**High pollinator population connectivity in heavily disturbed landscapes: substantial gene flow despite large urban areas and intensive agriculture in two hoverflies**

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Potential destinations:

Landscape and Urban Planning (8000 words with refs; IF: 8.1)

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**ABSTRACT**

**KEYWORDS**

Landscape genetics; Spatial ecology; Diptera; Urbanization; Machine learning

# INTRODUCTION

**Pollinators provide a key ecosystem service to agricultural crops and wild plants, and their importance for food security is widely acknowledged (Potts et al., 2015).** It has been estimated that, globally, the economic value of pollination is worth a total of €153 billion (Gallai et al., 2009). The vast majority of European crops and of temperate wildflowers benefit from insect pollination by, in particular, bees (Anthophila) and hoverflies (Syrphidae) (Potts et al., 2015). Besides being essential to the maintenance of plant diversity, pollinators also provide enormous added-value by indirectly supporting an immense range of other organisms, from microbes and parasites, to specialist predators, herbivores, fruit- and seed-eating animals, among others (Ollerton, 2017). The maintenance of pollinator abundance and diversity is therefore of critical importance for both ecosystems and agricultural services. However, evidence of the loss of pollinators is clear-cut: wild pollinators are declining at local, regional and global scales, in both diversity and abundance. Numerous species are threatened with extinction, primarily as consequence of human activities (Gill et al., 2016; Ollerton, 2017; Potts et al., 2016). This is a serious cause for concern because pollinators are an integral part of ecosystems and their precipitous decline presents a crisis for food security and human wellbeing.

**Pollinator declines are frequently attributed to multiple interacting causes.** The main underlying drivers are the intensification of land-use, climate change, and the spread of invasive species and parasites/pathogens (Dicks et al., 2021; Gill et al., 2016; Vanbergen et al., 2013). Especially land-use change and the resulting habitat loss and homogenization are often seen as major individual factors causing the problem (Vanbergen et al., 2013). The spread of urban areas and the intensification of agriculture have resulted in the destruction and fragmentation of many of the natural habitats that pollinators depend on for feeding and nesting resources (Potts et al., 2010; Vanbergen et al., 2013). While it appears that the rapid man-made landscape alterations of recent decades were associated with declines in the species richness of insect pollinators (Senapathi et al., 2015), there is a considerable lack of knowledge on the mechanisms underlying the responses of invertebrate pollinators to land-use change (Winfree et al., 2011). This makes it difficult to reliable quantify the interactive effects with other drivers of decline and to develop effective approaches to conserve pollinator populations and the associated ecosystem services (Gill et al., 2016).

**Dispersal capability is a key life-history trait affecting an organism’s ability to deal with habitat fragmentation.** It is required to maintain connectivity between distant habitat patches, to colonize new habitats and to allow re-colonization after local extinction. It thus impacts species distribution, community structure, (meta-)population dynamics, gene flow and extinction risk (Bowler and Benton, 2005). Species with high dispersal ability generally are better able to move efficiently between suitable habitat patches and may exploit fragmented resources more efficiently (Öckinger et al., 2010). Beyond a species’ intrinsic dispersal ability, however, dispersal between remnant habitat patches will be influenced by the functional connectivity of the landscape, which refers to how the behavior of an organism is affected by the distance between patches and the composition of the intervening habitat matrix (Baguette and Van Dyck, 2007; Jauker et al., 2009).

**We only have a limited understanding of the dispersal ability of most insect pollinators and about their functional connectivity in fragmented habitats (Dicks et al., 2013; Vanbergen et al., 2013)**. Specifically, further insights are needed into distances moved in different landscapes as well as the features and environmental factors that hinder or facilitate movement through the habitat matrix (Dicks et al., 2013; Gill et al., 2016; Vanbergen et al., 2013). A particular difficulty with evaluating the impact of land-use change relates to the fact that flying ability differs significantly between different insect pollinator species (Greenleaf et al. 2007). Even closely related species can respond differently to habitat fragmentation (Jauker et al., 2009; Steffan-Dewenter et al., 2002). Further studies on the impact of fragmentation on different pollinator groups/species in contrasting landscapes are thus needed. These would be of key importance for answering questions relative to the landscape structure and composition necessary to support insect pollinators, as well as the geographic scale at which maintenance measures should be implemented.

**One important group of plant pollinators are hoverflies (Syrphidae), a biologically diverse family of flower-visiting flies (Bickel et al., 2009; Speight, 2017; Wardhaugh, 2015).** Adults feed on nectar to gain energy and adult females on pollen to gain nutrients for egg production (van Rijn and Wäckers, 2016; Wäckers and van Rijn, 2012). Species do not display strict selectivity for specific flower species (Branquart and Hemptinne, 2000; Lucas et al., 2018). However, preferences do exist (Cowgill et al., 1993), and these preferences have an effect on hoverfly fitness (Amorós-Jiménez et al., 2014; Laubertie et al., 2012; van Rijn and Wäckers, 2016). Their dependence on floral resources makes hoverflies the most important pollinators besides bees, providing a major contribution to plant diversity and agricultural production (Hodgkiss et al., 2018; Jauker et al., 2009; Pekas et al., 2020; Rader et al., 2016; Ssymank et al., 2008). Hoverfly larvae use a diverse array of habitats and feeding modes, including fungal fruiting bodies, nests of social Hymenoptera, decaying wood, dung and different water bodies. Many larvae also feed on aphids and are very effective biocontrol agents, especially in agricultural landscapes (Speight, 2017). Given the ecological and economic importance of hoverflies, it would thus be important to gain a more thorough understanding of their movement ecology in fragmented landscapes.

**Little is known about dispersal of hoverflies in general and the effects of landscape fragmentation on their dispersal in particular.** In Europe, some 30 species migrate southwards in the autumn, some covering long distances and crossing mountain ranges in the process (Aubert and Goeldlin de Tiefenau, 1981; Gatter and Schmid, 1990; Lack and Lack, 1951; Odermatt et al., 2017; Wotton et al., 2019) likely using the sun as a compass (Massy et al., 2021). The majority of hoverfly species, however, are non-migratory (Keil et al., 2008; Schweiger et al., 2007; Speight, 2017) and not much is known about their intrinsic dispersal ability. Schweiger et al. (2007) assumed that hoverflies with large body sizes had high dispersal abilities. In a mark-recapture study on the aspen hoverfly (Hammerschmidtia ferruginea, Fallén 1817), Rotheray et al. (2014) found wing length to be positively correlated with dispersal, but only in males. There is also little knowledge about dispersal distances. While Rotheray et al. (2014) recovered some H. ferruginea individuals at up to 5 km from the release site, during their normal foraging activity, hoverflies move a few hundred meters at most and tall vegetation, bare soil (dirt tracks, asphalt roads or ploughed fields) can act as barriers (Lövei et al., 1998; Wratten et al., 2003). Studies investigating hoverfly richness in relation to habitat patch isolation suggest that hoverflies are significantly impacted by habitat fragmentation (Jauker et al., 2019; Moquet et al., 2018; Ouin et al., 2006).

**Molecular genetic methods are powerful tools to investigate the effect of fragmentation on target species where dispersal capability cannot be studied directly, or only with great difficulty.** In particular, investigating the spatial organization of genetic variation can help to clarify the degree of isolation of different habitat patches and identify landscape elements that hinder or facilitate gene flow (Holderegger and Wagner, 2006; Manel et al., 2003; Manel and Holderegger, 2013; Peterman, 2018). Frequently, abrupt genetic discontinuities are linked with elements in the landscape that may disrupt dispersal in a species of interest. For example, motorways and large water bodies can act as gene flow barriers for different vertebrate (Frantz et al., 2012, 2010) and insect species (Pérez-Espona et al., 2012; Vandergast et al., 2009). However, methods that detect abrupt genetic discontinuities can provide only limited information on how animals move through a landscape. By statistically relating the genetic distance, or relatedness, to landscape characteristics, it is possible to relate gene-flow patterns to landscape structure and develop rigorous empirical models of the functional connectivity of a landscape (Peterman, 2018).

**There are only very few studies that use genetic methods to investigate the effect of habitat fragmentation on dispersal of insect pollinators, particularly at the landscape scale.** Studies on hoverflies either looked at large spatial scales and/or did not statistically evaluate the effect of environmental features on dispersal (Raymond et al., 2013; Schauer et al., 2018). Nevertheless, the results from work on Apiformes suggest that even good dispersers can be impacted by habitat fragmentation. Bumblebee (Bombus) species normally exhibit very little genetic structure at smaller spatial scales (Dreier et al., 2014; Lozier et al., 2011), and sometimes even at very large scales . However, impervious cover associated with built-up areas significantly limited gene flow in a North American bumblebee (Jha and Kremen, 2013). Even at larger spatial scales, urban areas can be a substantial gene flow barrier for rare pollinators (Davis et al., 2010).

**Because of demographic growth, land use change for new infrastructure and urban development is expected to be considerable.** This, in turn, will lead to further loss and fragmentation of natural and semi-natural habitats (Jaeger & Madrinan 2011). Luxembourg has recognised that habitat loss and fragmentation are threatening its biodiversity in general and insect pollinators in particular. Key strategies to counteract the negative effects of habitat fragmentation include the design of a network of ecological corridors as well as land set-a-side to support pollinators within the agricultural landscape (Ministère du Développement durable et des Infrastructures 2017). In order for these mitigating measures to be successful, however, it is important to understand the functional connectivity of the landscape from the viewpoint of the pollinator (Dreier et al., 2014; Rands, 2014).

**In this study, we investigate the genetic structure of two species of hoverflies as well as how landscape features affect their genetic connectivity in urbanized landscapes.** First, we describe the genetic clustering and patterns of isolation-by-distance (IBD) of *S. pipiens* and *M. florea*, based onthousands of individuals in two Western Europe urban centers. We expect some genetic structure and IBD at the landscape scale due to the large extent and the anthropogenic nature of the study areas. If connectivity is enabled by unexpectedly large population sizes or unforeseen facilitation of dispersal by anthropogenic features, both genetic structure and IBD are expected to be weak. Second, we identify which landscape features are key in determining connectivity in each species, in each focal urban area, based on a machine-learning optimization algorithm, given the large gaps in expert knowledge regarding dipteran pollinator connectivity. We predict that parts of the landscape with large impervious surfaces would constitute a stronger barrier for *S. pipiens*, due to its much smaller size and XXXdispersal capacity. Similarly, we predict that although it could promote connectivity in both species, higher forest cover could facilitate gene flow in *M. florea* more than in *S. pipiens* due to higher habitat preference. Finally, to understand how general the relationships between gene flow and structural connectivity are across hoverfly species and parts of their ranges, we evaluated model transferability between species (same study area) and between study areas (same species). We predict lower model transferability between study areas, relative to between species, due to the generalist nature of the two species but the homogenization of biodiversity due to disturbances associated with urbanization and peri-urban intensive agriculture could enhance overall model transferability.

# METHODS

## | Study areas, study organisms, and sampling

To ensure successful We chose two hoverfly species likely to occur across the whole study areas based on preliminary field experience and previous inventories. Syritta pipiens (Linnaeus, 1758) is a widespread

Occurrence: Widespread and abundant. MNHNL: 14th most common species; the species has been trapped in different suburban areas of Cologne; Flight time NL/B: April to October, with peaks in abundance in June to September. Identification: Unmistakable, greatly enlarged hind femora, thorax dusted ash-grey. Wing length: 4.25-7 mm; Preferred habitat: wetland, most farmland, suburban gardens and urban parks. Larvae: live in moist, decaying, vegetable matter, including cow dung and garden compost heaps.

## | Laboratory procedures

## | Genetic diversity, clustering and isolation-by-distance

## | Landscape genetics approach

## | Optimization of resistance surfaces and model selection

## 2.6 | Model transferability

# RESULTS

## | Genotyping and filtering

## | Genetic diversity, clustering and isolation-by-distance

## | Single environmental surface optimizations

## | Composite environmental surface optimizations

## | Properties of the best surface

## | Model transferability

# DISCUSSION

## | High large-scale population connectivity

We did not find evidence for large-scale spatial genetic structure in either hoverfly species. STRUCTURE analyses always supported *K* = 1 genetic cluster.

, but we did find some fine-scale spatial genetic structure.

## | Constraints on gene flow within urbanized landscapes

## | Implications for hoverfly biodiversity and pollination services

## | Methodological limits and future directions

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# SUPPLEMENTARY MATERIAL