



## Short communication

## Meadow orchards as a good practice example for improving biodiversity in intensive apple orchards



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## ABSTRACT

Changes in agricultural land use and management are largely responsible for the current global biodiversity crisis. Addressing this crisis necessitates a change in management practices that are considered to limit biodiversity. Comparing intensive land-use forms with their extensive and traditional counterparts can help define good practice example for integrated conservation.

We compare remnants of traditional meadow orchards with intensively managed apple orchards in a mountain region by investigating the multi-taxonomic diversity of seven groups (including vascular plants, wild bees, diurnal butterflies, orthopterans, spiders, birds, and bats) and macro-invertebrates inhabiting four habitat strata (soil, ground-dwelling, herb, and tree layer). Each group and stratum was sampled with a target sampling method.

We found a consistent trend of higher abundance, diversity, and presence of threatened species in meadow orchards compared to apple orchards. Specifically, wild bees, butterflies, orthopterans, and birds showed significantly lower diversity in apple orchards across different diversity indices. Furthermore, multi-taxonomic indices of all taxa and most habitat strata followed the same trend, supporting the conclusion that these findings are applicable to the entire orchard ecosystem.

We conclude that traditional agroforestry systems, such as meadow orchards, could represent a well-suited good-practice example for integrated biodiversity conservation in the agricultural landscape. Finally, we emphasize the importance of maintaining traditional management practices through effective conservation measures such as subsidies as part of agri-environmental schemes.

## 1. Introduction

Intensive agriculture is widely recognised as a major cause of biodiversity loss worldwide (Jauregui et al., 2022; Sánchez-Bayo and Wyckhuys, 2019; Wagner et al., 2021). National and international institutions and organisations are calling for changes to shift the overall

agricultural impact towards a more sustainable and conservation-friendly scenario (CBD, 2010; Cuadros-Casanova et al., 2023; Cunningham et al., 2013; FAO et al., 2019). To prevent an ecological collapse, conserve life in and around agricultural areas, and support the long-term provision of related ecosystem functions and services, novel approaches are requested (Dainese et al., 2019; Hooper et al., 2012).

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Achieving this objective involves the identification, conservation and monitoring of high nature value agricultural land-use types (Cuadros-Casanova et al., 2023). A promising approach is to consider traditional, extensive agricultural management practices, that have been developed and implemented over a long time. Land-use types subjected to such extensive management regimes have in fact frequently evolved to high nature value land-use types, harbouring high levels of biodiversity and communities of organisms well adapted to exploit and withstand these type of land-uses (Edo et al., 2023; Halada et al., 2011).

One example of these production systems are traditional fruit orchards, also named meadow orchards. This traditional form of agroforestry, characterized by scattered, mostly high-stem and old-grown fruit trees with a grassland understory (Tojanko et al., 2011), was widespread across central Europe until the mid-20th century (Forejt and Syrbe, 2019). The industrialization in agriculture has led to homogenized landscapes and the gradual abandonment or conversion of meadow orchards into more intensive land-use types (Nerlich et al., 2013; Tojanko et al., 2011). This trend is widespread across Europe (Forejt and Syrbe, 2019) and is particularly noticeable in the study region, where a 95 % loss of traditional meadow orchard area has been reported over the last 75 years, with 69 % area being replaced by intensive apple orchards (Schönafinger, 2023). These highly profitable apple plantations represent intensive production systems (Tappeiner et al., 2020), that require frequent management and substantial inputs of fertilizers and pesticides. These chemicals have been detected at considerable distances from the apple orchards (Brühl et al., 2024) and are expected to have a negative impact on biodiversity at various scales (Sánchez-Bayo and Wyckhuys, 2019), raising conservation (van der Meer et al., 2020), and human health concerns (Linhart et al., 2019). Conversely, meadow orchards have gained recently increasing recognition for their cultural significance and ability to provide diverse ecosystem functions and services (Nerlich et al., 2013; Plieninger et al., 2013). Furthermore, the low intensity of grassland management and the presence of old fruit trees make meadow orchards particularly rich in biodiversity, since both grassland and forest-associated species can occur in meadow orchards (Edo et al., 2023; Ernst et al., 2017).

Most studies have compared different management intensities in meadow orchards (Deuschle and Glück, 2008) or compared them with other land-use types, such as grasslands and forested areas (Ernst et al., 2017). These studies consistently highlight meadow orchards as exceptionally biodiversity-rich. However, only a few studies compared meadow orchards with intensive orchards, focussing on single taxa, such as birds and soil macro-invertebrate communities (e.g. Kajtoch, 2017; Guariento et al., 2020). Other taxonomic groups that occupy different ecological niches are often neglected (Sattler et al., 2024). To develop and improve conservation strategies, it is important to assess multiple taxa for a more comprehensive understanding of ecosystem functioning and resilience, as pointed out in a recent review on meadow orchards by Sattler et al. (2024).

Comparing these management types from a multi-taxonomic perspective represents a promising strategy for highlighting differences and defining the biodiversity potential that could be supported by an extensification of this type of land-use (Cuadros-Casanova et al., 2023; Guariento et al., 2020). To this end, we compared the supported biodiversity between traditional extensive meadow orchards and intensive apple orchards following a multi-taxonomic approach. We expected (1) higher diversity values across all taxa and habitat strata in meadow orchards compared to apple orchards. The disturbances associated with management in intensive orchards are expected to limit the presence of species throughout the trophic chain and in each habitat stratum. Furthermore, (2) we expect a higher portion of threatened taxa in meadow orchards, as rare and potentially threatened species often rely on habitats with minimal human disturbance.

## 2. Material and methods

### 2.1. Study area

The study was performed in South Tyrol (Province of Bolzano-Südtirol in Northern Italy), a mountainous region and major apple-growing region in Europe (Südtiroler Apfelkonsortium, 2023). The modern industrialised apple orchards (AOs) cover a considerable part of the valley floors, while remnants of traditional meadow orchards (MOs) are scattered (Schönafinger, 2023). Ten sites distributed over the study region were selected, five MOs and five AOs (Fig. 1). MOs represented the traditional extensive fruit production system and included apple, pear, and plum trees. AO sites investigated in this study were all organically managed and carefully selected to minimize variations between sites (for further details on site management see Appendix file A1).

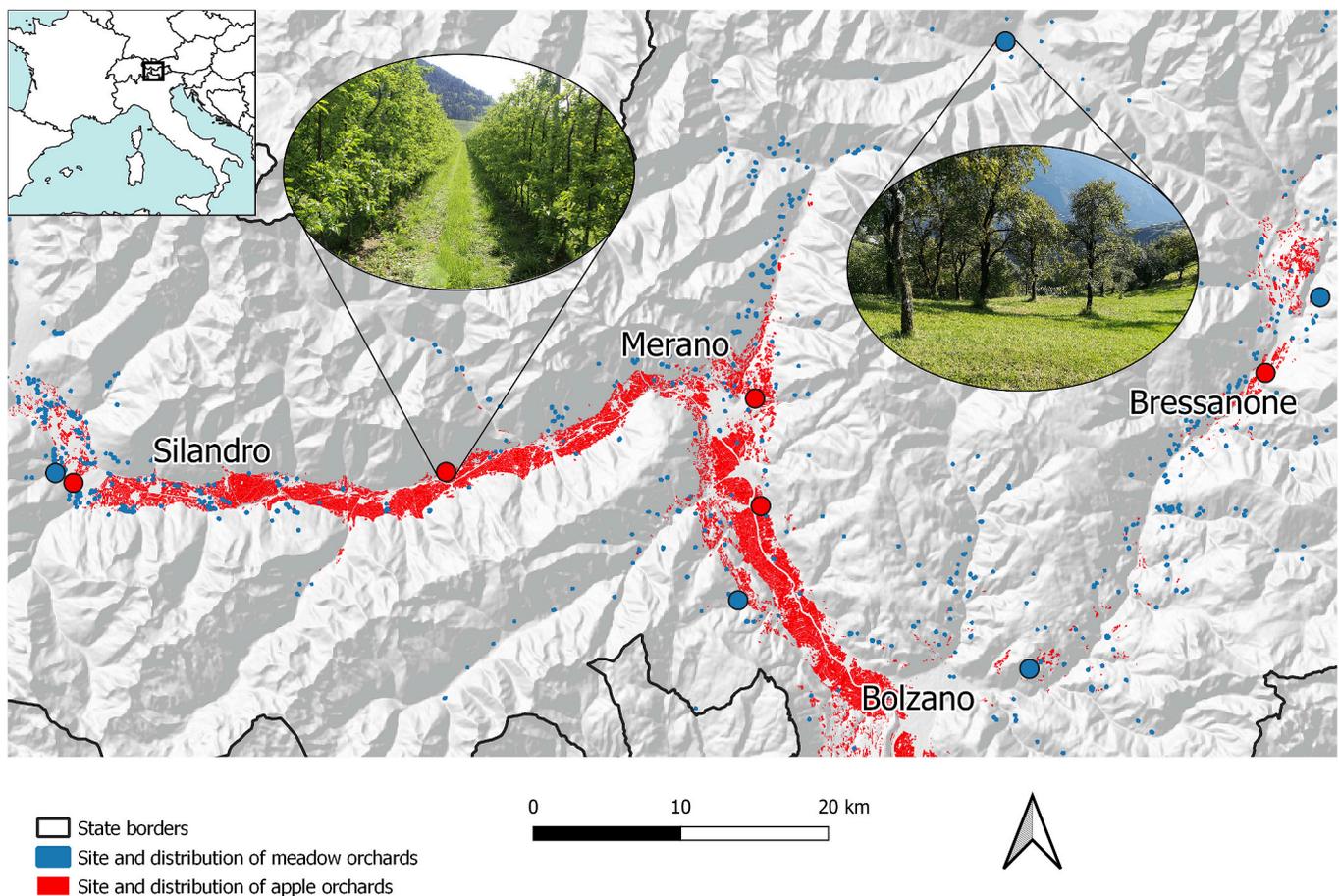
### 2.2. Sampling

AO sites are part of the sampling scheme of the Biodiversity Monitoring South Tyrol (Hilpold et al., 2023), while MO sites were newly selected for this study. Standardised sampling protocols were used to sample the target taxa and the different habitat strata which are briefly explained below (detailed description in Hilpold et al., 2023).

Vascular plants were surveyed by compiling a complete species list on a 100 m<sup>2</sup> area and assigning cover values for every species, following the method described in Hilpold et al. (2023). Wild bees were collected using three sets of yellow, white, and blue UV-painted pan traps, deployed three times for 24 h between May and August 2021 (described in more detail in Obwegs et al., 2023). Butterflies were sampled with a time area count (for 30 min on 1000 m<sup>2</sup>) replicated four times in one season from May to August and respecting minimal weather conditions (Barkmann et al., 2023). Orthopterans were sampled once in a season in an area of 100 m<sup>2</sup> using a combination of sweep netting and acoustic assessment. Species abundances were recorded in abundance classes within an areas of 100 m<sup>2</sup> (for more info see Hilpold et al., 2020). Spiders were retrieved for each site from the four habitat stratum sampling protocols (see below). Birds were sampled within a 100 m-radius from the site centre for 10 min using point counts, three times during the breeding period (from 15th April to 15th July), starting shortly after sunrise (5.30 a.m.) and ending at 11 a.m. The maximum abundance over the replicates was used (Anderle et al., 2022). Bat activity was recorded with a bat detector (Elekon Batloggers A+ ([www.batlogger.ch](http://www.batlogger.ch))), which was active for three consecutive nights from sunset to sunrise between May and September. Soil layer was sampled with four (10 × 10 × 15 cm) soil core samples per site from which macro-invertebrates were heat-extracted using a modified Kempson apparatus (Kempson et al., 1963). Ground layer macro-invertebrates were sampled with four pitfall traps (two in spring and two in autumn) per site, which were exposed for four weeks each. Herb layer invertebrates were sampled using two sweep netting transects of 50 sweeps performed in early summer using a 50 cm diameter round entomological net. Tree layer invertebrates were sampled with five energetic beatings on 10 different tree branches using a beating net. Vascular plants, wild bees, butterflies, orthopterans, spiders, birds, and bats were, as far as possible, identified to species level. Macro-invertebrates collected in the different habitat strata were identified to higher taxonomic levels, where possible to family level. Whereas wild bees, butterflies and orthopterans collected within the habitat strata were not further identified to species level.

### 2.3. Statistical analyses

Data on vascular plants (coded in cover classes) and orthopterans (coded in abundance classes) were transformed to count data to allow for direct comparison with other taxonomic group abundances. Vascular plants cover values were directly used as abundances as they are suggested to be the best abundance proxy for vegetation (Dengler et al.,



**Fig. 1.** Partial map of the study region South Tyrol, Italy (extending over 750,000 ha). The sampling sites (dots) and distribution area (shades) of traditional extensive meadow orchards (blue; extending over 296 ha) and intensive apple orchards (red; extending over 17,494 ha) are shown. Map based on data from Schönafinger (2023) and Anderle et al. (2022). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

2016). For the abundances of orthopterans, the median of each abundance class was used (for more details of abundance classes see Hilpold et al., 2020). For bats the number of bat passes during three consecutive nights was considered a proxy of bat activity (Runkel et al., 2021). Regarding the habitat strata, only target taxa bound to the relative stratum and routinely collected with the respective sampling methodology were considered (Santos and Fernandes, 2021). Macro-invertebrate abundances in soil samples were averaged for each site and scaled up to an area of 1 m<sup>2</sup> to provide standardised and comparable values. Animals from four pitfall traps were averaged and standardised to activity density per day of exposure. Sweeping data were retrieved by summing the arthropod abundances of two parallel transects of 50-sweep each.

Abundance data of every taxon and habitat stratum were used to estimate sampling coverage using species accumulation curves and to compare the total supported diversity between the two orchard types for each taxonomic group. When referring to total diversity in this study we mean the supported diversity by each management type as depicted only in the accumulation curves (Fig. A2, Fig. A4). For all other analysis, indices were computed at site level. Hill numbers (H0: Species richness, H1: Exponential of Shannon entropy – Shannon Diversity, H2: Inverse Simpson concentration – Simpson Diversity) for each taxonomic group were computed to the relative 85 % sampling coverage and for habitat strata to 95 % sampling coverage at site level (package iNEXT; Hsieh et al., 2016) to allow for optimal comparison among sites by accounting for the different abundances and detectability of taxa.

Red List (RL) scores were collected for all taxonomic groups

prioritizing locally available lists: vascular plants (Wilhelm and Hilpold, 2006), wild bees (Nieto et al., 2014), butterflies (Huemer, 2004), orthopterans (Hilpold et al., 2017), spiders (Gepp, 1994 and for missing species Blick et al., 2016), birds (Ceresa and Kranebitter, 2020) and bats (Rondinini et al., 2022). The RL scores were coded from 0 (least concern) to 4 (critically endangered) for each species. For each taxon and within each site an abundance-weighted RL score was computed. Species coded as DD or NE were excluded from the calculation.

Finally, min-max scaling was used to compute an overall indicator for abundance, Hill numbers and RL score for each site over all seven taxonomic groups. This approach avoids the dominance of abundant and species rich groups in determining a score over all taxa (Allan et al., 2014). Differences between orchard management types ( $N = 2$ ,  $df = 1$ ) were tested for all sites ( $N = 10$ ,  $df = 9$ ), all taxa ( $N = 7$ ), habitat strata ( $N = 4$ ) and indices ( $N = 5$ ) using unparametrized Wilcoxon rank-sum tests, corrected with Benjamini-Hochberg to avoid for false discovery rates (Benjamini and Hochberg, 1995). All analyses and graphs were computed using R environment (R Core Team, 2023) using the packages ggplot2 (Wickham, 2016), vegan (Oksanen et al., 2022) and iNEXT (Hsieh et al., 2016).

### 3. Results

Overall, we recorded 385 species spanning across seven taxonomic groups comprising vascular plants (123 species), wild bees (368 individuals of 85 species), butterflies (527 individuals of 38 species), orthopterans (238 individuals of 26 species), spiders (435 individuals of

49 species), bats (1561 bat passes of 15 taxonomic groups) and birds (412 individuals of 49 species). In the different habitat strata, a total of 13,446 macro-invertebrates identified at higher taxonomic levels were recorded, subdivided in soil layer (535 individuals of 22 taxa), ground layer (5052 individuals of 45 taxa), herb layer (7349 individuals of 39 taxa) and tree layer (510 individuals of 26 taxa).

The species diversity of each taxonomic group displayed different patterns, with higher scores observed in MOs for wild bees (H1,H2), butterflies (abundance, H0, H1, H2), orthopterans (abundance, H0, H1, H2) and birds (H0,H1). Conversely, no index scored significantly different between management type for vascular plants at site level, spiders, and bats (Fig. 2, Fig. A1). The total diversity supported by each management type resulted significantly higher for all individual taxa (also for vascular plants) in MOs compared to AOs, with the only exception of bats, which showed no significant differences (Fig. A2). Notably, the species richness (H0) accumulation curves for vascular plants, wild bees and spiders did not reach a visible saturation, suggesting an incomplete sampling for these taxonomic groups in the present study (Fig. A2).

The site level macro-invertebrate diversity within each habitat stratum resulted significantly higher in MOs for the soil layer (H0), the herb layer (abundance, H0 and H1) and the tree and shrub layer (H0). Ground layer consistently showed no significant differences between management types (Fig. 3; Fig. A3). The total supported diversity of each habitat stratum (Fig. A4) revealed a higher animal diversity in MOs at tree and herb layer (Fig. 3)

Min-max standardised indicators for abundance and Hill numbers clearly support a higher abundance and diversity in MOs compared to AOs (Fig. 4). RL scores resulted higher in MOs than in AOs, however, the proportion of endangered species was not significantly higher than in AOs in the summarized version (Fig. 4; Wilcoxon test:  $p = 0.056$ ) and for each single taxon (Fig. A1), respectively.

#### 4. Discussion

To halt and turn the trend of agricultural industrialization of the last century, high nature value agricultural land-use forms need to be defined and preserved (Cuadros-Casanova et al., 2023). In this regard,

MOs hold great potential for the conservation of biodiversity and ecosystem services in an otherwise impoverished agricultural landscape.

##### 4.1. The case of meadow orchards

The main expectation of an overall higher diversity in MOs in comparison to AOs was largely confirmed. If a significant difference in any indices was detected it was only by an increased score of MOs over AOs. These results lend support to studies that show a similar pattern underlining the potential hotspot of biodiversity supported by MOs (Sattler et al., 2024; Torralba et al., 2016) and the detrimental effect of intensive orchards on overall biodiversity (Guariento et al., 2022; Stoate et al., 2009; Zabel et al., 2019). This conclusion is remarked by the fact that almost all investigated taxa are considered important bioindicators for biodiversity and different ecosystem functions (i.e., predators, pest control, pollinators and primary producers), representing the food chain of an agricultural landscape (Chowdhury et al., 2023; Padoa-Schioppa et al., 2006; Park, 2015; Schindler et al., 2013). Moreover, the consistency of outputs across the surveyed habitat strata further supports the conclusion that these findings apply to the entire orchard habitat. Differences between taxa, habitat strata and indices support the notion that it is important to consider multiple aspects of biodiversity to capture an overarching effect (Anderle et al., 2024).

##### 4.2. What makes the difference?

In MOs, management involves fewer mowing events with less invasive machinery (e.g., bar mower; Humbert et al., 2010), reduced fertilization, the preference for organic fertilizers over synthetic ones, and the avoidance of pesticide use compared to AO (as listed in Appendix file A1). The generally high biodiversity scores in MOs likely result from the lower management intensity compared to the AOs (Appendix file A1), as management intensity is known to negatively impact biodiversity both directly and indirectly (Emmerson et al., 2016; Felipe-Lucia et al., 2020; Tsiafouli et al., 2015; Winter et al., 2018). The frequent use of heavy machinery in AOs likely causes soil compaction and a reduced soil biodiversity, as supported by other studies (Guariento et al., 2020). Increased and repeated mulching, mowing and fertilizing events have

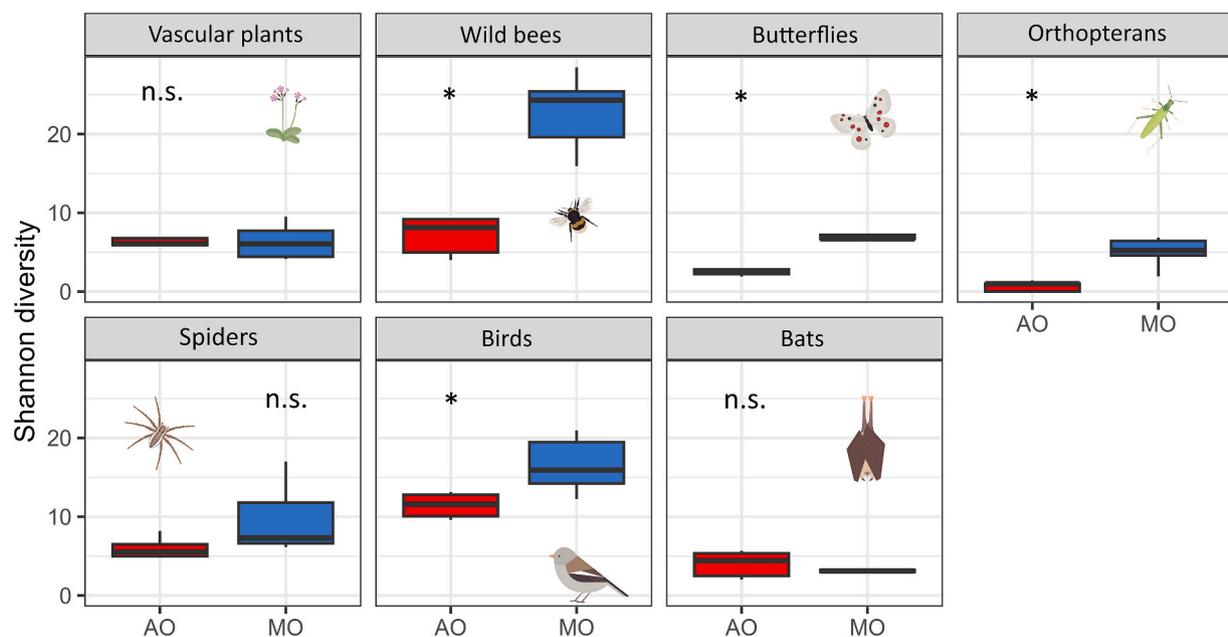
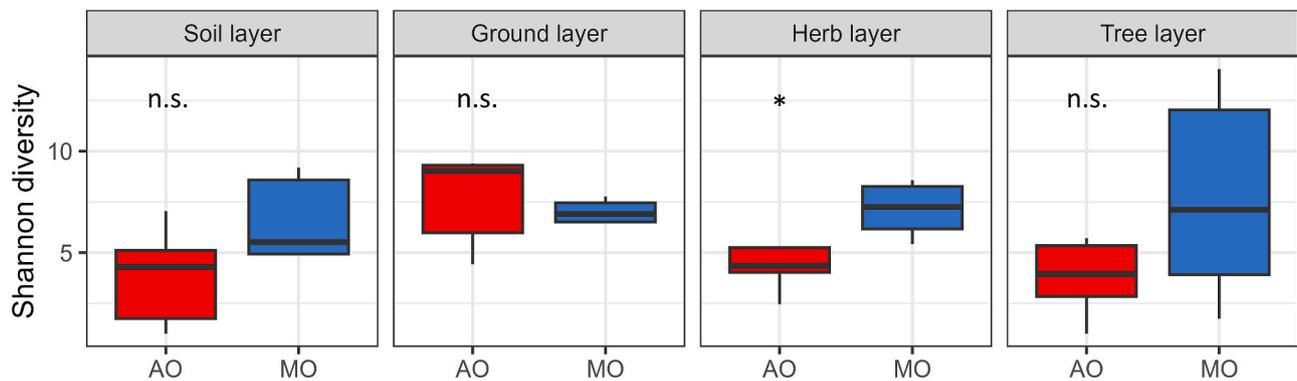
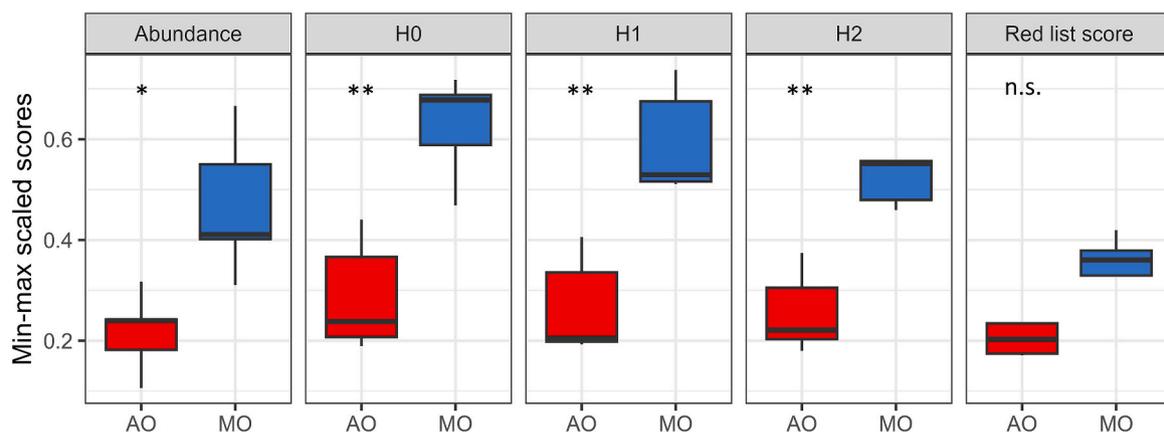


Fig. 2. Diversity of each taxonomic group identified to species level. Shannon diversity (Hill number 1) was computed to the relative 85 % coverage on each site for meadow orchards (MO; blue) and apple orchards (AO; red). Wilcoxon rank-sum tests corrected with Benjamini-Hochberg for false discovery rates were performed, \*  $p < 0.05$ . (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)



**Fig. 3.** Diversity of macro-invertebrates collected in each habitat stratum. Shannon diversity (Hill number 1) was computed to the 95 % coverage on each site. Differences between meadow orchards (MO; blue) and apple orchards (AO; red) were computed with a Wilcoxon rank-sum test corrected with Benjamini-Hochberg for false discovery rates, \*  $p < 0.05$ . (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)



**Fig. 4.** Min-max standardised indicators considering all taxonomic groups identified to species level and scaled between 0 and 1. Hill numbers (H0,H1,H2) are standardised on site level to 85 % coverage. Red List scores were computed for every taxon using IUCN categories scored as numbers and weighted upon abundance of individuals (except for vascular plants where only incidence was used). Wilcoxon rank-sum test corrected with Benjamini-Hochberg for false discovery rates were performed, \*  $p < 0.05$ ; \*\*  $p < 0.01$ . Apple orchards (AO; red), meadow orchards (MO; blue). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

been shown to negatively affect the lower vegetation (Hall et al., 2020) and associated animal communities living in and from the herb layer (Humbert et al., 2009). This likely explains the generally lower diversity of wild bees, butterflies, orthopterans and birds in AOs (Simons et al., 2016). Furthermore, the tree layer in MOs is characterized by less densely planted, older trees that exhibit a high structural diversity, providing microhabitats such as dead wood, tree cavities and a grassland understory. This agroforestry type is especially biodiversity-rich since it provides refugia for various animal groups (such as cavity-nesting birds and extensive grassland butterflies; Bas et al., 2009; Guariento et al., 2022) bound both to grasslands and forests (Edo et al., 2023). In contrast, large and old trees in AOs have been replaced to facilitate mechanization and increase production at the expense of certain ecosystem services, such as pest control (Lindell et al., 2018). Above all, additional chemicals, such as insecticides, herbicides, and fungicides, were more applied in AOs, even though the selection of sites was limited to organically managed sites (Appendix file A1). As reported by other studies, these are known to have a detrimental effect on insects (Serrão et al., 2022), bats (Stahlschmidt and Brühl, 2012) and biodiversity in general (Geiger et al., 2010).

#### 4.3. Limitations

While AOs are typically cultivated as monocultures over large areas in valley floors, MOs are remnants usually found on slopes between

settlements, other agricultural areas and forests. Some species are more affected by direct management practices at site level, while others also respond to the surrounding landscape. For instance, birds are also affected by landscape habitat diversity, configuration and composition (Anderle et al., 2023). Furthermore, the location of MOs and AOs along mountain slopes, leads to variations in (micro)climate and topography, further shaping communities. Future research should incorporate topography, landscape features, and microclimate alongside land-use to further explore these effects. A further limitation of our study is the limited number of sites. However, consistent patterns were observed across multiple taxa, habitat strata, and diversity indices in our multi-taxon approach. Despite varying habitat and landscape requirements among species, the results consistently point to the overall impact of management practices.

#### 4.4. Conclusions and conservation implications

The global biodiversity crisis can partially be attributed to land-use change and intensification (Jaureguiberry et al., 2022). This trend aligns well with the drastic area decline (95 %) of MOs and the concomitant increase of AOs observed in the study region over the last 75 years (Schönafinger, 2023). To mitigate the negative impact of AOs, alternative management strategies, such as organic management and biological pest control, have been proposed and partially implemented (Porcel et al., 2018; Samnegård et al., 2019). Further, since biodiversity

conservation in Europe necessarily includes agriculture as part of the solution (Batary et al., 2015), defining best practice models of land management that support large portion of biodiversity is of central importance. In this study, we propose traditional agroforestry systems, such as MOs, as a good practice example for biodiversity conservation within the agricultural landscape. Our research underlines the importance of remnant MOs as biodiversity hotspots in agricultural landscapes otherwise dominated by monocultures of AOs. Therefore, studying these traditional agroforestry systems represents an opportunity to understand which orchard characteristics and management practices lead to desirable biodiversity outcomes and ecosystem services. The insights gained could inform good management practices within AOs, thereby enhancing biodiversity conservation and ecosystem service provision while avoiding potential intensification traps (Burian et al., 2024).

Demonstrating the role of MOs as an example of traditional agroforestry system in sustaining and increasing local biodiversity is crucial for increasing also their appeal, and consequently their conservation as multifunctional yet declining extensive traditional management type. Finally, agri-environmental schemes to compensate for financial losses associated with extensive farming – as available in some countries – can help to maintain and promote threatened forms of traditional biodiversity-friendly farming.

#### CRediT authorship contribution statement

**Elia Guariento:** Writing – review & editing, Writing – original draft, Visualization, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Lisa Obwegs:** Writing – review & editing, Writing – original draft, Visualization, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Matteo Anderle:** Writing – review & editing, Writing – original draft, Visualization, Methodology, Investigation, Data curation. **Alex Bellé:** Writing – review & editing, Methodology, Data curation. **Paolo Fontana:** Writing – review & editing, Methodology. **Chiara Paniccia:** Writing – review & editing, Writing – original draft, Visualization, Methodology, Investigation, Formal analysis, Data curation. **Julia Plunger:** Writing – review & editing, Methodology, Investigation, Data curation. **Johannes Rüdiss:** Writing – review & editing. **Simon Stifter:** Writing – review & editing, Methodology, Data curation. **Valentina Giombini:** Writing – review & editing, Resources. **Lukas Egarter Vigl:** Writing – review & editing, Funding acquisition. **Ulrike Tappeiner:** Writing – review & editing, Funding acquisition. **Andreas Hilpold:** Writing – review & editing, Supervision, Project administration, Methodology, Investigation, Funding acquisition, Data curation, Conceptualization.

#### Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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#### Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.biocon.2024.110815>.

#### Data availability

Data provided in the online repository under [10.5281/zenodo.13933190](https://doi.org/10.5281/zenodo.13933190).

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