruralis	31	0	0	1	3	Larva	0	1	0	1
Plodia_interpunctella	17	0	0	1	3	n/a	0	1	1	1
Plutella_xylostella	14	0	1	0	3	Larva	0	1	0	1
Polyphaenis_sericata	42	0	1	0	3	Larva	0	1	0	1
Propiromorpha_rhodophana	16	0	0	1	2	Pupae	0	0.5	0	1
Pseudargyrotoza_conwagana	12.5	1	0	0	2	Pupae	0	1	0	1
Pseudoips_prasinana	32.5	0	1	0	3	Pupae	0	1	0	1
Pseudotelphusa_scalella	13	0	1	0	2	Pupae	0	1	0	1
Pterostoma_palpina	45	0	1	0	3	Pupae	0	0	0	1
Pyralis_farinalis	26	0	0	1	2	Larva	0	1	0	1
Pyrausta_aurata	19	0	0	1	3	Larva	0	1	0.5	0.5
Pyrausta_despicata	16.5	0	0	1	3	Larva	1	1	0.5	0.5
Pyrausta_purpuralis	17.5	0	0	1	3	Larva	0	1	0.5	0.5
Pyroderces_argyrogrammos	14	1	0	0	3	Larva	0	1	0	1
Rhigognostis_hufnagelii	11	0	0	1	2	Adult	0	1	0	1
Rhodometra_sacraria	22.5	0	1	0	3	n/a	0	1	1	1
Rhodophaea_formosa	19.5	0	0	1	2	Larva	0	1	0	1
Rhyacionia_buoliana	20	0.5	0	0.5	2	Larva	0	0	0	1
Rivula_sericealis	20	0	1	0	3	Larva	0	1	0.5	0.5
Schoenobius_gigantella	36	1	0	0	3	Larva	0	0	0	1
Schrankia_costaestrigalis	19	0	1	0	3	Larva	0	1	0	1
Sciota_rhenella	22.5	0	0	1	3	Pupae	0	1	0	1
Sclerocona_acutella	26.5	0	0	1	2	Pupae	0	1	0	1
Scoparia_basistrigalis	21.5	0	0	1	2	Larva	0	1	0	1
Scopula_emutaria	23	0	1	0	3	Larva	0	1	0	1
Scopula_imitaria	22.5	0	1	0	3	Larva	0	1	0	1
Scopula_nigropunctata	25	0	1	0	3	Larva	0	1	0	1
Scopula_rubiginata	18.5	0	1	0	3	Larva	0	1	1	1
Scythropia_crataegella	13.5	0	0	1	3	Egg	1	0	0	1
Senta_flammea	36	0	1	0	2	Pupae	0	1	0	1
Sideridis_rivularis	28.5	0.5	0.5	0	3	Pupae	0	1	0	1
Sitochroa_palealis	29	0	0	1	3	Larva	1	1	0	1
Spatalia_argentina	35.5	0	1	0	3	Pupae	0	0	0	1
Spilonota_ocellana	14.5	0	0	1	2	Larva	0	0	0	1
Spilosoma_lubricipeda	41	0	1	0	2	Larva	0	1	0	1
Spilosoma_lutea	34	0	1	0	2	Larva	0	0	0	1
Spodoptera_exigua	29	0	1	0	3	Larva	0	1	0	1
Stauropus_fagi	52.5	0	1	0	3	Pupae	0	0	0	1
Stegania_trimaculata	19.5	0	1	0	3	Pupae	0	1	0.5	1
Stemmatophora_brunnealis	20	0	0	1	2	Larva	0	0.5	0	1
Subacronicta_megacephala	42	0	1	0	3	Pupae	0	1	0	1
Symmoca_signatella	16	0	0	1	2	Larva	0	1	0	1
Synaphe_punctalis	24.5	0	0	1	2	Larva	0	0	0	1
Tegostoma_comparalis	17	0	0	1	3	Larva	0	1	0	1
Teleiodes_luculella	11	0	0	1	3	Pupae	0	1	0	1
Tethea_ocularis	35	0	1	0	3	Pupae	0	1	0	1
Thalera_fimbrialis	27.5	0	0	1	2	Larva	0	1	1	1
Thaumetopoea_pityocampa	38.5	0	1	0	2	Larva	1	0	0	1
Thetidia_smaragdaria	35	0	1	0	3	Larva	0	1	0	1
Thumatha_senex	17.5	0	1	0	2	Larva	0	0	0	1
Timandra_comae	27.5	0	1	0	3	Larva	0	1	1	1
Trachea_atriplicis	40	0	1	0	3	Pupae	0	1	0	1
Trachonitis_cristella	19.5	0	0	1	3	Larva	0	1	0	1
Trichoplusia_ni	35	0	1	0	3	Larva	0	1	0	1
Tyta_luctuosa	23.5	0	1	0	3	Pupae	0	1	1	1
Udea_ferrugalis	20	0	1	0	3	Larva	0	1	0	1
Watsonalla_binaria	24	0	1	0	3	Pupae	0	1	0	1
Xestia_cnigrum	38.5	0	1	0	3	Larva	0	1	0	1
Yponomeuta_cagnagella	22.5	0.5	0	0.5	2	Larva	1	1	1	1
Yponomeuta_evonymella	20.5	0.5	0	0.5	2	Larva	1	1	1	1
Yponomeuta_irrorella	22	0.5	0	0.5	2	Larva	1	1	1	1
Yponomeuta_plumbella	18	0.5	0	0.5	3	Egg	1	1	1	1
Ypsolopha_nemorella	22.5	0	0	1	2	Egg	1	1	0	1
Zebeeba_falsalis	18	0	1	0	3	Larva	0	1	0	1
Zeiraphera_griseana	19.5	0	0	1	2	Larva	0	0.5	0	1
Zeuzera_pyrina	47.5	1	0	0	1	Larva	0	0	0	1

Appendix 9.2: Moth trait matrix (Part 16: Species A-Chi, Traits „Migrating” - „Northern distribution”)

		Habitat type				Northern distribution				
Species	migrating	Forest	Scrub	Grassland	Reed	N 46-50	N 51-55	N 56-60	N 61-65	N 66-70
Abrostola_asclepiadis	0	0.5	1	1	0	1	1	1	0	0
Acentria_ephemerella	0	0	0	0	1	1	1	1	1	0
Acleris_kochiella	0	1	1	0	0	1	1	1	0	0
Acleris_rhombana	0	0.5	1	0	0	1	1	1	1	0
Acleris_variegana	0	0.5	1	0	0	1	1	1	1	0
Acontia_lucida	1	0	1	1	0	1	0	0	0	0
Acontia_trabealis	0	0.5	0.5	1	0.5	1	1	1	0	0
Acrobasis_advenella	0	1	1	0	0	1	1	1	0.5	0
Acrobasis_consociella	0	1	1	0	0	1	1	1	0	0
Acrobasis_fallouella	0	1	1	0	0	0.5	0	0	0	0
Acrobasis_marmorea	0	0.5	1	0	0	1	1	0.5	0	0
Acrobasis_suavella	0	1	1	0	0	1	1	0	0	0
Acronicta_aceris	0	1	0.5	0	0	1	1	1	0	0
Acronicta_cuspis	0	1	0	0	0.5	1	1	1	0	0
Acronicta_psi	0	1	1	0	0	1	1	1	1	0
Acronicta_rumicis	0	0.5	1	1	0.5	1	1	1	1	0
Aedia_leucomelas	0	0	1	1	0	0.5	0	0	0	0
Agapeta_hamana	0	0	0	1	0	1	1	1	0	0
Agapeta_zoegana	0	0	0	1	0	1	1	1	0	0
Agdistis_tamaricis	0	0	1	0	0	0.5	0	0	0	0
Agriphila_brioniellus	0	0	0	1	0	1	0	0	0	0
Agriphila_geniculea	0	0	0	1	0	1	1	0.5	0	0
Agrotera_nemoralis	0	1	1	0	0	1	1	1	0	0
Agrotis_bigramma	1	0	0.5	1	0	1	1	0	0	0
Agrotis_exclamationis	1	0.5	1	1	0.5	1	1	1	1	0
Agrotis_ipsilon	1	1	1	1	1	1	1	1	1	0
Agrotis_segetum	1	0	1	1	0	1	1	1	0.5	0
Alabonia_geoffrella	0	1	0	0	0	1	0.5	0	0	0
Aleimma_loeflingiana	0	0	1	1	0	1	1	1	0	0
Amphipyra_pyramidea	0	1	1	0	0	1	1	1	0.5	0
Anacampsis_populella	0	1	1	0	0	1	1	1	1	1
Anania_crocealis	0	0	0.5	0.5	1	1	1	1	0	0
Anarta_trifolii	0	0	0	1	0	1	1	1	0	0
Ancylis_apicella	0	1	1	0	0.5	1	1	1	0.5	0
Ancylis_mitterbacheriana	0	1	1	0	0	1	1	1	0	0
Ancylis_obtusana	0	0.5	1	0	0	1	1	1	0	0
Ancylis_selenana	0	0.5	1	0	0	1	1	1	0.5	0
Ancylis_unculana	0	0.5	1	0	0	1	1	1	0	0
Apeira_syringaria	0	1	0	0	0	1	1	1	0	0
Apoda_limacodes	0	1	1	0	0	1	1	1	0	0
Araeopteron_ecphaea	0	0	0	0	1	0.5	0	0	0	0
Archips_betulana	0	1	1	0	0	1	1	1	0	0
Archips_podana	0	1	1	0	0	1	1	1	0	0
Archips_rosana	0	1	1	0	0	1	1	1	1	0
Archips_xylosteana	0	1	1	0	0	1	1	1	0	0
Arctia_villica	0	1	1	0	0	1	1	0	0	0
Ascotis_selenaria	0	0.5	1	0.5	0	1	0.5	0	0	0
Athetis_hospes	1	1	1	1	0	1	0	0	0	0
Autographa_gamma	1	1	1	1	1	1	1	1	1	1
Bactra_robustana	0	0	0	0.5	1	1	1	1	0	0
Blastobasis_glandulella	0	1	1	0	0	1	1	0	0	0
Cacoecimorpha_pronubana	0	1	1	0	0	1	1	0	0	0
Cadra_figulilella	0	0.5	1	0.5	0	1	0	0	0	0
Calamotropha_paludella	0	0	0	0	1	1	1	1	0	0
Callopistria_juventina	0	1	0	0	0	1	1	0.5	0	0
Calophasia_platyptera	0	0	1	1	0	0.5	0	0	0	0
Caloptilia_alchimiella	0	1	1	0	0	1	1	1	0	0
Capperia_loranus	0	0	0.5	1	0	1	0	0	0	0
Caradrina_aspersa	0	0.5	1	1	0	0.5	0	0	0	0
Caradrina_morpheus	0	0	1	1	0.5	1	1	1	1	0
Carcina_quercana	0	1	1	0	0	1	1	1	0	0
Carpatolechia_aenigma	0	1	0	0	0	1	1	0	0	0
Cataclysta_lemnata	0	0	0	0	1	1	1	1	1	0
Catarhoe_rubidata	0	1	1	1	0	1	1	1	0	0
Catephia_alchymista	0	1	0.5	0	0	1	0	0	0	0
Catocala_conversa	0	1	0.5	0	0	0.5	0	0	0	0
Catocala_promissa	0	1	0	0	0	1	1	1	0	0
Catoptria_falsella	0	1	0.5	0	0	1	1	1	1	0
Catoptria_pinella	0	1	1	0	0.5	1	1	1	1	0
Celypha_flavipalpana	0	0	1	1	0	1	1	0	0	0
Cerura_erminea	0	1	0.5	0	0.5	1	1	1	0	0
Charanyca_ferruginea	0	1	1	0	0	1	1	1	1	0
Charanyca_trigrammica	0	0	0.5	1	0.5	1	1	1	0	0
Chiasmia_aestimaria	0	0	0.5	1	0	1	0	0	0	0
Chiasmia_clathrata	0	0	0.5	1	0	1	1	1	1	1
Chilo_luteellus	0	0	0	0	1	0.5	0	0	0	0
Chilo_phragmitella	0	0	0	0	1	1	1	1	1	0
Chilodes_maritima	0	0	0	0	1	1	1	1	0.5	0

Appendix 9.2: Moth trait matrix (Part 17: Species Chl-Et, Traits „Migrating” - „Northern distribution”)

		Habitat type				Norhern distribution				
Species	migrating	Forest	Scrub	Grassland	Reed	N 46-50	N 51-55	N 56-60	N 61-65	N 66-70
Chloantha_hyperici	0	0.5	1	1	0	1	1	1	0	0
Chloroclystis_vata	0	1	1	1	0	1	1	1	1	1
Chrysocrambus_linetella	0	0	0	1	0	0.5	0	0	0	0
Chrysoteuchia_culmella	0	0	1	1	0	1	1	1	1	1
Cilix_glaucata	0	1	1	0	0	1	1	1	0	0
Clepsis_consimilana	0	1	1	0	0	1	1	0.5	0	0
Clepsis_rurinana	0	1	1	1	0	1	1	1	1	0
Clostera_pigra	0	1	1	0	0.5	1	1	1	1	1
Cnaemidophorus_rhododactyla	0	0.5	1	0	0	1	1	1	0	0
Cnephasia_pasiuana	0	0.5	1	1	0	1	1	1	0	0
Coleophora_colutella	0	0	1	1	0	1	1	1	1	0
Colobochyla_salicalis	0	1	1	0	0	1	1	1	0.5	0
Comibaena_bajularia	0	1	0.5	0	0	1	1	1	0	0
Conisania_luteago	0	0	1	1	0	1	1	1	0	0
Cosmia_affinis	0	1	0.5	0	0	1	1	1	0	0
Cosmia_trapezina	0	1	0.5	0	0	1	1	1	1	0
Cosmopterix_lienigiella	0	0	0	0	1	1	1	1	1	0
Cosmopterix_orichalcea	0	0	0	1	1	1	1	1	1	0
Cosmopterix_scribaiella	0	0	0	0	1	1	1	1	0	0
Cosmorhoe_ocellata	0	0.5	1	0	0	1	1	1	1	0
Cossus_cossus	0	1	1	0	0	1	1	1	1	1
Costaconvexa_polygrammata	1	0	0.5	1	0.5	1	1	1	0.5	0
Craniophora_ligustri	0	1	0.5	0	0	1	1	1	0	0
Crocallis_elinguaria	0	1	1	0.5	0	1	1	1	1	0
Crombrugghia_distans	0	0	1	1	0	1	1	1	0	0
Cryphia_algae	0	1	1	0	0	1	1	0	0	0
Cryphia_ochsi	0	1	0	0	0	0.5	0	0	0	0
Cyclophora_annularia	0	1	1	0	0	1	1	1	0	0
Cyclophora_punctaria	0	1	0.5	0	0	1	1	1	0	0
Cyclophora_puppillaria	1	1	0.5	0	0	1	1	0	0	0
Cydia_amplana	0	1	0	0	0	1	1	0.5	0	0
Cydia_fagiglandana	0	1	0	0	0	1	1	1	0	0
Cydia_pomonella	0	1	0.5	0	0	1	1	1	0.5	0
Deltote_bankiana	0	0	0	1	0.5	1	1	1	0	0
Deltote_pygarga	0	1	0	0	0	1	1	1	0.5	0
Denticucullus_pygmina	0	0	0	1	1	1	1	1	0.5	0
Diaphora_mendica	0	0	0	1	0	1	1	1	1	0
Dichomeris_alacella	0	0.5	1	1	0	1	1	1	0	0
Dichomeris_derasella	0	1	1	0	0	1	1	1	0	0
Dichomeris_marginella	0	0	1	0	0	1	1	0	0	0
Dioryctria_abietella	0	1	0.5	0	0	1	1	1	0.5	0
Dioryctria_pineae	0	1	0	0	0	0.5	0	0	0	0
Dioryctria_sylvestrella	0	1	0	0	0	1	1	1	0	0
Ditula_angustiorana	0	0.5	1	0	0	1	1	0.5	0	0
Dolicharthria_punctalis	0	1	1	1	0.5	1	1	0.5	0	0
Donacaula_forficella	0	0	0	0	1	1	1	1	0.5	0
Drymonia_dodonaea	0	1	0	0	0	1	1	0.5	0	0
Duponchelia_fovealis	1	0	0	0.5	1	1	1	1	0	0
Dypterygia_scabriuscula	0	0.5	0.5	1	0.5	1	1	1	0.5	0
Dysauxes_ancilla	0	1	1	1	0	1	1	0	0	0
Dysauxes_famula	0	0	1	1	0	0.5	0	0	0	0
Dysauxes_punctata	0	0	1	1	0	0.5	0	0	0	0
Dysgonia_algira	1	0	1	1	0	0.5	0	0	0	0
Dyspessa_ulula	0	0	0.5	1	0	1	0	0	0	0
Earias_clorana	0	0.5	0.5	0	0.5	1	1	1	0	0
Earias_vernana	0	1	0	0	0.5	1	1	0	0	0
Eilema_caniola	0	1	1	1	0	1	1	0	0	0
Eilema_complana	0	1	1	1	0	1	1	1	0.5	0
Eilema_depressa	0	1	1	0	0	1	1	1	0.5	0
Eilema_sororcula	0	1	1	0	0	1	1	1	0	0
Elaphria_venustula	0	0.5	1	1	0.5	1	1	1	0	0
Elegia_similella	0	1	0	0	0	1	1	1	0	0
Emmelina_monodactyla	0	0	0.5	1	0	1	1	1	0	0
Endotricha_flammealis	0	0.5	1	0	0	1	1	0	0	0
Epagoge_grotiana	0	1	1	0	0	1	1	1	1	0
Ephestia_woodiella	0	0.5	1	0.5	0	1	1	0	0	0
Epiblema_foenella	0	0	1	1	0	1	1	1	1	0
Epicallima_formosella	0	1	1	0	0	1	1	0	0	0
Epinotia_festivana	0	1	1	0	0	1	0	0	0	0
Epione_repandaria	0	1	0	0	0	1	1	1	1	0
Epirrhoe_alternata	0	1	1	1	0	1	1	1	1	1
Ethmia_bipunctella	0	0.5	1	1	0	1	1	1	0	0
Ethmia_quadrillella	0	1	0.5	0	0	1	1	1	1	0
Ethmia_terminella	0	0	0	1	0	1	1	1	0	0
Etiella_zinckenella	0	0	0	1	0	1	1	1	0	0

Appendix 9.2: Moth trait matrix (Part 18: Species Eu-Mac, Traits „Migrating” - „Northern distribution”)

		Habitat type				Northern distribution				
Species	migrating	Forest	Scrub	Grassland	Reed	N 46-50	N 51-55	N 56-60	N 61-65	N 66-70
Eublemma_parva	1	0	0	1	0	1	1	0	0	0
Euchromius_superbellus	0	0	0	1	0	0.5	0	0	0	0
Eucosma_cana	0	0	1	1	0	1	1	1	1	0
Eucosma_conterminana	0	0	1	1	0	1	1	1	0	0
Eucosma_metzneriana	0	0	0	1	0	1	1	1	0	0
Eudonia_delunella	0	0	1	1	0	1	1	0	0	0
Eudonia_lacustrata	0	1	1	0	0	1	1	1	1	0.5
Eudonia_mercurella	0	1	1	0	0	1	1	1	0.5	0
Eudonia_pallida	0	0.5	0.5	1	0.5	1	1	1	0.5	0
Eupithecia_centaureata	0	0	1	1	0	1	1	1	1	0
Eupithecia_haworthiata	0	0.5	1	0	0	1	1	0.5	0	0
Eupithecia_ultimaria	0	0	1	0	0	1	0.5	0	0	0
Euplagia_quadripunctaria	1	0	1	1	0	1	0.5	0	0	0
Euplexia_lucipara	0	1	0.5	0	0	1	1	1	1	0
Euproctis_chrysorrhoea	0	1	1	0	0	1	1	0	0	0
Eutelia_adulatrix	0	1	1	0	0	0.5	0	0	0	0
Euzophera_fuliginosella	0	1	0.5	0	0	1	1	1	0	0
Evergestis_extimalis	1	0	1	1	0	1	1	1	1	0
Furcula_bifida	0	1	1	0	0.5	1	1	1	0.5	0
Galleria_mellonella	0	1	1	1	0	1	1	1	0	0
Gastropacha_quercifolia	0	1	1	0	0.5	1	1	1	0	0
Glyptoteles_leucacrinella	0	0	0	1	1	1	0	0	0	0
Gymnoscelis_rufifasciata	0	1	1	1	0	1	1	1	0.5	0
Gypsonoma_aceriana	0	1	1	1	0	1	1	0.5	0	0
Gypsonoma_minutana	0	1	1	1	0	1	1	1	0	0
Habrosyne_pyritoides	0	1	1	0	0	1	1	1	0.5	0
Hadena_bicruris	0	0	0.5	1	0	1	1	1	0	0
Harpyia_milhauseri	0	1	0	0	0	1	1	0.5	0	0
Hedya_nubiferana	0	1	1	0	0	1	1	1	1	0
Hedya_pruniana	0	1	1	0	0	1	1	1	0	0
Helicoverpa_armigera	1	0	1	1	0	1	1	1	0	0
Heliothis_viriplaca	1	0	1	1	0	1	1	1	0	0
Hellinsia_inulae	0	0	1	1	0.5	0.5	0	0	0	0
Hemistola_chrysoprasaria	0	1	1	0	0	1	1	1	0	0
Hemithea_aestivaria	0	1	1	0	0	1	1	1	0	0
Herminia_tarsicrinalis	0	1	1	0	0	1	1	1	0	0
Herminia_tarsipennalis	0	1	1	1	0	1	1	1	0.5	0
Herminia_tenuialis	0	0.5	1	0	1	1	0	0	0	0
Heterogenea_asella	0	1	0	0	0	1	1	1	0	0
Homaloxestis_briantiella	0	1	0.5	0	0	0.5	0	0	0	0
Homoeosoma_sinuella	0	0	1	1	0	1	1	1	0	0
Hoplodrina_ambigua	0	0.5	1	1	0	1	1	0.5	0	0
Horisme_tersata	0	1	1	0	0	1	1	1	0.5	0
Horisme_vitalbata	0	0.5	1	1	0	1	1	1	0	0
Hypomecis_punctinalis	0	1	1	0	0	1	1	1	1	0
Hypsopygia_costalis	0	1	0.5	0	0	1	1	1	0	0
Hypsopygia_glaucinalis	0	1	1	0	0	1	1	1	0	0
Idaea_aversata	0	0.5	1	0.5	0	1	1	1	1	0
Idaea_degeneraria	0	0.5	1	1	0	1	0.5	0	0	0
Idaea_dimidiata	0	0.5	1	0	0	1	1	1	1	0
Idaea_filicata	0	0	1	0	0	0.5	0	0	0	0
Idaea_fuscovenosa	0	0	1	1	0	1	1	0.5	0	0
Idaea_muricata	0	1	1	1	0	1	1	1	0	0
Idaea_politaria	0	0	0.5	1	0.5	0.5	0	0	0	0
Idaea_rusticata	0	0.5	1	0	0	1	1	0	0	0
Idaea_seriata	0	0.5	1	0.5	0	1	1	1	0	0
Idaea_subsericeata	0	0	1	1	0	1	1	0	0	0
Ipimorpha_subtusa	0	1	0.5	0	0	1	1	1	0.5	0
Isturgia_arenacearia	0	0	0.5	1	0	0.5	0	0	0	0
Lacanobia_oleracea	0	0.5	1	1	0	1	1	1	1	0
Lacanobia_wlatinum	0	0.5	1	1	0	1	1	1	0	0
Laelia_coenosa	0	0	0	0	1	1	1	0	0	0
Lamoria_anella	0	1	1	1	0	0.5	0	0	0	0
Laothoe_populi	0	0	1	0	0	1	1	1	1	0
Lasiocampa_quercus	0	1	1	1	0	1	1	1	1	0
Laspeyria_flexula	0	1	0.5	0.5	0	1	1	1	0.5	0
Leucania_loreyi	0	0	0	1	1	1	1	0	0	0
Leucania_obsoleta	0	0	0	0	1	1	1	1	0.5	0
Ligdia_adustata	0	1	1	0	0	1	1	1	0	0
Lithosia_quadra	0	1	1	0	0	1	1	1	0.5	0
Lomaspilis_marginata	0	1	1	0	0	1	1	1	1	1
Lomographa_bimaculata	0	1	1	0	0	1	1	1	0.5	0
Loxostege_sticticalis	1	0	0.5	1	0	1	0	0	0	0
Lygephila_craccae	0	0.5	0.5	1	0	1	1	1	0	0
Lymantria_dispar	0	1	1	0	0	1	1	1	0	0
Macaria_alternata	0	1	1	0	0	1	1	1	0.5	0
Macaria_liturata	0	1	0	0	0	1	1	1	1	1
Macaria_notata	0	1	0	0	0	1	1	1	1	0

Appendix 9.2: Moth trait matrix (Part 19: Species Mal-Phe, Traits „Migrating” - „Northern distribution”)

		Habitat type				Northern distribution				
Species	migrating	Forest	Scrub	Grassland	Reed	N 46-50	N 51-55	N 56-60	N 61-65	N 66-70
Malacosoma_castrensis	0	0	0.5	1	0	1	1	1	0	0
Mecyna_asinalis	0	0	0	1	0	0.5	0	0	0	0
Meganola_albula	0	1	1	0	0.5	1	1	1	0	0
Meganola_togatulalis	0	1	1	0	0	1	0.5	0	0	0
Menophra_abruptaria	0	1	1	0	0	1	1	0	0	0
Mesapamea_secalis	0	1	1	1	0	1	1	1	1	0
Metachrostis_velox	0	0	0.5	1	0	0.5	0	0	0	0
Metasia_ophialis	0	0	1	1	0	0.5	0	0	0	0
Metendothenia_atropunctana	0	1	1	0	0	1	1	1	1	1
Miltochrista_miniata	0	1	1	1	0	1	1	1	0.5	0
Mimas_tiliae	0	1	1	0	0	1	1	1	0	0
Minoa_murinata	0	1	1	0	0	1	0.5	0	0	0
Minucia_lunaris	0	1	0.5	0	0	1	1	0.5	0	0
Moma_alpium	0	1	0	0	0	1	1	1	0	0
Monopis_monachella	0	1	1	1	0	1	1	1	0	0
Monopis_obviella	0	1	1	0.5	0	1	1	1	0	0
Mormo_maura	0	0.5	1	0	1	1	0.5	0	0	0
Morophaga_choragella	0	1	0	0	0.5	1	1	1	0.5	0
Morophaga_morella	0	1	1	0	0	0.5	0	0	0	0
Myelois_circumvoluta	0	0	1	1	0	1	1	1	0	0
Mythimna_albipuncta	1	0	1	1	0.5	1	1	1	0	0
Mythimna_congrua	0	0	0	0	1	1	0	0	0	0
Mythimna_pallens	0	0	0	1	1	1	1	1	1	0
Mythimna_riparia	0	0	0	0	1	0.5	0	0	0	0
Mythimna_sicula	0	0	0	1	0	1	1	0	0	0
Mythimna_straminea	0	0	0	0	1	1	1	1	0	0
Mythimna_turca	0	1	0.5	0	1	1	1	1	0	0
Mythimna_vitellina	1	0	0	1	0	1	1	0	0	0
Nephopterix_angustella	0	0.5	1	0.5	0	1	1	1	0	0
Neurothaumasia_ankerella	0	1	0	0	0	1	1	0	0	0
Noctua_fimbriata	1	0.5	1	1	0	1	1	1	0.5	0
Noctua_janthina	0	1	1	0	0	1	1	1	0	0
Noctua_pronuba	1	1	1	1	1	1	1	1	1	0
Noctua_tirrenica	1	1	1	1	0	0.5	0	0	0	0
Nola_aerugula	0	1	1	0	0	1	1	1	0.5	0
Nola_chlamitulalis	0	0	1	1	0	0.5	0	0	0	0
Nomophila_noctuella	1	0	0	1	0	1	0	0	0	0
Notocelia_cynosbatella	0	0	1	0	0	1	1	1	1	0
Notocelia_roborana	0	0.5	1	0	0	1	1	1	1	0
Notocelia_rosaecolana	0	0.5	1	0	0	1	1	1	0	0
Notocelia_uddmanniana	0	0.5	1	0	0	1	1	1	1	0
Notodonta_tritophus	0	1	0	0	0	1	1	1	0	0
Nyctegretis_lineana	0	0	1	1	0	1	1	1	0.5	0
Nycterosea_obstipata	1	0	1	1	0	1	1	1	1	1
Nyctobrya_muralis	0	0	1	1	0	1	1	0	0	0
Ochropleura_plecta	0	0	1	1	0	1	1	1	1	0
Ocneria_rubea	0	1	1	0	0	0.5	0	0	0	0
Oligia_latruncula	0	0	1	1	0.5	1	1	1	1	0
Oncocera_semirubella	0	0	1	1	0	1	1	1	1	0
Opisthograptis_luteolata	0	1	1	0	0	1	1	1	1	0.5
Orgyia_antiqua	0	1	1	0	0	1	1	1	1	0
Ostrinia_nubilalis	1	0	0.5	1	0	1	1	1	0	0
Palpita_vitrealis	1	0.5	1	0.5	0	0.5	0	0	0	0
Pammene_fasciana	0	1	0	0	0	1	1	1	0	0
Pandemis_cerasana	0	1	1	0	0	1	1	1	1	1
Pandemis_heparana	0	1	1	0	0	1	1	1	1	0
Paradoxus_osyridellus	0	0	1	0	0	0.5	0	0	0	0
Parahypopta_caestrum	0	0.5	1	1	0	1	0	0	0	0
Parapoynx_stratiotata	0	0	0	0	1	1	1	1	0.5	0
Parascotia_fuliginaria	0	1	0	0	0	1	1	1	1	0
Paraswammerdamia_albicapitella	0	1	1	0	0	1	1	1	0	0
Paraswammerdamia_nebulella	0	0.5	1	0	0	1	1	1	0	0
Paratalanta_pandalis	0	1	1	1	0.5	1	1	1	1	0
Parectopa_robiniella	0	1	1	0	0	1	1	0	0	0
Pasiphila_chloerata	0	0.5	1	0	0	1	1	1	1	0
Pasiphila_rectangulata	0	0.5	1	0	0	1	1	1	1	0
Pechipogo_plumigeralis	0	1	0	0	0	1	0.5	0	0	0
Pediasia_contaminella	0	0	0	1	0	1	1	1	0	0
Pelochrista_mollitana	0	0	1	1	0	1	1	1	0	0
Pelosia_muscerda	0	1	0.5	0	0.5	1	1	1	0	0
Pempelia_palumbella	0	0	1	1	0	1	1	1	0	0
Penestoglossa_dardoinella	0	0	0	1	0	0.5	0	0	0	0
Peribatodes_rhomboidaria	0	1	1	0.5	0	1	1	1	0	0
Peridea_anceps	0	1	0	0	0	1	1	1	0	0
Petrophora_chlorosata	0	1	0.5	0	0	1	1	1	0	0
Phalera_bucephala	0	1	1	0	0	1	1	1	1	0
Phalonidia_albipalpana	0	0	0	1	0	0.5	0	0	0	0
Pheosia_tremula	0	1	1	0	0	1	1	1	1	0

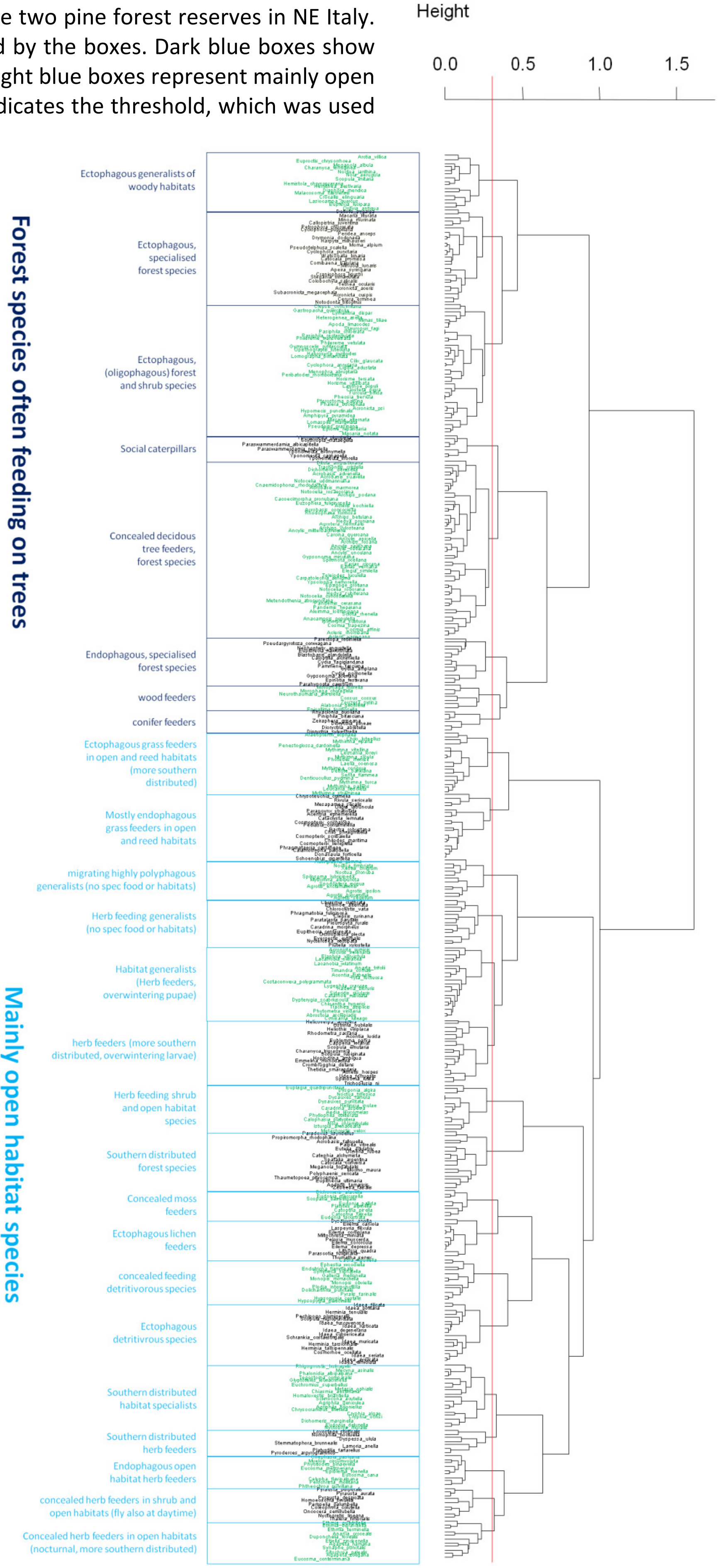
Appendix 9.2: Moth trait matrix (Part 20: Species Phi-Z, Traits „Migrating” - „Northern distribution”)

		Habitat type				Northern distribution				
Species	migrating	Forest	Scrub	Grassland	Reed	N 46-50	N 51-55	N 56-60	N 61-65	N 66-70
Philereme_transversata	0	0.5	1	0	0.5	1	1	1	0	0
Philereme_vetulata	0	1	1	0	0	1	1	1	0	0
Photedes_morrisii	0	0	0	1	0	1	1	0	0	0
Phragmataecia_castaneae	0	0	0	0	1	1	1	1	0.5	0
Phragmatobia_fuliginosa	0	1	1	1	0	1	1	1	1	1
Phtheochroa_pulvillana	0	0	1	1	0	1	1	0	0	0
Phycitodes_binaevella	0	0	1	1	0	1	1	1	0	0
Phyllophila_obliterata	0	0	1	1	0	0.5	0	0	0	0
Phytometra_viridaria	0	0	1	1	0.5	1	1	1	0	0
Piniphila_bifasciana	0	1	0	0	0	1	1	1	1	0
Platyptilia_farfarellus	0	0.5	1	1	0	1	0	0	0	0
Platytes_alpinella	0	0	0	1	0	1	1	1	1	0
Pleuropyta_ruralis	0	1	1	1	0.5	1	1	1	1	1
Plodia_interpunctella	0	1	1	1	0	1	1	1	1	0
Plutella_xylostella	1	0	1	1	0	1	1	1	1	1
Polyphaenis_sericata	0	1	1	0.5	0	1	0	0	0	0
Propiromorpha_rhodophana	0	0	1	0	0	1	0	0	0	0
Pseudargyrotoza_conwagana	0	1	1	1	0	1	1	1	1	0
Pseudoips_prasinana	0	1	0	0	0	1	1	1	0.5	0
Pseudotelphusa_scalella	0	1	0	0	0	1	1	1	0	0
Pterostoma_palpina	0	1	1	0	0	1	1	1	1	0
Pyralis_farinalis	0	0.5	1	0.5	0	1	1	1	0.5	0
Pyrausta_aurata	0	0	1	1	0	1	1	1	0	0
Pyrausta_despicata	0	0	1	1	0	1	1	1	0.5	0
Pyrausta_purpuralis	0	0	1	1	0	1	1	1	1	0
Pyroderces_argyrogrammos	0	0.5	0.5	1	0	1	0	0	0	0
Rhigognostis_hufnagelii	0	0	1	1	0	1	0	0	0	0
Rhodometra_sacraria	1	0	1	1	0	1	1	0.5	0	0
Rhodophaea_formosa	0	1	1	0	0	1	1	1	0	0
Rhyacionia_buoliana	0	1	0	0	0	1	1	1	0.5	0
Rivula_sericealis	0	0	1	1	1	1	1	1	1	0
Schoenobius_gigantella	0	0	0	0	1	1	1	1	0.5	0
Schrankia_costaestrigalis	0	1	1	0	1	1	1	1	0.5	0
Sciota_rhenella	0	0	1	1	0	1	1	1	0	0
Sclerocona_acutella	0	0.5	0	0.5	1	1	1	0	0	0
Scoparia_basistrigalis	0	1	1	0	0	1	1	1	0	0
Scopula_emutaria	0	0	0.5	0.5	0.5	1	1	0	0	0
Scopula_imitaria	0	0.5	1	0	0	1	1	0	0	0
Scopula_nigropunctata	0	1	1	0	0	1	1	0	0	0
Scopula_rubiginata	0	0	0.5	1	0	1	1	1	0	0
Scythropia_crataegella	0	0.5	1	0	0	1	1	1	0	0
Senta_flammea	0	0	0	1	1	1	1	1	0	0
Sideridis_rivularis	0	0.5	1	1	0	1	1	1	1	0
Sitochroa_palealis	0	0	0.5	1	0	1	1	1	0	0
Spatalia_argentina	0	1	0	0	0	1	0	0	0	0
Spilonota_ocellana	0	0.5	1	1	0	1	1	1	0	0
Spilosoma_lubricipeda	0	1	1	1	0	1	1	1	1	0
Spilosoma_lutea	0	1	1	1	0	1	1	1	0	0
Spodoptera_exigua	1	0.5	1	1	0.5	1	1	1	0	0
Stauropus_fagi	0	1	1	0	0	1	1	1	0	0
Stegania_trimaculata	0	1	0	0	0.5	1	1	0	0	0
Stemmatophora_brunnealis	0	0	0.5	1	0	1	0	0	0	0
Subacronicta_megacephala	0	1	0	0	0.5	1	1	0.5	0	0
Symmoca_signatella	0	1	1	0	0	1	0.5	0	0	0
Synaphe_punctalis	0	0	0	1	0	1	1	1	0	0
Tegostoma_comparalis	0	0	0	1	0	0.5	0	0	0	0
Teleiodes_luculella	0	1	0	0	0	1	1	1	0	0
Tethea_ocularis	0	1	0	0	0.5	1	1	1	0.5	0
Thalera_fimbrialis	0	0	1	1	0	1	1	1	0	0
Thaumetopoea_pityocampa	0	1	1	0	0	0.5	0	0	0	0
Thetidia_smaragdaria	0	0	0.5	1	0	1	1	1	0	0
Thumatha_senex	0	1	1	0	1	1	1	1	1	0
Timandra_comae	0	0	1	1	0.5	1	1	1	0.5	0
Trachea_atriplicis	0	0.5	1	1	0	1	1	1	0.5	0
Trachonitis_cristella	0	0.5	1	0	0	1	1	0	0	0
Trichoplusia_ni	1	1	1	1	0	1	1	1	0	0
Tyta_luctuosa	0	0	0	1	0	1	1	1	0	0
Udea_ferrugalis	1	1	1	1	0	1	0	0	0	0
Watsonalla_binaria	0	1	0	0	0	1	1	1	0	0
Xestia_cnigrum	1	0.5	1	1	0.5	1	1	1	1	0
Yponomeuta_cagnagella	0	0.5	1	0.5	0	1	1	1	0	0
Yponomeuta_evonymella	0	1	1	0	0	1	1	1	1	1
Yponomeuta_irrorella	0	1	1	0	0	1	1	1	0	0
Yponomeuta_plumbella	0	1	1	0	0	1	1	1	0	0
Ypsolopha_nemorella	0	1	0	0	0	1	1	1	0	0
Zebeeba_falsalis	0	0	1	1	0	0.5	0	0	0	0
Zeiraphera_griseana	0	1	0	0	0	1	1	1	1	1
Zeuzera_pyrina	0	1	1	0	0	1	1	1	0	0

Appendix 9.3: Factor loadings of the two PCAs. Local factors are circumscribed by the axes of the first PCA (white background), while landscape-scale factors are represented by the PC-axes of the second PCA (grey background). Loadings <-0.5 and >0.5 are marked in bold.

Local factors	Humidity-nutrient gradient	Old, open forest	Plant diversity	Conifer cover	Tree health
Plant species richness	0.24	0.24	**0.65**	-0.07	0.20
Functional dispersion of plants	-0.18	0.00	**0.80**	0.17	-0.16
Herb layer heterogeneity	-0.14	-0.18	-0.06	**0.62**	0.47
Shrub layer heterogeneity	-0.24	-0.23	**0.60**	-0.06	0.22
Ellenberg indicator “Nutrients”	**0.86**	0.13	-0.04	-0.08	0.10
Ellenberg indicator “Humidity”	**0.87**	0.14	-0.20	-0.06	0.05
Ellenberg indicator “Temperature”	**-0.51**	-0.31	0.10	0.09	0.40
Forest density	0.12	**-0.87**	-0.11	0.24	0.10
Crown density	**0.77**	-0.26	-0.04	0.22	-0.04
Cover of deciduous trees	0.42	-0.07	**-0.54**	-0.22	0.15
Cover of conifer trees	-0.01	0.09	0.34	**0.83**	-0.18
Mean basal area	0.21	**0.83**	0.02	0.36	-0.17
Standard deviation of basal areas	0.13	**0.58**	-0.16	**0.58**	0.07
Proportion of dead trees	-0.10	0.07	-0.05	0.03	**-0.83**
Landscape factors	Habitat diversity	Anthropogenic influence	Landscape diversity	Landscape fragmentation	Open habitats
Distance to edges	-0.19	**-0.89**	-0.12	0.13	0.11
Distance to canals	**-0.65**	-0.12	-0.10	**-0.59**	0.10
Distance to industry	**-0.72**	0.05	-0.18	-0.15	-0.23
Diversity of natural habitats (200m)	**0.79**	0.24	0.19	0.08	0.39
Proportion of open habitats (200m)	0.16	-0.05	-0.02	0.08	**0.96**
Proportion of reed habitats (200m)	**0.78**	0.20	0.30	0.05	-0.14
Edge density (1000m)	0.16	0.07	0.16	**0.89**	0.12
Diversity of natural habitats (1000m)	0.38	0.37	**0.80**	0.19	0.01
Proportion of forest areas (1000m)	-0.33	**-0.77**	-0.48	-0.12	0.07
Proportion of open areas (1000m)	0.10	0.16	**0.66**	0.36	0.23
Proportion of reed areas (1000m)	0.24	-0.12	**0.87**	-0.05	-0.14
Proportion of modified areas (1000m)	-0.07	**0.87**	-0.11	0.28	0.12

Appendix 9.4: Functional dendrogram of the whole observed moth species pool (387 species) in the two pine forest reserves in NE Italy. Functional groups are indicated by the boxes. Dark blue boxes show forest affiliated species, while light blue boxes represent mainly open habitat species. The red line indicates the threshold, which was used to separate functional groups.



Appendix 9.5: Results of the bivariate linear mixed effects models. Each row reports one model with the used response FD index in the first column and the predictor named in the second column. Reserve ID was included as random factor in each model. Significant correlations are marked in bold. Landscape-scale variables have grey background, while local predictors have white background.

response	Pc-axis	Predictor (Pc-Axis-Name)	t-value	p-value	Beta coefficient	Marginal R^2	Conditional R^2
FRic	Land 1	Habitat diversity	0.22	0.83	0.03	0.001	0.07
	Land 2	Anthropogenic influence	1.17	9.25	0.15	0.02	0.11
	Land 3	Landscape diversity	**3.75**	**<0.001**	**0.44**	**0.19**	**0.19**
	Land 4	Landscape fragmentation	-0.39	0.70	-0.05	0.002	0.08
	Land 5	Open habitats	-1.80	0.08	-0.23	0.05	0.16
	Local 1	Shady, nutrient rich sites	**2.11**	**0.04**	**0.26**	**0.07**	**0.10**
	Local 2	Old, open forest	-0.54	0.59	.0.07	0.005	0.09
	Local 3	Plant diversity	**2.93**	**0.005**	**0.36**	**0.12**	**0.15**
	Local 4	Conifer sites	0.42	0.68	0.05	0.003	0.07
	Local 5	Tree health	-1.45	0.15	-0.19	0.03	0.14
Trait space occupancy	Land 1	Habitat diversity	0.05	0.96	0.01	<0.001	0.15
	Land 2	Anthropogenic influence	1.55	0.13	0.19	0.03	0.20
	Land 3	Landscape diversity	**2.81**	**0.01**	**0.34**	**0.12**	**0.17**
	Land 4	Landscape fragmentation	-0.50	0.62	-0.06	0.004	0.15
	Land 5	Open habitats	-1.82	0.07	-0.23	0.05	0.24
	Local 1	Shady, nutrient rich sites	1.73	0.09	0.22	0.04	0.15
	Local 2	Old, open forest	0.62	0.54	0.08	0.006	0.12
	Local 3	Plant diversity	**2.12**	**0.04**	**0.26**	**0.06**	**0.16**
	Local 4	Conifer sites	0.63	0.53	0.08	0.006	0.14
	Local 5	Tree health	**-2.35**	**0.02**	**-0.29**	**0.07**	**0.28**
Functional redundancy	Land 1	Habitat diversity	-0.71	0.48	-0.12	0.01	0.22
	Land 2	Anthropogenic influence	1.28	0.21	0.16	0.02	0.16
	Land 3	Landscape diversity	**2.88**	**0.01**	**0.35**	**0.12**	**0.16**
	Land 4	Landscape fragmentation	-0.05	0.96	-0.007	<0.001	0.10
	Land 5	Open habitats	-1.26	0.21	-0.16	0.02	0.17
	Local 1	Shady, nutrient rich sites	**3.00**	**0.004**	**0.36**	**0.13**	**0.19**
	Local 2	Old, open forest	-0.54	0.59	-0.07	0.005	0.14
	Local 3	Plant diversity	**2.20**	**0.03**	**0.27**	**0.07**	**0.15**
	Local 4	Conifer sites	0.01	0.99	0.001	<0.001	0.11
	Local 5	Tree health	-1.52	0.13	-0.20	0.03	0.19
FDis	Land 1	Habitat diversity	1.40	0.17	0.23	0.04	0.31
	Land 2	Anthropogenic influence	0.13	0.89	0.02	<0.001	0.10
	Land 3	Landscape diversity	0.35	0.73	0.05	0.002	0.12
	Land 4	Landscape fragmentation	0.56	0.58	0.07	0.005	0.12
	Land 5	Open habitats	-0.22	0.83	-0.03	<0.001	0.10
	Local 1	Shady, nutrient rich sites	-1.19	0.24	-0.15	0.02	0.11
	Local 2	Old, open forest	0.65	0.52	0.09	0.006	0.14
	Local 3	Plant diversity	1.79	0.08	0.22	0.05	0.19
	Local 4	Conifer sites	-0.03	0.97	-0.004	<0.001	0.10
	Local 5	Tree health	-0.40	0.69	-0.05	0.003	0.10

(Continued on next page)

Appendix 9.5 (continued): Results of the bivariate linear mixed effects models. Each row reports one model with the used response FD index in the first column and the predictor named in the second column. Reserve ID was included as random factor in each model. Significant correlations are marked in bold. Landscape-scale variables have grey background, while local predictors have white background.

response	Pc-axis	Predictor (Pc-Axis-Name)	t-value	p-value	Beta coefficient	Marginal R^2	Conditional R^2
Weighted FEve	Land 1	Habitat diversity	0.57	0.57	0.09	0.007	0.20
	Land 2	Anthropogenic influence	-0.10	0.92	-0.01	<0.001	0.11
	Land 3	Landscape diversity	-1.82	0.07	-0.23	0.05	0.11
	Land 4	Landscape fragmentation	1.75	0.09	0.22	0.04	0.19
	Land 5	Open habitats	0.57	0.57	0.07	0.005	0.13
	Local 1	Shady, nutrient rich sites	-1.22	0.23	-0.15	0.02	0.11
	Local 2	Old, open forest	0.88	0.38	0.12	0.01	0.16
	Local 3	Plant diversity	-0.02	0.98	-0.002	<0.001	0.11
	Local 4	Conifer sites	-1.14	0.26	-0.14	0.02	0.13
	Local 5	Tree health	0.43	0.67	0.06	0.003	0.13
Unweighted FEve	Land 1	Habitat diversity	1.99	0.05	0.25	0.06	0.06
	Land 2	Anthropogenic influence	1.67	0.10	0.21	0.04	0.14
	Land 3	Landscape diversity	0.26	0.80	0.03	0.001	0.07
	Land 4	Landscape fragmentation	-1.13	0.26	-0.15	0.02	0.12
	Land 5	Open habitats	-1.75	0.08	-0.22	0.05	0.17
	Local 1	Shady, nutrient rich sites	**2.41**	**0.02**	**0.30**	**0.09**	**0.13**
	Local 2	Old, open forest	0.41	0.68	0.05	0.003	0.06
	Local 3	Plant diversity	1.94	0.06	0.24	0.06	0.10
	Local 4	Conifer sites	0.92	0.36	0.12	0.01	0.09
	Local 5	Tree health	-1.72	0.09	-0.22	0.04	0.17
FDiv	Land 1	Habitat diversity	1.93	0.06	0.32	0.08	0.32
	Land 2	Anthropogenic influence	0.60	0.55	0.08	0.01	0.03
	Land 3	Landscape diversity	-0.38	0.70	-0.05	0.002	0.03
	Land 4	Landscape fragmentation	0.32	0.75	0.04	0.002	0.04
	Land 5	Open habitats	-2.05	0.05	-0.26	0.07	0.07
	Local 1	Shady, nutrient rich sites	-1.16	0.25	-0.15	0.02	0.04
	Local 2	Old, open forest	0.48	0.63	0.06	0.004	0.06
	Local 3	Plant diversity	1.27	0.21	0.16	0.03	0.08
	Local 4	Conifer sites	1.51	0.14	0.19	0.04	0.07
	Local 5	Tree health	0.28	0.78	0.03	0.001	0.05