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Pollinator conservation in the Anthropocene

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Padua, 29 September 2023

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Summary

Pollinators play a key role in ecosystems, ensuring the reproduction of most wild and cultivated flowering plant species. However, pollinator communities are rapidly changing due to multiple anthropogenic drivers, with potential effects also on the fundamental ecosystem service they provide. Through the chapters of my thesis, I analysed how the factors that shape the abundance, diversity and distribution of pollinators in landscapes and thus determine their thriving or decline, *i.e.*, land-use changes, the use of pesticides, urbanization, and the introduction of managed species, affect both managed and wild pollinators.

After a brief introduction on pollinators and the key determinants of their abundance, diversity and distribution (*Chapter 1*), I investigated the effects of landscape composition and seasonality on the properties of pollen collected by managed honey bees, in particular on pollen diversity (*Chapter 2*) and pollen contamination by pesticides (*Chapter 3*), both of which strongly impact bee health. For both works, we collected pollen samples monthly, from April to September, for two consecutive years at 13 locations in Northern Italy. We highlighted that landscape composition affected both pollen features, and in particular that a high amount of semi-natural habitats in landscapes helped both to increase the heterogeneity of pollen collected by honey bees and to minimise contamination by pesticides.

I then focused on the effects of urbanization on wild pollinators (*Chapter 4*). In particular, I explored how increasing temperatures and the amount of green areas affected wild bee communities and their functional traits in the city of Rome, in central Italy. We sampled wild bees 7 times during spring and summer in 36 sites. We found that higher temperatures were generally associated with a higher abundance and species richness of wild bees, but they also led to a homogenisation of wild bee community traits, favouring a few traits such as small body size and polylectic diet. On the other hand, the amount of green areas did not affect wild bee communities.

In the following chapter, I examined the potential impacts of massively-introduced managed species on wild pollinator communities (*Chapter 5*). Through the study of 51 plant-pollinator networks sampled in northern Italy, I examined how potential competition between managed honey bees and wild pollinators was influenced by the functional traits of both pollinators and the plants they forage on. We highlighted that plant communities characterised by high functional richness could help mitigate potential competition between managed and wild pollinators by providing alternative resources on which wild pollinators can forage, and that pollinators characterised by functional traits similar to those of the honey bee were more prone to potential competition.

Last, I analysed how two pollinator-friendly measures, *i.e.*, habitat restoration and habitat enhancement for pollinators, affected pollinator diversity and ecosystem multi-functionality (*Chapter 6*). We selected 96 sites in northern Italy belonging to three habitat types (crop field margins, semi-natural patches, and urban green areas) with a gradient of flower coverage. We sampled wild pollinators and a large number of ecosystem services, mostly biodiversity-based, using which we calculated two indices of ecosystem multi-functionality. We found that while habitat restoration from intensive to semi-natural habitats benefited both pollinators and multiple ecosystem services, habitat enhancement for pollinators promoted pollinator diversity, but did not affect ecosystem multi-functionality.

In conclusion, the results obtained from my thesis could help develop targeted strategies for the conservation of both wild and managed pollinators. I highlighted that semi-natural areas play a key role in supporting pollinators, that honey bees may pose a threat to specific categories of pollinators, and that rising temperatures will lead to drastic changes in pollinator communities. I also showed that functional traits of both plants and pollinators have a strong influence on pollinator responses to the factors that threaten their survival. Finally, I pointed out how conservation measures for pollinators may – or may not – also impact other fundamental ecosystem services. It is therefore clear that multiple factors must be considered in order to get a clear picture of how pollinator communities are changing and what we can do to slow, stop or reverse their decline. Species conservation is a complex science, and further studies are needed to investigate the potential effects of interactions between drivers threatening managed and wild pollinators in the Anthropocene.

Riassunto

Gli insetti impollinatori svolgono un ruolo fondamentale negli ecosistemi, consentendo la riproduzione della maggioranza delle specie di angiosperme sia selvatiche che coltivate. Tuttavia, le comunità di impollinatori stanno rapidamente cambiando a causa di molteplici fattori di origine antropica, con potenziali effetti anche sul fondamentale servizio ecosistemico che questi insetti forniscono. Attraverso i capitoli della mia tesi ho analizzato nel dettaglio come i fattori che determinano l'abbondanza, la diversità e la distribuzione degli impollinatori nei paesaggi, in particolare i cambiamenti nell'uso del suolo, l'uso di pesticidi, l'urbanizzazione e l'introduzione di specie esotiche e gestite, influenzino sia gli impollinatori gestiti che quelli selvatici.

Dopo una breve introduzione sugli impollinatori e sui fattori che determinano la loro abbondanza, diversità e distribuzione (*Capitolo 1*), ho indagato gli effetti della composizione del paesaggio e della stagionalità sulle caratteristiche del polline raccolto dalle api mellifere gestite, in particolare sulla diversità del polline (*Capitolo 2*) e sulla sua contaminazione da prodotti fitosanitari utilizzati in agricoltura (*Capitolo 3*), due fattori che possono impattare fortemente la salute delle api. Per entrambi i lavori, abbiamo raccolto campioni di polline mensilmente, da aprile a settembre, per due anni consecutivi in 13 località in Nord Italia. Abbiamo evidenziato come la composizione del paesaggio abbia un effetto molto forte su entrambe le caratteristiche del polline, e in particolare come una elevata percentuale di habitat semi-naturali nel paesaggio possa contribuire sia ad aumentare l'eterogeneità del polline raccolto dalle api mellifere, sia a minimizzare la contaminazione da prodotti fitosanitari.

Mi sono poi concentrata sugli effetti dell'urbanizzazione sugli impollinatori selvatici (*Capitolo 4*). In particolare, abbiamo esplorato l'effetto dell'aumento delle temperature e della quantità di aree verdi sulle comunità di api selvatiche e i loro tratti funzionali nella città di Roma, in Italia centrale. Abbiamo campionato le api selvatiche per 7 volte durante la primavera e l'estate in 36 siti. Abbiamo riscontrato che temperature elevate erano associate a una maggiore abbondanza e ricchezza di specie di api selvatiche, ma anche a un'omogeneizzazione dei tratti della comunità di api, favorendo specifici tratti come dimensioni del corpo limitate e dieta generalista. Non abbiamo invece evidenziato alcun effetto della quantità di aree verdi sulle comunità di api selvatiche.

Nel capitolo successivo ho esaminato i potenziali impatti degli impollinatori gestiti sulle comunità di impollinatori selvatici (*Capitolo 5*). Attraverso lo studio di 51 network di interazione tra piante e impollinatori in Nord Italia, abbiamo indagato come la potenziale competizione tra api mellifere gestite e impollinatori selvatici fosse influenzata dai tratti funzionali degli impollinatori e delle piante fiorite su cui foraggiano. Abbiamo sottolineato come comunità di piante caratterizzate da alta ricchezza funzionale possano aiutare a mitigare la potenziale competizione tra impollinatori gestiti e selvatici, e come gli impollinatori caratterizzati da tratti funzionali simili a quelli dell'ape mellifera siano più inclini alla potenziale competizione.

Infine, ho analizzato come due misure *pollinator-friendly*, cioè il ripristino degli habitat semi-naturali e il miglioramento degli habitat per gli impollinatori, influissero sulla diversità di impollinatori e sulla multifunzionalità degli ecosistemi (*Capitolo 6*). Abbiamo selezionato 96 siti in Nord Italia in tre habitat diversi (margini di campo, aree semi-naturali, e aree verdi urbane) con copertura di piante fiorite variabile. Abbiamo campionato gli impollinatori selvatici e un elevato numero di servizi ecosistemici, per la maggior parte legati alla biodiversità, con i quali abbiamo calcolato due indici di multi-funzionalità ecosistemica. Abbiamo rilevato che mentre il ripristino degli habitat da intensivi a semi-naturali può favorire sia gli impollinatori che molteplici servizi ecosistemici, il miglioramento degli habitat può beneficiare gli impollinatori, ma non ha alcun effetto sulla multi-funzionalità ecosistemica.

I risultati ottenuti dalla mia tesi si configurano come uno strumento utile per l'elaborazione di precise strategie per la conservazione degli impollinatori sia selvatici che gestiti. Ho sottolineato che le aree seminaturali svolgono un ruolo chiave per il benessere degli impollinatori, che le api mellifere possono rappresentare una minaccia per specifiche categorie di impollinatori selvatici, e che l'aumento delle temperature può portare a cambiamenti drastici nelle comunità di impollinatori. Ho anche mostrato che i tratti funzionali, sia delle piante che degli impollinatori, possono avere una forte influenza sulle risposte degli impollinatori ai fattori che ne minacciano la sopravvivenza. Infine, ho evidenziato come misure di conservazione per gli impollinatori possano – o meno – aver un impatto anche su altri fondamentali servizi ecosistemici. È quindi evidente come sia necessario considerare numerosi fattori per avere un quadro chiaro di come le comunità di impollinatori stiano cambiando e cosa possiamo fare per rallentare, arrestare o invertirne il declino. La conservazione delle specie è una scienza complessa, e ulteriori studi sono necessari per indagare gli effetti delle possibili interazioni tra i fattori che minacciano gli impollinatori gestiti e quelli selvatici nell'Antropocene.

Introduction

Chapter 1: Introduction

Chapter 1: Introduction

1.1. Wild and managed pollinators

Pollination is a vital ecosystem service. Animal pollination, in particular, is fundamental for the reproduction of more than 85% of angiosperms (Ollerton et al. 2011), including 75% of global food crop types (Potts et al. 2016). In temperate regions, insects are the most important group of pollinators, with a monetary value of their contribution to crop production of about €153 billion (Gallai et al. 2009). Among them, bees (Hymenoptera: Anthophila) and hoverflies (Diptera: Syrphidae) stand out for their efficiency. Bees include more than 20,000 species worldwide, classified into 7 families (Michener 2007). Since both adults and larvae of most species feed on nectar and pollen, bees are strongly specialized for collecting these resources. Most bee species are characterized by specific pollen-carrying structures on their legs or abdomen, called *scopa* or *corbicula*, which make them particularly efficient in transporting pollen from one flower to another (Michener 2007). The western honey bee (*Apis mellifera* Linnaeus) is the most widespread bee species, as it has been managed for millennia (Roffet-Salque et al. 2015), mostly for the production of honey. The honey bee is a super-generalist pollinator and it is fundamental for the pollination of a large proportion of wild and cultivated plant species (Garibaldi et al. 2013; Hung et al. 2018), despite being less efficient than wild pollinators in some contexts (Rollin and Garibaldi 2019; Eeraerts et al. 2020). Hoverflies are a relatively large family of flies, including about 6,000 species worldwide (Rotheray and Gilbert 2011). Hoverflies have different lifestyles and habitat preferences in different stages of their life cycle: while larvae could be saprotrophs, insectivores, phytophagous or coprophagous and therefore linked to a high variety of habitat types, almost all adults feed on nectar and pollen and often prefer open habitats (Vujić et al. 2022). Many hoverfly species migrate and, as opposed to bees, they do not build nests for their larvae. Therefore, hoverflies usually have large home ranges and are able to transport pollen over considerable distances – even up to 100 km (Wotton et al. 2019; Doyle et al. 2020; Fisler and Marcacci 2023).

In the past 50 years, the demand for insect pollination in crops has tripled (Goulson et al. 2015). Nevertheless, several works showed that pollinators are declining due to multiple anthropogenic causes (Potts et al. 2010). A global study highlighted that the number of collected and observed bee species has been declining since 1990, with 25% fewer species found in recent years (Zattara and Aizen 2021). Also, regional studies showed that pollinators strongly declined in the Netherlands and Great Britain in the last 40 years (Biesmeijer et al. 2006; Carvalheiro et al. 2013; Powney et al. 2019; Van Strien et al. 2019), and bumblebee

community composition changed in red clover fields in Sweden in the last 70 years (Bommarco et al. 2012). Some bumblebee species have declined up to 90% and have contracted their surveyed geographic ranges by 23-87% in North America in the last decades (Cameron et al. 2011; Bartomeus et al. 2013; Jacobson et al. 2018; Richardson et al. 2019), while declines in abundance and richness of non-bumblebee wild pollinators in the United States seem to be modest (Bartomeus et al. 2013). Besides this decline, pollinator communities in general are undergoing major alterations: Bartomeus et al. (2013) showed that 56% of wild pollinator species significantly changed their relative abundance in the United States over the last century, while Mathiasson and Rehan (2020) highlighted profound changes also in plant-pollinator interactions.

However, not all pollinator species are impacted by environmental changes in the same way. Changes may negatively affect some species, while others, more adaptable to the new conditions, may be favoured and become dominant (Bartomeus et al. 2013). These differences in species responses are mostly related to their functional traits. For example, species characterized by oligolecty (high resource specialization), univoltinism (one generation per year), small phenological breadth, and large body size may be more prone to decline (Biesmeijer et al. 2006; Bartomeus et al. 2013). On the other hand, short-tongued bumblebees became prevalent in bumblebee communities of Northern Europe (Biesmeijer et al. 2006; Bommarco et al. 2012; Jacobson et al. 2018; Richardson et al. 2019), and dominant crop pollinators increased their abundance by 10% in Great Britain in the last 30 years, potentially following agri-environment scheme management for pollinators (Powney et al. 2019).

1.2. Pollinators in dynamic landscapes

Managed and wild pollinators live in dynamic, rapidly evolving landscapes. Depending on their features, landscapes will host specific pollinator communities which will change over time, being affected by several anthropogenic drivers that shape species abundance and diversity. These drivers are the same potentially determining pollinator decline and include, among the most relevant ones, land-use changes and habitat loss, the use of pesticides, urbanization, and the introduction of managed species (Potts et al. 2010; Goulson et al. 2015).

Land-use changes related to human activities include modifications in land cover, configuration and management that may result in the loss of suitable habitats for pollinators (Potts et al. 2016). Semi-natural habitats are of crucial importance for pollinators, being especially rich in floral resources and areas suitable

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for nesting or where larvae can develop. Therefore, the conversion of semi-natural habitats to intensive agriculture is known to strongly negatively affect pollinator communities (Carvalheiro et al. 2013; Koh et al. 2016; Habel et al. 2019), and increasing distance from semi-natural areas reduces wild pollinator abundance and richness (Ricketts et al. 2008; Moquet et al. 2018). Moreover, habitat loss and fragmentation can influence the foraging activity of pollinators, for example by increasing search and travel times to gather resources, with potential negative effects on pollinator health (LeBuhn and Vargas Luna 2021). Oligolectic and ground-nesting bees appear to be more vulnerable to habitat loss than polylectic and cavity-nesting bees (LeBuhn and Vargas Luna 2021), while hoverflies and dipterans in general are more resilient because of their polylecty and high mobility (Millard et al. 2021). Clarify how pollinators and their foraging activity are affected by land-use changes and habitat loss is a central theme in conservation ecology, as evidenced by the large body of literature on the topic (Winfree et al. 2009; Tonietto and Larkin 2018; Millard et al. 2021; Raven et al. 2021; Liang et al. 2023). Nevertheless, significant knowledge gaps remain to be addressed even for the most well-studied species, such as the honey bee (Härtel and Steffan-Dewenter 2014).

The conversion of habitats from semi-natural to agricultural also involves changes in management practices. Due to the sharp increase in cultivated areas in the last 50 years, nowadays pesticides are applied more than ever (Bernhardt et al. 2017). Pesticides are commonly used for crop protection and include, among the most important categories, insecticides, fungicides, and herbicides (Zioga et al. 2020). The toxicity of these compounds is highly variable, based on the target species, pollinator species sensitivity, pesticide formulation, and landscape context. In general, insecticides include compounds that pose major threats to pollinators, since they are specifically formulated to negatively affect insect health. Neonicotinoids, in particular, are systemic insecticides that have been largely shown to have important negative effects on non-target insects (Tooker and Pearsons 2021) and have therefore been banned in most EU countries. Nevertheless, newly formulated insecticides have also been shown to negatively impact pollinators (Siviter and Muth 2020). Fungicides are usually characterized by lower toxicity compared to other groups of pesticides, but they can interact synergistically among themselves and with other pesticides to exacerbate negative effects on pollinators (Siviter et al. 2021). Herbicides, on the other hand, could affect pollinator health both directly and indirectly, *i.e.*, by reducing the abundance and diversity of flowering plants (Potts et al. 2016). However, pollinators foraging in landscapes are exposed to multiple pesticides, which can synergistically interact to exacerbate the

negative effects on pollinator health (Zhao et al. 2020). While it is crucial to investigate the toxicity of single compounds for pollinators, it is also essential to understand how the mixes of compounds to which insects are exposed are modulated by landscape structure and composition.

In addition to the conversion of semi-natural habitats to agricultural habitats, the development and expansion of urban areas are among the major land-use changes that characterized the 20th century, and nowadays more than 50% of the world population lives in cities (OECD 2015). Urbanization, however, has strong impacts on biodiversity and pollinators for multiple causes. The increase in built-up areas is the most obvious and direct effect of urbanization, as it leads to the loss or reduction of green areas suitable for pollinators (Herrmann et al. 2023). Moreover, increased impervious surfaces can result in the so-called "urban heat island effect", making cities warmer than surrounding rural areas (Polidori et al. 2023). Warmer and drier climates associated with high urbanization can lead to homogenization of pollinator communities (Ganuza et al. 2022), and most pollinator groups, such as hoverflies and butterflies, struggle to adapt to urban environments (Burdine and McCluney 2019; Theodorou et al. 2020; Piano et al. 2020; Fenoglio et al. 2020). However, some species, characterized for example by high thermal limits, could adapt more easily and seem to thrive in cities (Papanikolaou et al. 2017; Hamblin et al. 2017). Since urban sprawl is predicted to further increase in the next decades (OECD 2015), additional studies are needed to understand how pollinators respond and adapt to urban environments.

Recently, another potential threat to wild pollinators has emerged. The presence in landscapes of the so-called "Massively Introduced Managed Species" (MIMS) (Geslin et al. 2017), which include the honey bee and a few other species, can cause major changes in pollinator communities and plant-pollinator interactions. The density of managed honey bee colonies increased exponentially in the last 50 years in the Mediterranean areas (Herrera 2020), and each honey bee colony can host more than 50,000 bees. As a result, honey bees are often dominant in pollinator communities (Hung et al. 2019; Herrera 2020). Despite being essential for crop pollination, extremely high abundances of honey bees found in areas where beekeeping is widely practised could potentially threaten wild pollinators (Mallinger et al. 2017; Geldmann and González-Varo 2018; Wojcik et al. 2018; Ropars et al. 2019; Angelella et al. 2021). These negative effects could be direct, *i.e.*, via competition for floral and nesting resources or spread of diseases and pathogens, or indirect, *i.e.*, via changes in plant communities to which wild pollinators are not able to adapt (Traveset and Richardson 2006; Mallinger et al. 2017). However, these potential negative effects are often context-dependent, and it is still unclear which pollinator groups might be most affected by a high abundance of managed honey bees, and how local conditions might mitigate this potential competition.

1.3. Pollinator conservation

Changes in pollinator communities related to land-use changes, the use of pesticides, urbanization and the introduction of managed pollinators potentially impact both human well-being and biodiversity (Potts et al. 2016). Pollination deficit resulting from drastic changes in pollinator communities and pollinator decline may endanger wild plant reproduction and diversity (Clough et al. 2014). Moreover, in agricultural landscapes, it could cause yield loss and a reduction in the quality of produced food, but also impair the long-term resilience of food production systems (Olhnuud et al. 2021). Equally important, however, are the potential negative effects on the so-called *bio-cultural diversity* (IPBES 2016; Dicks et al. 2021), a concept which recognises that culture and biodiversity are linked and may be mutually constituted (Hill et al. 2019). It is therefore clear how crucial it is to develop specific conservation plans to protect these key organisms.

Improving land management with pollinator-friendly measures is a key action to safeguard pollinator populations, for example through habitat restoration and habitat enhancement for pollinators (Kennedy et al. 2013; Van Strien et al. 2019; Warren et al. 2021). Habitat restoration involves the transformation from intensively managed habitats, such as croplands, to semi-natural habitats (Ricketts et al. 2008), and the presence in the landscape of different types of semi-natural habitats in particular has been shown to boost wild pollinator richness (Pindar and Raine 2023). Habitat enhancement involves the creation of flower strips, flower-rich margins, and hedgerows, usually in agricultural or urban-dominated landscapes (Wratten et al. 2012). Both flower strips and hedgerows showed important conservation benefits for pollinators (Ouvrard et al. 2018; Buhk et al. 2018; Ponisio et al. 2019) and for biodiversity in general (Albrecht et al. 2020). However, it is also essential to ensure that semi-natural habitat patches, flower strips or hedgerows are not isolated within intensive agricultural landscapes but are adequately connected, in order to allow pollinator movement in the landscape (Potts et al. 2016).

Conservation actions aimed at protecting one group of pollinators do not necessarily benefit another, since different pollinators have different necessities. For example, the presence of green roofs in urban environments has been shown to increase wild bee populations, but not hoverfly populations (Jacobs et al.

2023). In fact, different pollinator groups often require specific resources. For central-place foragers, the availability of nesting resources is also crucial. Interventions such as leaving patches of bare ground – since nearly 75% of wild bees nest on the ground (Antoine and Forrest 2021) – or providing suitable nesting cavities have been shown to boost pollinator populations (Potts et al. 2005). Also, for some species, other types of resources such as resin and floral oils can be limiting (Requier and Leonhardt 2020). Similarly, conservation measures for pollinators can impact other key ecosystem services, such as biological control and water quality regulation, thus underscoring how critical it is to carefully evaluate the most appropriate interventions to implement in order to maximize the benefits not only for different pollinator groups but also for multiple ecosystem services.

1.4. Research objectives and thesis structure

The overall aim of my PhD thesis was to analyse how land-use changes, the use of pesticides, urbanization, the introduction of managed species, and conservation measures for pollinators shaped the relative abundances and species diversity of pollinator communities, focusing on both managed and wild pollinators.

In *Chapter 2*, we explored how the provision of pollen by managed honey bees was influenced by landscape composition and seasonality. For two consecutive years, we collected pollen samples monthly, from April to September, from apiaries placed in 13 locations in a mountainous area of Northern Italy, and identified pollen grains to the lowest possible taxonomic level. We determined landscape composition at two different spatial scales using regional land cover maps. Then, we tested how landscape composition and seasonality shaped the diversity of pollen collected by honey bees.

In *Chapter 3*, we analyzed the effect of landscape composition and seasonality on pesticide contamination of pollen collected by honey bees. Similarly to *Chapter 2*, we collected pollen samples monthly from apiaries placed in 13 locations in a mountainous area of Northern Italy for two consecutive years. Using a multi-residual analysis, we searched for almost 400 compounds in pollen, including insecticides, herbicides, and fungicides. For each pollen sample, we calculated the Pollen Hazard Quotient, a measure of potential pollen toxicity, and then tested how it changed depending on landscape composition, seasonality, and pesticide category.

In *Chapter 4*, we investigated the effects of urbanization on wild bee communities and their functional diversity. We sampled bees using pan-traps in 36 sites in the city of Rome (central Italy) characterized by

independent gradients of temperature and amount of open habitat cover. We considered four functional traits of bees, *i.e.*, body size, nesting strategy, diet breadth, and social behaviour. We then tested how wild bee communities changed in relation to temperature and open habitat cover in terms of abundance of individuals, species richness, and functional diversity.

In *Chapter 5*, we used a combination of ecological network analysis and functional traits analysis to disentangle the relationships between managed honey bees and wild pollinators in semi-natural habitats. We sampled plant-pollinator networks in 51 grasslands in Northern Italy and calculated the resource overlap between managed honey bees and wild pollinators. We analyzed both functional traits of plants, *i.e.*, corolla length, flower shape and flower colour, and of pollinators, *i.e.*, tongue length, body size, type of foraging range, and taxonomic family. Then, we tested how the resource overlap was influenced by managed honey bee abundance, functional composition of plant communities, and pollinator traits.

In *Chapter 6*, we explored how two pollinator-friendly measures, *i.e.*, habitat restoration and habitat enhancement, affected pollinators and multiple ecosystem services. We sampled 96 sites belonging to three habitat types, *i.e.*, semi-natural patches, urban green areas, and crop field margins. We sampled pollinators using pan-traps and measured seven ecosystem services: honey bee-related ecosystem services, grounddwelling arthropod-related ecosystem services, pest control, seed predation, disease control, soil nutrient cycling, and flood control. We calculated ecosystem multi-functionality using two approaches and then tested how ecosystem multi-functionality and pollinator diversity were shaped by habitat type (habitat restoration) and increasing flower cover (habitat enhancement for pollinators).

Finally, in *chapter 7*, I summarized the results of my PhD thesis.

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Seasonality and landscape composition drive the diversity of pollen collected by managed honey bees

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Chapter 2: Seasonality and landscape composition drive the diversity of pollen collected by managed honey bees

2.1. Abstract

The western honey bee, *Apis mellifera*, is the most important and widespread managed pollinator species. Honey bee diet is based on nectar and pollen, and pollen diversity and composition, in particular, affect colony health and fitness. As landscape composition is strongly linked to floral resource heterogeneity, it could influence the resource intake of honey bees. This work aimed to explore how the composition of pollen collected by honey bees was modulated by seasonality and landscape composition heterogeneity in a mountainous cultivated area of Northern Italy. We selected 13 locations, and at each location, we placed two honey bee colonies from which we collected pollen samples every month during the whole flowering season for two consecutive years. We then analyzed pollen samples in the laboratory and determined the Shannon diversity index of each pollen sample and the temporal pollen taxon replacement. We extracted the cover of the main habitat types at three spatial scales and tested the effect of landscape diversity and composition using Principal Component Analysis. Honey bees foraged on a high number of floral resources, however, they mostly collected pollen from a small number of taxa, with pollen type composition changing throughout the flowering season. In early spring and late summer, most pollen grains were collected from a few plant species, while from May to August the number of collected pollen types was significantly higher. Landscape composition affected pollen diversity only at the end of the flowering season. While honey bees were able to collect highly diverse pollen throughout spring and summer regardless of landscape composition, in late summer, when pollen collected is fundamental for the overwintering of the colony and its development in the following season, semi-natural areas became crucial for honey bee foraging activities, with pollen diversity increasing with increasing percentages of semi-natural areas. Our research highlighted the importance for honey bees of certain seasonal resources and of semi-natural habitats at the end of the flowering season, which ensure the subsistence of their colonies throughout the year.

2.2. Introduction

In recent years, pollinator abundance and diversity faced a strong decline due to multiple anthropogenic pressures (Potts et al. 2010). One of the main causes of this decline is the loss and fragmentation of natural areas, which led to a decrease in plant diversity, potentially determining insufficient nutrition for pollinators (Goulson et al. 2008). In particular, the honey bee, *Apis mellifera* Linnaeus, is the most widespread managed pollinator species and its presence is crucial not only for ensuring the reproduction of plant species in natural habitats but also for crop production, which is positively impacted by honey bee pollination both in terms of quantity and quality (Hung et al. 2018; Rollin et al. 2019).

The honey bee is a eusocial species whose colonies can host more than 50,000 individuals (Von Frisch 1954; Fontana 2019). Its diet is based on nectar and pollen. Nectar is a source of energy and, after being transformed into honey, it constitutes the food stock through which the colony survives during winter. Pollen is a source of protein and lipids, and in addition to direct feeding of larvae and adult workers, it is necessary for the secretion of two substances essential for the life of the colony, *i.e.*, the royal jelly, which is the food for all the larvae in the first 3 days and for queens during their whole life (Winston 1991), and the wax, of which honeycombs are made (Hepburn 1986; Tautz 2008). Pollen availability not only influences the development and reproduction of the colony in the short term, but as for honey, it is also fundamental for the overwintering of the colony and its development in the following season (Alaux et al. 2017).

The quality of pollen in terms of nutrient content varies from one plant species to another (Roulston and Cane 2000), and for this reason, honey bees must have access to diverse pollen sources in order to assure colony health. Only landscapes with a certain degree of floristic diversity can therefore guarantee adequate resources for honey bees (Di Pasquale et al. 2016). Recent studies showed that the proportion of semi-natural habitat within the landscape is positively related to honey bee pollen diversity and protein content (Donkersley et al. 2014; Cannizzaro et al. 2022) and to the probability of winter survival of the colonies (Rutschmann et al. 2022), while habitat fragmentation negatively affects the abundance of pollen collected by honey bees (Ochungo et al. 2021). Moreover, heterogeneous landscapes have been shown to support honey bees also by reducing their foraging distances, therefore allowing them to consume fewer resources to obtain food (Danner et al. 2017).

In this work, we aimed to understand the effect of landscape composition and seasonality on the diversity of pollen collected by honey bees in a mountainous cultivated area in Northern Italy. We selected 13 locations, from which we collected pollen samples monthly from two honey bee colonies during the spring and summer of 2019 and 2020. After analyzing pollen samples in the laboratory, we determined the Shannon diversity index for each pollen sample and the temporal β-diversity of pollen at each location. To assess landscape heterogeneity, we calculated the cover of the main habitat types at 1, 3, and 5 km radius buffers around the sampling locations, and analyzed landscape composition through Principal Component Analysis and Shannon diversity index. We hypothesize that pollen composition would change throughout the flowering season, following plant phenology at least in early spring and late summer when floral resources are relatively scarce. Moreover, we expect that landscape composition would strongly affect pollen composition, with highdiverse landscapes supporting honey bee colonies by offering a wider range of pollen types in comparison to homogeneous landscapes.

2.3. Materials and methods

2.3.1. Study area

The study was carried out in the Trentino province, an area in Northern Italy covering about 6,214 km². The area is generally mountainous, but it is characterized by a considerable landscape heterogeneity, with about 80% semi-natural areas, 15% agricultural areas, and 5% urban areas. As a result, the climate is highly variable. The mean annual temperature is about 9 °C, and the mean annual precipitation at 200 m a.s.l. is 1,200 mm.

We selected 13 sampling locations, which were characterized by great variability in landscape composition (Table S2.1; Figure 2.1). Three sites were close to apple orchards, three were close to vineyards, three were in an urban setting, and three were far from agricultural areas. The average elevation of the sampling locations was 533 m a.s.l. (min = 93 m a.s.l., max = 1,481 m a.s.l.). The mean air temperature at the sampling sites during the sampling periods, *i.e.*, from April to September of 2019 and 2020, was 17 °C.

Figure 2.1: Map of the 13 sampling locations, also showing the landscape composition at 3 km radius buffers around the sampling locations using CORINE Land Cover classes. Abbreviations for locations are ALA (Ala), BOV (Borgo Valsugana), CAL (Caldonazzo), CAV (Cavalese), CLE (Cles), FAE (Faedo), GIO (Giovo), PEI (Peio), PEV (Pergine Valsugana), RDG (Riva del Garda), ROM (Romagnano), ROV (Rovereto), and TDS (Tiarno di Sopra). See Table S2.1 for additional information on sampling locations.

2.3.2. Experimental design

In 2019 and 2020, we placed one small apiary consisting of two honey bee colonies at each sampling location. All colonies originated from the livestock managed by the Edmund Mach Foundation and had sister queens of *A. m. carnica* x *A. m. ligustica*. The colonies were managed directly by Edmund Mach Foundation personnel according to the local beekeeping practice. From April to September, we carried out pollen samplings every month, for a total of six pollen samples collected per colony per year. At some locations, however, the number of pollen samples was lower due to adverse climatic conditions. In particular, in 2019, at one location only three samples could be collected, and only five at two others. In 2020, only five samples were collected at three locations. Pollen samples were collected by activating pollen traps at the hive entrance for 48 h, Pollen samples were then stored at -20 °C.

2.3.3. Landscape composition

For each sampling location, we extracted the cover of the main habitat types using the CORINE Land Cover (CLC) database (© European Union, Copernicus Land Monitoring Service 2018, European Environment Agency) at three spatial scales, *i.e.*, the local foraging scale of honey bees (1 km radius buffer around the sampling locations) and two landscape foraging scales of honey bees (3 and 5 km radius buffers around the

sampling locations). Following the CLC classification, we considered a total of 24 land-use classes (Table S2.2). Landscape composition was heterogeneous across sites. In 3 km radius buffers around the sampling locations, an average of 33% of the land was covered by agricultural areas (min = 7%, max = 52%), 51% by semi-natural areas (min = 26% , max = 92%), 13% by urban areas and other artificial surfaces (min = 0, max $= 30\%$), and 2% by other areas (min = 0, max = 13%) (Table S2.1).

As most of these classes were highly correlated, we performed a Principal Component Analysis (PCA) to extract the landscape composition at each of the three spatial scales. We extracted the first two eigenvalues, PC1 and PC2, which explained 38, 48, and 45% of the total landscape variability at 1, 3, and 5 km radius buffers around the sampling locations (Table S2.3). PC1 was positively related to semi-natural areas, in particular coniferous forests, natural grasslands, and areas with sparse vegetation, and negatively related to intensive areas, in particular urban areas and vineyards (Table S2.3). Therefore, high values of PC1 can be interpreted as a high proportion of semi-natural areas within the landscapes.

Moreover, we calculated the Shannon diversity index for landscape composition using the 24 land-use classes at each of the three spatial scales. Shannon diversity index quantifies the heterogeneity of landscapes, taking into account both richness and evenness of land-use classes, with low values of the index indicating a low landscape heterogeneity. Shannon diversity index was calculated using the *R* package *vegan* (Oksanen et al. 2019). All statistical analyses were performed using the *R* software version 3.6.1 (R Development Core Team 2019).

2.3.4. Pollen analysis

From each pollen sample, we extracted two grams of pollen pellets, which were dissolved in distilled water and mixed using an advanced vortex mixer (VELP Scientifica, ZX3). We took 20 μl of the obtained suspension and placed it on a microscopic slide. Once the suspension of water and pollen was dry, we placed a drop of glycerin jelly on top of the sediment and covered it with a slide. Pollen was then observed under the optical microscope (Optika, B500PPH). For each sample, we counted about 500 pollen grains by applying the "transect" method (Tamic et al. 2011). Pollen grains were identified at the lowest possible taxonomic level according to available literature (Ricciardelli d'Albore 1998; Bucher 2004; El-Labban 2020) and palynological databases (PalDat 2000; PollenAtlas 2021). The identified pollens were classified following the "pollen types" nomenclature proposed by Persano Oddo and Ricciardelli d'Albore (1989).

For each pollen sample, we calculated the Shannon diversity index. As for landscape composition, the Shannon index for pollen reflects both the richness and evenness of pollen samples, with lower values indicating a lower diversity in pollen sample composition. Moreover, to understand how pollen composition changed throughout the flowering season, we calculated the mean β-richness and replacement at each location over the six sampling months, based on presence/absence data. All pollen indices were calculated using the *R* package *vegan* (Oksanen et al. 2019).

2.3.5. Statistical analysis

First, to determine the effect of landscape composition and seasonality on pollen diversity, we built two linear mixed-effect models for each spatial scale using the R package *nlme* (Pinheiro et al. 2019). In all models, the response variable was pollen Shannon index. Selected explanatory variables were collection month, year, landscape Shannon index, and the interaction between month and landscape Shannon index for the first model, and collection month, year, landscape PC1, landscape PC2, and the interactions between month and landscape PC1 and between month and PC2 for the second model. We also included the sampling location as random factor in all models. Starting from each full model, we used a backward deletion procedure, removing one-byone the interactions with p value > 0.05 , and re-ran the model to correctly interpret model main effects.

Second, to explore the effect of landscape composition on temporal β-diversity of pollen, we built four linear models for each spatial scale. We selected β-richness and replacement of pollen as response variables, PC1 and PC2 as explanatory variables for the first model, and landscape Shannon index as explanatory variable for the second model.

2.4. Results

We analyzed a total of 116,979 pollen grains in 224 samples collected during 2 years. We identified 122 plant taxa, most of them $(n = 93)$ at the genus level (Table S2.4). We observed 48 pollen types in April, 80 in May, 77 in June, 67 in July, 69 in August, and 50 in September. The most abundant types were *Hedera* spp. (n = 16,896 pollen grains), Plantaginaceae (n = 10,303 pollen grains), and *Malus*/*Pyrus* spp. (n = 7,826 pollen grains). On the other hand, the most prevalent taxa were Compositae T-form, which includes the genera *Taraxacum* and *Cichorium* (found in 149 pollen samples), Compositae H-form, which includes the genera *Helianthus*, *Petasites*, and *Senecio* (found in 117 pollen samples), and *Trifolium repens* group (found in 110 pollen samples).

The monthly pollen samples were dominated by a handful of taxa, and there was a strong temporal turnover in the composition of pollen samples (Figure 2.2). In spring, honey bees mostly collected pollen on *Malus*/*Pyrus* spp. (21% of total pollen grains), *Salix* spp. (18%), and Compositae T-form (12%), with only three species making up half of the collected pollen grains (Figure 2.2 *a*, *b*). In June, *Castanea sativa* became the prevalent pollen type (29%), together with *T. repens* group (8%), *Filipendula* spp. (7%), and *Vitis* spp. (6%) (Figure 2.2 *c*). In July, the most visited taxa were Plantaginaceae (39%), *T. repens* group (9%), *Clematis* spp. (7%), and *Parthenocissus* spp. (7%) (Figure 2.2 *d*). Plantaginaceae were also found in August (16%), but pollen was mostly collected on *Artemisia* spp. (22%) and, to a lesser extent, on Compositae H-form (9%) and *Thalictrum* spp. (8%) (Figure 2.2 *e*). In September, almost all pollen was collected on *Hedera* spp. (79%) (Figure 2.2 *f*).

Figure 2.2: Rank abundance plots showing the relative proportion of the taxa found in pollen samples collected in *a)* April, *b)* May, *c)* June, *d)* July, *e)* August, and *f)* September of 2019 and 2020. Black lines represent single sampling locations and red lines represent the average of all locations for each sampling month. Species are ranked on the X-axis from left to right from the most to least abundant. The Y-axis was log-transformed to improve clarity.

Pollen Shannon index was strongly influenced by the collection month (Table 2.1). Pollen diversity was higher in May, July, and August, while pollen samples of April and particularly September were more homogeneous (Figure 2.3 *a*). Moreover, pollen Shannon index responded to the interaction between month and landscape PC1 at 3 and 5 km. Landscape composition had no effect on pollen diversity from April to August, however, in September the diversity of collected pollen increased with increasing landscape PC1, suggesting a positive effect of semi-natural habitat on pollen collection in late summer (Figure 2.3 *b*, *c*).

Table 2.1: Results of the linear mixed-effect models testing the response of pollen Shannon index to month, year, landscape Shannon index, and the interaction between month and landscape Shannon index; and month, year, landscape PC1 and PC2, and the interactions between month and landscape PC1 and month and landscape PC2. Landscape Shannon index, PC1 and PC2 were calculated at the three spatial scales, *i.e.*, a) 1 km radius buffer, *b*) 3 km radius buffer, and *c*) 5 km radius buffer around the sampling locations. Values in bold indicate significant effects (*p* value < 0.05). Only significant results after a backward stepwise model

selection procedure are reported.

Figure 2.3: Plots showing the effect on pollen Shannon index of *a)* collection month, *b)* the interaction between month and landscape PC1 calculated at 3 km radius buffer around the sampling locations, and *c)* the interaction between month and landscape PC1 calculated at 5 km radius buffer around the sampling locations. Small points represent raw data points, large black points and coloured lines represent model estimates and black bars represent the 95% confidence intervals.

Temporal β-richness and replacement did not change in response to landscape composition at any of the selected spatial scales (Table 2.2 *a*, *b*). In general, β-richness values were high at all locations (min = 0.783, max = 0.880), while β-replacement values were particularly low (min = 0.235, max = 0.342).

Table 2.2: Results of the linear models testing the response of *a)* mean β-richness and *b)* mean β-replacement of pollen samples to landscape PC1 and PC2, and landscape Shannon index, at the three spatial scales, *i.e.*, 1 km, 3 km, and 5 km radius buffers around the sampling locations.

Response variable	Spatial	Explanatory	Estimate	SE	t value	<i>p</i> value
	scale	variable				
a) Mean β -richness	1 km	Landscape PC1	0.002	0.007	0.302	0.769
		Landscape PC2	0.001	0.008	0.104	0.919
		Landscape Shannon	0.035	0.023	1.558	0.147
		index				
	3 km	Landscape PC1	-0.010	0.005	-2.060	0.066
		Landscape PC2	-0.004	0.006	-0.643	0.535
		Landscape Shannon	0.032	0.031	1.057	0.313
		index				
	5 km	Landscape PC1	-0.009	0.005	-2.062	0.066
		Landscape PC2	-0.001	0.006	-0.119	0.908
		Landscape Shannon	0.017	0.036	0.482	0.639
		index				
$b)$ Mean β - replacement	1 km	Landscape PC1	0.005	0.006	0.966	0.357
		Landscape PC2	-0.005	0.007	-0.670	0.518
		Landscape Shannon	0.025	0.022	1.164	0.269
		index				
	3 km	Landscape PC1	-0.007	0.005	-1.403	0.191
		Landscape PC2	0.004	0.006	0.585	0.571
		Landscape Shannon	0.035	0.028	1.285	0.225
		index				
	5 km	Landscape PC1	-0.006	0.005	-1.300	0.223
		Landscape PC2	-0.003	0.006	-0.516	0.617
		Landscape Shannon	0.023	0.033	0.720	0.487
		index				

2.5. Discussion

The survival, prosperity, and reproduction of honey bee colonies depend on the ability of honey bees to collect and store honey and pollen (Brodschneider and Crailsheim 2010). In this study, by observing almost 117,000 pollen grains, we were able to collect information on honey bee foraging behaviour from early spring to late summer. Moreover, we highlighted how pollen diversity was strongly shaped by seasonality, while landscape composition affected pollen diversity only at the end of the flowering season.

2.5.1. Effect of seasonality on honey bee foraging preferences and pollen diversity

Honey bees, despite being extraordinarily polylectic, usually select a limited number of flowering plant species to forage on (Lau et al. 2019). Here, we observed a strong temporal turnover in the composition of pollen collected by honey bees, which partly reflects honey bee foraging preferences, and partly reflects plant phenology and pollen availability in the study area, at least in the early and late flowering season. In particular, trees were revealed to be a key resource for honey bees in spring. *Salix* spp. in April, *Malus*/*Pyrus* spp. in May, and *Castanea sativa* in June were the main pollen taxa collected by honey bees. The importance of trees for honey bees is well-known (Donkersley 2019) as they are often among the early-flowering species. We showed that Compositae such as *Taraxacum* spp., *Helianthus* spp., and *Senecio* spp., and the legume *Trifolium repens* strongly supported honey bees throughout spring and summer. In August, *Artemisia* spp. pollen was highly represented, as this taxon is common in fallows and urban areas. In September, almost all pollen was collected on *Hedera* spp., which was the most abundant flowering plant species in late summer in the study area (Prosser et al. 2019).

Pollen diversity was also shaped by seasonality. We observed that the start and end of the flowering season, *i.e.*, April and September, were characterized by a dearth of floral resources, while we observed a peak of pollen diversity in May. Interestingly, despite the high percentage of agricultural areas in certain landscapes, we did not highlight a strong effect of mass flowering crops such as apple, which flowers in April and May, which can potentially reduce the diversity of pollen collected by honey bees, as bees tend to focus on these resources. The diversity of pollen collected in August was surprisingly high, given that resources are usually relatively scarce at the end of summer (Garbuzov et al. 2015; Requier et al. 2015; Danner et al. 2017; Sponsler et al. 2020). The high diversity found in August could be explained by the mid-elevation of sampling sites, which causes a shift in pollen decline from August to September.

Since many of the pollen taxa that we collected were grouped at the family level, and almost all the remaining ones were identified at the genus level, pollen diversity could have been even higher in some seasons, if we had been able to achieve species-level identifications of pollen.

2.5.2. Interactive effect of seasonality and landscape composition on pollen diversity

Our results highlighted that the diversity of pollen collected by honey bees was influenced by the interaction between collection month and landscape composition, *i.e.*, the proportion of semi-natural areas.

Pollen diversity was independent of the proportion of semi-natural areas from April to August. Several studies found that pollen composition was not affected by landscape composition (Danner et al. 2017; Guzman et al. 2019; Simanonok et al. 2020; Jones et al. 2021). This can be explained by both the structure of selected landscapes and the foraging behaviour of the honey bee. Even if some landscapes were strongly modified by anthropogenic activities, they always included a certain proportion of semi-natural habitats, ranging from 25 to 83%, which comprised both open habitats and forests. Moreover, many agricultural areas, which ranged from 7 to 52%, were intermixed with semi-natural habitats. In all landscapes, honey bees were therefore able to collect pollen in areas that offered a high amount of resources, at least until mid-summer. Moreover, honey bees can travel more than 10 km from their hive, although they usually forage < 1 km away from the hive (Von Frisch 1967; Visscher and Seeley 1982; Tautz 2008; Seeley 2019). Several studies highlight that landscape composition affects the distance to which honey bees forage, and in particular that their foraging distance increases in simplified landscapes (Steffan-Dewenter and Kuhn 2003; Abou-Shaara 2014; Danner et al. 2017). A study from the UK reports that in landscapes dominated by the common heather (*Calluna vulgare*), the average distance of foraging honey bees strongly changed during the season: while in May it was about 1 km, in August, during the flowering period of the common heather, the average foraging distance increased up to 5.5 km (Beekman and Ratnieks 2000). In our study, however, we did not collect data on how far honey bees travelled to collect pollen. In some areas, honey bees may need to travel much further to obtain food resources, with potentially negative consequences for colony fitness.

On the other hand, in September, pollen diversity increased with increasing proportion of semi-natural habitats at 3 and 5 km radius buffers. While honey bees are able to collect heterogeneous pollen independently of landscape composition from spring to mid-summer, the scarcity of floral resources in late summer may turn semi-natural areas into key habitats. In this part of the season, when nectar sources are decreasing (Tew et al. 2022), honey bees search for the most diverse pollen sources in order to breed winter individuals that must develop adequate fat bodies (Frias et al. 2016). Semi-natural areas in the landscape can promote late-season pollen protein and winter survival of honey bee colonies (Kuchling et al. 2018; Simanonok et al. 2020; Rutschmann et al. 2022). Therefore, the higher number of resources offered by these habitats can be crucial for honey bees at such a critical stage of the colony cycle.

2.6. Conclusions
Our work highlighted that the diversity of pollen was shaped by seasonality, as we observed a strong temporal turnover in the diversity of pollen collected by honey bees. Landscape composition only affected pollen diversity at the end of the flowering season. In spring and summer, honey bees were able to efficiently forage in all landscapes, probably even due to the presence of a few key plant species such as *Trifolium repens* that could strongly support colonies (Filipiak et al. 2017). In late summer, when resources were generally scarce, semi-natural areas became fundamental for honey bees, as they offered a wider range of floral resources. However, more research on this topic is needed, as landscape composition could also affect other aspects of honey bee ecology. For example, complementing this study with observations on foraging flight distances and colony fitness could help elucidate the potential effect of landscape simplification on honey bees. Moreover, another aspect that should be taken into account is the potential contamination of food sources for bees, as the presence of intensively cultivated areas can affect pollen quality due to pesticide presence (Zioga et al. 2020).

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Impact of landscape composition on honey bee pollen contamination by pesticides: A multi-residue analysis

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An adapted version of this chapter has been accepted by *Chemosphere*

Chapter 3: Impact of landscape composition on honey bee pollen contamination by plant protection products

3.1. Abstract

The honey bee is the most common and important managed pollinator of crops. In recent years, honey bee colonies faced high mortality for multiple causes, including the use of plant protection products (hereafter pesticides). This work aimed to explore how contamination by pesticides of pollen collected by honey bees was modulated by landscape composition and seasonality. We placed two honey bee colonies in 13 locations in Northern Italy in contrasting landscapes, from which we collected pollen samples monthly during the whole flowering season in 2019 and 2020. We searched for almost 400 compounds, including fungicides, herbicides, and insecticides and acaricides. We then calculated for each pollen sample the Pollen Hazard Quotient (PHQ), an index that provides a measure of multi-residue toxicity of contaminated pollen. Almost all pollen samples were contaminated by at least one pesticide. We detected 95 compounds, mainly fungicides, but insecticides and acaricides showed the highest toxicity. Fifteen % of the pollen samples had medium-high or high levels of PHQ, which could pose serious threats to honey bees. Fungicides showed a nearly constant PHQ throughout the season, while herbicides and insecticides and acaricides showed higher PHQ values in spring and early summer. Also, PHQ increased with increasing cover of agricultural and urban areas from April to July, while it was low and independent of landscape composition at the end of the season. The cover of perennial crops, *i.e.*, fruit trees and vineyards, but not of annual crops, increased PHQ of pollen samples. Our work highlighted that the potential toxicity of pollen collected by honey bees was modulated by complex interactions among pesticide categories, seasonality, and landscape composition. Due to the large number of compounds detected, our study should be complemented with additional experimental research on the potential interactive effects of multiple compounds on honey bee health.

3.2. Introduction

The honey bee, *Apis mellifera* Linnaeus, is the most important managed pollinator species, with an estimated economic value to crop yield of about \$6.4 billion in the USA alone (Reilly et al. 2020). Despite a global increase of 85% in the number of managed honey bee colonies since the 1960s, in recent years honey bees have been experiencing high mortality, especially in North America and Europe (Osterman et al. 2021). This syndrome is often referred to as Colony Collapse Disorder (CCD) (vanEngelsdorp et al. 2009), and it is related to several causes (Goulson et al. 2015). Among these causes, the most relevant ones seem to be the spread of parasites and pathogens, such as the parasitic mite *Varroa destructor* Anderson & Trueman and the fungus *Nosema ceranae* (Rosenkranz et al. 2010; Le Conte et al. 2010; Geffre et al. 2020), and nutritional stress related to a restricted diet due to limited availability of floral resources, often caused by semi-natural habitat loss (Naug 2009; Branchiccela et al. 2019). Moreover, the use of plant protection products (hereafter, pesticides) that could contaminate pollen and nectar can also play a key role in the decline of these pollinators (Henry et al. 2012; Sánchez-Bayo et al. 2016; Tsvetkov et al. 2017; Woodcock et al. 2017).

Agriculture has increased by c. 40% globally in the last 50 years (Aizen et al. 2019), and consequently the use of pesticides and their potential impact on bees (DiBartolomeis et al. 2019). Fungicides, herbicides and insecticides are commonly used for crop protection (Zioga et al. 2020). Insecticides include the compounds that pose major threats to arthropods, since they are designed to directly affect them (Fairbrother et al. 2014; Lundin et al. 2015; Tsvetkov et al. 2017; Woodcock et al. 2017; Wood and Goulson 2017; Holder et al. 2018). Few studies have investigated the effect of fungicides and herbicides on honey bees and pollinators in general, despite being the most widely used compounds in terms of applied tonnes (Tamburini et al. 2021, EUROSTAT, 2023). However, effects such as the reduction of bee foraging efficiency, longevity and survival rate, and changes in gut microbiota have been reported, with a large variability among compounds (Cullen et al. 2019; Rondeau and Raine 2022).

Since most pesticides are applied in crop fields, bees foraging in landscapes dominated by intensive farming should be more exposed to these compounds (David et al. 2016; Böhme et al. 2018). A high cover of semi-natural habitats could help dilute pollen contamination since honey bees could collect pollen from uncontaminated floral resources. The amount of crops in the landscape is known to potentially boost insecticide concentration in pollen, especially for some highly toxic neonicotinoids, such as thiamethoxam and

imidacloprid, and organophosphates, such as chlorpyrifos (Calatayud-Vernich et al. 2018; Wood et al. 2019). Also, the cover of specific crop categories in the landscape, such as apple and cherry orchards and blueberry plantations, could predict pesticide residue concentration in pollen (McArt et al. 2017; Graham et al. 2021, 2022). However, pesticide drift from crops could lead to high contamination also in surrounding areas, resulting for example in a high number of pesticides detected in pollen collected by bees in semi-natural habitats (Lambert et al. 2013; Calatayud-Vernich et al. 2018).

The use of pesticides is not continuous throughout the year. Therefore, seasonality can play a strong role in increasing or reducing the level of contamination by pesticides in pollen collected by honey bees, even because mechanisms of exposure to pesticides of honey bees might change throughout the season (Krupke et al. 2012). The highest concentration of pesticide residues in pollen collected by honey bees is usually observed in April and May since a large part of pesticide applications is made in spring (Lambert et al. 2013; Tong et al. 2018; Liu et al. 2022). However, some studies reported contamination peaks in mid-season or even later, *e.g.*, between July and September (Long and Krupke 2016; Tosi et al. 2018). Moreover, previous works reported a reduction in pesticide concentration after the blooming of focal crop species, which might be related to different foraging preferences, but also to the biodegradation of pesticides with increasing temperatures (David et al. 2016). Most of these studies, however, focused on specific pesticide categories such as insecticides, or a limited range of compounds, while multi-residue analyses on temporal and spatial variability of pollen contamination are largely still missing. This approach can provide a comprehensive picture of the importance of single crops and associated pesticides across heterogeneous agricultural landscapes.

In this work, we explored how pesticide residues in pollen collected by honey bees were affected by seasonality, landscape composition, and compound category. We selected 13 sampling locations in Northern Italy from which we collected pollen samples monthly for two consecutive years. For each pollen sample, we used liquid chromatography-tandem mass spectrometry and gas chromatography-tandem mass spectrometry to search for 375 compounds, including insecticides, acaricides, fungicides and herbicides. Then, for each compound and each pollen sample, we calculated the Pollen Hazard Quotient (PHQ), a measure of potential pollen toxicity for honey bees. We expected that insecticide would have a major impact on the potential toxicity of pollen, especially for some categories, such as neonicotinoids. We also expected higher pollen

contamination at the beginning of the season, especially in areas with a high cover of crops and fruit orchards in particular.

3.3. Materials and methods

3.3.1. Study area and site selection

The study was carried out in Northern Italy, in the Trentino-Alto Adige and Veneto regions (NE Italy), where we selected 13 sampling locations characterized by contrasting landscapes. In 3 km radius buffers around the sampling locations, the cover of semi-natural areas ranged from 1 to 92% (mean = 50%), the cover of agricultural areas ranged from 8 to 87% (mean = 38%), and the cover of urban areas ranged from 0 to 30% (mean = 12%) (Table S3.1, Figure S3.1). Site elevation ranged between 91 and 1,481 m a.s. l. (mean = 535 m a.s.l.). As a result, the climate in the sampling areas was highly variable: the mean annual temperature ranged between 6.8 °C (1500 m a.s.l.) and 13.5 °C (90 m a.s.l.) (mean = 10.8 °C), while the total precipitation ranged between c. 1,100 and 1,700 mm/year (mean = $1,260$ mm/year).

In 2019 and 2020, we placed two honey bee colonies at each location. Activating pollen traps at the hive entrance for 48 hours, we collected pollen samples monthly from April to September, for a total of six samples per year per location. Due to adverse climatic conditions, we were not able to collect pollen samples each month at a few locations: in 2019 we collected only five samples at two locations and three at one, while in 2020 we collected only five samples at three locations. Pollen samples were then stored at -20 °C.

3.3.3. Landscape composition

We extracted the cover of the main habitat types at each sampling location using the regional land-use map (\odot European Union, Copernicus Land Monitoring Service 2018, European Environment Agency) at two scales considering the foraging distance of honey bees, *i.e.*, 3 km and 5 km radius buffers around the sampling locations (Table S3.2). Since most of the 15 land-use classes were correlated with each other, we performed a Principal Component Analysis (PCA) to extract the landscape composition at each sampling location. We extracted the first three eigenvalues, PC1, PC2, and PC3, which respectively explained 25.9%, 18.9%, and 14.21% of the total landscape variability at 3 km radius buffers (Figure S3.2 *a*), and 31.2%, 20.6%, and 12.75% at 5 km radius buffers (Figure S3.2 *b*). All statistical analyses were performed using the *R* software version 3.6.1 (R Core Team 2019).

3.3.4. Pesticide analysis

We searched for 375 active ingredients in pollen samples, including insecticides and acaricides ($N = 169$), fungicides ($N = 117$), and herbicides ($N = 89$) (Table S3.3, Figure S3.3 *a*). For the chemical analyses, pollen was grounded using a mill in liquid nitrogen. From each sample, we extracted two grams of pollen according to the QuEChERS method (EN 15662:2018) (European Standard EN 15662:2018 2018). The extracts were then analysed using liquid chromatography-tandem mass spectrometry (LC-MS/MS) and gas chromatographytandem mass spectrometry (GC-MS/MS) (Tables S3.4, S3.5).

LC-MS/MS analyses were performed using an Acquity UPLC coupled with a XEVO TQ mass spectrometer equipped with an electrospray ion source (Waters Corporation, Milford, USA) and operating in MRM mode recording two specific transitions for each pesticide. The column used was an Acquity UPLC BEH C18 (1.7 μ m particle size, 100 × 2.1 mm), and the mobile phases were A (water with 0.1% formic acid) and B (methanol with 0.1% formic acid). The gradient conditions were as follows, based on times (t): $t_1 = 0$ -0.25 min, hold 95% A, 5% B; $t_2 = 0.25$ -6 min, ramp linearly to 70% B; $t_3 = 6$ -7.5 min, hold 70% B; $t_4 = 7.5$ -9.5 min, ramp linearly to 100% B; $t_5 = 9.5$ -12 min, hold 100% B.

GC-MS/MS analyses were performed by Agilent 8890 gas chromatograph coupled to a TQ 7010B mass spectrometer (Agilent Technologies Inc., USA) equipped with an electron impact ion source (ionization energy = 70 Ev EI). GC analysis was conducted on a Restek Rxi-5Sil MS capillary column (20 m \times 0.18 mm internal diameter \times 0.18 µm) (Restek, USA) and the following conditions were used: He constant flow 1 mL/min, inlet temperature 260 °C, injection volume 1 μ L (split, 1:10), MS transfer line temperature 280 °C, temperature program: 60 °C for 1 minute, then 60 °C/min ramped to 170 °C, followed by 20 °C/min ramped to 320 °C (held for 1 minute). The acquisition, as well as for the LC/MS system, was carried out in MRM mode.

Glyphosate was quantified following the QuPPe-PO-Method (M1.9, Version 12) (Anastassiades et al. 2020) which involves the use of an LC-MS/MS (Acquity UPLC coupled with a XEVO TQ mass spectrometer) system equipped with a Raptor Polar X column.

3.3.5. Validation method

Analytical parameters of the pollen multi-residue method such as matrix effect, limits of quantification (LOQs), limits of detection (LODs), linearity, precision and trueness were evaluated according to SANTE guidelines (SANTE/12682/2019; European Commission, 2020) (Tables S3.6, S3.7). All pesticide parameters

were quantified using five-point matrix-matched calibration curves $(R^2 > 0.98)$ and triphenyl phosphate as internal standard. Matrix effects were evaluated by comparing the slope of the calibration curve done in solvent and the slope of that prepared in the extract of the pollen matrix. To verify the recovery (Rec%) and the repeatability (RSD%) of the method, a blank pollen matrix (no pesticide contamination) was used. Pesticides were added to the matrix at three concentration levels: 10, 50, and 200 µg/kg, and each added concentration level was analysed sixfold. Average values of Rec% and RSD% over three concentration levels complied with the SANTE guidelines (Rec % 70-120% and RSD% < 20%) (European Commission, 2020). The sensitivity of the method was estimated by establishing the LOQs according to SANTE guidelines, and LODs were estimated as one-third of the quantification limit. According to the SANTE guidelines, all obtained pesticide data were not corrected by the recovery since it was found to be between 80% and 120%.

3.3.6. Pesticide risk assessment

After determining the concentration in ppm, we calculated the Pollen Hazard Quotient (PHQ) (Stoner and Eitzer 2013) for each compound in each pollen sample. PHQ is a measure of hazard from pesticide residues in pollen in relation to acute toxicity to honey bees, and it is calculated as the ratio between the compound concentration in ppb (μ g/kg) and the oral or contact LD₅₀ for honey bees. We retrieved oral LD₅₀ from the University of Hertfordshire Pesticide Properties DataBase (Lewis et al. 2016). However, we used contact LD_{50} for five compounds (bromophos ethyl, emamectin benzoate, fluazifop-p-butyl, piperonyl butoxide, and tetradifon), for which we could not obtain oral LD_{50} . Then, we determined the total PHQ of each pesticide category (fungicides, herbicides, and insecticides/acaricides) in each pollen sample by summing PHQ values of each category in each sample, and the total PHQ for each pollen sample by summing PHQ values of all compounds in each sample. We assumed additive toxic effects of multiple pesticides due to the lack of information on possible synergistic or antagonistic effects.

In addition, we calculated the acute risk quotient (RQ) for honey bees for each compound in each pollen sample using the US Environmental Protection Agency BeeREX model. While PHQ is ideal for evaluating the effect of specific drivers on multi-residue contamination of pollen, it does not take into account the amount of pollen consumed by honey bees, as opposed to the BeeREX model. First, we calculated the total dose of each compound consumed by each bee as the product between the concentration of the compound in μg/mg and the dose of pollen consumed by the honey bee in mg/day. Since we were not interested in testing how pesticide toxicity varied for different bee castes, we considered the highest consumed dose, which is 9.6 mg/day for nurse workers. Second, we calculated the acute RQ as the ratio between the total dose of pollen consumed by each bee and the oral LD_{50} for the compound. An acute $RQ > 0.4$ exceeds the concern threshold and indicates high toxicity of the compound for honey bees.

3.3.7. Statistical analyses

In order to determine the effect of seasonality, landscape composition, and pesticide category on PHQ of each pollen sample, we used linear mixed-effects models. We included the total PHQ of each pesticide category (fungicide, herbicide, and insecticide/acaricide) as response variable (ln-transformed), while selected explanatory variables were the year and the interaction between the sampling month and pesticide category, between the sampling month and landscape PC1, between the sampling month and landscape PC2, and between the sampling month and landscape PC3. Landscape PC1, PC2 and PC3 were calculated at both spatial scales, *i.e.*, 3 km and 5 km radius buffers around the sampling locations. To account for the repeated measures, we included the sample ID nested within the location ID as random factor. Then, starting from the full model, we used a backward deletion procedure, removing one-by-one interactions with *p*-value > 0.05, and re-ran the model to correctly interpret the main effects. We tested whether model residuals were spatially auto-correlated using Moran's I in the *R* package *ape* (Paradis and Schliep 2019) and we detected no spatial autocorrelation (global test, p -value = 0.859).

Then, we focused on the effect of specific crop categories on PHQ of pollen samples. We built two linear mixed-effects models using the total PHQ of pollen samples as response variable, and the cover of annual crops (including non-irrigated arable land, complex cultivation patterns, and agriculture with significant areas of natural vegetation) and perennial crops (including fruit trees, berry plantations, and vineyards) in the landscape at 3 km and 5 km radius buffers around the sampling locations as explanatory variables. We also included the location ID as random factor. Since the results of the models at the two spatial scales were similar, we presented in the main text only the results of the models at the 3-km radius scale.

3.4. Results

Out of the total 147 samples, only 4% were free of pesticide residues. We detected a total of 97 compounds in pollen samples, mostly fungicides ($N = 48$), followed by insecticides ($N = 32$) and only a few herbicides ($N =$

17) (Figure S3.3 *a*). The proportion of the detected compounds was similar throughout the season (Figure S3.3 *b*). On average, we detected 11 compounds in each pollen sample.

The concentration of detected pesticides was significantly higher for fungicides than for insecticides/acaricides and herbicides (Figure 3.1 *a*). The most abundant compounds were all fungicides, *i.e.*, captan, found in 30% of samples with a total concentration (summed across all pollen samples) of 320.135 ppm (max = 142 ppm, mean = 2.178 ppm); folpet, found in 10% of samples with a total concentration of 28.409 ppm (max = 15.6 ppm, mean = 0.193 ppm); and zoxamide, which was the most common detected compound, found in 80% of samples, with a total concentration of 16.955 ppm (max = 3.99 ppm, mean = 0.115) ppm) (Table S3.3). The fungicides spiroxamine and penconazole were also commonly detected in our samples, respectively found in 62% and 50% of samples (Table S3.3).

However, the overall toxicity of fungicides was low, as these compounds are mostly characterized by high LD_{50} values. The highest contribution to the total PHQ of pollen samples was made by insecticides/acaricides, in particular neonicotinoids and organophosphates (Figure 3.1 *b*). The compounds with the highest total PHQ (summed across all pollen samples) were all insecticides, *i.e.*, dimethoate, imidacloprid, and indoxacarb (Table S3.3). Dimethoate showed a total PHQ of 31,870 and, despite its toxicity, it was very common, being found in 23% of samples, with a total concentration of 3.187 ppm (max $= 1.370$ ppm, mean $=$ 0.022 ppm). Three pollen samples showed particularly high dimethoate concentrations, which led to PHQ values for the compound of 13,700, 7,470, and 4,840, corresponding to 137%, 75%, and 48% of the oral LD $_{50}$, respectively. Dimethoate in these three pollen samples exceeded the concern threshold for acute RQ, with acute RQ values of 0.132, 0.072, and 0.046, respectively. Imidacloprid showed a total PHQ of 25,405, and it was also common, being found in 20% of samples, with a total concentration of 0.094 ppm (max = 0.038 ppm, mean = 0.001 ppm). One pollen sample showed a peak of imidacloprid concentration, which led to a PHQ value of 10,270, corresponding to 102% of the oral LD_{50} , and an acute RQ value of 0.099, beyond the concern threshold. Indoxacarb showed a total PHQ of 4,821 and was less common than dimethoate and imidacloprid, being found in 7% of samples with a total concentration of 1.119 ppm ($max = 0.812$ ppm, mean = 0.008 ppm). One sample showed a peak of indoxacarb concentration, which led to a PHQ value of 3,500, corresponding to 35% of the oral LD₅₀, which however did not exceed the concern threshold for acute RQ.

Figure 3.1: Bar plots showing *a)* total concentrations in ppm of pesticide categories for each sampling month and *b)* total PHQ of pesticide categories for each sampling month.

Although the toxicity of single compounds in terms of acute RQ was relatively low, total PHQ values of pollen samples were high (total PHQ > 1000) in 8% of samples, medium-high (500 < total PHQ < 1000) in 7% of samples, medium (50 < total PHO < 500) in 22% of samples, and low (total PHO < 50) in 58% of samples. Total PHQ was influenced by the interactions among seasonality, landscape composition, and pesticide category at both 3 km and 5 km radius buffers around the sampling locations (Tables 3.1, S3.8). PHQ of pollen samples changed throughout the season based on the pesticide category. The peak of PHQ of fungicides was in July, but PHQ was approximately constant in all months. On the other hand, PHQ of herbicides and insecticides and acaricides was higher from April to June, and it decreased, especially for insecticides and acaricides, at the end of the season (Figure 3.2).

Table 3.1: Results of the linear mixed-effects model testing the effect of the interaction between the sampling month and pesticide category, the interaction between the sampling month and landscape PC1, the interaction between the sampling month and landscape PC2, and the sampling year on PHQ of pollen samples (ln-transformed). Landscape PC1, PC2 and PC3 were calculated using the regional land-use map categories in 3 km radius buffers around the sampling locations. Values in bold indicate significant effects (*p* value < 0.05). Only significant results after a backward stepwise model selection procedure are reported.

Figure 3.2: Plots showing the effect of the interaction between the sampling period and the pesticide category on PHQ of pollen samples (ln-transformed). Small coloured points represent raw data points, large black points represent model estimates, and bars represent the 95% confidence intervals.

PHQ was also influenced by the interaction between the sampling month and landscape PC1 calculated at both 3 km and 5 km radius buffers around the sampling locations. PHQ increased with increasing landscape PC1 from April to July, while in August and September, landscape composition did not affect PHQ of pollen samples (Figures 3.3, S3.4). Low values of landscape PC1 were related to semi-natural areas, in particular coniferous forests, natural grasslands, and sparsely vegetated areas, while high values of landscape PC1 were related to both agricultural and urban areas (Figure S3.2 *a*, *b*).

Figure 3.3: Plot showing the effect of the interaction between the sampling period and landscape PC1 on PHQ of pollen samples (lntransformed). Landscape PC1 was calculated using the regional land-use map categories in 3 km radius buffers around the sampling locations. Points represent raw data points and lines represent model estimates.

Total PHQ of pollen samples increased with increasing cover of perennial crops, *i.e.*, fruit trees and berries plantations and vineyards, at both 3 km and 5 km radius buffers around the sampling locations (Tables 3.2, S3.9, Figures 3.4, S3.5). However, total PHQ was only marginally affected by the cover of annual crops

in 3 km radius buffers around the sampling locations (Table 3.2), and the effect was not significant at a larger

scale (Table S3.9).

Table 3.2: Results of the linear mixed-effects model testing the effect of the percentage of annual and perennial crops in 3 km buffers around the sampling locations on PHQ of pollen samples (ln-transformed). Values in bold indicate significant effects (*p* value < 0.05).

Figure 3.4: Plot showing the effect of the percentage of perennial crops (fruit trees and vineyards) in 3 km radius buffers around the sampling locations on PHQ of pollen samples (ln-transformed). Points represent raw data points, the line represents model estimates, and the shaded area represents the 95% confidence interval.

3.5. Discussion

Contamination by pesticides of pollen collected by honey bees can seriously threaten the health of honey bees and their colonies. Here, we performed a multi-residue analysis, testing for almost 400 compounds, and explored how the potential toxicity of pollen changed based on the pesticide category and how it could be modulated by landscape context and seasonality. For the first time, we demonstrated the interactive effects of these three variables on the potential toxicity of pollen collected by honey bees. In particular, we found that the peak of potential toxicity of pollen for honey bees changed for fungicides, herbicides, and insecticides and acaricides. Moreover, the effect of landscape composition, in particular of agricultural and urban areas, was modulated by the sampling month. Also, a high cover of perennial crops in the landscape, but not of annual crops, was associated with a higher potential toxicity.

We detected at least one compound in 96% of analysed pollen samples. The few pesticide-free pollen samples were all collected in the areas with the highest cover of semi-natural areas. Similar works carried out in Italy found a lower rate of pollen sample contamination, with 50-62% of samples contaminated by pesticides (Tosi et al. 2018; Martinello et al. 2019), however, a study conducted in our same study region found no samples free of pesticides (Favaro et al. 2019). Out of the 375 compounds searched in pollen samples, we identified 97 compounds (26%), a percentage similar to the one reported by Böhme et al. (2018) but much higher than Favaro et al. (2019), which only detected 13% of the searched compounds. Our surveys were done halfway through each month, but we had no information on whether pesticide treatments were applied in the surrounding areas before our surveys due to the high number of farmers and fields. Although the investigated areas were mainly mountainous and characterized by a relatively high cover of semi-natural areas, the agricultural and urban areas around the hives boosted the presence of pesticides in pollen.

Herbicides were rare in our pollen samples and comprised the least toxic compounds, despite their toxicity being considered moderate for honey bees (Iwasaki and Hogendoorn 2021). By far, the most common and abundant pesticides detected in pollen samples were fungicides, as also found in other works (Mullin et al. 2010; Friedle et al. 2021). The most commonly detected were zoxamide, which affects cytoskeleton and motor proteins, and spiroxamine and penconazone, which affect sterol biosynthesis in membranes. These fungicides are used for the control of fungal pathogens in a variety of crops, in particular vineyards, fruit orchards and cereal fields. The toxicity of fungicides for honey bees is generally low since they do not directly impact insects, and therefore their potential negative effects on honey bees are still debated (Iwasaki and Hogendoorn 2021). For example, Tamburini et al. (2021) highlighted no effect of azoxystrobin, a systemic broad-spectrum fungicide, on honey bee colonies at field-realistic exposure, while Al Naggar et al. (2022) showed that the same compound could have detrimental effects on the gut microbiota of bees. However, the major threat of fungicides is related to their interaction with other compounds (Iwasaki and Hogendoorn 2021; Ward et al. 2022): for example, the acute toxicity of some insecticides dramatically increases in the presence of fungicides (Tsvetkov et al. 2017). Moreover, even low doses of pesticide mixtures, considered not harmful for honey bees, may reduce the efficiency of insects exposed in early development stages (Prado et al. 2019). While laboratory experiments are fundamental to test the effect of single pesticides, it is crucial to also investigate the effect of multiple pesticides to which bees could be exposed in nature.

In general, only a few single compounds exceeded the concern threshold for the acute RQ. However, multi-residue analysis showed that 15% of analysed pollen samples had medium or high levels of PHQ, which could pose serious threats to honey bees. Insecticides and acaricides were less common than fungicides, however, they contributed most to the total PHQ of pollen (Friedle et al. 2021; Knapp et al. 2023). This result was expected since insecticides and acaricides are specifically formulated to negatively affect arthropods, therefore including non-target species. The most toxic insecticide categories were neonicotinoids, especially abundant in April and May, and organophosphates, which boosted PHQ of pollen in June and July. Neonicotinoids are highly efficient in controlling target species, but consequently also highly toxic to bees. These insecticides are known to strongly negatively impact bee survival, also during overwintering, and bee general health, especially the immune and reproductive systems (Tsvetkov et al. 2017; Woodcock et al. 2017). Since the use of neonicotinoids has led to higher risks to bees in the last decades (Goulson et al. 2018), strict regulations have been imposed. In the analysed pollen samples, imidacloprid was the neonicotinoid with the highest PHQ, as also found by Tosi et al. (2018). Imidacloprid is an insecticide with immunosuppressive activity, that also showed detrimental effects on bee memory (Williamson and Wright 2013; Di Prisco et al. 2013; Delkash-Roudsari et al. 2022, but see Dai et al. 2019). Despite a shift towards neonicotinoids in the last few years (DiBartolomeis et al. 2019), organophosphates are still commonly used in Italy (Porrini et al. 2016), as demonstrated by the widespread use of dimethoate.

3.5.1. Banned pesticides

In our pollen samples, we detected a few compounds that were banned for use in the EU because of health and environmental concerns, as already reported in Italy (Perugini et al. 2018). We identified the fungicide carbendazim, which was banned in the EU since 2014, at 6 locations and in 14 samples, 7 from 2019 and 7 from 2020, at higher concentrations in 2020 (mean = 0.002 ppm) than in 2019 (mean = 0.0003 ppm). The use of carbendazim is still widespread in the EU (Pesticide Action Network Europe, 2020), and it was also detected in food produced in Italy (EFSA 2022). However, carbendazim is also a metabolite of thiophanate-methyl, a fungicide which was still legal to use until 2021 and was also found in our samples. Therefore, the contamination of some of our pollen samples by carbendazim could be related to thiophanate-methyl conversion - although carbendazim and thiophanate-methyl were not found in association in two pollen samples, pointing out the need for stricter controls on pesticide use in Europe. The fungicide quinoxifen and the insecticide chlorpyrifos were banned in Italy in March and April 2020 respectively, and after these dates, we detected them in 2 samples from 2 locations and 4 samples from 4 locations respectively. Some highly toxic compounds were banned in Italy after our surveys, *e.g.*, the neonicotinoid insecticides thiamethoxam and imidacloprid, and the oxadiazine insecticide indoxacarb, which was one of the compounds with the highest total PHQ. Lastly, in June 2020, the use of dimethoate was banned in Italy following the EU Regulation 2019/1090, however, its use was allowed in olive orchards until October 2020, after our samplings.

3.5.2. Interactive effect of pesticide category and seasonality on pollen toxicity

Seasonality differently affected PHQ of the three pesticide categories. For herbicides and insecticides and acaricides, PHQ was higher in spring and early summer and started to decrease in July. While herbicide contamination was generally low, the result for insecticides is probably largely related to applications in apple orchards, which in Italy are mainly made in spring and early summer (Garthwaite et al. 2015) and may have boosted pollen contamination. Similarly, other works found that pollen contamination by insecticides decreased at the end of summer (Tong et al. 2018; Friedle et al. 2021; Murcia-Morales et al. 2021). Some studies highlighted a peak of acaricide PHQ at the end of the season caused by treatments against *Varroa* mites (Murcia Morales et al. 2020), which we did not observe since our honey bee colonies were only treated with oxalic acid.

On the other hand, PHQ of fungicides slightly decreased in August and September, but it was more uniform throughout the season. The presence of fungicides in pollen samples was probably related to both apple orchards and vineyards in the landscapes. In apple orchards, fungicides are mainly applied to control diseases such as powdery mildews, apple scab, and cankers, while in vineyards they are used to prevent downy mildew, powdery mildew, and grey mould. These treatments are usually applied throughout the season, from the beginning of the vegetative growth to post-flowering of crops, and therefore caused little seasonal variation in fungicide PHQ.

3.5.3. Interactive effect of landscape composition and seasonality on pollen toxicity

The effect of landscape composition on PHQ of pollen collected by honey bees was modulated by the sampling month. PHQ increased with increasing cover of agricultural and urban areas from April to July, while it was lower in August and September and unrelated to landscape composition. It is well known that seasonality can have a strong effect on the detection of pollen contaminations (Koech et al. 2023), with fewer pesticides found

at the end of the season according to plant protection practices (Murcia-Morales et al. 2021). On the other hand, the effect of landscape context on honey bee pollen contamination is still debated. For example, some works highlighted that pesticide contamination was independent of landscape composition (Raimets et al. 2020; Koech et al. 2023; Knapp et al. 2023), while others showed that samples collected from hives placed in agricultural areas exhibited a higher concentration of pesticides (David et al. 2016; Meikle et al. 2020; Zaller et al. 2022). Our honey bee hives were not placed in intensive agricultural landscapes, since all selected landscapes were characterized by a certain cover of semi-natural areas (mean cover = 50%). Nevertheless, pollen contamination was high in areas with a higher cover of urban and agricultural areas, emphasizing that even a small amount of these areas may seriously threaten bees (Main et al. 2020).

An additional factor that should be considered when exploring the effect of landscape composition on pollen contamination is pesticide drift, which could increase risks to honey bees in agricultural-dominated landscapes. Pesticide residues could drift from focal crops to surrounding areas, contaminating pollen and nectar of wildflowers at field margins (Ward et al. 2022). Since a high diversity of floral resources could be related to a higher contamination risk of pollen collected by bees (Bednarska et al. 2022), the lower diversity of floral resources typical of the end of the season could have also minimized pollen contamination by pesticides.

Unexpectedly, urban areas emerged as key pathways of pollen contamination by pesticides. Contamination is usually lower in urban areas compared to rural areas (David et al. 2016, Siviter et al. 2023). However, recent studies underlined that urban habitats could be associated with high pollen contamination by pesticides, which may exceed that of agricultural habitats in some sampling periods (Benner et al. 2023), in particular for specific compounds such as neonicotinoid insecticides (Botías et al. 2017, Kavanagh et al. 2021). In addition, urban areas pose additional risks to honey bee health due to air pollution, which can negatively affect odour learning and memory (Leonard et al. 2019). The impacts of pesticide applications and pollution in general on pollinators in urban areas are still largely unexplored, despite the widespread use of pesticides in public and private gardens and the growing interest in urban beekeeping in most cities (Matsuzawa and Kohsaka, 2021), underscoring the need for further studies on this topic.

3.5.4. Effect of annual and perennial crops on pollen toxicity

The cover of annual crops, which in the study area mostly included maize, did not affect pollen contamination, as also found by Wintermantel et al. (2020). On the other hand, pollen collected in landscapes with a high cover of perennial crops, *i.e.*, fruit orchards and vineyards, was characterized by a higher PHQ. Böhme et al. (2018) analysed pesticide residues in pollen collected by honey bees in different habitats, highlighting the lowest pollen contamination in semi-natural habitats, intermediate contamination in grain fields, and the highest contamination in fruit orchards, similar to what we observed. Most of the perennial crops in our landscapes were apple orchards, which are crucial for the economy of our study area, and covered a large portion of our landscapes, ranging between 0 and 45% (mean = 9%). Apple is one of the most sprayed crops, with an average of 25 pesticide applications per year (Garthwaite et al. 2015), and therefore pollen collected in apple orchards often shows high levels of pesticide contamination (Knapp et al. 2023). However, it is also important to emphasize that most pesticide applications, especially for insecticides, are not permitted during blooming to safeguard pollinators. The high PHQ observed during apple blooming could be therefore related to pre-blooming pesticide applications, since most treatments in apple orchards in the study region are made between mid-March and the end of May (Garthwaite et al. 2015), but also to contamination at non-focal crops, as also highlighted by McArt et al. (2017).

3.5.5. Study limitations

Like most of the works performed under field conditions, we were not able to account for the potential interactive effects among pesticides, thus considering only additive effects when estimating multi-residue pollen toxicity, and potentially underestimating the negative effects on bee health. In fact, laboratory trials showed that the toxicity of pesticide mixtures can increase synergistically and also lead to an amplification of the sub-lethal effects of the least-toxic compounds, resulting in detrimental effects on bee health and colony longevity (Di Prisco et al. 2013). Therefore, future studies should also consider possible synergies among pesticides, in order to have an accurate and realistic assessment of the impacts of pesticides on honey bees.

3.6. Conclusions

Honey bees are key pollinators and are seriously threatened by pesticide applications. Here, we showed that the potential toxicity of pollen was related to the interaction of multiple factors, *i.e.*, the pesticide category, seasonality, and landscape composition. We highlighted that contamination was generally higher in spring and early summer, and that semi-natural areas can contribute to decreasing pollen contamination. We also found that pesticide applications in urban and agricultural areas, especially in perennial crops, were probably responsible for a high contamination of pollen. To ensure the well-being not only of pollinators but also of humans, without overlooking crop protection, specific actions can be implemented. For example, farmers should decrease their dependency on pesticides, moving towards more sustainable management practices such as the use of pheromones and biopesticides (Pretty 2018, Baker et al. 2020). Agrochemical companies should formulate compounds that are more selective and less toxic to non-target organisms, focusing on new technologies such as controlled release systems (Singh et al. 2020). Lastly, beekeepers should always carefully assess where to place honey bee hives, preferring whenever possible areas surrounded by semi-natural habitats, in order to provide potentially uncontaminated resources for bees.

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Temperature and not landscape composition shapes wild bee communities in an urban environment

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Chapter 4: Temperature and not landscape composition shapes wild bee communities in an urban environment

4.1. Abstract

More than half of the world's population lives in urban areas, a proportion that is expected to increase. Even if urbanisation is widely regarded as a major threat to global biodiversity, recent research highlighted the potential ecological importance of cities for pollinators. Key determinants of cities' ability to sustain pollinators are the presence of green areas and the connectivity between them. However, also temperature is expected to be of primary importance for pollinator activities. Here, we aimed to disentangle the effects of temperature, open habitat cover, and distance from the city centre on wild bee communities in the city of Rome (Italy). We selected 36 sites along two statistically independent gradients of temperature and open habitat cover, and we sampled wild bee communities using pan-traps for 4 months. Then, we measured functional traits of wild bee species, that is, body size, social behaviour, nesting strategy, and diet breadth. Temperature emerged as the main driver of wild bee communities, with communities richer in species and individuals at warmer temperatures. We found little species replacement between cold and warm sites. In addition, with increasing temperatures, bee communities were dominated by polylectic and small-bodied species. Here, we showed that in a highly urbanised environment, temperature shapes pollinator communities irrespective of other landscape metrics. Even if warming seemed beneficial for urban pollinator abundance and richness, it might strongly homogenise bee communities by selecting those traits that make species more easily adaptable.

4.2. Introduction

Globally, urban areas are expanding, while natural habitats shrink and become more remote (Grimm et al. 2008). Today, more than half of the world's population lives in urban landscapes, a proportion that is expected to increase to 85% by 2100 (OECD 2015). Urbanisation is widely regarded as a major threat to global biodiversity (Sala et al. 2000; Grimm et al. 2008); however, high levels of biodiversity may also thrive inside cities (Beninde et al., 2015). In particular, recent research highlighted the ecological importance of cities for pollinators (Hall et al. 2017; Theodorou et al. 2020; Wenzel et al. 2020). Urbanisation generally enhanced pollinator diversity compared to more intensified agricultural landscapes (Wenzel et al. 2020). Moreover, urbanisation appeared to shift the functional diversity of bee assemblages (Fournier et al. 2020). Over the last few years, it has been well established that insect pollinators are declining worldwide, mostly due to habitat fragmentation, loss and land-use intensification (Potts et al. 2010; Kennedy et al. 2013). In this context, understanding the potential role of cities as pollinator refuge becomes fundamental.

Key determinants of cities' ability to sustain pollinators are often related to the amount of green areas that are rich in nesting and food resources and to the connectivity between green fragments (Beninde et al. 2015; Wenzel et al. 2020; Biella et al. 2022). Moreover, besides the well-known positive effects of flower availability and high landscape connectivity, temperature is expected to be of primary importance for pollinator activities (Kühsel and Blüthgen 2015). As for ectotherms in general, temperature is one of the main drivers of insect pollinators' activities (Bale et al. 2002; Kühsel and Blüthgen 2015). Warmer environments are expected to be associated with higher growth rates, reduced development time, and increased probability of survival (Zuo et al. 2012). However, excessive climate warming can also lead to negative effects such as increased desiccation impairing insect growth, reproduction, and survival (Hamblin et al. 2018; Dale and Frank 2018). For pollinators, changes in climate are also expected to cause spatial and temporal mismatches with their food plants (Papanikolaou et al. 2017). The urban heat island effect makes cities warmer than surrounding natural areas (Oke 1973), providing an ideal system to study warming effects.

Considering the high diversity of bee life-history strategies, different species might respond to environmental changes in different ways (Bale et al. 2002). Because certain traits can be favoured in different environmental conditions, pollinator communities are likely to exhibit shifts in functional group composition in response to urbanisation and warming. Usually, under warming temperatures, organisms show a smaller

body size because warmer temperature increases metabolic rates and the associated costs for a given body size (Brown et al. 2004; Eggenberger et al. 2019). However, responses to increasing temperatures can be different from taxon to taxon, for example, bumblebees and Halictidae bees showed dissimilar thermal limits and desiccation tolerances (Burdine and McCluney 2019). In contrast, the relationship between wild bees' traits and urbanisation is more variable. However, most studies highlighted that urban areas act as a strong environmental filter on wild bees and that some functional traits are particularly beneficial to thrive in urban areas (Buchholz and Egerer 2020; Gathof et al. 2022). For example, cavity-nesting and polylectic species seemed to profit more from urbanisation than ground-nesting and oligolectic species (Wenzel et al. 2020; Sexton et al. 2021).

In this study, we aimed to disentangle the effects of temperature, open habitat cover, and distance from the city centre on wild bee communities in the metropolitan city of Rome (Italy). Mediterranean ecosystems are among the most vulnerable to climate change and belong to the world biodiversity hotspots for wild bees (Orr et al. 2021). In particular, Italy hosts an incredible diversity of bee species: more than half of the species listed for the entire Europe (Quaranta et al. 2018). However, few studies focus on Mediterranean bees and even less on bees in Mediterranean urban environments. Here, we selected 36 sites along two statistically independent gradients of temperature and open habitat cover and we sampled bee communities using pan-traps for 4 months. We then measured several functional traits of pollinator species. We hypothesised that wild bee diversity and abundance would increase with warmer temperatures and with a higher cover of open habitat at the landscape scale. In addition, we expected that communities would be dominated by species adapted to warm conditions at higher temperatures. In particular, we hypothesised traits to be filtered by the environment, with small bees being favoured at warmer temperatures near the city centre and below-ground nesters and oligolectic bees in areas with a higher cover of open habitat.

4.3. Materials and methods

4.3.1. Study area

The study area was the metropolitan city of Rome (Italy, 41.889956 N, 12.492286 E) (Figure 4.1 *a*), defined as the territory circumscribed by the great motorway ring (c. 360 km²). Rome is the third most populated city in the European Union, with a population estimated at 3.8 million, and a density of 2,232 people/ km^2 in 2016 (World Population Review 2016). The climate is temperate, with mild wet winters and warm summers. From

1970 to 2000, maximum mean annual temperature was 21.4 °C, minimum mean annual temperature was 9.1 °C, and mean precipitation was 140.9 mm. Over the last 40 years in Italy, summer temperatures increased on average by 0.52 °C every 10 years (Fioravanti et al. 2020). Approximately 54% of the study area is represented by urban areas (residential, industrial, and commercial areas), 16% by urban green areas (non-agricultural green areas, both artificial and semi-natural, including historical and archaeological sites, public parks and gardens, grasslands, shrublands, and forests), and the remaining 30% is covered in agricultural lands, pastures and water.

Figure 4.1: *a)* Study area in the city of Rome, Italy; *b)* spatial distribution of the 36 selected sampling sites (black points) along a gradient of urbanisation (shaded); *c)* example of open green habitat cover (in green) in a 500 m buffer. The centroid of the buffer is the point where pan-traps were placed. Maps were obtained from OpenLayers Plugin, QGIS.

4.3.2. Sampling design

We selected 36 sampling sites with open grassland vegetation with 2 km minimum and 26 km maximum distance from each other (Table S4.1, Figure 4.1 *b*). Sampling sites were chosen along two independent gradients: a gradient of median surface temperatures from 34 to 43 °C, and a gradient of open habitat cover in a buffer of 500 m radius spanning from 4% to 53%. We selected a 500 m radius because it emerged from several studies as the most appropriate landscape scale for wild bees (Gathmann and Tscharntke 2002; Steffan-Dewenter et al. 2002).

To obtain surface temperatures, we extracted the radiative skin temperature of the land surface, using Landsat 8 images with 30 m resolution. For each pixel, we calculated the median of the temperatures recorded over the sampling period, from June to September 2016, using Google Earth Engine (Ermida et al. 2020). This temperature metric is considered very relevant for insects and it has been used as a source of temperature data in several insect population models (Chuang et al. 2012; Blum et al. 2015).

To quantify the cover of the main habitat categories in a radius of 500 m around each sampling site, we identified urban, woody, and open habitat areas (*i.e.*, covered in herbaceous vegetation) and digitised polygons in Google Earth Pro manually (Google Earth 7.1.5.1557, 2015). Then, with a field survey, we validated the habitat classification obtained digitised polygons (Figure 4.1 *c*).

Moreover, we calculated the distance of each site from the city centre, that is, the Colosseum (41.890149 N, 12.492298 E). For Rome, this variable is a good proxy of decreasing disturbance along an urban-rural gradient (Fattorini 2014), as suburban areas are richer in semi-natural habitats than the central areas (Figure 4.1 *b*). Lastly, we assessed collinearity between all landscape variables, that is, land surface temperature, open habitat cover, urban cover, woody habitat cover, and distance from the city centre (Figure S4.1 *a*).

4.3.3. Wild bee sampling

At each sampling site, we collected wild bees (Apoidea: Anthophila) using a set of six yellow pan-traps, composed of plastic cups (750 ml, Ø 12.5 cm, h 4.5 cm) filled with a solution of water and 2% biodegradable dish detergent. As the vegetation in the sampling sites was below 50 cm, we placed pan-traps on the ground approximately 10 m apart, in two parallel lines of three pan-traps each. Due to the well-documented relationship between pollinator diversity and flower cover, we chose our sampling sites to reflect a similar amount of flower availability, allowing us to focus on the broader landscape context, that is, open habitat cover and temperature. We placed the pan-traps in small patches of open grassland vegetation characterised by similar plant composition and similar vegetation height (between 20 and 50 cm). Fieldwork was carried out every 2 weeks from mid-June to mid-September 2016, for a total of seven sampling rounds. For each sampling round, pan-traps were set out for 48 h. We excluded honey bees from this study because in our sampling area most honey bees are managed; therefore, their abundance strongly depends on beehive presence. The material was sorted by D.C. and identified by M.M. using identification keys (Additional references in Supplementary Information) and the reference collection of the Museum of Zoology of Sapienza, University of Rome. Species names follow Discover Life (Perlmutter 2010). Specimens are preserved at the Museum of Zoology of Sapienza, University of Rome.

Pan-trap sampling is a well-established method of collecting Hymenoptera and it usually captures a greater diversity of bee species compared to netting (Boyer et al. 2020). Even if the potential bias was constant

across all sites, by using pan traps to sample wild bees we may have under-sampled certain taxa (Prendergast et al. 2020), in particular larger bees (Roulston et al. 2007). In addition, several studies assessed colour preference in Hymenoptera, showing that trap colour affects the diversity of sampled bees and that, in most cases, yellow pan traps collected the largest numbers of bees (Buffington et al. 2021; Krahner et al. 2021). To evaluate the completeness of our sampling effort, we estimated the rarefaction curves using a coverage-based method (Chao et al. 2020) (Figure S4.2 *a*, *b*). With a few exceptions, the curves presented similar slopes and did not cross indicating that our species richness estimates were comparable across sites. However, the quick saturation showed by most curves stressed again that some groups of bees might have been under-sampled (Prendergast et al. 2020).

4.3.4. Wild bee functional traits

To investigate how life history and ecological characteristics mediate bee response to temperature, open habitat cover, and distance from the city centre, we sorted all recorded species based on functional traits. For each bee species, we collected 1) body size, 2) social behaviour (solitary or social), 3) nesting strategy (above-ground or below-ground), and 4) diet breadth (oligolectic or polylectic) (Table S4.2, Additional references in Supplementary Information). We selected the most informative functional traits in predicting bee responses to environmental change according to current literature and our knowledge (Williams et al. 2010). For body size, we measured body length of pinned specimens from head to metasoma end using graph paper. We measured one to five individuals, proportionally to how many specimens we collected in the field. For each species, whenever possible, we measured at least one female and one male. We then calculated the mean body size value for each species. We considered semi-social, social, and eusocial bees as social. Concerning nesting strategies, nesting categories were collapsed to below-ground and above-ground nesting to increase sample size and provide greater generality (Williams et al. 2010). Above-ground nesting bees included those species which build their nests in stems or pre-existing cavities. For diet breadth, we classified as oligolectic those bee species that are specialised to forage on one specific plant taxon, for example, one single plant family (Cane 2021). Finally, we assessed collinearity between all functional traits of wild bees (Figure S4.1 *b*).

4.3.5. Statistical analyses

First, we estimated the effects of surface temperature, open habitat cover, and distance from the city centre on wild bee abundance, species richness, and community evenness. We calculated wild bee community evenness

using the *R* package *codyn* (Hallett et al. 2016) with the default settings that calculate evenness as *Evar* (Smith and Wilson 1996). Then, we fitted three linear regressions using surface temperature, open habitat cover, distance from the city centre, and their two-way interactions as fixed factors and wild bee abundance, species richness, and community evenness as response variables. We used a natural logarithmic transformation of wild bee abundance and species richness to meet the assumption of normally distributed residuals. Pan-traps were placed in herbaceous open habitats that are considered to be the most influential habitat types for wild bees (Michener 2007; Winfree et al. 2011). However, some oligolectic species, in particular the ones nesting in wood, might be associated with trees. Therefore, we tested also the effect of woody cover on wild bees and wood-nesting bees, separately. As woody cover was negatively correlated with surface temperature $(r = -0.49)$, *p* value = 0.002), we could not test for the effect of both variables in the same models. Woody cover did not affect the abundance, species richness, and community evenness of either wild bees or wood-nesting bees (Table S4.3). Therefore, we decided to present in the main text only models testing for the effects of open habitat, surface temperature and distance from the city centre on all wild bees.

Second, we measured changes in the community composition. Based on presence/absence community data, we calculated richness and replacement, the two components of pairwise Jaccard dissimilarity, using the function *betadiver* in the *R* package *vegan* (Oksanen et al. 2019). Then, we generated a temperature distance matrix, a habitat cover distance matrix, and a distance from the city centre distance matrix using the *vegdist* function with Euclidean distance, and a geographical distance matrix using the *R* package *geosphere* (Hijmans 2019). To test the effects of temperature, open habitat cover and geographic distance on wild bee community dissimilarity, we performed multiple regressions on the obtained distances using the *MRM* function in the *R* package *ecodist* with 1000 permutations (Goslee and Urban 2007). We used richness and replacement dissimilarities as response variables.

Third, to measure functional diversity, we used functional dispersion (FDis) and functional evenness (FEve). Functional dispersion represents the dispersion of bee species in a multi-dimensional trait space, that is, the distance of species to the centroid of all species in the community, weighted by their abundance (Laliberté and Legendre 2010). Functional evenness describes the regularity of species distribution in the trait space weighted by their abundance. First, we created a distance matrix using Gower distance for traits. Then, we calculated both indices based on abundance data and Gower distances for traits using the *R* package *FD*

(Laliberté et al. 2014). Finally, we fitted two linear models using functional dispersion and functional evenness as response variables and surface temperature, open habitat cover, distance from the city centre, and their twoway interactions as fixed factors.

Fourth, to assess shifts in trait values within communities due to environmental selection, we used community-weighted means (CWMs), which allow extracting community-level trait values weighed by species abundances. CWMs are particularly useful as the distribution of traits is one of the best methods to describe the community functional composition (Moretti et al. 2009). We calculated CWM for all wild bee functional traits, expanding nominal traits, that is, social behaviour, nesting strategy, and diet breadth, into binary traits (Podani 2005). Then, we fitted four linear regressions using surface temperature, open habitat cover, distance from the city centre, and their two-way interactions as fixed factors and CWMs for each of the four traits as response variables. We excluded kleptoparasite species from all models of functional traits, as they lack pollen-collecting structures and do not build their nests, and morphospecies from social behaviour and diet breadth models, as we lack these data. Moreover, when analysing nesting strategy, we excluded one site because it contained extreme values of above-ground nesting bees compared to all other sites, distorting our analysis (Grubbs test for outlier *p* value < 0.001), and violating assumption of residual normality.

Starting from each of the full linear models, we used a backward deletion procedure, removing oneby-one the interactions with *p* value > 0.05, and re-ran the model with all main effects to avoid overfitting and to correctly interpret the main effects. Moreover, in all models, we estimated variance inflation factors (VIFs) to assess possible collinearity issues between fixed effects. All VIF values were close to 1, indicating very little collinearity among predictors (Akinwande et al. 2015). All statistical analyses were performed using the *R* software version 3.5.1 (R Development Core Team 2019).

4.3.6. Multi-model inference

To evaluate the uncertainty of model selection, we also performed a multi-model inference analysis and compared the fit of all possible candidate models nested within each of the full models presented above. Within each set, models were ordered based on their second-order Akaike information criterion (AICc), with the bestfitting model showing the lowest AICc. For each model, we calculated the difference between the model AICc and the lowest AICc of the entire set of models $(\Delta AICc_i = AICc_i - AICc_{min})$. A model in a set can be considered plausible if its ΔAICc is below 2. Multi-model inference analyses were performed with the *MuMIn* package

(Burnham et al. 2011; Barton 2020). The final models selected according to the backward stepwise deletion were consistent with the ranking of the plausible models based on AICc (Tables S4.4, S4.5). Hence, we presented the results of the reduced models from the backward deletion procedure in the main text and reported the multi-model inference analyses only in the Supplementary Information.

4.4. Results

Overall, we collected 3,280 individuals of 96 species and morphospecies of wild bees (Table S4.2, Figure S4.3). The most abundant species was *Lasioglossum malachurum* (Kirby, 1802) (n = 897 individuals), followed by *Lasioglossum glabriusculum* (Morawitz, 1853) (n = 456 individuals) and *Seladonia gemmea* Dours, 1872 (n = 275 individuals). Among the collected species, 77% were polylectic bees, 22% showed a social lifestyle and 38% nested above ground.

Surface temperature was the only factor affecting wild bee abundance and richness (Table 4.1). Both abundance and species richness increased with increasing temperatures (Figure 4.2 *a*, *b*), while community evenness did not respond. Open habitat cover and distance from the city centre did not affect wild bee abundance, species richness, and community evenness (Table 4.1).

Response variable	Explanatory variable	Estimate	SE	t value	p value
a) Wild bee	Intercept	0.278	1.775	0.157	0.877
abundance (ln)	Temperature	0.107	0.045	2.389	0.023
	Open habitat cover	-0.011	0.009	-1.164	0.253
	Distance from the city centre	0.015	0.041	0.362	0.720
b) Wild bee richness	Intercept	1.154	0.765	1.509	0.141
(ln)	Temperature	0.048	0.020	2.418	0.016
	Open habitat cover	-0.007	0.004	-1.814	0.081
	Distance from the city centre	${}_{0.001}$	0.018	-0.015	0.988
$c)$ Community	Intercept	1.070	0.366	2.919	0.006
evenness	Temperature	-0.015	0.009	-1.567	0.127
	Open habitat cover	-0.004	0.008	-0.512	0.612
	Distance from the city centre	0.001	0.002	0.715	0.480

Table 4.1: Results of the linear models testing the effect of temperature, open habitat cover, and distance from the city centre on *a)* wild bee abundance (ln-transformed), *b*) species richness (ln-transformed), and *c*) community evenness. Values in bold indicate significant effects (p value < 0.05). No significant interactions were found.

Figure 4.2: Plot showing the effect of surface temperature on *a*) abundance (ln-transformed) and *b*) species richness (ln-transformed) of wild bees. Points represent raw data points, lines represent model estimates, and the shaded areas represent the 95% confidence intervals.

Multiple regressions on distance matrices showed that temperature distance affected only community dissimilarity related to species richness difference (Table 4.2). Species richness difference increased with increasing temperature distance, that is, sites with similar temperatures shared a subset of the occurring species and showed more similar bee communities (Figure 4.3). In contrast, the species replacement component was not affected by temperature. In addition, open habitat distance, distance from the city centre and geographic distance did not have any effect on both richness and replacement components (Table 4.2).

Figure 4.3: Plot showing the effect of temperature distance on richness dissimilarity of wild bee communities among sites. Composition dissimilarity was calculated using the richness component of Jaccard index (Legendre 2014). The line represents the estimate of a multiple regression model on distance matrices.

Functional diversity analyses showed that functional evenness decreased at higher temperatures (Table

4.3 *a*, Figure 4.4) while it was not affected by open habitat cover or distance from the city centre (Table 4.3

a). Functional dispersion did not respond to temperature, open habitat cover or distance from the city centre

(Table 4.3 *b*).

Table 4.3: Results of the linear models testing the effect of temperature, open habitat cover, and distance from the city centre on *a)* functional evenness and *b)* functional dispersion of wild bee communities. Values in bold indicate significant effects (*p* value < 0.05). No significant interactions were found.

Response variable	Explanatory variable	Estimate SE		t value p value
a) Functional evenness	Intercept	1.190	0.223 5.338	${}< 0.001$
	Temperature	-0.014	$0.006 -2.488$	0.018
	Open habitat cover	0.001	0.001 0.737	0.467
	Distance from the city centre 0.001		0.005 0.289	0.774
b) Functional dispersion Intercept		0.359	0.119 3.004	0.005
	Temperature	-0.003	$0.003 -0.848$	0.403
	Open habitat cover	-0.001	$0.001 -1.183$	0.245
	Distance from the city centre -0.003		$0.003 - 1.024$	0.314

Figure 4.4: Plot showing the effect of surface temperature on functional evenness of wild bee communities. Points represent raw data points, the line represents model estimate, and the shaded area represents the 95% confidence interval.

By analysing CWMs for body size, social behaviour, nesting strategy, and diet breadth, we found that communities were functionally diverse depending on temperature and distance from the city centre (Table 4.4). Communities were characterised by smaller individuals when they were close to the city centre or when temperatures were warmer (Figure 4.5 *a*, *b*). Moreover, bee communities showed a higher proportion of individuals of polylectic species with warmer temperatures (Figure 4.5 *c*). In contrast, CWMs for nesting strategy and social behaviour did not respond to surface temperature, open habitat cover or distance from the city centre. However, we found a positive trend between sociality and open habitat cover (Figure S4.4).

Figure 4.5: Plots showing the effects of *a*) temperature, *b*) distance from the city centre on CWM body size, and the effect of *c*) temperature on CWM diet breadth (polylecty) (arcsin(sqrt)-transformed). Points represent raw data points, lines represent model estimates, and the shaded areas represent the 95% confidence intervals.

4.5. Discussion

Here, we showed that in a highly urbanised environment, temperature was the key driver of wild bee diversity, abundance, composition and functional diversity, shaping pollinator communities irrespective of the cover of open habitat and the distance from the city centre. Warmer sites showed communities richer in individuals and species but dominated by similar traits. In response to warming and distance from the city centre, bee assemblages exhibited clear shifts in functional composition.

4.5.1. Temperature as the main driver of wild bee communities

Both wild bee abundance and species richness were driven by temperature, with a positive effect of warmer temperatures. In addition, temperature was the only factor filtering community composition and, even with a very high variability, it led to communities that differed because of the number of species, and not because of species turnover. Warm temperatures are often beneficial to insects, as they might increase growth rate and survival, and reduce development time (Zuo et al. 2012). Most studies investigating the relationship between temperatures and pollinators found that warm temperatures increased insect activities, abundance, diversity or biomass (Kühsel and Blüthgen 2015; Schürch et al. 2016; Burdine and McCluney 2019; Welti et al. 2022, p. 20; but see Papanikolaou et al. 2017; Hamblin et al. 2018; Casanelles‐Abella et al. 2022). However, the reported positive effect of warming should be taken with caution. Large deviations from long-term temperature averages were found to negatively affect flying insects, as rapid temperature rises may exceed locally established tolerance (Welti et al. 2022). To assess more precisely temperature warming effects on bees, we should gain knowledge on mid- and long-term effects of temperature and on species thermal optima. However, little is still known about bee thermal and humidity limits, besides that they could strongly differ from species

to species and even from one population to another (Burdine and McCluney 2019; Sánchez-Echeverría et al. 2019; Martinet et al. 2021).

Cities usually experience much warmer temperatures than nearby rural or semi-natural areas because of heat-absorbing and impervious building materials (Oke 1973). In contrast, increasing vegetation cover decreases temperatures (De Frenne et al. 2013). Also in this study, we found a negative correlation between temperature and tree cover, that is, warmer sites were embedded in highly urbanised landscapes, while colder sites showed a lower percentage of urbanisation. Besides increasing local temperatures with a potentially positive effect on bee growth and survival, high urbanisation might provide locally a large amount of floral resources, for example, in parks, gardens and roadsides, therefore sustaining a high number of species and individuals (Hall et al. 2017; Baldock et al. 2019; Wilson and Jamieson 2019). However, in our study, wild bee abundance and diversity did not respond to open green habitat cover and distance from the city centre. Therefore, it is likely that different sites offered a similar amount of floral resources irrespective of the amount of open habitat in the landscape. Another hypothesis is that all sampled species had been already selected for intensive anthropogenic habitat types (Corcos et al. 2019). In cities, wild bee communities should be the result of centuries of human disturbance and therefore, they might be composed mostly of species adapted to an urban environment. Many studies revealed that only a subset of species, consisting of the most tolerant to anthropogenic activities, is able to survive in highly disturbed environments (Banaszak-Cibicka and Żmihorski 2012; Gámez-Virués et al. 2015; Fournier et al. 2020). In particular, it has been found that insect diversity increases with the age of an urban settlement (Sattler et al. 2010), as its insect fauna has probably been selected for high tolerance to fragmentation and colonisation potential.

4.5.2. Warm urban communities are dominated by specific functional traits

Our results show that in warmer sites, functional evenness decreased. This means that at high temperatures, the most abundant species shared similar traits different from the rest of the community. Probably, few species characterised by specific traits can cope better with warm conditions. As a consequence, these few dominant species may be better adapted to future climate change scenarios, while others, characterised by different traits, may disappear. By analysing community mean traits, we were able to identify which traits seemed beneficial with increasing temperatures. Community mean trait values shifted depending on temperature and distance from the city centre. As expected, we found that mean body size decreased with increasing temperatures, that
is, communities adapted to warm conditions showed on average smaller individuals. Similar results were reported for spiders, beetles, and aquatic taxa in urban environments (Merckx et al. 2018). It is well known that usually smaller animals dissipate heat better (Burdine and McCluney 2019). Larger wild bee species might be therefore negatively affected by increasing temperatures in cities (Wilson and Jamieson 2019). In addition, mean body size increased further away from the city centre, irrespective of the cover of open habitat. Similar results were reported in other studies, where mean body size of several invertebrate species increased with increasing distance from the city centre regardless of local site characteristics (Tóth and Hornung 2019; Braschler et al. 2021). For ground-dwelling arthropods, the decrease in body size has been related to a combination of reduced soil moisture and increased soil contamination (Braschler et al. 2021). However, for mobile flying organisms such as wild bees, this result is probably linked to foraging distances. Larger bee individuals forage further away, while smaller individuals travel closer to their nest (Greenleaf et al. 2007). Cities seem to favour smaller-bodied species because small bees may be more likely to use local and isolated floral spots in the city centre (Braschler et al. 2021; Prendergast et al. 2022). An additional possible explanation is that smaller species require a much limited amount of resources compared to larger species (Winfree et al. 2011; Eggenberger et al. 2019).

Besides filtering for smaller body sizes, warm temperatures increased the number of individuals of polylectic species in the community. In our study, all wild bee communities showed a high level of generalisation, with most species having a polylectic diet. This is typical of highly urbanised environments, where oligolectic species are usually uncommon (Lizée et al. 2011; Casanelles-Abella et al. 2022). Polylectic wild bee species are better able to exploit resources in urban areas as they can access and forage on a great variety of flowers. In this study, the few oligolectic species occurring at colder temperatures disappeared at warmer temperatures. A possible explanation for this might be that specialised species strongly depend on a particular range of conditions and are, consequently, more vulnerable to habitat disturbance in general and warming in particular (Winfree et al. 2011; Hopfenmueller et al. 2014; Martinet et al. 2021). It might also be that the abundance of the favoured host plants of some oligolectic species decreased at warmer temperatures but, unfortunately, we lack the data to confirm this hypothesis.

Finally, we did not find any effect of temperature, open habitat cover, and distance from the city centre on nesting strategy and social behaviour, except for a positive trend between sociality and open habitat cover.

Williams et al. (2010) also found that social species responded strongly to the amount of natural habitat. In our study, most social species nested below ground and, therefore, the availability of bare ground in open areas might have been a key resource for them.

4.6. Conclusions

In a highly urbanised environment, such as the metropolitan city of Rome, wild bee abundance and diversity did not change in response to open habitat cover or distance from the city centre. In contrast, temperature was the main driver shaping wild bee communities. Under future global warming, we expect that heat-tolerant wild bee species will benefit from increasing temperatures in urban settlements and that warm-temperature communities will be dominated by polylectic and small-bodied bees. Further research is needed to understand the potential role of cities as pollinator refuge under global change, focusing not only on wild bees, but even on other fundamental pollinator taxa such as Coleoptera, Diptera, and Lepidoptera.

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Functional traits of plants and pollinators explain resource overlap between honey bees and wild pollinators

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5.1. Abstract

Managed and wild pollinators often cohabit in both managed and natural ecosystems. The western honey bee, *Apis mellifera*, is the most widespread managed pollinator species. Due to its density and behaviour, it can potentially influence the foraging activity of wild pollinators, but the strength and direction of this effect are often context-dependent. Here, we observed plant-pollinator interactions in 51 grasslands, and we measured functional traits of both plants and pollinators. Using a multi-model inference approach, we explored the effects of honey bee abundance, temperature, plant functional diversity, and trait similarity between wild pollinators and the honey bee on the resource overlap between wild pollinators and the honey bee. Resource overlap decreased with increasing honey bee abundance only in plant communities with high functional diversity, suggesting a potential diet shift of wild pollinators in areas with a high variability of flower morphologies. Moreover, resource overlap increased with increasing trait similarity between wild pollinators and the honey bee. In particular, central-place foragers of family Apidae with proboscis length similar to the honey bee exhibited the highest resource overlap. Our results underline the importance of promoting functional diversity of plant communities to support wild pollinators in areas with a high density of honey bee hives. Moreover, greater attention should be paid to areas where pollinators possess functional traits similar to the honey bee, as they are expected to be more prone to potential competition with this species.

5.2. Introduction

As a managed and super-generalist pollinator, the western honey bee, *Apis mellifera* Linnaeus, plays a fundamental role in the pollination of both crops (Garibaldi et al. 2013) and wild plants (Hung et al. 2018). However, managed honey bees might adversely impact wild pollinator communities, as they are often extremely abundant, have a prolonged flight season, and tend to forage on the most abundant and rewarding floral resources (Goulson 2003). Nevertheless, observed effects are often idiosyncratic and seem to depend on local conditions, the composition of wild pollinator communities, and the different methodological approaches adopted (Goulson 2003; Cane and Tepedino 2017; Mallinger et al. 2017).

Against this background, functional traits of both plants and pollinators can help to identify the likelihood, strength and direction of the interactions between managed and wild pollinators (Violle et al. 2007; Eklöf et al. 2013; Schleuning et al. 2015; Bergamo et al. 2020). Floral morphological traits are fundamental in shaping plant-pollinator interactions (Junker et al. 2013). Plant species with greater flower size and longer flowering periods are usually more generalist, being attractive to many pollinator species, while flowers with deep corolla are usually accessible only to a few specialized pollinator species (Lázaro et al. 2020). Although the effect of functional diversity of plant communities on pollinators is still debated (Fornoff et al. 2017; Uyttenbroeck et al. 2017; Goulnik et al. 2020), one expectation is that increased functional diversity should reduce the plant resource overlap between wild pollinators and a dominant species such as the honey bee by providing a larger number of alternative nectar and pollen resources (Figure 5.1).

Similarly, pollinator traits can affect both how pollinators interact with plant species and how they interact with each other (Albrecht et al. 2012; Garibaldi et al. 2015; Woodcock et al. 2019). In particular, the competition of wild pollinators with honey bees in areas with a high abundance of managed pollinators could be stronger for central-place foragers, which are forced to collect pollen and nectar near their nest (Walther-Hellwig et al. 2006), and for oligolectic pollinators, which have a limited ability to shift to alternative resources (Cane and Tepedino 2017). On the contrary, large-sized pollinators with longer proboscis usually have a larger diet breadth, as they are able to exploit a wider range of resources compared to smaller ones (Greenleaf et al. 2007; Lara-Romero et al. 2019). Hence, we expect that a high trait similarity between wild pollinators and the honey bee should increase their resource overlap (Figure 5.1).

Environmental variables can also have a strong effect on species phenology and behaviour. Air temperature and weather, in particular, modulate the activity of pollinators (Trøjelsgaard and Olesen 2013; Giannini et al. 2015). For example, bumblebees are often active at low temperatures and under unfavourable weather conditions (Goulson 2010), while butterflies are strongly negatively affected by low air temperatures (Abrahamczyk et al. 2011). Honey bees are more sensitive to low temperatures than many wild pollinators (Jaffé et al. 2010), so potential competition between wild pollinators and honey bees should be more severe at high temperatures (Figure 5.1).

Figure 5.1: Expected effects of functional diversity of plant community and trait similarity between wild pollinator community and the honey bee on plant-pollinator interactions. We hypothesise that: a) in sites with a low functional diversity of plant community and a low trait similarity between wild pollinator community and the honey bee, the resource overlap between wild pollinators and the honey bee would be generally low, as pollinator species with functional traits different from those of the honey bee would exploit different resources; *b)* in sites with a high functional diversity of plant community and a low trait similarity between wild pollinator community and the honey bee, the resource overlap would be even lower, as pollinator species would spread on different floral resources; *c)* in sites with a low functional diversity of plant community and a high trait similarity between wild pollinator community and the honey bee, pollinator species would share an important portion of plants with the honey bee, therefore, resulting in a high resource overlap; *d)* in sites with a high functional diversity of plant community and a high trait similarity between wild pollinator community and the honey bee, the resource overlap would decrease, as pollinator species would have much more resources to forage on. Increasing honey bee abundance and higher temperatures would intensify the observed effects.

A promising approach to elucidate potential mechanisms shaping the interactions between plants and pollinators is the use of network tools integrated with functional trait analysis. Here, we investigated how functional traits of both plants and pollinators, together with the abundance of honey bees and temperature, affected the foraging behaviour of wild pollinators. In particular, this study aimed to explore how functional richness and dispersion of plant communities influenced the resource overlap between wild pollinators and the honey bee, also testing the effect of trait similarity between wild pollinators and the honey bee. We observed plant-pollinator networks in 51 grasslands in Northern Italy and computed the resource overlap between each wild pollinator species and the honey bee. We calculated functional richness and functional dispersion of plant communities using flower corolla length, flower colour, and flower shape, while trait similarity between wild pollinators and the honey bee was calculated using proboscis length, body size, type of foraging range, and taxonomic family.

5.3. Materials and methods

5.3.1. Sampling design

Fieldwork was carried out in 51 grasslands in Northern Italy (Alps and Prealps), approximately 50×30 m in size. Grasslands were selected across a steep elevational gradient ranging from 150 to 2100 m a.s.l., and had a wide range of honey bee abundance (Table S5.1, Figure S5.1). The selection of the sites was adjusted during the sampling season to have statistical independence between temperature and honey bee abundance (Pearson's correlation = 0.11, p value = 0.41). Each sampling site was at least 0.53 km from the nearest one (mean = 4.60 km). We were not able to determine the exact number of beehives near the sampling sites, but the mean density in the study area was c. 5 beehives per km² (data provided by the National Data Bank of the Zootechnical Registry established by the Ministry of Health at the National Service Centre of the "G. Caporale" Institute of Teramo).

5.3.2. Sampling of ecological interactions

Between May and September 2019, we observed plant-pollinator interactions in the selected sites. Sampling occurred between 9:00 and 17:00 only with air temperature > 15 °C, low wind, no rain, and cloud coverage < 70%. Each site was visited only once. At each site, we identified all flowering plant species and assessed their relative abundance. All the individuals of each plant species were then observed for 15 min in total, during which all hymenopterans and dipterans touching the reproductive parts of flowers were counted and collected. Both plant and pollinator species were identified in the field when possible, otherwise, plants were collected and prepared in a herbarium, while pollinators were placed in vials filled with 70% ethanol. Later identification was entrusted to experts (Filippo Prosser and LM for plants, and AC, MM, DP, and PC for pollinators). During the sampling, we also measured the air temperature using a Tinytag Plus 2 TGP-4017 data logger.

5.3.3. Resource overlap between wild pollinators and the honey bee

Starting from the observed interactions, we built 51 bipartite plant-pollinator networks, one for each sampling site. For each network, we calculated the resource overlap between each wild pollinator species (*i.e.*, excluding the honey bee) and the honey bee using Morisita's index (Morisita 1959) in the *R* package *spaa* (Zhang 2016). The index ranges from 0 to 1, with increasing values indicating an increase in the plant resource overlap between the two pollinator species. In each network, we then calculated the community weighted mean (hereafter, CWM) resource overlap between wild pollinators and the honey bee as the mean resource overlap value of all wild pollinator species weighted by their abundance. We used CWM resource overlap instead of resource overlap values of single species as no model using species as replicates met statistical assumptions, even after changing the distribution or transforming the variables. All analyses were performed using *R* version 3.6.1 (R Development Core Team 2019).

5.3.4. Functional traits of plant species

For each flowering plant species, we measured flower corolla length with a calliper, and recorded flower type after Kugler (1970) and flower colour (Table S5.2). These are among the most important morphological traits for the definition of pollinator feeding niches: flower colour affects the attractiveness and selectivity of flowers, while flower type and corolla length determine the accessibility of flowers to pollinators (Junker et al. 2013). We then calculated two indices of functional diversity of plant communities for each network, *i.e.*, the standardized functional richness and the functional dispersion, which provide complementary information (Villéger et al. 2008; Laliberté and Legendre 2010). First, for each network, we built an Euclidean distance matrix by projecting flowering plant species into a three-dimensional trait space with each axis corresponding to a functional trait. The distance matrix was analysed through Principal Coordinate Analysis (PCoA), and the PCoA axes were then used as new combined traits to compute the functional diversity indices. Categorical variables were transformed into dummy variables (*i.e.*, binary). Functional richness measures the functional space filled by the plant community, *i.e.*, the volume of the convex hull. For each network, we standardized the index value by the "global" functional richness, including all plant species in all networks (Laliberté and Legendre 2010). Its value ranges from 0 to 1, with increasing values of the index indicating an increase in community functional richness. Functional dispersion additionally takes into account the relative abundance of plant species. The index represents the dispersion of plant species in the trait space, *i.e.*, the distance of species to the centroid of all species in the community, weighted by their relative abundance. Its value ranges

from 0 to infinity, with increasing values indicating an increase in functional dispersion, *i.e.*, a strong difference in traits between dominant plant species and low abundant ones. Both indices were calculated using the *R* package *FD* (Laliberté et al. 2014).

5.3.5. Functional traits of pollinator species

For each pollinator species, we selected one to four individuals, depending on the availability, and extracted the proboscis which was measured along with total body length (body size). We derived from the literature two additional traits: type of foraging range (two classes: central-place forager, for species which build a nest, and non-central-place forager), and taxonomic family (Table S5.3, Additional References in Supplementary Information). Asfor corolla shape and length, proboscis length and body size affect the way a pollinator species can exploit a floral resource. The type of foraging range does not directly influence resource selection, but it determines how far pollinators can travel to collect pollen and nectar. Finally, the taxonomic family is often linked to floral preferences or particular mouthpart morphology. Using these traits, we estimated the trait similarity between each wild pollinator species and the honey bee using Gower's similarity coefficient (Gower 1971) as described by Podani (1999), calculated using the *R* package *FD* (Laliberté et al. 2014). For each site, we then determined the CWM trait similarity between the community of wild pollinators and the honey bee by calculating the mean trait similarity value of all wild pollinator species (*i.e.*, excluding the honey bee) weighted by their abundance.

5.3.6. Potential collinearity between predictors

Before performing the statistical analyses described below, we analysed potential collinearity in our data by computing the variance inflation factors (VIFs) using the *R* package *car* (John and Weisberg 2019). Plant species richness and standardized functional richness of plant community were strongly correlated (Pearson's correlation = 0.876, *p* value < 0.001), as well as temperature and elevation (Pearson's correlation = 0.751, *p* $value < 0.001$). We, therefore, chose to build our models using plant standardized functional richness and temperature as explanatory variables. Functional traits of pollinators were also correlated with each other (Table S5.4, Figure S5.2), so their effect on resource overlap was analysed separately. The explanatory variables of the six global models described in the next paragraph fitted without the interactions had VIFs < 1.5, indicating low collinearity.

5.3.7. Statistical analyses

For the statistical analyses, we followed an information-theoretic approach (Burnham and Anderson 2002), which allows comparing the fit of a set of models rather than selecting one single best model based on *p* values. The first global model (Model 1) included resource overlap between wild pollinator community and the honey bee as response variable, and the main effects of honey bee abundance, temperature, standardized functional richness of plant community, and trait similarity between wild pollinator community and the honey bee as explanatory variables. The model also included all the interactions that could strongly affect the resource overlap, *i.e.*, the two-way interactions between honey bee abundance and plant standardized functional richness, between honey bee abundance and trait similarity between wild pollinator community and the honey bee, between plant standardized functional richness and trait similarity between wild pollinator community and the honey bee, and the three-way interaction between honey bee abundance, plant standardized functional richness and trait similarity between wild pollinator community and the honey bee. The structure of the second model (Model 2) was similar, but standardized functional richness of plant community was replaced by functional dispersion of plant community.

Second, we explored the effect of single pollinator traits on resource overlap. We, therefore, built four linear mixed-effect models, one for proboscis length (Model 3), one for body size (Model 4), one for type of foraging range (Model 5), and one for taxonomic family (Model 6). Proboscis length and body size of wild pollinators were categorized according to trait values of the honey bee, which possesses a proboscis of c. 5 mm and body size of about 12 mm. Proboscis length categories for wild pollinators were: proboscis shorter than the honey bee ≤ 3.9 mm, proboscis similar to the honey bee = 4-6.9 mm, and proboscis longer than the honey bee > 7 mm. Body size categories for wild pollinators were: smaller than the honey bee < 7.9 mm, similar to the honey bee $= 8-14.9$ mm, and larger than the honey bee > 15 mm. We categorized continuous trait variables due to the poor outcome of model residual diagnostics using traits as continuous variables. For taxonomic family, we aggregated families with less than ten collected individuals, *i.e.*, Cimbicidae, Megalodontesidae, Melittidae, and Scoliidae. For each network, we calculated the CWM resource overlap between wild pollinators and the honey bee for each trait category, *e.g.*, for body size, we had one value of CWM resource overlap for wild pollinators smaller than the honey bee, one for wild pollinators similar in size, and one for wild pollinators larger than the honey bee. Each global model included honey bee abundance, temperature, trait category, and the interaction between honey bee abundance and trait category as explanatory

variables, and network identity as random factor. In all models described above, the continuous explanatory variables were scaled to mean 0 and standard deviation 1 to make slopes comparable (Gelman 2008). For a summary of the six global models, see Table S5.5.

Within each set, models were ordered based on their second-order Akaike information criterion corrected for small sample size (AICc), with lower values indicating models that better fit the data. For each model, we calculated the ΔAICc, *i.e.*, the difference between the model AICc and the lowest AICc of the entire set of models (with the best model having $\Delta AICc = 0$), and the Akaike model weight, which indicates the probability that the model is the best one. As a measure of goodness-of-fit, we estimated the $R²$. Lastly, we calculated the model-averaged partial coefficient for each explanatory variable using all models within each set and estimated the 95% confidence intervals around model-averaged partial coefficients. We presented in the tables all models with ΔAICc < 6 (Harrison et al. 2018). All multi-model analyses were conducted using the *R* package *MuMIn* (Barton 2020).

Lastly, we tested for potential spatial autocorrelation of residuals of all models using Moran's I in the *R* package *ape* (Paradis and Schliep 2019). The analyses highlighted no spatial autocorrelation in any of the model (Model 1 *p* value = 0.692; Model 2 *p* value = 0.478; Model 3 *p* value = 0.336; Model 4 *p* value = 0.842; Model 5 *p* value = 0.539; Model 6 *p* value = 0.075).

5.3.8. Methodological considerations

In this study, we opted to sample many sites with a single visit, as we wanted to include a wide range of plant and pollinator functional traits and temperatures. In network ecology, it is common practice to aggregate data collected in multiple sampling events within a single plant-pollinator network (*e.g.*, Montero-Castaño and Vilà 2017; Norfolk et al. 2018; Valido et al. 2019). However, this operation can potentially create artificial species assemblages, *i.e.*, cumulative communities composed of species observed on different days, weeks or seasons, often with non-overlapping phenology (CaraDonna et al. 2020; Schwarz et al. 2020). Using single-visit networks, we aimed at exploring the realized interactions between co-occurring individuals of honey bees and wild pollinators, rather than achieving high sampling completeness of pollinator species or interactions. Our interactions can, therefore, be interpreted as short-term, behavioural responses.

5.4. Results

5.4.1. General results

Across the 51 networks combined, we observed 262 plant species (Table S5.2) and 325 pollinator species or morphospecies (Table S5.3), for a total of 10,841 pollinator visits to flowers. During the 255 h of observation, we recorded 1497 unique plant-pollinator interactions. We identified to the species level 99% of collected wild pollinators (Table S5.3). We observed an average of 81 wild pollinator individuals (min = 16, max = 332), and 24 pollinator species (min = 9, max = 49) per site (Table S5.1). The honey bee was found in all sites and was the most abundant pollinator with 6718 collected individuals (min = 2, max = 768, mean = 132), and the most generalist one, visiting 111 flowering plant species. Other common, abundant and generalist species were *Eristalis tenax* (Linnaeus), a hoverfly species found at 39 sites with 597 individuals that visited 76 flowering plant species, *Bombus pascuorum* (Scopoli), a bumblebee species found at 35 sites with 411 individuals that visited 45 flowering plant species, and *Sphaerophoria scripta* (Linnaeus), a hoverfly species found at 37 sites with 366 individuals that visited 77 flowering plant species. Pollinator proboscis length ranged from 0.4 mm for *Entomognathus brevis* (Vander Linden) to 16 mm for *Bombus gerstaeckeri* Morawitz, while body length ranged from 4 mm for *Hylaeus taeniolatus* Förster and *H. imparilis* Förster to 22.5 mm for *Xylocopa violacea* Linnaeus (Table S5.3).

We observed an average of 20 flowering plant species (min = 8, max = 35) per site (Table S5.1). The most frequently visited species were *Rubus* sp. L. (931 total visits, 97% by the honey bee), *Centaurea nigrescens* Willd. (823 total visits, 84% by the honey bee), and *Epilobium angustifolium* L. (560 total visits, 93% by the honey bee), while the species most frequently visited only by wild pollinators were *Galeopsis pubescens* Besser (278 visits), *Leucanthemum vulgare* Lam. (191 visits), and *Erigeron annuus* (L.) Pers. (153 visits). Few plant species $(N=9)$ were exclusively visited by honey bees, while many species were exclusively visited by wild pollinators (N = 102), among which there were many umbellifers such as *Daucus carota* L., *Anthriscus sylvestris* (L.) Hoffm., and Heracleum sphondylium L. The most generalist plant species were *Ranunculus acris* L. (attracting 40 pollinator species), *Trifolium pratense* L. (attracting 39 pollinator species), and *E. annuus* (attracting 37 pollinator species). Flower corolla length ranged from 0.05 mm of open disc flowers to 33 mm of *Calystegia sepium* (L.) R. Br. (Table S5.2).

5.4.2. Overall functional traits of plants and pollinators

For Model 1, fifteen models showed a ΔAICc < 6 (Table S5.6). Model averaging indicated that both plant and pollinator functional traits affected the resource overlap between wild pollinator community and the honey bee (Figure 5.2). The impact of plant functional traits on resource overlap varied with honey bee abundance: resource overlap decreased as honey bee abundance increased in sites with high plant functional richness, while there was no change in resource overlap with increasing honey bee abundance in sites with low plant functional richness (Figure 5.3 *a*). Moreover, resource overlap increased as trait similarity between wild pollinator community and the honey bee increased (Figure 5.3 *b*). Temperature and other interactions did not affect the resource overlap (Table S5.6, Figure 5.2).

Figure 5.2: Model estimates from the model-averaging procedure based on the set of models with all functional traits of both plants and pollinators (Model 1). Explanatory variables of the global model are honey bee abundance (*Apis*, ln-transformed), temperature (Temp), standardized functional richness of plant community (FRic), trait similarity between wild pollinator community and the honey bee (TSim), and the interactions *Apis* × FRic, *Apis* × TSim, FRic × TSim, and *Apis* × FRic × TSim. All explanatory variables were scaled to mean 0 and standard deviation 1. Points represent model estimates and bars represent the 95% confidence intervals. The variable effect is supported when the confidence interval does not include zero.

Figure 5.3: Plots showing the effect of *a*) the interaction between honey bee abundance (ln-transformed) and standardized functional richness of plant community, with the three standardized functional richness levels representing the $10th$, $50th$, and $90th$ percentiles, and *b*) trait similarity between wild pollinator community and the honey bee on resource overlap between wild pollinator community and the honey bee (ln-transformed) (Model 1). Points represent raw data points, lines represent model estimates, and the shaded areas represent the 95% confidence intervals.

For Model 2, twenty-eight models showed a ΔAICc < 6 (Table S5.7). The resource overlap was affected only by the trait similarity between wild pollinator community and the honey bee (Figure S5.3).

5.4.3. Single functional traits of pollinators

For Model 3, the multi-model inference analysis selected five models with a ΔAICc < 6 (Table S5.8 *a*). Proboscis length was the only variable affecting the resource overlap between wild pollinator community and the honey bee (Figure 5.4 *a*), *i.e.*, pollinators with proboscis length similar to the honey bee showed the highest overlap (Figure 5.5 *a*).

For Model 4, five models had a ΔAICc < 6 (Table S5.8 *b*). Body size was the only variable affecting resource overlap between wild pollinator community and the honey bee (Figure 5.4 *b*), *i.e.*, resource overlap increased with increasing body size (Figure 5.5 *b*). Models for body size showed the highest values of \mathbb{R}^2 compared to other functional traits (Table S5.8).

For Model 5, six models had a ΔAICc < 6 (Table S5.8 *c*). Again, only the trait category strongly affected resource overlap between wild pollinator community and the honey bee (Figure 5.4 *c*), *i.e.*, centralplace foragers showed a higher overlap with honey bees compared to non-central-place foragers (Figure 5.5 *c*).

For Model 6, four models showed a ΔAICc < 6 (Table S5.8 *d*). The taxonomic family strongly affected resource overlap between wild pollinator community and the honey bee (Figure 5.4 *d*). Bees of family Apidae showed a higher resource overlap than the other families (Figure 5.5 *d*), but the resource overlap was also relatively high for other families such as Conopidae, Halictidae, Megachilidae, and Syrphidae (Figure 5.5 *d*). We did not find an interactive effect of honey bee abundance and trait category in any of the models (Figure 5.4), meaning that the difference in resource overlap between trait categories was independent of honey bee abundance.

Figure 5.4: Model estimates from the model-averaging procedure based on the four sets of models considering single traits of pollinators, *i.e.*, *a)* proboscis length (Model 3), *b)* body size (Model 4), *c)* type of foraging range (Model 5), and *d)* taxonomic family (Model 6). Explanatory variables of the four global models are honey bee abundance (*Apis*, ln-transformed), temperature (Temp), the levels of the four trait categories (Prob_S = proboscis similar to the honey bee, Prob_L = proboscis longer than the honey bee, Body_S = body size similar to the honey bee, $Body_L = body$ size larger than the honey bee, $Force = non-central forager$, Apid = Apidae, Coll = Colletidae, Cono = Conopidae, Crab = Crabronidae, Hali = Halictidae, Mega = Megachilidae, other = other families, *i.e.*, Cimbicidae, Megalodontesidae, Melittidae, and Scoliidae, Syrp = Syrphidae, Tach = Tachinidae, Tent = Tenthredinidae, Vesp = Vespidae) and the interactions between honey bee abundance and each levels of the traits. All continuous explanatory variables were scaled to mean 0 and standard deviation 1. Points represent model estimates and bars represent the 95% confidence intervals. The variable effect is supported when the confidence interval does not include zero.

Figure 5.5: Plots showing the effect of *a)* proboscis length (Model 3), *b)* body size (Model 4), *c)* type of foraging range (Model 5), and *d)* taxonomic family (Model 6) on resource overlap between wild pollinator community and the honey bee (ln-transformed). Small black points represent raw data points, large black points represent model estimates, and black bars represent the 95% confidence intervals.

5.5. Discussion

Incorporating functional traits into ecological network analyses helped to elucidate the degree of resource overlap between wild pollinators and the honey bee. In particular, a low functional diversity of plant community combined with a high trait similarity between wild pollinators and the honey bee appeared to increase the risk of potential negative impacts of a high honey bee abundance on wild pollinator communities.

In areas with a high abundance of managed pollinators, resource overlap between wild pollinators and the honey bee could be mitigated by a high functional richness of plant community, in which pollinators could shift to alternative food resources, as opposed to areas with a low functional richness. To our knowledge, this is the first time that plant functional diversity was used to explore the changes in the resource overlap between wild pollinators and the honey bee. Previous works highlighted a similar effect of plant diversity and honey bee abundance on pollinator communities, with a reduction of potential competition in sites rich in plant species despite an increase in honey bee abundance (Rodríguez et al. 2021). Similarly, heterogeneous landscapes have been shown to support wild pollinators by reducing competition with honey bees (Herbertsson et al. 2016), while a lower availability of differentiated floral resources might increase competition among pollinator species (Thomson 2016; Wignall et al. 2020a, b). However, in contrast with previous research, we found that the resource overlap between wild pollinators and the honey bee never increased with increasing honey bee abundance (Lindström et al. 2016 but see Hudewenz and Klein 2015), even in sites with low plant functional diversity. This might be related to the honey bee foraging behaviour, as it often focuses on the most abundant and rewarding resources, especially in areas with low diversity of plants (Magrach et al. 2017). On the other hand, the lower resource overlap observed in sites with high functional diversity of plant community and high honey bee abundance could be related to the foraging behaviour of wild pollinators that could be forced to forage on plants that are not visited by honey bees. However, while we found an effect of functional richness of plant community, we observed no effect of functional dispersion. This could be partly explained by the fact that many sites were characterized by the same dominant plant species (*e.g.*, *E. annuus* and *Melilotus albus* Medikus) and many different species with lower abundances, so functional dispersion values were similar across sites.

As expected, the resource overlap increased with increasing trait similarity between wild pollinators and the honey bee. Species with similar functional traits usually exploit similar floral resources (Fontaine et al. 2006; Albrecht et al. 2012), so potential competition is expected to be higher for wild pollinators which share traits with the honey bee. First, proboscis length is one of the main constraints of resource selection, affecting whether a pollinator species can obtain nectar from specific flowers. Pollinators are usually more efficient when foraging on plants with flower corolla length matching their mouthpart length (Inouye 1980; Madjidian et al. 2008; Klumpers et al. 2019). For example, hoverflies with a short proboscis tend to prefer flowers that are flat or have a shallow corolla (Fontaine et al. 2006), while long-tongued bumblebees tend to forage on flowers with deep corolla (Balfour et al. 2013). While pollinator species with proboscis shorter or longer than the honey bee mostly foraged on plant species that were not visited by honey bees, pollinators with a similar proboscis visited the same plant species, therefore, increasing their potential competition. Second, body size determines how far pollinators are able to forage, with large pollinators usually having a longer

foraging range compared to small species (Gathmann and Tscharntke 2002; Greenleaf et al. 2007). Here, we found that body size was a key functional trait, driving the resource overlap between wild pollinators and the honey bee. The latter increased with increasing body size, even if we expected a higher overlap for species similar in size to the honey bee. Potential competition with honey bees was, therefore, higher for large species, such as bumblebees. Third, we also observed an increase in resource overlap for central-place foragers. These species are obliged to forage relatively near the nest, based on their foraging range, and are, therefore, unable to expand their foraging area, even when the local density of honey bees is high (Walther-Hellwig et al. 2006). Fourth, many Hymenoptera families such as Apidae, Halictidae, and Megachilidae showed a high level of resource overlap with honey bees. Surprisingly, both thick-headed flies (Diptera: Conopidae) and hoverflies (Diptera: Syrphidae), which we expected to mostly visit open disc flowers, also showed a relatively high resource overlap. While the potential negative effects of honey bees on wild pollinators have often focused on wild bees (*e.g.*, Mallinger et al. 2017), other groups of insects might also be affected.

As the honey bee is not particularly active at low temperatures (Jaffé et al. 2010), we expected that its effect on wild pollinators would be stronger in sites with relatively high temperatures. However, similarly to what was observed in other works (*e.g.*, Corcos et al. 2020; Seoane et al. 2021), we did not find any effect of temperature on resource overlap between wild pollinators and the honey bee, even if the observed temperature range was large (min = 18 °C , max = 38 °C).

5.6. Conclusions

Honey bees have been introduced worldwide, and, therefore, often cohabit with wild pollinators. As their hives can host more than 50,000 individuals, their abundance in natural and managed habitats can be extremely high. Here, we showed that the potential interactions between wild pollinators and honey bees depended on functional traits of both plants and pollinators. In particular, our results highlight the potential role of plant functional diversity in supporting wild pollinators in areas with high honey bee density by decreasing the resource overlap between wild pollinators and the honey bee. Moreover, as pollinator species with traits similar to those of the honey bee tended to visit the same plant species, they could be more vulnerable to potential competition. From a conservation point of view, particular attention should be paid to the potential effects of beekeeping in sites where pollinator species of conservation concern possess functional traits similar to those

of the honey bee. More research is needed to quantify potential short- and long-term effects of high honey bee abundance on fitness, health, and population dynamics of wild pollinators.

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Does pollinator conservation promote environmental co-benefits?

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Chapter 6: Does pollinator conservation promote environmental co-benefits?

6.1. Abstract

The decline of pollinators is an urgent issue that has gained global attention and many initiatives have been implemented to promote conservation actions. However, interventions aimed at safeguarding pollinators can have ripple effects on multiple ecosystem services that are equally important for human well-being. In this work, we investigated whether environmental conditions favouring pollinators are positively associated with the provision of multiple ecosystem services across three different habitats. We selected 96 sites belonging to three habitat types with different roles in supporting pollinators, *i.e.*, crop field margins, semi-natural patches, and urban green areas. We sampled wild pollinators and seven ecosystem services, which included provisioning, cultural, and regulatory services, using which we calculated two ecosystem multi-functionality metrics. Semi-natural patches and crop field margins exhibited both the highest diversity of pollinators and ecosystem multi-functionality, *i.e.*, habitats that supported pollinators also delivered a higher number of environmental co-benefits. However, increasing habitat quality for pollinators did not result in increased multifunctionality, indicating that single ESs exhibited non-linear responses. Therefore, improving local conditions for wild pollinators did not enhance ecosystem multi-functionality, while specific habitat types have been shown to have the potential to improve pollinator diversity while generating multiple environmental cobenefits.

6.2. Introduction

Pollination is one of the most valuable ecosystem services (ESs), with an estimated overall monetary value of about US\$195 billion (Bauer and Sue Wing 2016). Animal pollination, in particular, is essential for ensuring wild plant reproduction (Aguilar et al. 2006; Ollerton et al. 2011) and maintaining crop productivity (Klein et al. 2007; Garibaldi et al. 2013). Since the decline of pollinators could strongly impact pollination (Reilly et al. 2020), maintaining or increasing pollinator diversity and abundance has become a central target in biodiversity conservation (Brittain et al. 2013; Hallmann et al. 2017; Lemanski et al. 2022). Common interventions to support pollinators include management actions at the local scale, *e.g.*, improving habitat quality by increasing flower cover and diversity (Gill et al. 2016; Sutter et al. 2017; Klaus et al. 2021), but also the enhancement of landscapes, *e.g.*, by restoring natural and semi-natural habitats (Scheper et al. 2013; Tonietto and Larkin 2018). However, any intervention designed for pollinators should be carefully assessed, as it could affect multiple ESs both positively and negatively (Galler et al. 2015).

In the best-case scenario, habitat or landscape manipulations to boost pollinator diversity also increase multiple ESs, leading to enhanced ecosystem multi-functionality (EMF). EMF is the capacity of a landscape, habitat, or ecosystem to provide multiple functions at the same time, implying social, economic, and ecological benefits(Byrnes et al. 2014). Until now, most studies on EMF have focused on its association with biodiversity, highlighting positive relationships between EMF and above- and below-ground diversity (Maestre et al. 2012; Lefcheck et al. 2015; Mensah et al. 2020; Delgado-Baquerizo et al. 2020; Fan et al. 2023; but see Gamfeldt and Roger 2017). A key research gap concerns the response of EMF to conservation actions in different habitat types. In particular, it is not known yet the extent to which management actions designed to conserve pollinators in different environments will lead to positive effects on other ESs, potentially generating environmental co-benefits.

ES provision worldwide strongly depends on land use change (Millennium Ecosystem Assessment 2005; Haddad et al. 2015; Gomes et al. 2020). In general, habitats with a favourable conservation status enhance both regulating and cultural ESs (Maes et al. 2012), and a high amount of semi-natural areas enhances biodiversity-based ESs compared to urban and agricultural areas (Baral et al. 2014). For example, pest control is strongly related to the presence of semi-natural habitats in the landscape (Rusch et al. 2016; Holland et al. 2016; Rega et al. 2018), and pollinator diversity declines with increasing distance from semi-natural areas (Ricketts et al. 2008). However, even urban areas, especially those characterized by a moderate level of urbanization and rich in green areas, seem to better support pollinators and the ESs they provide than agricultural areas (Theodorou et al. 2020; Wenzel et al. 2020, but see Baldock et al. 2015). Usually, agricultural areas are fundamental for crop production but are poor in delivering other ESs, particularly regulating ones (Maes et al. 2012; Laura et al. 2017; Tóth et al. 2018). Nonetheless, most of these studies analysed how single ES provisioning changed in different habitat types, without taking into account the possible interactions among ESs.

In this work, we measured wild pollinator diversity, flower cover and diversity and seven ESs, comprising provisioning, regulating and cultural ESs, through eight ES indicators. We selected 96 sampling sites in north-eastern Italy belonging to three habitat types, *i.e.*, crop field margins, semi-natural patches, and urban green areas. Selected habitats represent common land-use categories, each potentially suitable to support pollinators but characterised by a distinct degree of relevance to pollinators. Moreover, sites belonging to the same habitat were selected along a gradient of habitat quality for pollinators, estimated through flower cover and diversity. Our specific aims were 1) to understand how wild pollinator diversity and EMF varied among different habitat types, and 2) to test whether improving local conditions for pollinators would also boost EMF. We expect that both pollinator diversity and EMF would be higher in semi-natural patches and that EMF would increase with increasing flower cover and diversity, suggesting that both restoring semi-natural habitats and improving existing habitat quality for pollinators should produce multiple environmental co-benefits.

6.3. Materials and methods

6.3.1. Study area and sampling design

We selected four regions in north-eastern Italy (Table S6.1, Figure S6.1). Within each region, we selected 24 sampling sites representing three habitat types: crop field margins, which included simple herbaceous margins and complex margins; semi-natural patches, which included grasslands and open abandoned areas; and urban green areas, which included both private and public gardens. Within each region, we selected 8 sites for each habitat type. Within each habitat, sites were chosen a priori along a gradient of quality for pollinators, taking into account both the cover and diversity of floral resources. Sites belonging to the same habitat type were at least 500 m away from each other. Climatic conditions of sites were similar since elevation ranged between

10 and 550 m above sea level. Minimum annual temperatures ranged from 0 °C in January and 18 °C in July, maximum annual temperatures ranged from 6 °C in January and over 30 °C in July, and total annual precipitation ranged from 800 to 1100 mm.

6.3.2. Wild pollinator and plant sampling

We sampled wild pollinators, *i.e.*, wild bees (Hymenoptera: Apoidea: Anthophila) and hoverflies (Diptera: Syrphidae), using pan traps. At each site, we placed three pan traps (yellow, blue, and white; 750 ml capacity, 12.5 cm diameter, 4.5 cm height), 1 m apart from each other, filled with water and a drop of biodegradable dish soap with no fragrance. We did not perform standard transect observations since the sampling was performed by people with different skills, and due to COVID-19 restrictions, it was not possible to work in teams. Pan traps were placed on the ground, in areas with short grass, so that they were clearly visible to pollinators. Pan traps were exposed for 48 h during sunny days, with low wind and temperatures > 20 °C. Wild pollinators were morphologically identified to the species or morphospecies level by DP (hoverflies), and AC and MM (wild bees). Wild pollinator samplings were repeated three times, once per month, between May and July 2021. Since pan traps are considered an unreliable method for estimating pollinator abundance (Westphal et al. 2008; Portman et al. 2020), we focused on pollinator diversity. We calculated α-diversity, *i.e.*, the number of wild pollinator species at each site, and γ-diversity, *i.e.*, the total number of wild pollinator species for each habitat type.

The cover and diversity of flowering plant species are strong indicators of habitat quality for pollinators, and can therefore be used as proxies for habitat enhancement for pollinators (Wratten et al. 2012; Zamorano et al. 2020; von Königslöw et al. 2022). At each site, we identified all flowering plant species in a 10-m radius buffer around the pan traps and assessed their relative abundance. The sampling was repeated three times, once per month, between May and July 2021. At each site, we then calculated flowering plant species α-diversity and mean flower cover.

6.3.3. Assessment of multiple ESs

Between April and September 2021, we measured eight indicators of seven ESs at each site. ESs were chosen based on the Common International Classification of Ecosystem Services (CICES) 5.1 categories and included provisioning, regulating and cultural ESs, mostly related to biodiversity (Table 6.1) (Haines-Young and Potschin 2018). We chose a high number of ESs that are fundamental in both agricultural and natural areas (Garland et al. 2021), but are rarely assessed in urban environments (Pereira et al. 2023). Moreover, all selected

ESs could be quickly and easily measured in all habitat types.

Table 6.1: List of the assessed ESs, with information on the corresponding Common International Classification of Ecosystem Services (CICES) 5.1 category and code (Haines-Young and Potschin 2018) and the measured ES indicators.

6.3.3.1. Honey bee-related ESs

The honey bee (*Apis mellifera* Linnaeus) is the most important managed pollinator species (Hung et al., 2018). ESs provided by honey bees include several regulating, provisioning, and cultural services. Since large-sized pollinators are often under-sampled using pan traps (Roulston et al. 2007), we opted for direct observations of honey bees on flowering plants to assess their abundance. At each site, we counted honey bees on flowers for 10 min. Honey bee samplings were repeated three times, once per month, between May and July 2021. At each site, we then calculated the total honey bee abundance.

6.3.3.2. Ground-dwelling arthropod-related ESs

Ground-dwelling arthropods include key groups of pest and seed predators (Bohan et al. 2011; Nyffeler and Birkhofer 2017). We assessed ground-dwelling arthropod abundance using pitfall traps. At each site, we placed two pitfall traps, consisting of a buried plastic cup (500 ml capacity, 11 cm diameter, 15 cm height) protected by a plastic cover (Spence and Niemelä 1994). Traps were activated with 70% ethylene glycol for four weeks from June to August 2021, for a total of three sampling rounds. Collected arthropods were stored in 75% ethanol and sorted in the laboratory. At each site, we then determined the total abundance of target grounddwelling arthropods, *i.e.*, ground beetles (Coleoptera: Carabidae), rove beetles (Coleoptera: Staphylinidae), and spiders (Araneae).

6.3.3.3. Pest control

Pest control by natural enemies is a major regulating ES, especially in agroecosystems (Holland et al. 2016; Rega et al. 2018). Dummy caterpillars are commonly used to assess the intensity of pest predation by actively hunting sight predators (Howe et al. 2009). We moulded 30 mm \times 3 mm dummy caterpillars using green plasticine and glued the caterpillars on wood skewers. We placed eight dummy caterpillars at each site, which were exposed for 72 hours. The sampling was repeated two times, in June and July 2021. We then checked all predation marks on caterpillars and determined the mean predation rate of dummy caterpillars at each site.

6.3.3.4. Seed predation

We used seed cards to assess the intensity of predation of weed seeds by seed predators. Seed cards were made of small rectangles (8×3 cm) of P80 grit sandpaper, on which seeds were glued using a repositionable glue (3 M Spray Mount) (Westerman et al. 2003). On each seed card, we glued forty seeds of *Taraxacum officinale* (Weber) ex Wiggers, a native plant species, and forty seeds of *Oenothera biennis* L., an invasive exotic species. At each site, we placed three seed cards that were fixed to the ground using nails and were exposed for 72 hours, during sunny days with low wind. Then, we collected the seed cards and counted the remaining seeds of each species. The sampling was repeated twice, in June and July 2021. At each site, we then estimated the mean seed predation rate.

A limitation of this study is that we assumed that weed seeds removed from the cards were predated, thus indicating a service, although we cannot ensure that the organisms that removed the seeds actually destroyed them. However, seed cards have been used for decades to specifically assess seed predation rather than dispersal (Brust and House 1988; Westerman et al. 2003). Moreover, the most common predators of both *T. officinale* and *O. biennis* are insects (Honek et al. 2005; Anstett et al. 2014), such as ground beetles, which are key seed predators (Kulkarni et al. 2015; Carbonne et al. 2020). Seeds of both species are relatively small in size (weight of 1000 seeds for both species: 0.45 gr) and birds and rodents probably predated them to a minimal extent (Hulme 1998).

6.3.3.5. Disease control

We used ovitraps to estimate the abundance of Asian tiger mosquitoes, *Aedes albopictus* (Skuse), a species of medical importance (Benedict et al. 2007). Ovitraps consisted of a small dark container (400 ml capacity, 8 cm diameter, 10 cm height) filled with water and containing a masonite stick where mosquitoes laid their eggs. At each site, we placed one ovitrap on the ground and exposed it for two weeks at the end of July 2021, during

the peak season of egg laying (Petrić et al. 2021). Ovitraps were collected, and the number of eggs was counted using a stereoscope.

6.3.3.6. Soil nutrient cycling

We estimated the decomposition rate of organic matter in soil using the Tea Bag Index (TBI) methodology (Keuskamp et al. 2013). We weighed the green tea and rooibos before placing the bags in the field. At the end of April 2021, we buried two pairs of bags in two 8-cm-deep holes at each site. For each pair, we used one green tea bag and one rooibos bag. After three months, at the end of July 2021, bags were collected, ovendried at 65 °C for 48 h, and their contents were weighed. At each site, following the TBI protocol, we calculated the stabilisation factor *S* and the decomposition rate *k* (Keuskamp et al. 2013).

Since we were not able to collect all green tea and rooibos bags after three months, we had a few missing values for both the stabilisation factor and the decomposition rate, which we replaced with the respective averaged values to have the same number of measured ESs in all sites. However, to ensure that the use of averaged values would not affect the results of our models, we also performed all the statistical analyses excluding sites with missing bags, *i.e.*, those for which it was not possible to calculate soil stabilisation factor and/or soil decomposition rate. This sensitivity analysis indicated that all models did not show significant differences, therefore, we only present the results of models including averaged values.

6.3.3.7. Flood control

We assessed flood control by measuring the rate of water infiltration in soil (United States Department of Agriculture 2014). The measurements were taken after the soil had been saturated by rain, in September 2021. At each site, we selected a spot with short grass, where we hammered a plastic tube (20 cm diameter) in the ground for about 10 cm. Then, we poured 1 L of water into the plastic tube and assessed the water depth at the beginning of the experiment and after 6 min to obtain the water infiltration rate. We repeated the process three times per site. At each site, we then calculated the mean water infiltration rate as the average value of the three trials.

6.3.4. Assessment of EMF

We assessed EMF at each site including measures for honey bee-related ESs, ground-dwelling arthropodrelated ESs, pest control, seed predation, disease control, soil nutrient cycling, and flood control. We used two approaches: 1) the averaging approach (Mouillot et al. 2011), and 2) the multiple threshold approach (Byrnes et al. 2014). All statistical analyses were performed using *R* version 3.6.1 (R Core Team, 2019).

Using the averaging approach, we calculated a simple EMF index based on normalized values for each ES indicator. First, we normalized each ES indicator value by its maximum, using the formula $X_{\text{norm}} = (X_{\text{raw}} X_{\min}$ / ($X_{\max} - X_{\min}$), where X_{norm} is the normalized ES indicator value, X_{raw} is the raw ES indicator value, X_{\min} is the minimum ES indicator value and X_{max} is the maximum ES indicator value. We considered as X_{min} and Xmax the minimum and maximum ES indicator values observed over the whole dataset, including all three habitat types. For the abundance of Asian tiger mosquito eggs, the only indicator for which low values indicate higher levels of the ES, raw indicator values were reflected before normalization as $X_{ref} = X_{max} - X_{raw}$. Second, we calculated the averaged EMF index for each site as the mean value of all normalized indicator values. Averaged EMF was calculated using the *R* package *caret* (Kuhn 2008).

The multiple threshold approach allows for evaluating whether multiple functions are simultaneously performing at high levels. We considered the full range of thresholds, from 1% to 99% of the maximum value of each ES indicator, and then counted the number of ES indicators that surpassed each threshold at each site. To compute the multiple threshold EMF, we used the *R* package *multifunc* (Byrnes et al. 2014).

6.3.5. Statistical analyses

First, we visually assessed the differences among the three habitat types for wild pollinator α -diversity, flower cover, flowering plant α-diversity and ES indicators. To do so, we compared normalized variable values among the three habitat types using a radar plot.

Second, we analysed how wild pollinator α -diversity and EMF changed in the three habitat types (indicator of habitat restoration) and in relation to flower cover (indicator of habitat enhancement). As flower cover and flowering plant α-diversity were strongly correlated (Pearson's correlation coefficient = 0.606, *p* value < 0.001), we could not include both in the same models. Therefore, all models were run twice, first using flower cover as explanatory variable, and then using flowering plant α-diversity as explanatory variable. All models including flower cover showed a lower AIC, therefore, we chose flower cover as an indicator of habitat enhancement for pollinators. We built two linear mixed-effect models using wild pollinator α -diversity and averaged EMF as response variables, and habitat type and flower cover as explanatory variables. We also included the region ID as random factor. To run these models, we used the *R* package *nlme* (Pinheiro et al.

2019). Moreover, using the multiple threshold approach, we analysed the effect of habitat type and flower cover on the number of ESs beyond a certain level of performance. To visually assess the significance of each threshold, we calculated the slope of these relationships and plotted them against the corresponding threshold value. Figures were plotted using the *R* package *ggplot2* (Wickham 2016).

Third, to quantify the relationships between wild pollinator α-diversity, flower cover, flowering plant α-diversity and ES indicators and test how these relationships changed among the three habitat types, we calculated the Pearson's correlation coefficients between pairs of variables within each habitat type. Correlations were plotted using the *R* package *corrplot* (Wei et al. 2017).

Landscape context, in particular the amount of semi-natural areas, could affect both wild pollinators and EMF. However, our study was not designed to explore the effect of landscape context, since due to COVID-19 restrictions during fieldwork, we could only sample sites relatively close to the area where the authors who did the fieldwork resided. Therefore, we decided to reduce as much as possible the variation in landscape composition during site selection. To evaluate any potential effect of landscape variables, we fitted three models for each response variable, *i.e.*, wild pollinator α-diversity and averaged EMF, using maximized log-likelihood and compared them using ΔAICc. Model 1 included as explanatory variables habitat type and flower cover. Model 2 included as explanatory variable only the percentage of semi-natural habitats in a 250 m radius buffer around the sampling sites. Model 3 included as explanatory variables habitat type, flower cover, and the percentage of semi-natural habitats in a 250 m radius buffer around the sampling sites. For all response variables, the ΔAICc between Model 1 and Model 3 was below 2, indicating little improvement with the addition of landscape variables, while the difference between Model 1 and Model 2 was always above 2, indicating a better predictive power of local variables (Table S6.2).

6.4. Results

6.4.1. Wild pollinators

We collected 1516 wild pollinator individuals belonging to 144 species or morphospecies (Table S6.3). The most represented wild pollinator family was Halictidae, with 1,080 individuals and 45 species collected, which included the three most abundant wild pollinator species, *i.e.*, *Lasioglossum glabriusculum* (Morawitz) (295 individuals), *L. malachurum* (Kirby) (125 individuals), and *L. minutissimum* (Kirby) (118 individuals). While wild bees were relatively common, we only collected 96 hoverfly individuals belonging to 30 species.

6.4.2. Effect of habitat type on wild pollinators and EMF

Semi-natural patches were characterized by a higher provision of most ESs compared to crop field margins and urban green areas, and results were similar for pollinators and flowering plants (Table S6.4, Figure 6.1). However, the abundance of ground-dwelling arthropods was higher in crop field margins. Urban green areas generally showed the lowest variable values, except for honey bee abundance, flower cover and flowering plant α-diversity. Soil-related ESs were comparable among the three habitat types.

Figure 6.1: Radar plot showing the mean normalized value of each variable at each habitat. Abbreviations are: "Wild poll α-div" for wild pollinator α-diversity, "Flower cover" for flowering plant cover, "Flower α-div" for flowering plant α-diversity, "Honey bee ab" for managed honey bee abundance (honey bee-related ESs), "Ground arth ab" for ground-dwelling arthropod abundance (grounddwelling arthropod-related ESs), "Cat pred rate" for dummy caterpillar predation rate (pest control), "Seed pred rate" for seed predation rate (seed predation), "Mosq egg ab (ref)" for Asian tiger mosquito egg abundance (reflected) (disease control), "TBI S" for soil stabilisation factor S and "TBI k" for soil decomposition rate k (soil nutrient cycling), and "Inf rate" for water infiltration rate in soil (flood control).

Habitat type affected both wild pollinator diversity and EMF. Wild pollinator α -diversity was comparable in semi-natural patches and crop field margins, and it was lower in urban green areas (Table 6.2 *a*, Figures 6.2 *a*, S6.2 *a*). However, wild pollinator γ-diversity was higher in semi-natural patches than in other habitats. We observed 111 wild pollinator species in semi-natural patches, 77 species in crop field margins, and only 59 species in urban green areas.

Figure 6.2: Plots showing the effect of habitat type on *a)* wild pollinator α-diversity and *b)* averaged EMF. Small coloured points represent raw data points, large black points represent model estimates, and bars represent the 95% confidence intervals.

Averaged EMF was also higher in semi-natural patches and crop field margins (Table 6.2 *b*, Figures 6.2 *b*, S6.2 *b*). EMF calculated using the multiple threshold approach showed a similar response to habitat type. EMF in semi-natural patches and crop field margins was generally comparable at low thresholds, but their differences increased at higher thresholds, with semi-natural patches providing higher levels of multiple ESs (Table S6.5 *a*, Figure 6.3 *a*, *d*). We observed no differences in multiple threshold EMF between crop field margins and urban green areas (Table S6.5 *b*, Figure 6.3 *b*, *e*), while the comparison between semi-natural patches and urban green areas revealed higher values of EMF in semi-natural patches (Table S6.5 *c*, Figure 6.3 *c*, *f*).

Table 6.2: Results of the linear mixed-effect models testing the effect of habitat type and flower cover on *a)* wild pollinator αdiversity and *b)* averaged EMF. Values in bold indicate significant effects (*p* value < 0.05).

Response variable	Explanatory variable	Estimate	SЕ	df	t value	<i>p</i> value
a) Wild pollinator α -diversity	Intercept (Crop field margin)	8.113	0.782	89	10.380	${}_{0.001}$
	Semi-natural patch	-1.902	1.136	89	-1.674	0.098
	Urban green area	-3.822	1.023	89	-3.735	< 0.001
	Flower cover	0.128	0.047	89	2.751	0.007
b) Averaged EMF	Intercept (Crop field margin)	0.377	0.015	89	25.371	${}_{\leq 0.001}$
	Semi-natural patch	0.037	0.022	89	1.626	0.108
	Urban green area	-0.049	0.020	89	-2.434	0.017
	Flower cover	0.001	0.001	89	1.558	0.123

Figure 6.3: Plots showing the effect of habitat type on multiple threshold EMF, *i.e.*, the number of ESs maximized at a certain threshold level. Panels *a)* and *d)* compare crop field margins and semi-natural patches, panels *b)* and *e)* compare crop field margins and urban green areas, and panels *c)* and *f)* compare semi-natural patches and urban green areas. Panels *a)*, *b)*, and *c)* show the relationship between pairs of habitats and the number of functions that performed higher than a certain threshold. We considered the full range of thresholds, from 1% to 99% of the maximum value of each ES indicator, and each line represents a given threshold. Panels *d*), *e*), and *f*) show the corresponding relationship between the threshold value and the slope of the relationship between habitat type and the number of functions reaching a certain threshold. Black points represent fitted values and the shaded areas represent the 95% confidence intervals. For each threshold, the relationship with habitat type is significant if the confidence interval does not overlap zero.

6.4.3. Effect of flower cover on wild pollinators and EMF

Wild pollinator α-diversity strongly increased with increasing flower cover (Table 6.2 *a*, Figure 6.4). On the other hand, flower cover did not affect averaged and multiple threshold EMF (Tables 6.2 *b*, S6.6, Figure S6.3). To explain this result, we analysed the correlations between wild pollinator α-diversity, flower cover, flowering plant α-diversity, and ES indicators (Figure S6.4). We highlighted several co-benefits (positive correlations) and only a few trade-offs (negative correlations) among variables in all habitat types. However, correlations changed depending on habitat type. In crop field margins, wild pollinator α-diversity showed a trade-off with infiltration rate, but we also observed synergies between honey bee abundance and flower cover, flower cover and soil decomposition indices, and abundance of ground arthropods and predation rate of dummy caterpillars (Figure S6.4 *a*). Semi-natural patches showed the lowest number of significant correlations among variables, of which only one was a trade-off, and we observed no significant relationships between wild pollinator αdiversity and other variables (Figure S6.4 *b*). In urban green areas, wild pollinator α-diversity was positively

correlated to flowering plant α-diversity and ground-dwelling arthropod abundance, and negatively correlated to the abundance of Asian tiger mosquito eggs (Figure S6.4 *c*).

Figure 6.4: Plot showing the effect of flower cover on wild pollinator α-diversity. Points represent raw data points, the line represents model estimate, and the shaded area represents the 95% confidence interval.

6.5. Discussion

To our knowledge, this is the first study investigating how conservation actions for pollinators, *i.e.*, habitat restoration and enhancement, affected EMF calculated using a considerable number of ESs. We found that habitat types supporting a higher diversity of wild pollinators were also associated with higher EMF. On the other hand, we did not find any relationship between flower cover and EMF in the three habitat types, meaning that improving local conditions for pollinators did not lead to higher EMF and indicating non-linear responses of multiple ESs.

6.5.1. Effect of habitat type on wild pollinators and EMF

Contrary to our expectations, we found that semi-natural patches and crop field margins hosted a comparable number of wild pollinator species. However, even if the number of species at each site was similar, the total species diversity of crop field margins was considerably lower, with 34 fewer pollinator species than in seminatural patches, *i.e.*, species assemblages of field margins were more homogeneous and characterized by a low spatial turnover. Wild pollinators are usually negatively affected by agricultural intensification (Le Féon et al. 2010; Williams et al. 2010) since floral resources are often insufficient and the use of pesticides can pose a serious threat (Goulson et al. 2015). However, unmanaged field margins can be a crucial resource for pollinators in agricultural areas (Arnold et al. 2021; Slupik et al. 2022). In our study, we sampled both simple herbaceous field margins and complex field margins characterized by hedgerows and trees that might have boosted pollinator diversity (Aviron et al. 2023). Also, we found that urban green areas hosted the lowest number of pollinator species. This result is quite unexpected since recent studies highlighted the potential importance of urban areas for pollinators (Hall et al. 2017; Wenzel et al. 2020). However, these positive effects have been mostly reported for wild bees (but see Herrmann et al. 2023), while other pollinator groups such as hoverflies are known to be negatively affected by urbanization (Lagucki et al. 2017; Theodorou et al. 2020; Herrmann et al. 2023).

EMF also changed among the three habitat types. Averaged EMF showed comparable values in seminatural patches and crop field margins and lower values in urban green areas. Semi-natural areas and, in general, habitats with a low management intensity have been shown to exhibit higher EMF (Lavorel et al. 2022; Moi et al. 2022; Olimpi et al. 2022). In particular, our crop field margins showed a high abundance of ground-dwelling arthropods and a high predation rate of seeds, as they often provide shelter and alternative prey (Allan et al. 2015; Samnegård et al. 2019). However, the multiple threshold approach revealed that at higher thresholds the difference between semi-natural patches and crop field margins was consistent, meaning that semi-natural patches, unlike crop field margins, were able to simultaneously provide high levels of multiple ESs. On the other hand, lower EMF values in urban green areas were expected, since regulating services have been shown to strongly decrease with increasing urbanization (Wang et al. 2019). Therefore, both wild pollinator diversity and EMF were maximized in semi-natural patches and crop field margins, also highlighting the potential role of field margins for sustaining pollinators while generating multiple environmental co-benefits (Mkenda et al. 2019). Habitat conversion from intensively managed to pollinatorfriendly habitats might not be the only way to increase pollinator diversity and EMF.

6.5.2. Effect of flower cover on wild pollinators and EMF

As expected, we found a positive relationship between flower cover and wild pollinator α-diversity. Habitat enhancement for pollinators, *i.e.*, the increase in diversity and cover of flowering plant species, is an effective measure specifically designed to boost pollinator abundance and diversity in different habitat types (Morandin and Kremen 2013; Woodcock et al. 2014; Andrieu et al. 2018; Zamorano et al. 2020; Dietzel et al. 2023; Hussain et al. 2023) since floral resources are one of the central factors in shaping pollinator populations.

Contrary to our expectations, we did not find any relationship between flower cover and EMF. This is in contrast with other studies since habitat enhancement seems to benefit not only pollinators but also other
ESs, especially those related to biodiversity (Wratten et al. 2012). Moreover, there is a large body of literature that showed positive relationships between biodiversity and EMF across different land use types, and most studies on the effect of above-ground biodiversity on EMF focused on plant species (Maestre et al. 2012; Jing et al. 2015; Lefcheck et al. 2015; Soliveres et al. 2016; Schittko et al. 2022; Zhou et al. 2022). However, here we did not sample the complete plant community, since we were only interested in understanding how flower cover and diversity, as indicators of habitat enhancement for pollinators, could affect EMF. Flower cover did not emerge as a good predictor of EMF, highlighting that improving the quality of existing habitats for pollinators does not positively affect EMF. Within the same habitat type, the analysis of the correlation among ESs indicated that probably the underlying drivers that promoted wild pollinator diversity were distinct from those promoting EMF. Moreover, the lack of consistent relationships among services within the three habitats suggested that specific drivers may lead to non-linear responses depending on the habitat type. For instance, pollinator-targeted interventions are often beneficial not only to pollinators but also to predators of pests (Albrecht et al. 2020; Savage et al. 2021). However, sown flower strips do not always benefit pollinator populations as their effects may vary depending on the chosen flower mixture (Wood et al. 2015), and they might also increase the abundance of herbivores, resulting in a trade-off between pollination and pest control (Wäckers et al. 2007). Therefore, the net effects of pollinator-targeted interventions are not straightforward, and it is crucial to investigate which drivers determine high levels of different ESs among habitats (Bullock et al. 2021)

6.6. Conclusions

Maximising the delivery of multiple ESs across different habitat types is a complex task, but it is of central importance for the well-being of humans and ecosystems across human-impacted landscapes. Here, we showed that both semi-natural patches and crop field margins were associated with higher pollinator diversity and EMF, highlighting not only the key role of undisturbed habitats but also the potential importance of field margins. Nevertheless, it is fundamental to emphasise that the total diversity of pollinator species collected in crop field margins was much lower than in semi-natural patches, which are therefore able to support more heterogeneous pollinator communities. Moreover, we found no association between flower cover and EMF in any of the three investigated habitats, meaning that improving habitat quality for pollinators proved to be insufficient to enhance EMF. Our study indicated that promoting pollinators does not always increase the number of co-benefits that could be delivered to society. Future investigations are needed to understand how pollinator interventions could affect ESs and EMF in different habitat types, and how landscape composition and structure could modulate these relationships.

6.7. Funding information

This project received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No. 101003476 (www.safeguard.biozentrum.uni-wuerzburg.de).

General conclusions

Through the chapters of my PhD thesis, I was able to analyse in detail how managed and wild pollinators are affected by the drivers that determine their abundance and diversity in dynamic landscapes, *i.e.*, land-use changes and habitat loss, urbanization, and the introduction of managed species. Landscape alterations are now unavoidable and usually occur rapidly, leaving pollinator communities little time to adapt. While some species, the more resilient ones, may continue to thrive, other species will not be able to cope with the new conditions and will therefore decrease in abundance or, in the worst case, disappear. Understanding how pollinators respond to these factors will allow us to counteract their negative effects through tailor-made conservation interventions, summarized in Table 7.1.

Table 7.1: Summary of conservation interventions for pollinators that emerged in the chapters of my thesis, including information on the pollinator groups that can benefit from them and the chapters of the thesis in which the topic was addressed.

7.1. The importance of protecting diverse semi-natural habitats and the resources they provide

Semi-natural habitats in landscapes are crucial for sustaining pollinator communities, as seen in *Chapter 2* and *Chapter 3*. However, semi-natural habitats are heterogeneous and not all of them support pollinators to the same degree. Maurer et al. (2022) showed that extensively and conventionally managed meadows, flower strips, hedgerows and forest edges hosted unique sets of pollinator species, and that the importance of these habitats changed throughout the flowering season. Bartual et al. (2019), on the other hand, showed that although forests and woodlands may be optimal for nest building and larvae development, they harboured the lowest abundance of bees compared to open semi-natural habitats. Different types of semi-natural habitats also

offer distinct nesting resources for wild bees, therefore, different bee taxa may benefit more from the presence of certain types of semi-natural habitats than others (Eeraerts and Isaacs 2023). These differences are mainly related to semi-natural habitat structure and vegetation composition, and thus to the amount of resources they can provide, particularly floral resources. For example, in *Chapter 2* we observed how plant phenology and bee preferences affected the composition of pollen collected by honey bees. Even if the abundance of pollinators in forests is generally low, we found that trees played a key role in supporting managed honey bees at the beginning of the flowering season, being replaced later in the season by herbaceous flowering plants, further confirming how different habitat types are needed for the well-being of pollinator populations.

The restoration of different types of semi-natural habitats, therefore, could be a key action to safeguard pollinator populations. However, whenever pollinator-friendly measures are implemented, the potential impact on other organisms and ecosystem services fundamental to our well-being should also be assessed, in order to maximise the positive effects of these conservation actions, as we observed in *Chapter 6*. In Europe, agrienvironment schemes in agricultural landscapes are widely sponsored not only for the protection of pollinators but also for biodiversity and their associated ecosystem services. However, these programmes are not sufficient even to protect pollinators: to effectively protect insects, we would need three times the amount indicated by the current policy guidelines of a diverse range of habitats (Pindar and Raine 2023). Targeted policies for pollinators and other key organisms are essential (Cole et al. 2020), however, to date no government worldwide has delivered specific legislation to address biodiversity decline (Hall and Steiner 2019; Van Der Sluijs 2020).

7.2. Conservation of pollinator functional traits

The analysis of pollinator functional traits can be crucial for accurately assessing the response of pollinators to the drivers that determine their abundance and diversity. In *Chapter 4*, we found that wild bees characterized by specific functional traits were threatened by high temperatures in cities, and in *Chapter 5* we highlighted that potential competition with managed honey bees changed based on wild pollinator functional traits. Indeed, the impacts of these drivers on pollinator species are not related to their taxonomic identity, but rather to their functional identity. We observed that wild pollinator responses were influenced by their morphological features such as body size and proboscis length, ecological features such as foraging and nesting preferences, and evolutionary history such as taxonomic family. For example, although bees are generally considered a thermophilic group, negative impacts of increasing temperatures have been highlighted for bumblebees

(Janousek et al. 2023; Sepúlveda and Goulson 2023) and for above-ground nesting bees (Ulyshen and Horn 2023), stressing how climate effects strongly depend on pollinator traits (Dorian et al. 2023). This also emphasises that, despite being a common practice, the clustering of large groups of pollinators, *e.g.*, considering wild bees or hoverflies as single groups, should be evaluated carefully, as it can lead to results that do not give an accurate picture of the actual changes in communities.

Exploring the functional composition of pollinator communities and how they change is also crucial because these modifications can strongly impact the ecosystem service pollinators provide (Gagic et al. 2015) and, therefore, ecosystem resilience (Mouillot et al. 2013). Functional traits determine species role in ecosystems (Coux et al. 2016) and, for pollinators, traits such as body size and proboscis length are strongly related to pollination efficacy (Chase et al. 2023). Pollinator communities characterized by a high functional diversity are generally more efficient, potentially leading to higher crop yield (Hoehn et al. 2008; Woodcock et al. 2019), and changes in the functional composition of pollinator communities can also impact plantpollinator networks and lead to major changes in plant communities (Simpson et al. 2022). Moreover, the loss of specific functional traits, for example large body size, could impact the reproduction of specific plantspecies (Zaragoza-Trello et al. 2023). It is therefore clear that not only the conservation of pollinator species but also the preservation of their functional traits should be a priority.

7.3. Managed and wild pollinators: Matching conservation strategies?

The honey bee is a key pollinator species, and the pollination and production of many crops depend on its activity. Therefore, it is crucial to ensure that honey bee colonies maintain optimal health, which could be achieved, for example, by placing their hives in landscapes with a high amount of semi-natural areas, as highlighted in *Chapter 2* and *Chapter 3*. However, honey bees are considerably different from other pollinators and bee species, being eusocial, competitive, super-generalist and, most importantly, managed by humans. These characteristics make managed honey bees potentially harmful to wild pollinators, as seen in *Chapter 5* – including feral honey bee populations, which in Europe are endangered due to the lack of nesting sites and transfer of pathogens and parasites from managed hives (Requier et al. 2019). In Europe, the vast majority of honey bees are managed and feral honey bee colonies are rare and scattered, with densities usually lower than 0.2 colonies km⁻² and a high rate of winter mortality (Rutschmann et al. 2022; Kohl et al. 2022). The density of managed hives is much higher in Europe, with more than 5 hives km⁻² in Italy (data provided by the National

Data Bank of the Zootechnical Registry established by the Ministry of Health at the National Service Centre of the "G. Caporale" Institute of Teramo). These unnatural abundances of managed honey bees could result, for example, in increasing competition for floral resources with wild pollinators: during the flowering season, a single honey bee colony could collect the pollen needed for the development of 100,000 wild solitary bees (Cane and Tepedino 2017).

Several strategies have been recommended to limit these potential negative effects on wild pollinators. For example, it has been proposed to limit the placement of bee hives in natural areas, or establish a threshold of hive density in landscapes (Geslin et al. 2017), however, some of these actions could be detrimental to managed honey bee health. Therefore, it is clear that we need an inclusive approach to find a balance between managed pollinator health and wild pollinator conservation (Kleijn et al. 2018). Specific legislation should be adopted that would lead to more sustainable and conscious beekeeping, without impacting bee health, crop pollination and honey production.

7.4. Knowledge of pollinator species

A key, but often neglected, aspect of pollinator conservation is that it cannot be accomplished without proper knowledge of pollinator species, their ecology, and distributions. Although pollinators are crucial for ecosystems and our well-being, our knowledge of some pollinator groups is extremely limited. Hoverflies are a relatively well-known group and for only 5% of European species, out of the total 890 species, the International Union for the Conservation of Nature (IUCN) could not evaluate the risk of extinction due to insufficient information (Vujić et al. 2022). For bees, on the other hand, the scenario is quite different: for more than half of the European species (55.6%), out of the total 1,965 species, we have too little information to define their overall population trend (Nieto et al. 2014). For instance, the Italian Red List of Bees only assessed the conservation status of less than 15% of the species reported for the country, and yet 55% were classified as "Data Deficient" (Quaranta et al. 2018). For the studies presented in *Chapter 4, Chapter 5* and *Chapter 6* we sampled managed and wild pollinators and gathered a large amount of data on species distribution and their floral and habitat preferences. By sampling for only three years and mostly in areas characterized by moderate or high anthropogenic pressure, we collected more than 400 pollinator species and morphospecies, including more than 100 hoverfly species and almost 250 bee species. These data are of critical

importance for our knowledge of pollinators and will contribute to future assessments of pollinator conservation status.

7.5. Future steps and final remarks

The factors that determine pollinator abundance and diversity are not independent of each other. For example, climate could interact with pesticides, either improving or worsening their effect on pollinator health (Kenna et al. 2023), but it can also interact with land-use changes, with effects changing from one pollinator guild to another (Ganuza et al. 2022). In my PhD thesis, I analyzed how pollinators were affected by individual factors, but future studies need to take into account the potential interactive effects among drivers in order to have a realistic and accurate overview of pollinator status that will allow us to effectively protect them. In addition, we know that even the more resilient pollinator species are experiencing change, *e.g.*, pollinator individuals of common species found in warmer urban areas are becoming smaller than those of the same species in cooler areas (Eggenberger et al. 2019; Tommasi et al. 2022). In my PhD thesis, I focused on community-level responses, which are the most easily observed in the short-term, but future studies should explore long-term adaptations at the intra-specific level.

Pollinator conservation is a multifaceted science and an ongoing challenge. The factors that determine the abundance and diversity of pollinators are multiple, complex, often context-dependent, and interconnected. It is our responsibility to work to slow, stop or reverse this process of decline, not only for their value for biodiversity but also because our well-being strongly depends on pollinators. To protect pollinators, the key ecosystem service they provide, and the fundamental contribution they make to biodiversity, tailored conservation actions are needed: to limit land consumption and restore natural and semi-natural habitats that are adequately connected – even in cities; to more strictly regulate beekeeping and become less dependent on honey bee pollination in favour of wild pollinators; to decrease the use of highly toxic pesticides, moving towards an integrated pest management approach, which could benefit not only pollinators and other organisms but also crops; and last, to pursue pollinator monitoring programs that allow determining how pollinator populations are changing over time.

Supplementary information

CHAPTER 2

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Table S2.1: List of the 13 sampling locations with information on coordinates (WGS84, decimal degrees), elevation (m a.s.l.), and percentage of agricultural (Agric), semi-natural (Semi-nat), man-made (Man-made), and other (Other) areas in 3 km radius buffers around the sampling locations.

Location	Lat (N)	Lon(E)	Elev	Agric	Semi-nat	Man-made	Other
Ala	45.782728	11.029251	291	20	73	5	
Borgo Valsugana	46.055169	11.455965	406	44	41	15	θ
Caldonazzo	45.997705	11.270409	462	33	42	12	13
Cavalese	46.283778	11.50333	894	37	55	8	$\boldsymbol{0}$
Cles	46.361671	11.039318	650	46	31	12	11
Faedo	46.194805	11.169871	700	18	79	3	θ
Giovo	46.143398	11.118596	339	52	25	21	0
Peio	46.38582	10.687238	1481	8	76	Ω	Ω
Pergine Valsugana	46.073691	11.231101	503	38	43	19	Ω
Riva del Garda	45.901052	10.852101	93	40	28	27	4
Romagnano	46.000702	11.113726	192	44	45	8	3
Rovereto	45.884123	11.021881	175	41	28	29	\mathfrak{D}
Tiarno di Sopra	45.893395	10.679264	747	13	83	3	θ

CLC code	CLC class	Category
111	Continuous urban fabric	Urban
112	Discontinuous urban fabric	
121	Industrial, commercial and public units	
122	Road and rail networks and associated land	
124	Airport	
131	Mineral extraction sites	
132	Dump sites	
211	Non-irrigated arable land	Crop
221	Vineyards	
222	Fruit trees and berries plantations	
231	Pastures	
242	Complex cultivation patterns	
243	Crop with significant amount of natural vegetation	
311	Broadleaved forest	Semi-natural
312	Coniferous forest	
313	Mixed forest	
321	Natural grassland	
322	Moors and heathland	
324	Transitional woodland-scrub	
332	Bare rock	
333	Sparsely vegetated areas	
335	Glaciers and perpetual snow	
511	Water courses	Other
512	Water bodies	

Table S2.2: CORINE Land Cover (CLC) classes and merged categories.

1 km 3 km 5 km PC1 PC2 PC1 PC2 PC1 PC2 Explained variability 22.4% 15.8% 26.1% 19.9% 28.8% 16.3% **CLC class** 111 - Continuous urban fabric -0.382 -0.277 0.231 0.272 -0.203 -0.087 112 - Discontinuous urban fabric -0.331 0.284 0.281 0.347 -0.266 -0.193 121 - Industrial, commercial and public units -0.308 0.178 $\begin{array}{|l} 0.255 \quad 0.227 \end{array}$ -0.233 0.098 122 - Road and rail networks and associated land - - - - -0.146 0.056 $124 -$ Airport $0.096 -0.288$ -0.029 0.343 131 - Mineral extraction sites 0.137 -0.094 0.070 -0.211 -0.092 0.087 132 - Dump sites - - - - -0.069 0.037 211 - Non-irrigated arable land -0.382 -0.277 | 0.078 0.157 | -0.065 -0.189 221 - Vineyards -0.019 -0.180 | 0.225 -0.260 | -0.178 0.360 222 - Fruit trees and berries plantations -0.064 0.393 $\begin{array}{|l} 0.000$ 0.145 \end{array} -0.017 -0.149 231 - Pastures 0.119 -0.098 -0.204 0.002 0.213 -0.107 241 - Crop with significant amount of natural vegetation 0.318 -0.019 0.161 0.259 -0.246 -0.099 242 - Complex cultivation patterns -0.176 0.202 0.195 0.282 -0.199 -0.204 311 - Broadleaved forest -0.043 -0.411 | 0.194 -0.363 | -0.164 0.377 312 - Coniferous forest 0.280 -0.028 -0.401 0.050 0.215 -0.247 $313 - Mixed forest$ 0.204 $-0.327 \mid 0.085$ $-0.220 \mid -0.173$ 0.050 321 - Natural grassland 0.213 0.016 -0.356 0.020 0.335 0.071 $322 -$ Moors and heathland $\qquad \qquad \qquad \qquad \qquad 0.267$ 0.262 324 - Transitional woodland-scrub -0.394 -0.281 | 0.109 -0.240 | -0.052 0.197 $332 -$ Bare rock $\begin{array}{ccc} - & - & - \end{array}$ $\begin{array}{ccc} -0.356 & 0.020 & 0.325 & 0.072 \end{array}$ 333 - Sparsely vegetated areas - - -0.347 0.044 0.321 0.064 335 - Glaciers and perpetual snow $\qquad \qquad$ - $\qquad \qquad$ - $\qquad \qquad$ - $\qquad \qquad$ 0.073 511 - Water courses -0.051 -0.081 | 0.187 -0.328 | -0.111 0.433 512 - Water bodies -0.102 0.354 0.001 0.131 -0.051 -0.210

Table S2.3: Results of the Principal Component Analysis (PCA) for 1, 3, and 5 km radius buffers around the sampling locations, showing variable loadings and their eigenvector values.

Table S2.4: Pollen types identified in pollen samples and their average proportion in the six sampling months and in total. The identified pollens were classified following the pollen types nomenclature proposed by Persano Oddo and Ricciardelli d'Arbore (1989).

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Table S3.1: List of the 13 sampling locations with information on coordinates (WGS84, decimal degrees), elevation (m a.s.l.), and percentage of semi-natural (Semi-nat), agricultural (Agric), and man-made (Manmade) areas calculated using the regional land-use map categories in 3 km radius buffers around the sampling locations.

Location	Lat (N)	Lon (E)	Elev	Semi-nat	Agric	Man-made
Ala	45.78273	11.02925	291	74	20	5
Borgo Valsugana	46.05517	11.45597	406	41	44	15
Caldonazzo	45.99771	11.27041	462	49	38	13
Cavalese	46.28378	11.50333	894	56	37	8
Cles	46.36167	11.03932	650	35	52	14
Cogolo di Peio	46.38582	10.68724	1481	92	8	θ
Faedo	46.19481	11.16987	700	79	18	3
Giovo	46.1434	11.1186	339	26	52	22
Pergine Valsugana	46.07369	11.2311	503	43	38	19
Rovereto	45.88412	11.02188	175	29	41	30
Salorno	46.24121	11.20504	216	47	45	7
Tiarno di Sopra	45.8934	10.67926	747	84	13	3
Valeggio sul Mincio	45.4085	10.72586	91		87	11

Table S3.2: Regional land-use map classes and corresponding categories used in the Principal Component Analysis.

Table S3.3: List of compounds searched in pollen samples, including information on the pesticide category (Cat; Fung = fungicide, Herb = herbicide, Ins = insecticide and/or acaricide), chemical group (Chem group), frequency at locations (Freq loc), frequency in samples (Freq sam), maximum and mean concentration (Conc max, Conc mean), maximum and mean PHQ (PHQ max, PHQ mean), and maximum risk quotient (RQ max).

Compound	Cat	Chem group	Freq	Freq	Conc	Conc	PHQ max	PHQ mean	RQ max
			loc	sam	max	mean			
$2, 4$ -DDD	Ins	NA	0	Ω	θ	$\overline{0}$	$\mathbf{0}$	$\mathbf{0}$	Ω
2, 4-DDE	Ins	NA		0	Ω	$\mathbf{0}$	Ω		Ω
$2, 4-DDT$	Ins	NA		θ	$\boldsymbol{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$		
3, 5-dichloroaniline	Fung	NA		0	θ	$\boldsymbol{0}$	0		θ
3-hydroxycarbofuran	Ins	NA		0	θ	θ	θ		$^{(1)}$
3-ketocarbofuran	Ins	Carbamates		0	θ	θ	θ		$^{(1)}$
4, 4-DDE	Ins	NA		θ	$\overline{0}$	θ	0		
4, 4-DDT	Ins	NA		θ	θ	$\overline{0}$	0		0
6-benzylaminopurine	Herb	NA	8	20	0.041	0.001619	0.698	0.027558	0.000007
Abamectin	Ins	Avermectins	θ	θ	θ	$\boldsymbol{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$	θ
		milbemycins							
Acephate	Ins	Organophosphates	$\overline{0}$	$\boldsymbol{0}$	$\mathbf{0}$	$\overline{0}$	$\mathbf{0}$	θ	$\boldsymbol{0}$
Acetamiprid	Ins	Neonicotinoid	10	57	0.267	0.009844	18.376	0.677476	0.000176
Acetochlor	Herb	α -chloroacetamides	θ	θ	θ	$\overline{0}$	θ	0	θ
Acibenzolar-S-methyl	Fung	Benzo thiadiazole	θ	Ω	$\overline{0}$	$\overline{0}$	θ	0	
Acrinathrin	Ins	Pyrethroids and	$\overline{0}$	$\mathbf{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$	0
		pyrethrins							
Alachlor	Herb	α -chloroacetamides	$\overline{0}$	θ	$\mathbf{0}$	$\mathbf{0}$	$\boldsymbol{0}$	0	θ
Aldicarb (sum)	Ins	Carbamates	Ω	θ	$\boldsymbol{0}$	$\mathbf{0}$	$\boldsymbol{0}$	θ	$_{0}$
Aldicarb sulfone	Ins	Carbamates	θ	θ	$\boldsymbol{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$		
Aldicarb sulfoxide	Ins	Carbamates	0	$\boldsymbol{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$	0
Aldrin	Ins	Cyclodiene	θ	$\mathbf{0}$	$\overline{0}$	$\mathbf{0}$	$\boldsymbol{0}$	θ	θ
		organochlorines							
Allethrin	Ins	Pyrethroids and	$\boldsymbol{0}$	$\boldsymbol{0}$	$\mathbf{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$
		pyrethrins							

Table S3.4: Instrument acquisition data for pesticides analysed by LC-MS/MS. The table reports the ionization mode and its polarity (Ion mode), cone voltage (CV, expressed as V), quantification trace (Quant trace), collision energy (CE, expressed as eV), and qualification trace (Qual trace).

<u>est</u>

Compound	Quant trace	CE	Qual trace	CE
2, 4-DDD	$235.0 \ge 165.1$	25	$\overline{235.0}$ -> 200.1	10
2, 4-DDE	$248.0 \ge 176.2$	30	$246.0 \ge 176.2$	30
2, 4-DDT	$237.0 \ge 165.2$	20	$235.0 \ge 165.2$	20
3, 5-dichloroaniline	$161.0 \ge 99.0$	20	$161.0 \ge 90.0$	20
4, 4-DDE	$246.1 \div 176.2$	30	$315.8 \ge 246.0$	15
4, 4-DDT	$237.0 \ge 165.2$	20	$235.0 \ge 165.2$	20
Acetochlor	$146.0 \ge 131.1$	10	$174.0 \ge 146.1$	10
Acrinathrin	$181.0 \ge 152.0$	30	$207.8 \rightarrow 181.1$	10
Alachlor	$188.1 \ge 160.1$	10	$160.1 \ge 132.1$	15
Aldrin	$262.9 \div 192.9$	35	$254.9 \ge 220.0$	20
Benfluralin	$292.0 \ge 264.0$	5 ⁵	$292.0 \ge 206.0$	10
Bifenox	$189.1 \div 126.0$	20	$340.9 \ge 309.9$	10
Bromophos-ethyl	$302.8 \ge 284.7$	15	$358.7 \ge 302.8$	15
Bromopropylate	$185.0 \ge 157.0$	15	$183.0 \ge 155.0$	15
Captan	$263.0 \div 79.0$	25	$149.0 \ge 70.0$	15
Chinomethionat	$206.0 \ge 148.1$	15	$233.9 \ge 206.1$	10
Chlorfenapyr	$137.0 \ge 102.0$	15	$247.1 \div 227.1$	20
Chlorfenson	$175.0 \ge 111.0$	10	$111.0 \ge 75.0$	15
Chlormephos	$121.1 \div 65.0$	10	$153.9 \ge 121.1$	$\overline{0}$
Chlorpropham	$127.0 \ge 65.0$	25	$213.0 \ge 127.0$	10
Chlorpyrifos-methyl	$78.9 \div 47.0$	10	$286.0 \ge 93.0$	15
Cyfluthrin I	$162.9 \ge 90.9$	15	$162.9 \ge 127.0$	5
Cyfluthrin II {CAS # 68359-37-5}	$162.9 \div 90.9$	15	$162.9 \div 127.0$	5
Cyfluthrin III $\{CAS \# 68359-37-5\}$	$162.9 \div 90.9$	15	$162.9 \ge 127.0$	5
Cyfluthrin IV {CAS # 68359-37-5}	$162.9 \div 90.9$	15	$162.9 \ge 127.0$	5
Cyhalofop-butyl	$120.1 \div 91.0$	15	$256.2 \div 120.1$	10
Cypermethrin I	$163.0 \ge 91.0$	10	$163.0 \ge 127.0$	5
Cypermethrin II $\{CAS \# 52315-07-8\}$	$163.1 \ge 127.1$	5 ⁵	$163.1 \div 91.0$	15
Cypermethrin III $\{CAS \# 52315-07-8\}$	$163.1 \div 91.0$	15	$163.1 \ge 127.1$	5
Cypermethrin IV $\{CAS \# 52315-07-8\}$	$163.1 \div 91.0$	15	$163.1 \div 127.1$	5
Cypermethrin, alpha-	$163.0 \geq 91.0$	15	$163.0 \ge 127.0$	5
Cypermethrin, beta- {CAS# 67375-30-8)	$163.0 \ge 91.0$	15	$181.0 \ge 152.0$	30
Deltamethrin	$252.9 \ge 93.0$	15	$181.0 \ge 152.1$	25
Dichlobenil	$171.0 \ge 100.0$	20	$171.0 \ge 136.0$	20
Dichlofenthion	$223.0 \ge 204.9$	15	$279.0 \ge 223.0$	15
Dichlofluanid	$123.0 \ge 77.0$	20	$123.0 \ge 51.0$	40
Dicloran	$206.1 \div 176.0$	10	$160.1 \ge 124.1$	10
Dicofol o, p'-	$139.0 \ge 75.0$	30	$139.0 \ge 111.0$	10
Dicofol p, p'-	$183.9 \ge 169.3$	5	$183.9 \ge 155.0$	30
Dieldrin	$262.9 \div 193.0$	35	$277.0 \ge 241.0$	5°
Diflufenican	$266.0 \ge 238.1$	15	$266.0 \ge 246.1$	15
Dioxathion	$124.9 \ge 96.9$	5 ⁵	$152.9 \ge 96.9$	10
Diphenylamine	$169.0 \ge 168.2$	15	$168.0 \ge 167.2$	15
Disulfoton	$88.0 \div 60.0$	5	$142.0 \ge 109.0$	5

Table S3.5: Instrument acquisition data for pesticides analysed by GC-MS/MS. The table reports quantification trace (Quant trace), collision energy (CE, expressed as eV), and qualification trace (Qual trace).

Table S3.6: Validation data of the QuEChERS method (EN 15662:2018) applied on the pollen matrix. Matrix-matched calibration was used to quantify spiked samples (5 concentration levels included in the range shown in the table). Six replicates were prepared for each level added, and recovery data shown represents the average of six replicates. For each compound, the table reports the limit of quantification (LOQ, expressed as µg/kg, estimated according to the SANTE guidelines), limit of detection (LOD, expressed as μ g/kg, estimated as one-third of the LOQs), the three concentration levels of added compounds (10, 50, and 200 μ g/kg), recovery (Rec, expressed as %) and repeatability (RSD, expressed as %) of the method, matrix effect (expressed as %), and linearity (R²).

Table S3.7: Validation data of the QuPPe-PO-Method applied to the pollen matrix. Matrix-matched calibration was used to quantify spiked samples (5 concentration levels included in the range shown in the table). Six replicates were prepared for each level added, and recovery data shown represents the average of six replicates. The table reports the limit of quantification (LOQ, expressed as μ g/kg, estimated according to the SANTE guidelines), limit of detection (LOD, expressed as μ g/kg, estimated as one third of the LOQ), the three concentration levels of added compound (100, 500, and 2000 ug/kg), recovery (Rec, expressed as %) and repeatability (RSD, expressed as %) of the method, matrix effect (expressed as %), and linearity (R^2) .

Table S3.8: Results of the linear mixed-effects model testing the effect of the interaction between the sampling month and pesticide category, the interaction between the sampling month and landscape PC1, the interaction between the sampling month and landscape PC2, the interaction between the sampling month and landscape PC3, and the sampling year on the PHQ of pollen samples (ln-transformed). Landscape PC1, PC2 and PC3 were calculated using the regional land-use map categories in 5 km radius buffers around the sampling locations. Values in bold indicate significant effects (*p*-value < 0.05). Only significant results after a backward stepwise model selection procedure are reported.

Table S3.9: Results of the linear mixed-effects model testing the effect of the percentage of annual and perennial crops in 5 km radius buffers around the sampling locations on the PHQ of pollen samples (lntransformed). Values in bold indicate significant effects (p -value < 0.05).

	value	SE	df	<i>t</i> -value	<i>p</i> -value
Intercept	0.779	1.061	64	0.734	0.466
Annual crop $\%$ (5 km)	6.227 3.825		10	1.628	0.135
Perennial crop % (5 km) 12.690 4.620			10	2.747	0.021

Figure S3.1: Map of the 13 sampling locations. Imagery © 2023 TerraMetrics, Map data © 2023 Google.

Figure S3.2: Principal Component Analysis loading plots showing landscape PC1, landscape PC2, and the regional land-use map categories at *a)* 3 km radius buffers around the sampling locations and *b)* 5 km radius buffers around the sampling locations.

Figure S3.3: Plots showing *a)* the number of searched and detected compounds for each pesticide category and *b)* the number of pollen samples containing each pesticide category found for each sampling month.

Figure S3.4: Plot showing the effect of the interaction between the sampling period and landscape PC1 on PHQ of pollen samples (ln-transformed). Landscape PC1 was calculated using the regional land-use map categories in 5 km radius buffers around the sampling locations. Points represent raw data points and lines represent model estimates.

Figure S3.5: Plot showing the effect of the cover of perennial crops (fruit trees and vineyards) in 5 km radius buffers around the sampling locations on PHQ of pollen samples (ln-transformed). Points represent raw data points, the line represents model estimate, and the shaded area represents the 95% confidence interval.

CHAPTER 4

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Table S4.1: List of the 36 sampling sites.

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community evenness of wild bees.

Tables S4.4, S4.5: Results of the multi-model inference analyses**.**

Figure S4.1: Correlations among predictors and among wild bee functional traits.

Figure S4.2: Species rarefaction and extrapolation curves.

Figure S4.3: Wild bee species abundance per site.

Figure S4.4: Effect of open habitat cover on CWM social behaviour (sociality).

Table S4.1: List of the 36 sampling sites with information on coordinates (WGS84, decimal degrees), distance from the city centre (km), area of open habitat in a 500 m buffer (ha), and surface temperature (°C).

Table S4.2: List of collected wild bee species with information on their abundance (Ab) and functional group assignments. Body size (Body) is the mean value in mm of the measured specimens. For social behaviour (Social), social species comprise semi-social, social, and eusocial bees. For nesting strategy (Nest), categories were collapsed to below-ground and above-ground nesting (which include those species which build their nests in stems or pre-existing cavities). For diet breadth (Diet), oligolectic bees (oligo) are specialized to forage on one specific plant taxon.

Table S4.3: Results of the linear models testing the effect of woody cover (km²) on abundance (lntransformed), species richness (ln-transformed), and community evenness of *a)* all wild bee species and *b)* wood nesting wild bee species.

	Response variable	Estimate	SE	t value	<i>p</i> value
<i>a</i>) All wild bee species	Wild bee abundance (ln)	-0.748	0.835	-0.895	0.377
	Wild bee richness (ln)	-0.203	0.375	-0.541	0.592
	Community evenness	0.1978	0.161	1.227	0.228
b) Wood nesting wild	Wild bee abundance (ln)	-0.694	0.431	-1.611	0.125
bee species	Wild bee richness (ln)	-0.526	0.360	-1.464	0.160
	Community evenness	0.219	0.746	0.294	0.778
Table S4.4: Results of the multi-model inference analysis testing the effects of distance from the city centre (Dist), open habitat cover (Open), temperature (Temp) and their interactions on *a*) wild bee abundance (ln-transformed), *b*) wild bee richness (ln-transformed), and *c*) community evenness. The table reports the estimate for each variable, the ΔAICc, and the Akaike weight (w) for each model of the set with ΔAICc < 4.

Response variable		Ranking Intercept Dist		Open					Temp Dist \times Dist \times Open \times Dist \times Open AAICc w		
							Open Temp Temp		\times Temp		
$a)$ Wild bee abundance (ln) 1		-0.131			0.114	\overline{a}				0	0.344
	2	0.237		-0.01	0.111	\blacksquare				1.195	0.189
	3	-0.129	0.003		0.113	$\overline{}$				2.535	0.097
	4	3.296		-0.125	0.033	$\overline{}$		0.003		3.456	0.061
	5	0.278	0.015	-0.011	0.108	$\overline{}$				3.761	0.052
b) Wild bee richness (ln)	$\mathbf{1}$	1.155		-0.007	0.049	\blacksquare	\blacksquare	$\overline{}$	\blacksquare	$\mathbf{0}$	0.310
	$\overline{2}$	0.888			0.051	\blacksquare				1.158	0.174
	3	2.326		-0.051	0.019	$\overline{}$		0.001		2.355	0.095
	4	1.154	θ	-0.007	0.049					2.709	0.080
	5	1.788	-0.069	-0.022	0.044	0.002				3.439	0.056
	6	0.882	$-0.008 -$		0.053	\blacksquare				3.476	0.055
$c)$ Community evenness	1	1.123			$-0.016 -$		\blacksquare	$\overline{}$		$\overline{0}$	0.260
	$\overline{2}$	0.509				$\overline{}$				0.709	0.182
	3	1.081		0.001	$-0.015 -$			-		2.129	0.090
	4	1.121	-0.003		$-0.015 -$					2.407	0.078
	5	0.476		0.001						2.584	0.071
	6	0.539	-0.005	$\overline{}$						2.717	0.067
	7	0.168	0.167		0.009	$\overline{}$	$-0.004 -$			3.516	0.045

Table S4.5: Results of the multi-model inference analysis testing the effects of distance from the city centre (Dist), open habitat cover (Open), temperature (Temp) and their interaction on CWMs for *a)* body size, *b)* nesting strategy, *c)* diet breadth and *d)* social behaviour. The table reports the estimate for each variable, the \triangle AICc, and the Akaike weight (w) for each model of the set with \triangle AICc < 4.

Response variable	Intercept	Dist	Open	Temp	Dist \times	Dist \times		Open \times Dist \times Open \triangle AICc w		
					Open	Temp	Temp	\times Temp		
a) CWM body size	10.919	0.095	\blacksquare	-0.115					$\overline{0}$	0.351
	6.915	0.810		-0.011	$\overline{}$	-0.018	L,		1.561	0.161
	10.892	0.094	0.001	-0.114	$\overline{}$				2.704	0.091
	10.848			-0.098	$\overline{}$				3.176	0.072
	6.512	0.079							3.833	0.052
$b)$ CWM nesting	0.044							$\overline{}$	$\boldsymbol{0}$	0.282
strategy (above ground)	0.061		-0.001						0.183	0.258
	0.051	-0.001							2.090	0.099
	0.029			0.000	$\overline{}$				2.376	0.086
	0.063	0.000	-0.001	$\overline{}$					2.704	0.073
	0.063		-0.001	\blacksquare	$\overline{}$	\blacksquare	$\overline{}$	$\overline{}$	2.741	0.071
c) CWM diet breadth	0.524	÷,	0.002	0.023	\blacksquare	\overline{a}		$\qquad \qquad \blacksquare$	$\boldsymbol{0}$	0.270
(polylecty)	0.616			0.022	$\overline{}$				0.708	0.189
	-0.244		0.031	0.042			-0.001		1.569	0.123
	0.620	0.006		0.021					2.332	0.084
	0.534	0.003	0.002	0.022					2.399	0.081
d) CWM social	0.601	$\overline{}$	0.004					$\qquad \qquad \blacksquare$	$\overline{0}$	0.176
behaviour (sociality)	-0.061		0.004	0.017	$\overline{}$				0.016	0.175
	0.713								1.461	0.085
	0.556	0.009	0.004						1.602	0.079
	-1.169		0.046	0.045			-0.001		1.753	0.073
	0.108			0.015					1.931	0.067
	0.631	0.013							2.020	0.064
	-0.042	0.007	0.004	0.015					2.196	0.059

Figure S4.1: Correlation matrices for *a)* predictors and *b)* wild bee functional traits based on Pearson's correlation. Right-oriented blue ellipses indicate positive correlations, while left-oriented red ellipses indicate negative correlations. Narrower ellipses indicate stronger correlations. Only significant correlations (*p* value < 0.05) are displayed.

Figure S4.2: Species rarefaction and extrapolation curves: *a)* sample completeness curve per site and *b)* coverage‐based sampling curve per site. Each site is shown in a different colour.

Figure S4.3: Wild bee species abundance per site. The size of each point is proportional to logarithmic transformed abundance. Sites are ordered according to increasing surface temperature, while species are ordered according to their overall abundance.

Figure S4.4: Plot showing the effect of open habitat cover on CWM social behaviour (sociality). Points represent raw data points, the line represents model estimate, and the shaded area represents the 95% confidence interval.

CHAPTER 5

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Table S5.1: List of the 51 sampling sites.

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Table S5.5: Summary of the six global models.

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Figure S5.1: Map of the 51 sampling sites.

Figure S5.2: Relationships between functional traits of pollinators.

Figure S5.3: Model estimates from the model-averaging procedure based on the set of models including all functional traits of both plants and pollinators.

Table S5.1: List of the 51 sampling sites with information on coordinates (WGS84, decimal degrees), elevation (m a.s.l.), recorded air temperature (°C), number of flowering plant species (Plant rich), number of pollinator species (Poll rich), abundance of honey bees (Honey bee ab), and abundance of wild pollinators (Wild poll ab).

Site ID	Lat (N)	Lon (E)	Elev	Temp			Plant rich Poll rich Honey bee ab Wild poll ab	
A	45.587007	11.468313	60	27.67	20	31	5	111
AA	46.487789	12.035109	2005	25.29	26	22	768	73
AB	46.490416	12.066126	1982	23.24	28	12	109	16
$\mathbf{A}\mathbf{C}$	46.518712	12.007109	2090	22.36	34	19	145	39
${\rm AD}$	46.533594	11.986739	2111	27.05	25	13	282	43
$\mathbf{A}\mathbf{E}$	46.565153	12.243253	1658	22.37	21	30	34	65
AF	46.548764	12.261756	1500	26.72	19	16	22	29
AG	46.396688	12.104436	1450	25.43	27	49	274	119
AH	46.420795	12.105355	1780	20.95	28	30	31	150
AI	46.484398	11.831885	2008	19.63	22	14	$\overline{2}$	93
${\rm AJ}$	45.82542	12.180076	175	27.99	13	27	44	63
AK	45.808239	12.111145	320	30.23	11	14	80	25
${\rm AL}$	46.485461	11.788397	1915	19.52	34	34	101	110
AM	46.549767	11.813354	2055	19.02	35	30	116	78
AN	46.339973	11.804519	2032	20.95	13	19	9	130
AO	46.195026	11.42058	1430	22.72	18	26	34	51
AP	46.348829	11.845274	1600	22.33	18	16	25	61
AQ	46.139193	11.472058	1250	24.49	16	24	149	332
AR	46.147208	11.771577	910	30.98	15	17	$\overline{4}$	31
AS	46.172563	11.441852	2040	19.65	16	22	227	64
AT	45.880301	11.794101	1665	21.37	18	24	$\overline{2}$	75
AU	45.755492	10.874539	1500	18.05	11	10	$\overline{3}$	25
AV	45.756764	10.920759	640	24.63	10	9	108	29
AW	45.803576	12.049459	200	35.54	8	28	201	67
AX	45.868023	12.009987	170	30.91	10	13	24	45
AZ	45.694425	10.926014	130	32.84	10	12	55	16
B	45.583447	11.463828	150	27.37	22	29	25	119
$\mathsf C$	45.747647	11.329589	670	24.04	19	35	113	109
D	45.755546	11.363854	630	24.65	17	29	64	69
E		45.711296 11.68899	76	30.6	15	32	302	94
$\boldsymbol{\mathrm{F}}$	45.760339	11.699603	106	36.89	12	25	508	73
G	45.595876	11.467499	150	37.89	22	22	19	121
H_{\rm}	45.622053	11.415189	165	33.93	16	19	19	103
Ι	45.862562	11.762562	1251	21.02	19	27	353	57
J	45.649502	11.7196	50	28.19	11	9	31	25
K	45.979623	12.730447	35	27.88	20	25	179	72
L	45.839134	11.736687	1000	25.27	15	17	550	51
M	45.848196	11.452165	943	26.37	29	29	119	93
${\bf N}$	45.824215	11.455581	1170	23.79	19	18	31	71
$\mathbf O$	45.760665	11.39284	1215	19.51	22	34	21	119

Table S5.2: Functional traits of flowering plant species: flower colour (six classes: blue, brown, pink/purple, red, white, yellow/orange), flower type (nine classes: bell/funnel/lip, brush, hidden disc, open disc, flag, flower head, NA, pollen, and stalk disc flower), and flower corolla length (mm).

Table S5.3: Functional traits of pollinator species: taxonomic family, proboscis length (mm; mean value of the measured specimens), body size in mm (mm; mean value of the measured specimens), and type of foraging range (*C* central-place forager, *NC* non-central-place forager).

Table S5.4: Functional traits of pollinator families: number of collected specimens (N), proboscis length (mm; mean and SD values of the measured specimens), body size (mm; mean and SD values of the measured specimens), and percentage of central and non-central forager species (*C* central-place foragers, *NC* noncentral-place foragers).

Family	N	Proboscis	Body	C species	NC species
Andrenidae	86	1.73(0.67)	9.33(2.17)	100	
Apidae	8045	6.88(2.66)	14.1(3.56)	78	22
Cimbicidae	$\overline{2}$	0.85(0.07)	10(2.83)	$\overline{}$	100
Colletidae	37	0.79(0.19)	5.13(0.88)	100	-
Conopidae	43	4.1(0.99)	8.78 (3.12)	$\overline{}$	100
Crabronidae	40	0.92(0.4)	7.62(2.38)	100	-
Halictidae	258	1.84(0.62)	7.87(1.73)	88	12
Megachilidae	116	3.9(1.11)	10.31(3.32)	94	6
Megalodontesidae	3	2.25(0.07)	12(0)	-	100
Melittidae	8	1.2 (NA)	9(NA)	100	-
Scoliidae	4	4.1 (NA)	19 (NA)		100
Syrphidae	2000	0.98(0.38)	9.66(2.49)	\overline{a}	100
Tachinidae	102	2.68(1.07)	8.74(2.72)	$\overline{}$	100
Tenthredinidae	81	0.91(0.29)	10.9(1.76)	\overline{a}	100
Vespidae	16	1.54(0.09)	13.58 (0.49)	83	17

Table S5.5: Summary of the six global models. Abbreviated explanatory variables are honey bee abundance (*Apis*, ln-transformed), temperature (Temp), standardized functional richness of plant community (FRic), functional dispersion of plant community (FDis), trait similarity between wild pollinator community and the honey bee (TSim), proboscis length category (Prob), body size category (Body), type of foraging range (For), and taxonomic family (Fam). The continuous explanatory variables were scaled to mean 0 and standard deviation 1 to make slopes comparable.

Table S5.6: Results of the multi-model inference analysis testing the effects on CWM resource overlap of honey bee abundance (*Apis*, ln-transformed), temperature (Temp), standardized functional richness of plant community (FRic), trait similarity between wild pollinator community and the honey bee (TSim), and the following interactions: Apis × FRic, Apis × TSim, FRic × TSim, and Apis × FRic × TSim. The table reports the estimates for each variable, the ΔAICc, the R², and the Akaike weight (w) for each model with ΔAICc < 6. All the explanatory variables were scaled to mean 0 and standard deviation 1.

Ranking	Intercept	<i>Apis</i>	Temp	FRic					TSim <i>Apis</i> × FRic <i>Apis</i> × TSim FRic × TSim <i>Apis</i> × FRic × TSim \triangle AICc R ²			W
$\mathbf{1}$	-1.471	-0.087	\sim	-0.010	0.143	-0.193				0.000	0.290	0.286
2	-1.474	$-0.084 -$		-0.008	0.155	-0.201	-0.058			1.917	0.300	0.110
3	-1.458	-0.087	$\overline{}$	0.000	0.159	-0.190	$\overline{}$	0.043		2.290	0.295	0.091
4	-1.472	-0.089	0.007	-0.007	0.144	-0.191				2.682	0.290	0.075
5	-1.472	$-0.087 -$		-0.056	\sim	-0.189				3.373	0.202	0.053
6	-1.517				0.158	\blacksquare	$\overline{}$			3.511	0.120	0.049
	-1.517	$-0.084 -$			0.152	$\overline{}$				3.884	0.154	0.041
8	-1.458	-0.083	\sim	0.006	0.177	-0.199	-0.069	0.055		4.065	0.310	0.037
9	-1.474	-0.084	0.000	-0.007	0.155	-0.201	-0.058			4.741	0.300	0.027
10	-1.517			-0.061	0.139	\sim				4.931	0.136	0.024
11	-1.459	-0.089	0.007	0.003	0.160	-0.188	$\overline{}$	0.043		5.099	0.295	0.022
12	-1.517		0.048	\blacksquare	0.159	$\overline{}$				5.226	0.131	0.021
13	-1.517	-0.093	0.061	$\overline{}$	0.152	$\overline{}$				5.270	0.172	0.021
14	-1.517	-0.075	\sim	-0.043	0.139	$\overline{}$				5.890	0.161	0.015
15	-1.471	-0.084	-0.015	-0.062	\blacksquare	-0.194				5.894	0.203	0.015

Table S5.7: Results of the multi-model inference analysis testing the effects on CWM resource overlap between wild pollinators and the honey bee of honey bee abundance (*Apis*, ln-transformed), temperature (Temp), functional dispersion of plant community (FDis), trait similarity between wild pollinator community and the honey bee (TSim), and the following interactions: *Apis* × FDis, *Apis* × TSim, FDis × TSim, and *Apis* × FDis × TSim. The table reports the estimates for each variable, the ΔAICc, the R², and the Akaike weight (w) for each model with $\Delta AICc \leq 6$. All the explanatory variables were scaled to mean 0 and standard deviation 1.

Ranking	Intercept	<i>Apis</i>	Temp	FDis	TSim	$Apis \times FDis$		$Apis \times TSim$ FDis $\times TSim$	<i>Apis</i> \times FDis	$\triangle AICc$	\mathbf{R}^2	W
									\times TSim			
	-1.517				0.171					0.000	0.141	0.144
2	-1.517	-0.082			0.165					0.436	0.173	0.116
3	-1.517			-0.082	0.143					0.635	0.169	0.105
4	-1.517	-0.087		-0.088	0.134	$\overline{}$				0.842	0.205	0.095
5	-1.517	$\overline{}$	0.038	\sim	0.170	\blacksquare				1.944	0.148	0.055
6	-1.517	-0.090	0.052	\blacksquare	0.161	\blacksquare				2.128	0.185	0.050
	-1.519	-0.081			0.168	\blacksquare	-0.023			2.793	0.174	0.036
8	-1.527			-0.067	0.140			-0.030		2.857	0.173	0.035
9	-1.519	-0.079		-0.084	0.135	-0.059				2.967	0.212	0.033
10	-1.517	-0.100		-0.134	$\overline{}$					2.981	0.130	0.033
11	-1.517	\sim	0.021	-0.077	0.144					2.982	0.171	0.032
12	-1.517	-0.092	0.034	-0.080	0.135	$\overline{}$				3.097	0.210	0.031
13	-1.527	-0.088		-0.072	0.130	$\overline{}$		-0.031		3.135	0.210	0.030
14	-1.518	-0.086		-0.087	0.137	$\overline{}$	-0.019			3.344	0.206	0.027
15	-1.517	$\overline{}$		-0.131						3.344	0.083	0.027
16	-1.518	-0.089	0.050	\sim	0.164		-0.016			4.650	0.186	0.014
17	-1.518	-0.092		-0.131	\blacksquare	-0.056				5.077	0.136	0.011
18	-1.517	-0.104	0.030	-0.127	\blacksquare					5.205	0.134	0.011
19	-1.528	$\omega_{\rm{max}}$	0.026	-0.058	0.140			-0.034		5.245	0.176	0.010
20	-1.530	-0.093	0.040	-0.059	0.130	\blacksquare		-0.039		5.377	0.217	0.010
21	-1.529	-0.079		-0.069	0.131	-0.058		-0.031		5.390	0.216	0.010
22	-1.517	-0.096								5.456	0.044	0.009

Table S5.8: Results of the multi-model inference analysis for single traits of pollinators, testing the effects on CWM resource overlap between wild pollinators and the honey bee of honey bee abundance (*Apis*, lntransformed), temperature (Temp), and *a)* proboscis length (Prob) and the interaction between honey bee abundance and proboscis length $(Apis \times Prob)$, *b*) body size (Body) and the interaction between honey bee abundance and body size (*Apis* × Body), *c)* type of foraging range (For) and the interaction between honey bee abundance and type of foraging range (*Apis* × For), and *d)* taxonomic family (Fam) and the interaction between honey bee abundance and taxonomic family (*Apis* × Fam). The table reports the estimate for each continuous variable or the presence of each categorical variable in the model, the $\Delta AICc$, the R^2 , and the Akaike weight (w) for each model of the set with $\triangle AICc \le 6$. All the continuous explanatory variables were scaled to mean 0 and standard deviation 1.

Figure S5.1: Map of the 51 sampling sites. Map credit: © OpenStreetMap contributors.

Figure S5.2: Plots showing the relationships between functional traits of pollinators, *i.e.*, *a)* proboscis length and body size, *b)* type of foraging range and proboscis length, and *c)* type of foraging range and body size. In all plots, proboscis length and body size were ln-transformed.

Figure S5.3: Model estimates from the model-averaging procedure based on the set of models including all functional traits of both plants and pollinators. Explanatory variables of the global model are honey bee abundance (*Apis*, ln-transformed), temperature (Temp), functional dispersion of plant community (FDis), trait similarity between wild pollinator community and the honey bee (TSim), and the following interactions: *Apis* × FDis, *Apis* × TSim, FDis × TSim, and *Apis* × FDis × TSim. All explanatory variables were scaled to mean 0 and standard deviation 1. Points represent model estimates and bars represent the 95% confidence intervals. The variable effect is supported when the confidence interval does not include zero.

CHAPTER 6

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Lasioglossum glabriusculum Lasioglossum griseolum Lasioglossum interruptum Lasioglossum laevigatum Lasioglossum laticeps Lasioglossum leucozonium Lasioglossum lucidulum Lasioglossum malachurum Lasioglossum marginatum Lasioglossum medinai Lasioglossum mesosclerum Lasioglossum minutissimum Lasioglossum minutulum Lasioglossum morio Lasioglossum nigripes Lasioglossum nitidulum Lasioglossum pauxillum Lasioglossum politum Lasioglossum puncticolle Lasioglossum pygmaeum Lasioglossum transitorium Lasioglossum tricinctum Lasioglossum villosulum Lasioglossum zonulum Nomiapis diversipes Nomioides facilis Seladonia confusa Seladonia smaragdula Seladonia subaurata Sphecodes alternatus Sphecodes ephippius Sphecodes gibbus Sphecodes longulus Sphecodes monilicornis Sphecodes niger Sphecodes scabricollis Sphecodes sp. *Systropha curvicornis* Megachilidae *Anthidium manicatum Anthidium oblongatum Chelostoma campanularum Chelostoma emarginatum Coelioxys elongatus Heriades rubicola Hoplitis adunca Hoplitis* cf. *papaveris Hoplitis leucomelana Lithurgus chrysurus*

Osmia sp. 2 *Osmia spinulosa Osmia submicans* Melittidae *Melitta haemorrhoidalis* Syrphidae *Chalcosyrphus nemorum Episyrphus balteatus Eristalinus sepulchralis Eristalis arbustorum Eristalis interrupta Eristalis similis Eristalis tenax Eumerus funeralis Eumerus ornatus Eumerus uncipes Eupeodes corollae Eupeodes latifasciatus Helophilus pendulus Heringia heringi Melanostoma mellinum Merodon albifrons Merodon equestris Merodon rufus Myathropa florea Neoascia podagrica Paragus pecchiolii Pipiza noctiluca Pipizella* sp. *Pipizella viduata Sphaerophoria infuscata Sphaerophoria scripta Syritta pipiens Syrphus ribesii*

Megachile apicalis Megachile centuncularis Megachile circumcincta Megachile ericetorum Megachile flabellipes Megachile pilidens Megachile pusilla Megachile rotundata Osmia andrenoides Osmia aurulenta Osmia bicornis Osmia caerulescens Osmia erythrogastra Osmia latreillei Osmia rufohirta Osmia sp. 1

Syrphus vitripennis Xylota segnis

Table S6.4: Summary table of the variables measured in the three habitat types (mean and SD). Abbreviations are: "Wild poll α-div" for wild pollinator α-diversity, "Flower cover" for flowering plant cover, "Flower α-div" for flowering plant α-diversity, "Honey bee ab" for managed honey bee abundance (honey bee-related ESs), "Ground arth ab" for ground-dwelling arthropod abundance (ground-dwelling arthropod-related ESs), "Cat pred rate" for dummy caterpillar predation rate (pest control), "Seed pred rate" for seed predation rate (seed predation), "Mosq egg ab (ref)" for Asian tiger mosquito egg abundance (reflected) (disease control), "TBI S" for soil stabilisation factor S and "TBI k" for soil decomposition rate k (soil nutrient cycling), and "Inf rate" for water infiltration rate in soil (flood control).

Habitat	Wild poll	Flower	Flower	Honey	Ground	Cat pred	Seed pred	Mosquito	TBIS	TBI k	Inf rate
type	α -div	cover	α -div	bee ab	arth ab	rate	rate	egg ab (ref)			
Crop field	8.94	6.44		4.31	317.56	0.26	0.68	92.22	0.23	0.02	34.63
margin	(3.83)	(3.19)	(3.16)	(4.41)	212.32	(0.19)	(0.18)	(79.24)	(0.06)	(0.01)	(39.67)
Semi-natural	8.66	19.09	12.53	23.31	223.06	0.38	0.71	70.72	0.26	0.02	51.81
patch	(4.8)	(12.9)	(4.48)	(39.04)	160.24	(0.16)	(0.18)	(104.49)	(0.05)	(0.01)	(53.37)
Urban green	6	13.34	9.75	20.28	140.34	0.2	0.51	114.34	0.26	0.02	40.94
area	(3.37)	(7.17)	(3.7)	(22.6)	87.73	(0.14)	(0.21)	(91.02)	(0.07)	(0.01)	(34.5)

Table S6.5: Model outputs for the multiple threshold analysis, testing the effect of habitat type, between *a)* crop field margins and semi-natural patches, *b)* crop field margins and urban green areas, and *c)* semi-natural patches and urban green areas. Values in bold indicate significant thresholds (*p* value < 0.05).

Threshold	Estimate	SE	Statistic	<i>p</i> value
$\mathbf{1}$	0.018	0.006	3.068	0.003
$\overline{\mathbf{c}}$	0.016	0.006	2.627	0.010
$\overline{\mathbf{3}}$	0.017	0.007	2.338	0.022
$\overline{4}$	0.016	0.008	2.005	0.048
5	0.018	0.009	2.028	0.045
6	0.012	0.009	1.385	0.169
7	0.013	0.008	1.524	0.131
8	0.013	0.009	1.426	0.157
9	0.015	0.010	1.527	0.130
10	0.014	0.010	1.373	0.173
11	0.010	0.010	0.953	0.343
12	0.013	0.010	1.260	0.211
13	0.013	0.011	1.258	0.212
14	0.013	0.011	1.206	0.231
15	0.014	0.011	1.269	0.208
16	0.020	0.011	1.804	0.074
17	0.019	0.010	1.855	0.067
18	0.015	0.010	1.448	0.151
19	0.015	0.010	1.478	0.143
20	0.014	0.011	1.286	0.202
21	0.007	0.011	0.657	0.513
22	0.011	0.011	0.984	0.328
23	0.007	0.012	0.546	0.586
24	0.005	0.012	0.441	0.660
25	0.004	0.012	0.298	0.766
26	0.003	0.012	0.236	0.814
27	0.000	0.012	0.021	0.984
28	-0.002	0.013	-0.155	0.877
29	-0.004	0.013	-0.342	0.733
30	-0.006	0.013	-0.491	0.625
31	-0.004	0.013	-0.280	0.780
32	-0.001	0.013	-0.058	0.954
33	0.003	0.013	0.235	0.815
34	0.007	0.013	0.574	0.568
35	0.008	0.013	0.600	0.550
36	0.006	0.013	0.479	0.633
37	0.007	0.012	0.559	0.577
38	0.005	0.013	0.368	0.713
39	0.002	0.013	0.131	0.896
40	0.001	0.013	0.101	0.919
41	0.004	0.013	0.285	0.776
42	0.004	0.013	0.281	0.779
43	0.008	0.014	0.549	0.584
44	0.006	0.012	0.491	0.624

Table S6.6: Model output for the multiple threshold analysis testing the effect of flower cover on the number of functions maximized at each threshold. Values in bold indicate significant thresholds (*p* value < 0.05).

Figure S6.1: Map of the 96 sampling sites. Imagery © 2023 TerraMetrics, Map data © 2023 Google.

Figure S6.2: Boxplots showing the relationships between habitat type and *a)* wild pollinator α-diversity and *b)* averaged EMF. Points represent raw data points.

Figure S6.3: Effect of flower cover on multiple threshold EMF. Panel *a)* shows the relationship between flower cover and the number of functions that performed higher than a certain threshold. We considered the full range of thresholds, from 1% to 99%, and each line represents a given threshold. Panel *b)* shows the slope of the relationship between flower cover and the number of functions reaching a certain threshold. Black points represent fitted values and the shaded areas represent the 95% confidence intervals. For each threshold, the relationship with flower cover is significant only if the confidence interval does not overlap 0.

Figure S6.4: Correlation matrices for pollinator α-diversity, flower cover, flowering plant α-diversity and ES indicators based on Pearson's correlation in the three habitat types, *i.e.*, *a)* crop field margins, *b)* semi-natural patches, and *c)* urban green areas. Right-oriented blue ellipses indicate positive correlations, while left-oriented red ellipses indicate negative correlations. Narrower ellipses indicate stronger correlations. Only significant correlations (*p* value < 0.05) are displayed. Abbreviations are: "Wild poll α-div" for wild pollinator α-diversity, "Flower cover" for flowering plant cover, "Flower α-div" for flowering plant α-diversity, "Honey bee ab" for managed honey bee abundance (honey bee-related ESs), "Ground arth ab" for ground-dwelling arthropod abundance (ground-dwelling arthropod-related ESs), "Cat pred rate" for dummy caterpillar predation rate (pest control), "Seed pred rate" for seed predation rate (seed predation), "Mosq egg ab (ref)" for Asian tiger mosquito egg abundance (reflected) (disease control), "TBI S" for soil stabilisation factor S and "TBI k" for soil decomposition rate k (soil nutrient cycling), and "Inf rate" for water infiltration rate in soil (flood control).

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