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# Semi-natural areas adjacent to vineyards increase the abundance of Hymenoptera parasitoids in a hill wine-growing area of Northern Italy

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## Abstract

Hymenoptera parasitoid communities were studied using Malaise traps in a hill wine-growing area of Northern Italy, dominated by extensive viticulture. Parasitoid abundance data were correlated with landscape composition around vineyards using geospatial analysis. A remarkable parasitoid fauna, comprising 71 taxa across families and subfamilies, was recorded, with Ichneumonidae (18%), Diapriidae (14%), Braconidae (11%), Mymaridae (9%), and Scelionidae (8%) being the most represented. Semi-natural habitats within 200 m were strongly associated with the abundance of several Hymenoptera taxa, including five families and six subfamilies. *Lobesia botrana* (EGVM) infestation was negatively correlated with the proportion of semi-natural habitats within 200 m, while parasitisation was not correlated with any of the landscape metrics tested at 200, 500, or 1000 m (vineyards and orchards, semi-natural, anthropised areas, and meadows and arable crops). Parasitoids emerged from collected EGVM larvae belonged to the genus *Diadegma* (Ichneumonidae, Campopleginae). These results highlight the importance of nearby semi-natural habitats as refuges for parasitoid diversity in viticultural landscapes. Integrating spatial scale with the ecological requirements of target taxa is crucial for promoting conservation strategies that support specific functional groups, in this case Hymenoptera parasitoids.

## Key Words

European grapevine, GIS analysis, Ichneumonidae, *Lobesia botrana* infestation, parasitoid wasps, semi-natural areas, vineyard

## Introduction

Viticulture has experienced a steady global growth over the past 30 years (Daane et al. 2018a). At the same time, the wine sector has become increasingly demanding of safer products, emphasizing the need to reduce chemical inputs, a principle advocated by EU policies such as the Farm to Fork Strategy (Cortignani et al. 2022), and promote functional taxa capable of providing multiple ecosystem services. In countries characterized by a long-standing viticultural tradition and the production of high-quality wines, the landscape is often dominated by vineyards. Many of these areas lie within regions of high natural value, shaped by Mediterranean biomes, usually associated with global biodiversity hotspots (Myers et al. 2000; Cuttelod et al. 2008). Although vineyards are crops potentially subjected to a relatively high input loads due to various phytosanitary problems (i.e., invasive species, pest infestations and diseases, insect vectors), they have a long-standing tradition in the development of management tools and practices aimed at restoring and maintaining functional biodiversity at a farm level (e.g. Duso et al. 2004; Altieri et al. 2010; Lucchi et al. 2019). Among farm habitat management techniques, ground cover, including the associated conservation and sowing practices, represents one of the most widely applied and validated approaches, demonstrating the potential to promote multiple ecosystem services (Berndt et al. 2006; Winter et al.

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2018; Daane et al. 2018b; Garcia et al. 2018; Zanettin et al. 2021; Di Giovanni et al. 2024). Some covers can positively affect vineyard pests, by changing nitrogen concentration (Muscas et al. 2017), however such response may be complex, as influenced by environmental conditions, soil, grape vigor and cultivar.

An increase in the proportion of non-cultivated areas within agroecosystems is generally positively correlated with the abundance and diversity of beneficial arthropods, as evinced by review papers on the relationship between pest natural enemies and landscape factors and/or connectivity (Chaplin-Kramer et al. 2011; Veres et al. 2013; Rusch et al. 2016). Natural and semi-natural habitats surrounding agroecosystems can enhance populations of beneficial insects by providing alternative hosts, nectar and pollen for adult parasitoids, overwintering sites and shelter when field conditions are unfavorable (e.g. Bianchi et al. 2006; Winkler et al. 2006; Tylianakis et al. 2008; Fahrig et al. 2011).

Despite this substantial body of evidence supporting the role of landscape complexity in promoting natural enemies, generalizations remain difficult and sometimes ambiguous: for example, crop pest and natural enemy species can interact differently with landscape composition, generating variable patterns and heterogeneity in species responses (Karp et al. 2018). It is thus advisable to gather data on the effects of landscape patterns on beneficial insects across a wide range of crops and geographical contexts, in order to detect specific and targeted effects.

Besides a strong interest in local vineyard management, as mentioned above, landscape diversity surrounding wine-growing areas can also play a key role in functional biodiversity conservation, providing ecosystem services (Thomson and Hoffmann 2009, 2010) and reducing insecticide inputs (Etienne et al. 2023). Moreover, in vineyard agroecosystems, landscape diversity may mediate, and in many cases outweigh, the influence of local diversification (Wilson et al. 2017).

A crucial aspect concerns the spatial scale at which landscape elements influence vineyard biodiversity – that is, the distance at which semi-natural habitats can affect functional biodiversity within vineyards. Compared to other cropping systems, relatively few studies have investigated these spatial effects in viticulture (Thomson and Hoffmann 2009, 2010; Altieri et al. 2010; Guenser et al. 2020; Zielonka et al. 2024). Existing evidence suggests that the influence of ecological infrastructures on functional diversity and potential pest control varies widely in relation to the distance of surrounding habitats, the geographic context, farm management, and particularly the target taxa, which may respond differently according to their mobility and body size. For example, in Napa Valley (USA), Hogg and Daane (2011) reported that oak woodlands surrounding vineyards increased the richness and abundance of local spider communities while reducing populations of the invasive spider *Cheiracanthium mildei* Koch, 1864 (Araneae, Cheiracanthiidae). In contrast, Rusch et al. (2015) observed no effect of landscape complexity on parasitoids within a radius of 1 km in Southern France vineyards. Conversely, semi-natural elements such as hedgerows adjacent to vineyard have repeatedly been shown to act as important reservoirs of alternative hosts for *Anagrus* spp. (Hymenoptera, Mymaridae), key parasitoid of leafhoppers in vineyards (Altieri et al. 2005; Wilson et al. 2017).

Understanding the spatial (or buffer) effect, in other words the range of influence of infrastructures surrounding vineyards, is therefore essential for predicting their potential contribution to functional biodiversity and for assessing the role that specific taxa may play in pest control. This knowledge allows local management practices to be tailored to the particular type of landscape context surrounding the vineyard. Furthermore, insights into the spatial effects of semi-natural habitats can support landscape planning within agro-environmental schemes, such as those promoted under the Nature Restoration Law (http://data.europa.eu/eli/reg/2024/1991/oj).

The main aim of this study was to investigate Hymenoptera parasitoids given their ecological importance as biological control agents of numerous agricultural pests, including key vineyard species. These beneficial taxa have also been the focus of a number of habitat management strategies on this crop aimed at enhancing parasitism rates (Begum et al. 2006; Berndt et al. 2006; Mansour et al. 2016; Hoffmann et al. 2017; Möller et al. 2020).

Specifically, the objective of this research was to assess the influence of semi-natural areas on Hymenoptera parasitoid communities and to identify the spatial scale at which these effects are most pronounced. We hypothesized that the presence of semi-natural habitats would positively influence parasitoid assemblages, although this effect may vary among families. Since many parasitoids – especially oophagous species – are very small and have limited flight-control abilities, relying largely on wind for dispersal (Strickland et al. 2017), we expected these effects to be detectable at a relatively fine spatial scale, particularly at the farm-level landscape.

# Materials and methods

## Vineyards

The study was conducted in the Colli Bolognesi hill near Bologna (Northern Italy), an area of notable viticultural importance that includes several Protected Designation of Origin (PDO) wines; among these, Pignoletto represents one of the most widely cultivated varieties. The landscape of this cultivation area is characterized by an extensive network of semi-natural habitats, including some protected areas, and by comparatively lower infestations of the European grapevine moth (EGVM), *Lobesia botrana* (Denis & Schiffermüller, 1775) (Lepidoptera, Tortricidae) and reduced pesticide inputs compared to surrounding lowland vineyards. These features make the area a relatively low-intensity wine-growing system, of-

fering favorable conditions for studying the relationship between semi-natural habitats and vineyard biodiversity.

The study was conducted in six pilot wine-growing farms (Table 1, Fig. 1) selected for their importance in local viticulture. A seventh vineyard (Molinari), located in a more lowland area, was included only for the assessment of EGVM infestation and associated parasitism.

The farms were selected to maximize variation of the semi-natural habitat density around each site. Only vineyards with well-documented management practices, monitored through the phytosanitary assistance programme of the Centro Agricoltura e Ambiente G. Nicoli (Crevalcore), were considered, as this guaranteed consistent information for the study. Besides these methodological aspects, farmers' willingness to implement an insect monitoring plan was also considered in the selection of the farms.

## Faunistic analysis

Insect sampling was carried out using Malaise traps (Fig. 2) (Skvarla et al. 2021). In each farm, two traps were set along the edge of a vineyard, near boundary hedges or other perimeter features. The edge position of the Malaise traps was also chosen with the aim of not hindering the passage of agricultural machinery and other farming equipment. The Malaise traps used were black and white colored and made of synthetic fiber. Each Malaise was 120 cm high, 150 cm long and 100 cm deep, and was activated with a 70% alcohol solution. The traps were active two weeks per month, from the beginning of June to the first half of October, for a total of seventy days of active insect collection. The insects collected were taken to the laboratory for identification every fifteen days.

Hymenoptera were identified to the family and subfamily level. Subfamily identification was chosen for Ichneumonidae (Broad et al. 2018) and Braconidae (van Achterberg, 1993), due to the exceptional diversity of these taxa and because of their importance in attacking many agricultural pests. Indeed, subfamily identification can enable interpretation of parasitisation of pest taxa, including, for example, EGVM (Scaramozzino et al. 2017, 2018).

Hymenoptera data collected in each farm were expressed as mean total abundance per trap per days of trap activation (mean abundance per trap $^{-1}$ per day $^{-1}$). In this way, each family and subfamily was described by an abundance parameter which took into account the sampling effort, allowing the standardization of data.

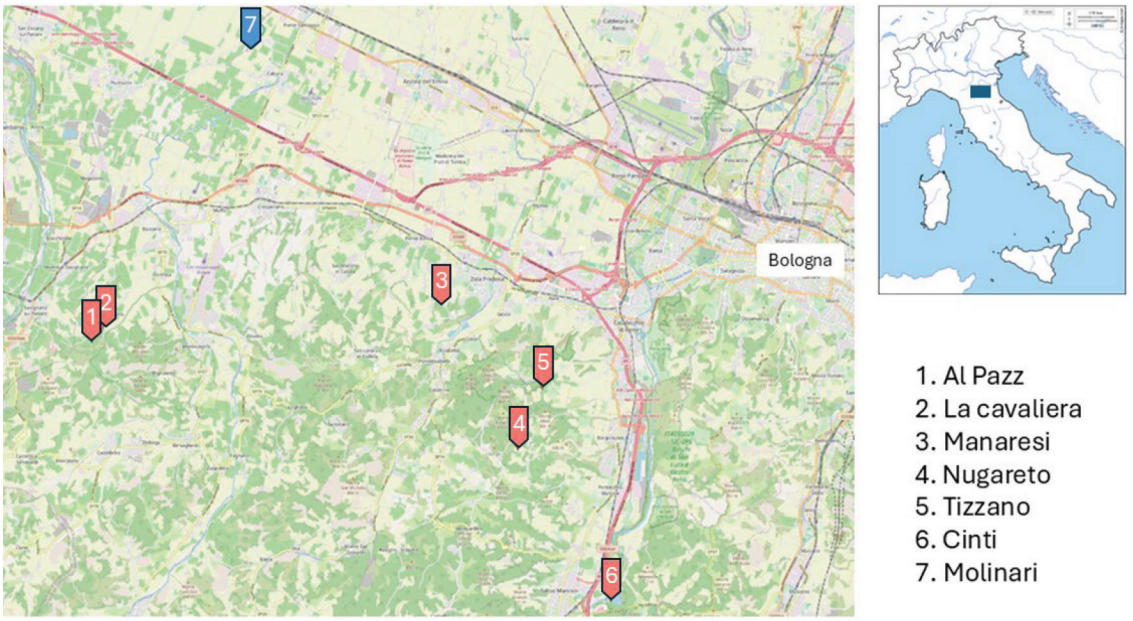



**Figure 1.** Location of the seven vineyards included in the study. Details on each site are provided in Table 1. In red the vineyards sampled both with Malaise traps and for EGVM parasitisation; in blue the vineyard sampled only for EGVM parasitisation.

**Table 1.** Main characteristics of the surveyed farms, including geographical coordinates, management type and predominant grape variety.

| Farm | Farm n. | GPS coordinates | Management | Prevalent wine variety |
|---|---|---|---|---|
| Al Pazz | 1 | 44°28'27.5"N, 11°03'28.1"E | IPM | Barbera |
| La Cavaliera | 2 | 44°28'38.0"N, 11°03'40.9"E | Organic | Albana |
| Manaresi | 3 | 44°29'06.5"N, 11°11'58.0"E | Organic | Pignoletto |
| Nugareto | 4 | 44°26'35.2"N, 11°13'49.9"E | Organic | Pignoletto |
| Tizzano | 5 | 44°27'38.3"N, 11°14'24.8"E | IPM | Merlot |
| Cinti | 6 | 44°23'57.7"N, 11°16'05.8"E | Organic | Pignoletto |
| Molinari | 7 | 44°33'36.5"N, 11°07'28.1"E | IPM | Pignoletto, Pinot bianco, Chardonnay |



**Figure 2.** Malaise trap with detail of the collecting jar.

## Landscape GIS analysis

Geospatial analysis was used to characterize the landscape features in the surroundings of each vineyard, based on metrics aimed at quantifying the presence and abundance of various habitats. The analysis was performed using ArcGIS 10 (ESRI) and the Land Use Database of the Emilia-Romagna Region 2008 ed. 2011, whose minimum mapped unit was 1.56 hectares. In particular, the analysis took into consideration the land use/land cover categories of the highest level of detail available in the regional geodatabase, i.e. the fourth level, which provides a further in-depth analysis into subclasses compared to the third level of the standard Corine Land Cover (CLC) legend. Therefore, the dataset allowed both a higher spatial resolution in terms of polygons digitization (1.56 hectares instead of 25 hectares minimum mapped unit), and a more specific classification, developed by considering territorial specificities of regional interest, compared to CLC datasets. Using proximity analysis in the GIS environment, to evaluate the effects of habitats on biodiversity at different scales, three concentric buffers were generated around the centroid of each vineyard, with radius equal to 200 m, 500 m and 1,000 m, covering an area of 12.56 ha, 78.5 ha, and 314 ha, respectively. Within each buffer, the land surfaces corresponding to each 4$^{th}$ level land use/land cover classes (as listed in the second column of Table 2) were calculated, by clipping land use polygons on each buffer, calculating the surface of each polygon using GIS geometry calculation tools, and summing the surfaces of all polygons with the same class in each buffer. Then these values were converted into percentages of territorial coverage, and subsequently summarized on the basis of the reclassification shown in Table 2, reorganizing land-use categories into habitat classes whose characteristics are known to be associated with biodiversity (Fig. 3).

## EGVM infestation

The first generation EGVM infestation and the associated parasitisation were assessed by collecting 400 randomly selected inflorescences in each vineyard. Inflorescences containing nests (also called glomerulae) with live larvae were considered infested. The sampling was carried out between the end of May and the first week of June.

**Table 2.** The classification of landscape categories.

| Reclassified categories | Original 4$^{th}$ level land use/land cover classes |
|---|---|
| Cultivated areas | Vineyards, orchards, other tree crops, areas mainly covered by agricultural crops with the presence of natural spaces, complex cultivation and parcel systems |
| Semi-natural areas | Non cultivated areas consisting of vegetation including both tree and shrub layers, herbeceous vegetation with shrubby and/or herbaceous vegetation with scattered trees, rivers and streams with riparian vegetation |
| Anthropised areas | Residential fabric, production settlements, other artificially modeled areas |
| Meadows and arable crops | Herbeceous vegetation including improved grasslands and arable crops |

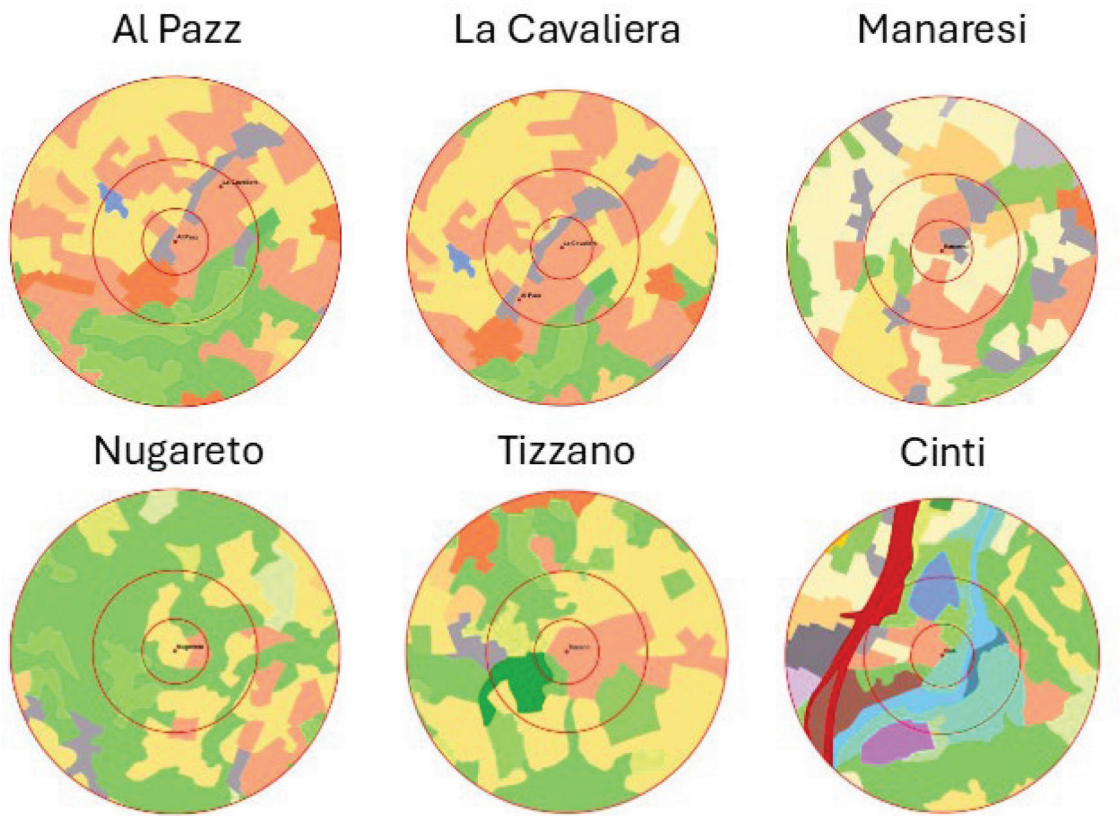



**Figure 3.** Landscape features of the six vineyards (From left to right farm N. 1, 2, 3, 4, 5, 6, see Table 1). Greens: semi-natural habitats; pinks: crops (orchards and vineyards); yellows: meadows and arable crops; blue: rivers and waterways; other colours include anthropised areas and streets.

The presence of the first larval generation was estimated using the phenological model implemented by the Regione Emilia-Romagna (2026). Infestation in each vineyard was estimated as the ratio between the number of infested inflorescences and the total number sampled. The first EGVM larval generation was selected to provide a reliable estimate of infestation intensity, for practical reasons. First of all, inflorescences can be easily detected and collected without production losses for growers; moreover, the first larval generation is not subjected to insecticide treatments, thus avoiding data bias due to control measures.

## EGVM parasitisation

Infested inflorescences were collected in plastic boxes to rear EGVM and potential parasitoids. To prevent mold formation, the boxes were equipped with metal mesh to keep the inflorescences raised and allow air circulation. Moreover, paper towels were positioned under the meshes to provide EGVM larvae with an appropriate substrate to pupate and to maintain suitable microclimatic conditions for their development. The boxes were wetted two to three times a week to ensure optimal humidity for EGVM development and were checked weekly to detect and count grapevine moth adults and/or parasitoids. Natural enemies were refrigerated and stored in Falcon tubes until their identification.

Parasitisation was estimated as the ratio between the number of emerged parasitoids and the total number of parasitoids and EGVM adults. This is also called apparent parasitisation since it does not account for potential hosts and parasitoid mortality.

## Data analysis

Canonical Discriminant Analysis (CDA) was performed on landscape metrics (Semi_Nat = % semi-natural areas; Cultiv = % vineyards and orchards; Mead = % permanent grassland and arable crops; Anthrop = % buildings and other anthropised areas), within each buffer range (200 m; 500 m; 1000 m) to explain trends and relationships among these variables and to detect those with the greatest discriminating power.

Redundancy Analysis (RDA) was used to correlate the contribution of landscape metrics (explanatory variables) within each buffer, to explain the abundances of Hymenoptera taxa (response variables).

This multivariate analysis aimed, given the high number of taxa involved in the analysis (more than 60), to select the most descriptive metric and buffer to be used in the subsequent statistical analysis. Indeed, this study adopts a pattern-oriented approach, focusing on identifying consistent ecological gradients rather than fitting predictive parametric models.

In this way, after the selection of the most relevant variables for explaining Hymenoptera parasitoid abundances, the landscape metric within the most predictive buffer range was correlated with the abundances of Hymenoptera families and subfamilies by means of non-parametric Spearman correlation test. It is worth noting that Spearman rank correlation coefficients - or Spearman's $\rho$ values - were not used as independent hypothesis tests but as a descriptive tool to rank and weight the contribution of the landscape metric(s) to explaining the Hymenoptera taxa abundances. In our analysis, the abundances of Hymenoptera taxa (families and subfamilies), expressed as counts of individuals, were treated as response variables. The explanatory variables were the landscape metrics (e.g. percentage of habitat types) calculated within the buffer identified as most predictive through multivariate approach.

The Spearman test was used also to correlate the most descriptive landscape metric and buffer against infestation and parasitisation of the first EGVM generation. Infestation and parasitisation levels of the first EGVM generation were also treated as response variables and were correlated with the landscape metric and buffer that emerged as most descriptive from the multivariate analyses.

Statistical analyses were performed with R 4.4.3 (R Core Team 2026), in particular, the Canonical Discriminant Analysis (CDA) was conducted using the "*candisc*" package, whereas the Redundancy Analysis (RDA) was performed using the "*vegan*" package. Statistica version 10 (StatsoftTM, Tulsa, OK, USA) was used for all non-parametric correlation analysis. Data visualization was implemented using the "*plotly*" package (Sievert 2020).

# Results

## Faunistic analysis

A total of 10,356 Hymenoptera parasitoid specimens belonging to 32 families were collected from the 12 Malaise traps over the 70-day monitoring period (Fig. 4). The most representative families, in decreasing order, were: Ichneumonidae (19%), Diapriidae (14%), Braconidae (11%), Mymaridae (9%), Scelionidae (8%) and Eulophidae (6%); the other families accounted for relative abundances lower than 5%. Further identification of Ichneumonidae and Braconidae revealed 24 and 17 subfamilies, respectively. Among Ichneumonidae, Cryptinae (35.6%), Campopleginae (17.2%) and Oxytorinae (9%) were the most represented subfamilies, while within Braconidae Alysinae (32.6%), Microgastrinae (21.8%), Blacinae (11.7%) and Aphidiinae (11.2%) were the most abundant.

## Landscape GIS analysis

The preliminary analysis performed with CDA and RDA was used to select the buffer range and the landscape metric that best explained the Hymenoptera family abundances. First, CDA calculated on landscape metrics showed lower canonical scores of the first canonical discriminant function (Can 1) within 200 m buffer compared with those calculated for 500 m and 1000 m buffers (Fig. 5, left panel). In other words, the first canonical function clearly separates the 200 m buffer from the 500 m and 1000 m buffers, while the latter two groups are less distinctly separated, providing the same information (Fig. 5). Moreover, CDA structure (Fig. 5, right panel) of Can 1 represents the Pearson correlation coefficients between each original variable and the canonical discriminant function. They therefore indicate how strongly each variable is associated with the canonical axis and are dimensionless because they are standardized by definition. In particular, Semi_Nat shows the strongest positive correlation with Can1, while Anthrop and Mead show moderate positive correlations; instead, Cultiv exhibits a strong negative correlation with Can1. Thus, structure analysis demonstrated higher discriminating power for Semi_Nat and Cultiv, which are clearly negatively correlated. Landscape features of the farms are shown in Fig. 3.

RDAs performed on Semi_Nat and Cultiv within the different buffers demonstrated that 200 m buffer (constrained inertia = 71.6%) better explained the abundances of Hymenoptera taxa than 500 m (constrained inertia = 17.4%) and 1000 m (constrained inertia = 16.6) buffers (Table 3). Eigenvalues for constrained axes of RDAs calculated on the different buffers are shown in Table 4.

**Table 3.** Model summary for RDA calculated on the different buffers (200-500-1000 m). Response variables: abundances of Hymenoptera taxa; explanatory variables: 1. Semi_Nat (semi-natural habitats); 2. Cultiv (vineyards and orchards).

| Buffer (m) | Inertia | Proportion (%) |
|---|---|---|
| 200 | 16.3 (total) | 100 |
| | 11.7 (constrained) | 71.6 |
| | 4.6 (uncostrained) | 28.4 |
| 500 | 16.3 (total) | 100 |
| | 2.8 (constrained) | 17.42 |
| | 13.5 (uncostrained) | 82.6 |
| 1000 | 16.3 (total) | 100 |
| | 2.7 (constrained) | 16.6 |
| | 13.6 (uncostrained) | 83.4 |

**Table 4.** Eigenvalues for constrained axes of RDA calculated on the different buffers (200–500–1000 m).

| Buffer (m) | RDA1 | RDA2 |
|---|---|---|
| 200 | 10.9 | 0.7 |
| 500 | 2.6 | 0.2 |
| 1000 | 2.5 | 0.2 |

Moreover, since RDAs plots (Suppl. material 1: figs S1–S3) showed that Semi_Nat correlated with abundances of most Hymenoptera families, this metric was selected for the further analysis with respect to Hymenoptera taxa. The vector Cultiv was in the opposite direction of Semi_Nat, demonstrating an inverse correlation between these two ecological metrics. The same results were ob-

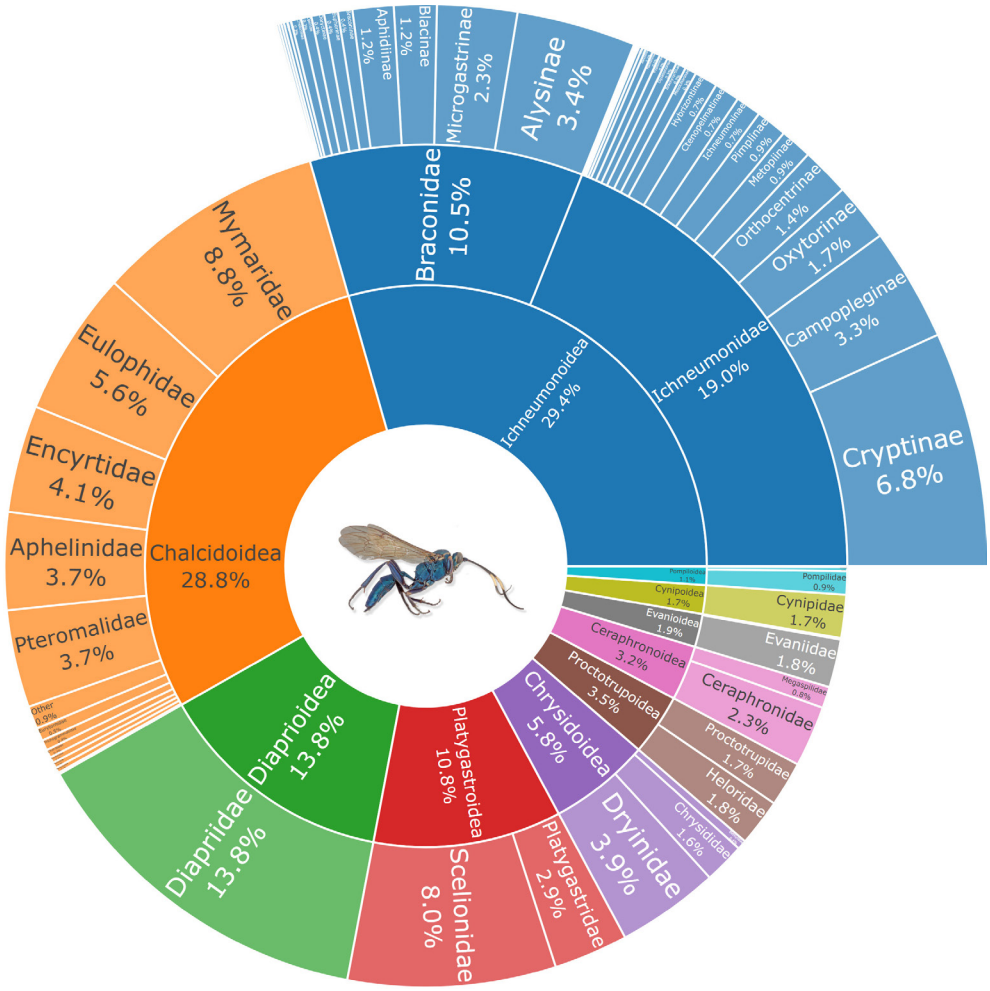



**Figure 4.** Relative abundances of Hymenoptera taxa collected in this study (N = 10,356). The sunburst diagram shows the hierarchical composition of the sampled community, with superfamilies in the inner ring, families in the middle ring, and subfamilies (when present) in the outer ring. Percentages indicate the proportion of each taxon relative to the total number of Hymenoptera specimens.

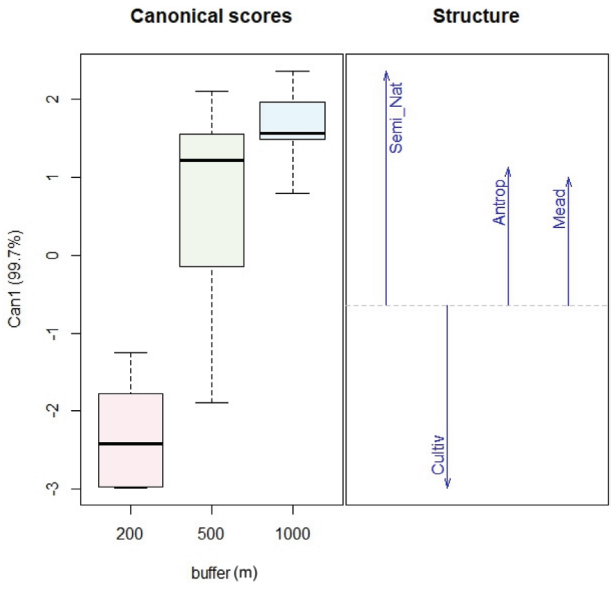



**Figure 5.** CDA canonical scores and structure of the landscape features (first axis) surrounding the vineyard within the three buffer ranges (m). Semi_Nat = %semi-natural areas; Cultiv = %vineyards and orchards; Anthrop = %anthropised areas including buildings and streets; Mead = %permanent meadows and arable crops.

tained with RDAs performed between Hymenoptera subfamilies and the same explanatory variables (not shown).

These analyses identified "semi-natural habitats within 200 m" as the most informative parameter for Spearman correlations with the abundances of Hymenoptera families and subfamilies.

## Relationship between Hymenoptera taxa abundances and landscape metrics

This Spearman correlation analysis generated a correlation matrix, whose $\rho$ values were used to rank the relative contribution of this metric for explaining the taxa abundances (Table 5). Most correlations showed positive $\rho$ values; only 4 taxa displayed negative $\rho$ values (Heloridae, Brachistinae, Miracinae, Banchinae), although not statistically significant.

A number of taxa displayed $\rho$ Spearman values > 0.60, which conventionally is considered a strong monotonic association between insect taxa and landscape metrics, including 11 families and 13 subfamilies (Table 5). Of these, 5 families and 6 subfamilies were characterized by significant

**Table 5.** Spearman $\rho$ and related P values from correlations between "200 m semi-natural habitats" and Hymenoptera families and subfamilies. Only taxa with $\rho$ values ≥ 0.60 are presented.

| Taxa | Taxonomic status | $\rho$ | P |
|---|---|---|---|
| Bethylidae | Family | 0.61 | 0.192 |
| Elasmidae | Family | 0.69 | 0.124 |
| Aulacidae | Family | 0.69 | 0.124 |
| Chrisididae | Family | 0.68 | 0.130 |
| Ceraphronidae | Family | 0.69 | 0.122 |
| Braconinae | Subfamily (Braconidae) | 0.70 | 0.115 |
| Other Chalcidoidea | Various families | 0.70 | 0.115 |
| Cynipoidea | Superfamily | 0.70 | 0.115 |
| Encyrtidae | Family | 0.70 | 0.115 |
| Euphorinae | Subfamily (Braconidae) | 0.70 | 0.115 |
| Hybrizontinae | Subfamily (Ichneumonidae) | 0.70 | 0.115 |
| Ichneumoninae | Subfamily (Ichneumonidae) | 0.70 | 0.115 |
| Metopinae | Subfamily (Ichneumonidae) | 0.70 | 0.115 |
| Eupelmidae | Family | 0.73 | 0.093 |
| Oxytorinae | Subfamily (Ichneumonidae) | 0.74 | 0.091 |
| Alysinae | Subfamily (Braconidae) | 0.75 | 0.080 |
| Campopleginae | Subfamily (Ichneumonidae) | 0.77 | 0.073 |
| Dryinidae | Family | 0.81 | 0.049 |
| Chalcididae | Family | 0.80 | 0.052 |
| Mesochorinae | Subfamily (Ichneumonidae) | 0.80 | 0.016 |
| Eurytomidae | Family | 0.83 | 0.040 |
| Adelognathinae | Subfamily (Ichneumonidae) | 0.87 | 0.020 |
| Opiinae | Subfamily (Braconidae) | 0.89 | 0.016 |
| Microgastrinae | Subfamily (Braconidae) | 0.94 | 0.005 |
| Rogadinae | Subfamily (Braconidae) | 0.98 | <0.005 |

(P < 0.05) or marginal P values very close to 5% level (i.e. 0.05 < P < 0.09). In particular, Dryinidae (P = 0.049), Chalcididae (P = 0.050), Eurytomidae (P = 0.040), Microgastrinae (P = 0.005), Rogadinae (P = 0.0003), Opiinae (P = 0.016), Adelognathinae (P = 0.020), Mesochorinae (P = 0.010) displayed statistically significant correlation, accounting for $\rho$ values higher than 0.80. Moreover, Campopleginae (P = 0.070), Alysinae (P = 0.080), Eupelmidae (P = 0.090), Oxytorinae (P = 0.090) indicated a clear directional pattern, with $\rho$ values between 0.74 and 0.77, showing a strong association with the semi-natural habitats within 200 m. It is interesting to point out that Ichneumonidae abundance, which was not significantly correlated with 200 m semi-natural habitats at family level (data not shown), included subfamilies (i.e. Adelognatinae, Mesochorinae, and in particular Campopleginae) that displayed a consistent monotonic response to the semi-natural habitats within 200 m.

Correlation matrices calculated for the 500 and 1000 m showed lower values and fewer significant correlations compared with those obtained for 200 m (data not shown), proving to be less informative, in agreement with the previous analyses obtained with RDA.

## EGVM infestation and parasitisation

The presence of EGVM first generation larvae was detected in five vineyards out of seven, and the mean infestation was generally low (3.5% of infested inflorescences) (Fig. 6); the most infested vineyard (no. 3) showed 15.2% infested inflorescences. The EGVM first generation infestation was negatively correlated with the proportion of semi-natural habitats within 200 m ($\rho$ = -0.83; P < 0.05) (Table 6).

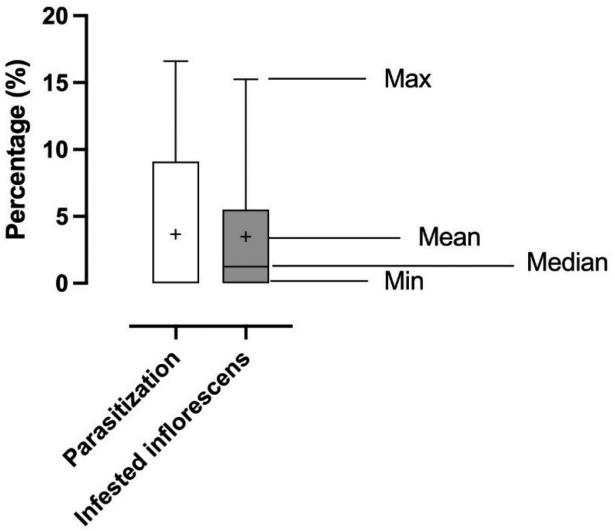



**Figure 6.** Infestation (% infested inflorescences) of first EGVM generation, and related parasitisation rate (%).

**Table 6.** Spearman $\rho$ and related P values of Spearman correlations between "200 m semi-natural habitats" and first EGVM infestation (% of infested inflorescences) and first generation parasitisation (%).

| EGVM parameters | $\rho$ | P |
|---|---|---|
| Parasitisation | -0.51 | 0.235 |
| Infestation | -0.83 | 0.019 |

First generation parasitisation was detected in two vineyards out of five with infestation, with a mean of 3.6% (Fig. 6); the highest parasitisation value was recorded in the vineyard no. 2 (16.6%). Parasitisation was found to be variable and discontinuous and was not correlated with any landscape metric (Table 6). Parasitoids emerged from collected EGVM larvae belonged to the genus *Diadegma* Förster, 1869 (Ichneumonidae, Campopleginae).

# Discussion and conclusions

This study revealed a remarkable parasitoid Hymenoptera fauna, comprising 71 taxa across families and subfamilies, highlighting the high biodiversity of this low-intensity, cultivated wine-growing area investigated. Several Hymenoptera taxa were significantly positively affected by the presence of semi-natural habitats within the 200 m buffer, which include infrastructures adjacent

to the vineyard. These findings are consistent with previous studies (Thomson and Hoffmann 2009, 2010), which showed that small parasitoids with limited dispersal ability are strongly influenced by green areas at a local scale. Notably, ecosystem services (i.e. predation) were also enhanced in vineyards bordered by remnant forests or planted woody vegetation (Thomson and Hoffmann 2010). Similarly, a significant positive correlation between the proportion of semi-natural habitats within a 400 m buffer and arthropod richness within vineyard plots has been reported (Guenser et al. 2020). In contrast, other studies have demonstrated that vineyard management practices, rather than the surrounding semi-natural habitats, are the key drivers of variation in arthropod and bird biodiversity across English vineyards (Zielonka et al. 2024); however, it is important to note that this latter study focused specifically on soil-dwelling arthropod communities.

Our results clearly show that semi-natural areas and vegetation patches adjacent to vineyards are crucial for the conservation of a diverse Hymenoptera parasitoid fauna that can potentially parasitize many important agricultural pests, including species infesting vineyards. Semi-natural habitats within wider buffers (in our study 500 and 1000 m) can play a role in the conservation of Hymenoptera diversity at the landscape level; however, the prevalent influence on vineyard diversity is driven by local non-crop areas in close proximity to the vineyard.

Among the taxa positively affected by semi-natural areas adjacent to vineyards, the subfamilies Campopleginae (Ichneumonidae) and Microgastrinae (Braconidae) deserve particular attention, as they include many parasitoid species of EGVM. In our study, first-generation EGVM larvae were parasitized by *Diadegma* spp. (Campopleginae), a result consistent with the positive correlation observed between semi-natural areas adjacent to vineyards and the abundance of this ichneumonid subfamily. In Italy, eleven Campopleginae species are reported as parasitoids of EGVM (Scaramozzino et al., 2018), including two species of *Diadegma* – *D. armillatum* (Gravenhorst, 1829) and *D. tenuipes* (Thomson, 1887) – as well as *Campoplex capitator* Aubert, 1960, which is considered a key species in the biological control of EGVM. A study conducted in vineyards in France and Switzerland also recorded ten parasitoid species associated with EGVM, including *Diadegma fenestrale* (Holmgren, 1860) (Moreau et al. 2010). Within Microgastrinae, two species are reported in Italy as parasitoids of EGVM, while the status of two additional taxa remains uncertain (Scaramozzino et al. 2017). Beyond primary parasitoids directly involved in vineyard pest suppression, several other Ichneumonidae subfamilies were also significantly correlated with semi-natural habitats within the 200 m buffer, reflecting the broader trophic complexity supported by these environments. Among these, Mesochorinae includes obligate hyperparasitoid species that primarily attack Braconidae and Ichneumonidae parasitoids. In addition, the monotypic subfamily Adelognathinae (Ichneumonidae) comprises ectoparasitoids of Symphyta larvae (Broad et al. 2018).

Other Ichneumonidae subfamilies showed weaker, non-significant responses to semi-natural habitats. For example, Oxytorinae exhibited a marginally positive association with semi-natural habitats within the 200 m buffer, suggesting a possible influence of local landscape features that did not reach statistical significance. Unfortunately, nothing is known about the biology and host association of this subfamily (Broad et al. 2018).

Moving beyond Ichneumonidae, 17 subfamilies of Braconidae were also recorded. To our knowledge, the subfamily Opiinae does not include parasitoids of vineyard pests, although a species, *Psyttalia concolor* (Szépligeti, 1910) is an important natural enemy of the olive fly, *Bactrocera oleae* (Rossi, 1790) (Diptera, Tephritidae). The subfamily Alysinae (Braconidae) includes species used in biological control programs (Murphy and LaSalle 1999; Heimpel and Meloche 2001). In addition, the subfamily Rogadinae (Braconidae), whose members are primarily parasitoids of Lepidoptera larvae, includes several taxa of potential relevance for biological control in agroecosystems, for example species attacking the genus *Spodoptera* Guenée, 1852 (Lepidoptera, Noctuidae) (Shimbori et al. 2023).

It is remarkable also the correlation of local semi-natural habitats with Dryinidae, a family that includes *Neodryinus typhlocybae* (Ashmead, 1893), an important parasitoid of *Metcalfa pruinosa* (Say, 1830) (Hemiptera, Flatidae). This parasitoid, employed in classical biological control programs also within vineyard agroecosystems, is usually released in hedgerows and semi-natural areas, which provide refuge sites crucial for multiplication of this beneficial species (Favaro et al. 2018).

Additional parasitoid families associated with semi-natural habitats adjacent to vineyards were also recorded. Eupelmidae, which also showed associations with semi-natural habitats adjacent to vineyards, includes *Anastatus bifasciatus* (Geoffroy, 1785) (Hymenoptera, Eupelmidae), an important parasitoid of the Brown Marmorated Stink Bug (BMSB), *Halyomorpha halys* (Stål, 1855) (Hemiptera, Pentatomidae), which is a potential vineyard pest. This parasitoid species has been used in the augmentative biological control of BMSB (Iacovone et al. 2022) and ecological infrastructures adjacent to crops are typically the focus areas for releases.

Chalcididae is an important family of parasitoids. While the majority of the species of Chalcididae are primary solitary endoparasitoids, some are secondary or gregarious parasitoids. Chalcididae parasitoids attack a wide range of hosts, including Lepidoptera, Diptera, Coleoptera and Hymenoptera; some species can attack Neuroptera, Orthoptera and Strepsiptera (Narendran and van Achterberg 2016).

Another parasitoid family associated with semi-natural habitats is Eurytomidae, whose members primarily attack seeds, gall-forming insects, and occasionally lepidopteran hosts (Gates et al. 2025). Although their role in vineyards is less well documented, Eurytomidae may contribute to regulating pest populations within surrounding

vegetation and maintaining overall parasitoid biodiversity in vineyard landscapes.

Loni and Lucchi (2014) sampled a rich community of Braconidae, in a grape-growing area of Tuscany region (Central Italy), finding that the abundance of some subfamilies was significantly related to the habitat variables and not negatively influenced by insecticides applications. In addition to serving as refuges and multiplication areas, semi-natural habitats adjacent to vineyards may act as buffer zones, protecting beneficial fauna from pesticide sprays. In our study, Ichneumonidae was the most represented family, followed by Diapriidae and Braconidae. As far as we know, these represent the only faunistic studies carried out in Italy specifically focused on the complex of Hymenoptera parasitoid in vineyards, alongside the targeted EGVM parasitoid recordings by Marchesini and Della Montà (1992) and the updated listings of Scaramozzino et al. (2017, 2018), which summarize faunistic information on EGVM parasitoids in Italy.

The negative correlation between infestation and the proportion of semi-natural habitats is consistent with the classic "resource concentration hypothesis" (Root 1973; O'Rourke and Petersen 2017). The generally low EGVM infestations observed in our study may reflect the extensive cultivation typical of the investigated wine-growing area, characterized by a high presence of ecological infrastructures. The discontinuous and patchy EGVM parasitism observed here may be explained by the overall low infestation levels of the grapevine moth. It should be noted that parasitism was assessed only in the first generation of EGVM, to avoid potential bias arising from the spray application, including mandatory control measures against *Scaphoideus titanus* Ball, 1932 (Hemiptera, Cicadellidae), which occur in mid-summer. For the same reason, collecting from the second- or third-generation larvae would have been challenging and potentially problematic, requiring the sampling of a large number of individuals. Given that parasitism may vary among EGVM generations (Marchesini and Della Montà 1992), our assessment may therefore represent a non-exhaustive estimate of this ecosystem service.

A recent national-level study in Italy demonstrated that climatic and landscape factors, particularly the presence of semi-natural habitats, explained variation in pesticide pressure independently of local management practices (Geppert et al. 2024). Notably, in this research, the increase in semi-natural areas surrounding vineyards was associated with reduced pesticide pressure and lower environmental impacts. This pattern may help explain the generally lower pesticide inputs observed in the wine-growing area of our study compared with vineyards located in lowland areas of this province or in more intensively managed vineyards elsewhere in the region (Bongiovanni S., personal communication).

Our study indicates that Hymenoptera parasitoid diversity can serve as an effective bioindicator of vineyard ecological sustainability, as also confirmed by other studies (i.e. Thomson and Hoffmann 2009, 2010; Loni and Lucchi 2014). On the other hand, a study based on these taxa typically requires Malaise trap sampling, the management of which is particularly time consuming. Identification of subfamilies of Ichneumonidae and Braconidae requires a certain level of taxonomic expertise, although it is considerably less demanding than identification to genus or species level and still allows for a more accurate interpretation of ecological patterns. For example, several Ichneumonidae subfamilies abundances were correlated with the 200 m landscape metric, even though the overall abundance of the whole family was not statistically correlated. It is clear that the subfamily-level identification within large families like Ichneumonidae and Braconidae can yield more informative insights, as it is more closely linked to biological and ecological patterns of these taxa.

In conclusion, this work reiterates the important role of semi-natural areas in the conservation of functional biodiversity. The strong dependence on habitats located within 200 m of the vineyard likely reflects the small body size and limited mobility of some of these taxa. The extent to which semi-natural habitats positively influence functional biodiversity ultimately depends on the functional groups considered in a study. Combining information on the spatial scale of landscape variables with the ecology of target taxa is, therefore, crucial for promoting the conservation of specific functional groups. Such knowledge is particularly valuable for guiding agroecological interventions aimed at enhancing functional diversity through targeted and well-planned management strategies.

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## Additional information

### Conflict of interest

The authors have declared that no competing interests exist.

### Ethical statement

No ethical statement was reported.

### Artificial Intelligence (AI) use

The authors accept full responsibility for the content of the manuscript, including the disclosure of any use of AI.
No AI tools were used in the preparation of this manuscript.

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### Author contributions

Conceptualization: GB, DS. Data curation: DS, DDP, CT. Formal analysis: DT, GB, DDP. Investigation: CT, DDP, DS, MP. Methodology: DT, GB, DS. Supervision: GB, DS. Writing - original draft: DS, GB. Writing - review and editing: DT, MP, DDP, CT.

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### Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information.

# Supplementary material 1

## Supplementary information

Authors: Giovanni Burgio, Daniele Torreggiani, Daniele Sommaggio, Carlo Tassini, Martina Parrilli, Davide Dal Pos
Data type: docx
Explanation note: **figure S1.** Redundant analysis which explains variations of Hymenoptera family abundances (response variables), using semi-natural habitats and crop habitat within 200 m as explanatory variables. **figure S2.** Redundant analysis which explains variations of Hymenoptera family abundances (response variables), using semi-natural habitats and crop habitat within 500 m as explanatory variables. **figure S3.** Redundant analysis which explains variations of Hymenoptera family abundances (response variables), using semi-natural habitats and crop habitat within 1000 m as explanatory variables.
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Link: https://doi.org/10.3897/bull.insectology.200939.suppl1