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From protected species to communities: citizen science and expert-based approaches to study saproxylic beetles under environmental changes

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Overview of the doctoral thesis

Abstract

English

Saproxylic beetles, organisms relying on dead or decaying wood during part of their life cycle or on other organisms depending from these resources, are among the most species-rich and functionally diverse components of forest biodiversity. By exploiting various microhabitats, they contribute to wood decomposition and nutrient cycling, while their dependence on specific substrates and microclimates makes them highly sensitive to environmental changes. The present thesis investigates different approaches that can be implemented for the study of this group, focused on: *i*. the potential of citizen science for monitoring protected saproxylic species at the national scale; *ii.* the evaluation of the influence that temporal changes of climatic variables can have on beetle community in terms of taxonomic and functional diversity; *iii.* The assessment of how forest structure and dynamics can influence communities in historically managed beech woodland areas. Within this framework, three case studies are presented. The first one concerns a national citizen science initiative (MIPP/InNat; 2014–2024) aimed at collecting distributional records of protected insect species across Italy. The study evaluates the increase in knowledge of the spatial distribution of the target species over time and explores the potential of georeferenced photographic records to support additional ecological investigations, with a particular focus on eco-ethological traits of *Lucanus cervus* Linnaeus, 1758. In addition, the social dimension of the project is also examined by characterising volunteer participation and engagement patterns, identifying motivation, social interaction and communication strategies as key factors in sustaining long-term involvement. The second case study compares, over an eleven-year period (2009–2010 and 2021–2022), the characteristics of a community of saproxylic beetles associated with tree cavities in a Spanish National Park. The study reveals a decline in total abundance and marked changes in structure and phenological patterns at community, functional groups and species levels, with heterogeneous responses, mainly influenced by temperature values. The third case study examines how forest structure and silvicultural practices affect saproxylic beetle communities in a central Italian beech forest undergoing conversion from coppice to high forest (i.e., natural evolution, periodic thinning, and anticipated seed cutting). Differences in community composition and diversity indices are observed among the stands, with the detection of structural key drivers of these patterns. The results also indicate that passive abandonment of historically intensively managed areas

may be insufficient to promote suitable habitats for biodiversity, highlighting the importance of active management that fosters tree growth and diverse deadwood to support saproxylic beetle diversity.

Overall, this thesis further highlights the vulnerability of saproxylic beetles and the challenges of conserving them under ongoing environmental pressures, including climate change and human-driven forest management. Overall, this study highlights the wide range of effects that environmental changes can have on saproxylic beetles and underscores the need to study them from multiple perspectives, including through interdisciplinary collaborations. This approach would, in fact, provide a more comprehensive understanding of the acting dynamics and thus enable the identification of effective strategies for the conservation of forest biodiversity.

Italiano

Gli organismi che, per almeno una fase del loro ciclo vitale, dipendono dal legno morto o in decomposizione sono detti *saproxilici* e, tra questi, i coleotteri rappresentano uno dei gruppi più ricchi di specie e funzionalmente diversificati. Essi svolgono un ruolo chiave nella decomposizione del legno e nel ciclo dei nutrienti, e, considerata la loro stretta dipendenza da substrati e condizioni microclimatiche specifiche, risultano essere altamente sensibili ai cambiamenti ambientali. La presente tesi esplora ed espone diversi approcci scientifici volti allo studio e alla valutazione dello stato di conservazione dei coleotteri saproxilici, dal monitoraggio di specie protette attraverso iniziative di scienza partecipata, fino alla valutazione che cambiamenti climatici e strutturali possono avere sulle comunità di coleotteri in termini di diversità tassonomica e funzionale. All'interno di questo quadro, vengono presentati tre casi studio. Il primo si basa su un'iniziativa nazionale di citizen science (MIPP/InNat; 2014–2024) finalizzata alla raccolta di dati distributivi di specie di insetti protetti su territorio nazionale. Lo studio valuta l'incremento di conoscenza della distribuzione spaziale delle specie target nel tempo ed esplora il potenziale dei dati fotografici raccolti per supportare ulteriori indagini ecologiche con particolare riferimento ai tratti eco-etologici di *Lucanus cervus* Linnaeus, 1758. Inoltre, viene analizzata la dimensione sociale del progetto attraverso l'analisi della partecipazione e dell'impegno dei volontari, evidenziando i fattori chiave per un loro coinvolgimento a lungo termine. Il secondo caso studio confronta, a distanza di undici anni (2009–2010 e 2021–2022), le caratteristiche di una comunità di coleotteri saproxilici associati alle cavità arboree in un Parco Nazionale in Spagna. Lo studio evidenzia un significativo calo nell'abbondanza totale di coleotteri, così come importanti cambiamenti nella struttura e nei pattern fenologici a

livello di comunità, gruppi funzionali e singole specie. Infine, il terzo caso studio si concentra sull'influenza della struttura forestale e delle pratiche selvicolturali sulle comunità di coleotteri saproxilici in una faggeta dell'Italia centrale in fase di conversione da ceduo a fustaia mediante diverse tipologie di trattamenti: evoluzione naturale, diradamento periodico e taglio anticipato di sementazione. Tra gli stand investigati si riportano differenze nella composizione delle comunità e negli indici di diversità, individuando alcuni fattori strutturali come principali driver di tali pattern. I risultati suggeriscono inoltre che l'abbandono passivo di aree storicamente gestite non è sufficiente a garantire habitat favorevoli alla biodiversità, evidenziando l'importanza di una gestione attiva che promuova la crescita degli alberi e la diversità di legno morto, tenendo conto sia della storia gestionale passata sia delle pratiche attuali.

Complessivamente, questo lavoro presenta alcuni approcci che si possono adottare per studiare lo stato di conservazione dei coleotteri saproxilici e gli effetti che i cambiamenti ambientali possono su questo gruppo. Evidenzia inoltre la necessità di studiare tali fenomeni da più prospettive, anche avvalendosi di collaborazioni interdisciplinari. È difatti sempre più necessario ottenere una visione completa delle dinamiche in atto, per individuare strategie efficaci per la conservazione di questi insetti chiave all'interno dell'ecosistema forestale.

Thesis aims

The overall objective of this PhD thesis is to explore different approaches related to saproxylic beetles species assessments, as well as community investigations, through the presentation of three case studies that consider the following aspects:

1. Is it citizen science an effective approach for the study and the assessment of protected species of insects? Which scientific and sociological impacts can be generated? (chapter 1)
2. Which are the effects of temporal variation in climatic factors on saproxylic beetles? Are there differences considering the community level, functional groups and single species?(chapter 2)
3. Can different silvicultural options shape saproxylic beetles community in a beech forest once exploited as coppice with standards? (chapter 3)

Chapters description and authors contribution details

Chapter 1

This chapter includes a general introduction (*pp* 25 – 28) and four subchapters corresponding to already published articles.

Subchapter 1 – Lenzi et al., 2025 (pp 28 – 34*)*

- Paper citation. Lenzi A, Gisondi S, Bardiani M, Hardersen S, Maurizi E, Mosconi F, Nardi G, Campanaro A (2025) Protected insect species in Italy: occurrence data from a 10-year citizen science initiative. Biodiv Data J 13: e151742. https://doi.org/10.3897/BDJ.13.e151742
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  Alice Lenzi. Conceptualization, Investigation, Formal Analysis, Writing – original draft, Visualization, Investigation. Silvia Gisondi: Conceptualization, Data curation, Writing – review and editing. Marco Bardiani: Conceptualization, Data curation, Writing – review and editing. Sönke Hardersen: Conceptualization, Data curation, Writing – review and editing. Emanuela Maurizi: Data curation, Writing – review and editing. Fabio Mosconi: Data curation, Writing – review and editing. Gianluca Nardi: Data curation, Writing – review and editing. Alessandro Campanaro: Conceptualization, Funding acquisition, Supervision, Writing – review and editing, Project administration

Subchapter 2 – Gisondi et al., 2025 (pp 35– 49*)*

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- Author contribution. Silvia Gisondi: Conceptualization, Data curation, Writing—original draft, Writing—review and editing. Fiorenza Augusta Spotti: Conceptualization, Data curation, Validation, Writing—review and editing. Alice Lenzi: Conceptualization, Data curation, Visualization, Writing—review and editing. Donato Antonio Grasso: Resources, Writing—review and editing. Alessandro Campanaro: Conceptualization, Project administration, Resources, Supervision, Writing—review and editing. Cristina Castracani: Conceptualization, Formal analysis, Supervision, Validation, Writing—original draft, Writing—review and editing

Subchapter 4 – Gisondi et al., 2025 (pp 69 – 88*)*

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- Author contribution. Silvia Gisondi: Data curation, Investigation, Writing – original draft, Writing – review and editing. Paolo Giardullo: Data curation, Formal analysis, Investigation, Writing – original draft, Writing – review and editing. Alice Lenzi: Writing – original draft, Validation, Visualization, Writing – review and editing.

Emanuele di Buccio: Formal analysis, Writing – review and editing. Pio Federico Roversi: Funding acquisition, Supervision. Alessandro Campanaro: Data curation, Project administration, Resources, Supervision, Writing – review and editing.

Chapter 2

This chapter includes one already published article

Lenzi et al., 2026 (pp 87 – 107*)*

- Paper citation. Lenzi A, Quinto J, Bajocco S, Martínez-Pérez S, Gisondi S, Padilla A, Sánchez-Almodóvar E, Campanaro A, Micó E. Temperature drives Trait-Dependent responses of saproxylic insect phenology in mediterranean woodland. Biodivers Conserv 35, 17 (2026). https://doi.org/10.1007/s10531-025-03209-4
- Author contribution. Alice Lenzi and Javier Quinto are co-first authors. Alice Lenzi: Data collection, Conceptualisation, Writing – original draft, Formal analysis, Visualization, Writing – review and editing. Javier Quinto: Data collection, Conceptualisation, Writing – original draft, Formal analysis, Writing – review and editing. Sofia Bajocco: Formal analysis, Writing – review and editing. Sandra Martínez-Pérez: Data collection, Visualisation. Silvia Gisondi: Conceptualisation, Writing – review and editing. Ascenciòn Padilla: Data collection, Formal analysis, Writing – review and editing. Esther Sánchez-Almodóvar: Data collection, Formal analysis, Writing – review and editing. Alessandro Campanaro: Conceptualisation, Writing – review and editing. Estefanìa Micó: Data collection, Conceptualisation, Writing – original draf, Funding acquisition, Supervision, Project administration, Writing – review and editing.

Chapter 3

This chapter includes one article currently in preparation for publication

Lenzi et al., in prep (pp 108 – 138*)*

All co-authors of the papers cited above have granted their permission for these articles to be incorporated into the present doctoral thesis.

Thesis introduction

Forest ecosystem

Forest distribution and diversity

Forests are among the most widespread and multifunctional ecosystems, playing a central role in ecological processes and human well-being. Beyond their economic value, forest ecosystems support a wide range of regulating and supporting services essential for environmental stability. Specifically, forests play a pivotal role in carbon storage, nutrient cycling, water regulation, soil protection and slope stabilization, as well as in moderating air temperatures. In addition to these regulating and supporting functions, forest ecosystems supply timber and a wide range of non-wood products that are essential for human societies (FAO, 2020).

In Europe, more than 40% of land surface is covered by woodlands (EEA, 2016) and in the last 25 years, forested areas have expanded by approximately 10%, reflecting ongoing land-use changes and forest management policies across the continent (Forest Europe and FAO, 2015). A remarkable diversification in terms of tree composition and structural characteristics can be observed encompassing a wide range of forest environments across Europe. In order to describe such heterogeneity, the European Environment Agency proposed the European Forest Type (EFT) classification in 2006, grouping 79 forest habitat types into 14 broader categories (EEA, 2006; Barbati et al., 2014). Within this framework, boreal and hemiboreal coniferous forests dominate northern Europe, together accounting for approximately 40% of the total forested area. Italy, encompassing Alpine, Continental and Mediterranean biogeographical regions, hosts nearly half of all EFT categories identified at the European scale (Borghi et al., 2024). Indeed, forests cover about 30.2% of the national territory, a proportion that rises to approximately 36.7% when other wooded lands are included (INFC, 2015). In addition, it is calculated that Italian forest totalised an increment of about 87% in the last century (Camarretta et al., 2018). Such a growth is largely attributable to abandonment of rural land, especially in mountainous and marginal agricultural zones, which has led to spontaneous forest expansion (Malandra et al., 2018).

Deadwood

Deadwood is an essential structural component of forest ecosystems and is generally defined as all non-living woody biomass that has not yet been integrated into the soil (FAO, 2025). It includes standing dead trees (snags), fallen logs, large branches, tree stumps and other woody fragments of different dimensions (i.e., coarse wood debris, CWD generally ≥ 10 cm) (Clark et al., 1998). This broad definition captures both aboveground and belowground deadwood arising from natural mortality and disturbance processes (e.g., windthrow, senescence, disease) as well as from anthropogenic influences (e.g., harvesting residues) and is central to quantifying structural complexity in forests (Paletto et al., 2012; Rondeux et al., 2012; Kunttu et al., 2015). Deadwood is ubiquitous in forests ecosystems worldwide, but its abundance and spatial distribution vary widely depending on forest type, disturbance history and management regime. At the global scale, recent assessments, indicate that it represents up to about 20% of living biomass in temperate forest regions (FAO, 2025), while, within Europe, forests show a pronounced geographical gradient in both the amount and spatial distribution of deadwood (Forest Europe, 2015; Alberdi et al., 2020). Indeed, harmonised data from the International Co-operative Programme on Assessment and Monitoring of Air Pollution Effects on Forests (ICP Forests[1]) indicate a continental mean deadwood volume of approximately 15–16 m³/ha, but with an uneven distribution (Puletti et al., 2017b; 2019): at regional scale, higher deadwood volumes are mainly associated with Central and Northern Europe (range from about 22 to more than 30 m³/ha), and in particular with mountainous and less intensively managed woodlands, where long rotation periods, high-forest systems and protected areas favour the accumulation of standing and lying deadwood (e.g., exceeding 100 m³/ha)). In contrast, lower deadwood amounts are typically observed in Southern and Mediterranean Europe and in parts of Western Europe, where historical and current management practices, such as coppicing systems and continuous timber removal, have reduced the persistence of large and old deadwood elements (Kirby, 1992; Puletti et al., 2017b). Within this framework, Italy reflects the general Mediterranean pattern, with comparatively low average deadwood volumes at the national scale and marked spatial variability, with higher values mainly restricted to mountain forests and protected areas, whereas lowland and traditionally managed stands generally contain much smaller deadwood amounts (Paletto and Tosi, 2010; Puletti et al., 2019).

Moreover, deadwood is recognised as a key element supporting multiple ecosystem functions and contributing to biogeochemical processes, biodiversity conservation and forest

[1] https://www.icp-forests.net/

resilience (Harmon et al., 1986; Fridman and Walheim, 2000; Müller and Bütler, 2010). In particular, deadwood represents a substantial carbon stock and an active reservoir in the forest carbon cycle: at the global scale it hosts approximately 10% of total forest biomass (FAO 2025) and contributes to long-term carbon storage, with a gradual release of carbon to the soil and the atmosphere during decomposition (Zell et al., 2009; Wijas et al., 2024). This processes, carried out by detritivores invertebrates, fungi, and bacteria, also plays a fundamental role in nutrient cycling and soil formation, releasing organic matter and nutrients and improving the physical structure of forest soils (Zalamea et al., 2007; Shannon et al., 2022; Błońska et al., 2024; Stokland and Alfredsen, 2024). Finally, the decaying wood strongly supports and enhances forest biodiversity by providing a wide variety of microhabitats whose characteristics depend on tree species, wood size, position, decay stage, exposure and microclimatic conditions (Siitonen, 2012; Stokland, 2012a; Larrieu et al., 2018). These niches are critical for a broad range of organisms, including vascular plants, bryophytes, lichens, fungi, arthropods and vertebrates, and contributes to higher levels of species richness and functional diversity within forest communities (Lassauce et al., 2011; Stokland et al., 2012c; Doerfler et al., 2018).

Climatic and human stressors

Nevertheless, these ecosystems are increasingly vulnerable, subject to a complex suite of pressures that compromise their health, structure and ecological functioning, (Romeiro et al., 2022). Three main categories have been identified, such as climate-related stressors, human actions and abandonment of traditional land-use practices (Seidl et al., 2017; Lecina-Diaz et al., 2021)

Meteorological anomalies, such as rising temperatures, changes in precipitation patterns, extended droughts and extreme events (e.g., wind, storms, heavy rainfall, wildfires) are having a relevant influence on European forest ecosystems (Calvin et al., 2023; Knutzen et al., 2025) and their impact seems to increase over time (Abbass et al., 2022; Wasserman and Mueller, 2023). Specifically, forests of central countries exhibited a significant increase in tree cover loss and defoliation (~9.4%), conversely southern ones appeared relatively more resilient, likely due to their historical adaptation to arid conditions, while alpine forests showed minor impacts (Knutzen et al., 2025). In addition, reduced soil moisture and repeated heat peack can lead to stress condition for trees, making them more weak and vulnerable to pest outbreaks, such as those by the bark beetle *Ips typographus* (Linnaeus, 1758) attacking Norway spruce (*Picea abies* (L.) H.Karst., 1881) woodlands (Seidl et al., 2017; Hlásny et al., 2021). Such phenomena lead to a reshaped forest structure, with variations in

productivity and carbon sequestration, but also could provide altered deadwood dynamics, also influencing habitat availability for species which rely on these resources (Štraus and Bončina, 2025).

Finally, it deserves to be emphasised that even ecosystems traditionally considered resilient are now approaching their physiological limits, underscoring the urgent need for region-specific forest management strategies and harmonised long-term monitoring frameworks aimed at mitigating future climate-induced damages (Lindner et al., 2010; Knutzen et al., 2025).

Beyond climatic stress, human management practices remain key drivers of forest dynamics, and thus conservation. Intensified logging, biomass extraction, planting trees for timber and maximising cutting for wood quality, are practices that deeply reshape forests, reducing diversity in terms of structure and heterogeneity, species composition and deadwood availability (Schall et al., 2018b; Hui et al., 2019; Latterini et al., 2023).

Worldwide humans started reshaping forest lands since Neolitic era (~8'000 years ago) with the advancement of agriculture and animal husbandry (Lambin and Meyfroidt, 2011; Ellis, 2021; Nogué et al., 2025). Actually, it is estimated that to date, approximately half of the world's pristine forests have been lost, with the remnants covering about 24% of global woodlands (Butler and Laurance, 2008; Laurance et al., 2009); whereas in Europe about 0.7% of the total forest area still retains the structural attributes of primary forests and hosting a valuable biodiversity (Eckelt et al., 2018; Sabatini et al., 2018). According to the latest FAO reports (FAO, 2016, 2020), global deforestation rates reached approximately 130,000 km² per year between 1990 and 2005. Nevertheless, the overall percentage of forest loss has remained relatively limited, as these losses have been partly offset by reforestation and afforestation activities worldwide. However, it should be emphasised that such processes cannot fully replicate the ecological dynamics and long-term equilibrium typical of old-growth forests. As a consequence, a substantial portion of forest structural complexity and associated biodiversity may be lost, even when overall tree cover changes only marginally (Betts et al., 2017; Hill et al., 2019).

In addition, traditional land uses (e.g., wood-pasture systems, open canopy forestry, mixed stands) often supporting higher structural complexity, are now under an increasing abandonment in favour of "efficient" timber plantations, leading again to a reduction of availability of such functional niches (Bughalho et al., 2011; Mantero et al., 2020; Micó et al., 2022).

Saproxylic organisms

Forests are among the most biologically diverse terrestrial ecosystems on Earth, hosting more than 80% of terrestrial species (FAO, 2020). They provide a wide array of habitats supporting organisms from microbes and fungi to plants, arthropods and vertebrates (Stokland et al., 2012a). This high diversity is largely driven by structural complexity, vertical stratification, canopy extension, features that in turn determine the presence and richness of wood-related microhabitats (Siitonen, 2012; Larrieu et al., 2018).

Considering all forest types, it is estimated that 25% of the inhabiting species are strictly dependent on the presence of dead or decaying wood to survive, at least for one phase of their life cycle. These organisms are called "saproxylics" (Speight, 1989; Stokland, 2012b). Such a term covers a wide range of taxa encompassing several species, nowadays not reliably quantifiable due to the lack of knowledge we have, consider, for instance, that the life cycle and ecological niche are fully known for only 900 saproxylic species. More accurate and comprehensive researches covering the available knowledge about the number of species depending on deadwood, refer to northern European countries: e.g., the Nordic Saproxylic Database (Stokland and Meyke, 2008) lists about 7,500 saproxylic species inhabiting boreal and continental forests (a conservative estimate) (Stokland, 2012b).

Saproxylic beetles

Beetles (Coleoptera) represent a quite diverse and ecologically significant group, including approximately a quarter of the known species (~ 400,000) (Zhang, 2013; Stork, 2018) and occupying all the terrestrial environments, as well as, some marine ones (Doyen, 1976). Globally, ~2,000 Coleoptera families are recognised (Figure 1), and it is estimated that around 2/3 of them are present in Europe, encompassing a total of 130,000 species (Audisio et al., 2015). Among saproxylic taxa, together with fungi, beetles represent the most important component of organisms related to dead wood, as well as the main characters dwelling the process of wood decomposition, predation and organism control, seed dispersal, and even pollination (Speight, 1989; Siitonen, 2012). Estimations focused on Nordic European area list a total of 1,447 saproxylic beetle species for those countries, while the European Red List of saproxylic beetles, stated that the total number of species in Europe could be close to 4,000 (Cálix et al., 2018).

Such a taxonomic diversity also reflects a great diversification and specialisation of evolutionary patterns which over time have led organisms to exploit as food or refuge a relevant number of forest niches and tree-related microhabitats (Stokland, 2012b; Stokland

et al., 2012c; Carpaneto et al., 2015) (Table 1) . Some saproxylic beetles develop beneath the bark, feeding on the outer and most nutrient-rich layers of wood (i.e., sap feeders and inner-bark consumers). Others exploit wood at various stages of decay: from recently dead substrates (i.e., xylophagous species) to those in advanced decomposition, where wood material is extensively mixed with fungal and microbial components (i.e., saproxylophagous species). Many taxa are associated with saproxylic fungi (i.e., fungivores), some feeding on fungal fruiting bodies (i.e., mycetophagous), while others consuming fungal mycelium developing within deadwood (i.e., mycophagous species). Remarkably, certain beetles have evolved mutualistic associations with fungi; they cultivate fungal mycelium within their galleries and actively transport fungal spores when moving from a host tree to another (the so-called "ambrosia beetles," including species of Lymexylidae and Curculionidae Platypodinae and Scolytinae). Finally, a diverse assemblage of species live at the expense of other saproxylic organisms, such as parasites, parasitoids and predators.

Table 1. List of trophic guilds characterising saproxylic beetle community. Carpaneto et al., 2015

Guild	Details
AR	Arecophagous, i.e., saprophytophagous or spermophagous on Arecaceae (palms)
CO	Commensal of SX/XY or of other saproxylic insects
HW	Saprophagous in small water pools inside hollow trees
MB	Mycetophagous on carpophora of large fungi (mostly Polyporales) growing on veteran trees or on old stumps
MF	Bryophytophagous developing on mosses growing on veteran trees or on old stumps
MM	Myrmecophilous o melittophagous inside hollow trees or stumps hosting colonies of ants or of other social Hymenoptera
MY	Mycophagous (developing on ifae of saproxylic fungi or on micromycetes, yeasts and Myxomiceta)
NI	Commensal in bird or small mammal nests, inside hollow trees larval
PA	Parasitoid of SX/XY or of other saproxylic insects
PR	Predator (as larvae or imagoes) of SX/XY or of other saproxylic insects
SF	Feeding on fermented sap and exudates (usually including a mixture of bacteria and yeasts) produced by trees attacked by XY, fungi or wounded by external physical agents
SP	Saprophytophagous on rotting vegetal matter associated with dead wood and wood debris
SS	Saproxylophagous in fragments of dead wood present in the soils among roots and stumps
SX	Saproxylophagous in dead wood during the whole process of its decomposition, including the wood mould inside hollow trees
UN	Trophic category unknown
WX	Saproxylophagous associated with dead wood completely or partially submerged in water (rivers, lakes, ponds, channels, wetlands, lagoons)
XB	Saproxylophagous associated with dead wood (trunks, branches and fragments) deposited by the sea along sandy beaches, shores and sand dunes
XY	Xylophagous (also developing on healthy trees)

Threats and conservation

Although much remains to be understood about saproxylic beetles, this group is nonetheless relatively well documented compared to many other insect taxa, including several beetle groups and entire insect orders that remain largely neglected in ecological research (Wilson, 2017). For instance, the International Union for Conservation of Nature (IUCN[2]) has produced reports assessing saproxylic beetles conservation status on different scales: European (Cálix et al., 2018), Mediterranean (García et al., 2019) and Italian (Carpaneto et al., 2015). All reports investigated a number of species (693, 320 and 2,049, respectively) resulting in 17.9% of species considered threatened across Europe, 32% across Mediterranean regions and 20.5% within Italy.

The above-mentioned assessments show that habitat loss and environmental degradation associated with intensive forest management represent major drivers of biodiversity decline (Nieto, 2010; Cálix et al., 2018). The most critical factors include the removal of deadwood and the reduction of veteran and over-mature trees, which represent essential substrates for forest organisms such as standing deadwood, fallen logs, tree hollows, and coarse woody debris (Stokland et al., 2012a). Among silvicultural practices, clear-cutting is regarded as one of the most invasive interventions, as it removes all trees within a stand and eliminates most woody material, thereby profoundly altering forest structure and functioning and causing severe impacts on saproxylic communities, including already rare and threatened species (Sverdrup-Thygeson and Ims, 2002; Heikkala et al., 2016; Norkute et al., 2025). Similarly, non-selective and production-oriented thinning represents a strong pressure on these organisms (Müller et al., 2008) because the systematic removal of medium- and large-sized trees prevents stands from developing the size, age and structural complexity that are known to be key drivers of forest biodiversity (Stokland et al., 2012b; Gossner et al., 2016). In addition, as previously mentioned, an important role is also played by the recent transition from traditional agriculture and grazing systems to agro-industrial systems. In fact, these landscapes were often characterised by large, old trees that provide habitats for numerous saproxylic species (often consisting in organisms extremely vulnerable to such changes) (Micó et al., 2022; Henneberg et al., 2025). Furthermore, these practices involve the removal of all dead wood present in the managed stands, including logging residues and stumps, and such a trend has also intensified in recent years as cutting residues have gained economic

[2] https://iucn.org/about-iucn

value for bioenergy production from forest biomass (Rudolphi and Gustafsson, 2005; Lin and Ge, 2020).

Given this, both national and international regulations have been established to protect several saproxylic species that are considered ecologically important and particularly vulnerable to habitat degradation, many of which are also regarded as umbrella and/or flagship species because of their ability to represent broader conservation needs and to promote habitat-level protection (Ducarme et al., 2013; Thomas-Walters and Raihani, 2017). A central instrument in Europe is the Habitats Directive (Council Directive 92/43/EEC), which aims to ensure the long-term conservation of natural habitats and species of Community interest and has led to the creation of the Natura 2000 network, an international coordinated network of protected areas across Europe (Commission et al., 2015).

Within this framework, a subset of saproxylic beetle species (Table 2) is legally protected at the EU level, with 21 species listed in Annex II and eight also included in Annex IV as strictly protected taxa (Council Directive 92/43/EEC). The Directive further requires Member States to monitor the conservation status of all listed species and habitats and to report every six years on their status and on the effectiveness of conservation measures (Council Directive 92/43/EEC, Art. 11 and 17 ;), by adopting harmonised standard protocols (DG Environment, 2023). For saproxylic beetles, meeting these obligations remains particularly challenging, mainly due to their cryptic life cycles and strong association with old growth and dead wood structures, requiring substantial field effort, in terms of time, spatial coverage, and financial resources. In addition, standardised survey protocols specifically designed for saproxylic beetles have only been developed in recent years, and this has so far limited the implementation of long-term monitoring schemes and the comparability of data among studies (Bardiani et al., 2017; Campanaro et al., 2017; Carpaneto et al., 2017; Hardersen et al., 2017; Redolfi De Zan et al., 2017)

Citizen science

Citizen science (CS) refers to a research approach in which members of the public, often non-professional volunteers, participate in systematic scientific data collection, analysis, interpretation, and sometimes dissemination of findings (Shirk et al. 2012). While precise definitions may vary (Heigl et al., 2019; Haklay et al., 2021), a CS initiative can be considered as such if it follows 10 fundamental principles provided in Table 2 (ECSA, 2015). The earliest forms of activities now recognized as CS can be traced when non-professional enthusiasts recorded observations to describe and better understand the natural world, with examples ranging from local experiences to overseas explorations of the 15th-19th centuries (Aono and Kazui, 2008; Frigerio et al., 2021). Subsequently, one of the first structured CS examples emerged in the early 20th century with the American volunteer-based initiatives Audubon Society's Christmas Bird Count[3], which since 1901 has been engaging volunteers in systematic bird observations on more than 2500 avian species (Dunn et al., 2005).

Today, CS is considered a highly adaptable approach implemented in hundreds of projects (ECSA[4]) across several scientific fields, e.g., astronomy, natural science, ecology, public health, as well as in the humanities (Kullenberg and Kasperowski, 2016; Fraisl et al., 2026). Based on the degree of involvement and participation of volunteers, CS projects can be classified in different categories (Shirk et al., 2012), such as: i. contractual projects, where participants commission professional researchers to conduct investigations; ii. contributory projects, usually designed by scientists, in which volunteers are involved in data collection; iii. collaborative projects, where participants contribute to project design, data analysis, or dissemination; iv. co-created projects, jointly developed by scientists and members of the public, where people actively conduct most or all stages of the research; v. collegial contributions, in which non-professionals independently carry out research with different levels of acceptance by scientific institutions and researchers.

In natural sciences, CS supports diverse applications, such as monitoring atmospheric and water quality (Jollymore et al., 2017; Lu et al., 2022), cataloguing species distributions (Feldman et al., 2021; Matutini et al., 2021; O'Neill et al., 2023), monitoring population of species of conservation interests and tracking changes (Chandler et al., 2017; Jollymore et al., 2017; Soroye et al., 2018; Fuccillo Battle et al., 2022), mapping non-native invasive organisms (Crall et al., 2015; Encarnação et al., 2021; Howard et al., 2022).

[3] https://www.usgs.gov/centers/eesc/science/north-american-bird-phenology-program
[4] https://www.ecsa.ngo/projects-2/

Table 2. Citizen science ten principle. From the European Citizen Science Association (www.ecsa.citizen-science.net)

N.	Definition
1	Citizen science projects actively involve citizens in scientific endeavour that generates new knowledge or understanding. *Citizens may act as contributors, collaborators, or as project leader and have a meaningful role in the project.*
2	Citizen science projects have a genuine science outcome *For example, answering a research question or informing conservation action, management decisions or environmental policy*
3	Both the professional scientists and the citizen scientists benefit from taking part. *Benefits may include the publication of research outputs, learning opportunities, personal enjoyment, social benefits, satisfaction through contributing to scientific evidence e.g. to address local, national and international issues, and through that, the potential to influence policy.*
4	Citizen scientists may, if they wish, participate in multiple stages of the scientific process. *This may include developing the research question, designing the method, gathering and analysing data, and communicating the results.*
5	Citizen scientists receive feedback from the project. *For example, how their data are being used and what the research, policy or societal outcomes are.*
6	Citizen science is considered a research approach like any other, with limitations and biases that should be considered and controlled for. *However unlike traditional research approaches, citizen science provides opportunity for greater public engagement and democratisation of science*
7	Citizen science project data and meta-data are made publicly available and where possible, results are published in an open access format. Data sharing may occur during or after the project, unless there are security or privacy concerns that prevent this.
8	Citizen scientists are acknowledged in project results and publications.
9	Citizen science programmes are evaluated for their scientific output, data quality, participant experience and wider societal or policy impact.
10	The leaders of citizen science projects take into consideration legal and ethical issues surrounding copyright, intellectual property, data sharing agreements, confidentiality, attribution, and the environmental impact of any activities.

Technological advancements have greatly enhanced the effectiveness of such initiatives, by enabling more accurate, scalable, and sophisticated data collection and analysis. Indeed, digital platforms and mobile applications, such as iNaturalist[5] and eBird[6], usually equipped with location and images recording system and automated identification features, serve as fundamental tools for engaging participants and standardising environmental data gathering (Hognogi et al., 2023; Rodríguez-Loinaz et al., 2024). Moreover, the integration of machine learning into CS applications has improved on-field guidance and data processing, allowing participants to collect higher-quality information even with limited prior expertise (Franzen et al., 2021). Given this, CS contributes to generate large volumes of occurrence data across broad geographic and temporal scales (Pocock et al., 2018), providing ecological insights that are often unattainable by professional scientists alone (Walker and Taylor, 2017; Alfeus

[5] https://www.inaturalist.org/
[6] https://ebird.org/home

et al., 2025; Mason et al., 2025). Finally, when these data are combined with professional analyses and statistical methods accounting for sampling biases, such occurrence data can serve as basis for more advanced investigations, including species distribution models (SDMs) (Robinson et al., 2020; Redolfi De Zan et al., 2023), trend analyses (Dennis et al., 2017; Horns et al., 2018; van Swaay et al., 2025), as well as for conservation planning (McKinley et al., 2017).

Despite such effectiveness, some challenges still characterise CS initiatives, starting from data quality to the retention of participants. For instances, especially projects that are less structured, may exhibit issues concerning standardisation of data collection and their validation (Johnston et al., 2023). In fact, observer behaviour can drive uneven sampling effort across space and time, with volunteers more likely to record data in accessible or preferred locations or daily times and seasons (Mair and Ruete, 2016; Johnston et al., 2020, 2023). Taxonomic bias is also common, with smaller, less detectable, or less charismatic taxa underrepresented in observations (Steger et al., 2017; Barbato et al., 2021; Callaghan et al., 2021). Considering data validation, different approaches can be implemented, such as a mandatory control performed by experts and professionals involved in the project, or a validation made by the community of participants, relying on a great number of people participating and the knowledge acquired through experience gained in the project (Callaghan et al., 2019). Lastly, a remarkable issue is the long-term engagement of participants (Frigerio et al., 2018), which requires a great deal of effort not only in promoting the initiative, but also in encouraging consistent contributions rather than one-off observations (Richter et al., 2018; Robinson et al., 2020).

As a final remark, beyond its scientific contributions, CS also has important personal, social and political implications (Walker et al., 2021). By actively involving participants in the research process, it promotes public engagement with science, enhances environmental awareness and learning, and contributes to the development and sharing of cultural and local knowledge (Bonney et al., 2016). In addition, CS supports the creation and strengthening of people communities by fostering collaboration and dialogue between citizens and researchers, thus helping to bridge the traditional gap between science and society (Strasser et al., 2018), Importantly, participation in CS initiatives can also increase individuals' sense of ownership and responsibility towards environmental issues, empowering citizens to engage more actively in decision-making processes and to support conservation actions (Schade et al., 2021; Walker et al., 2021).

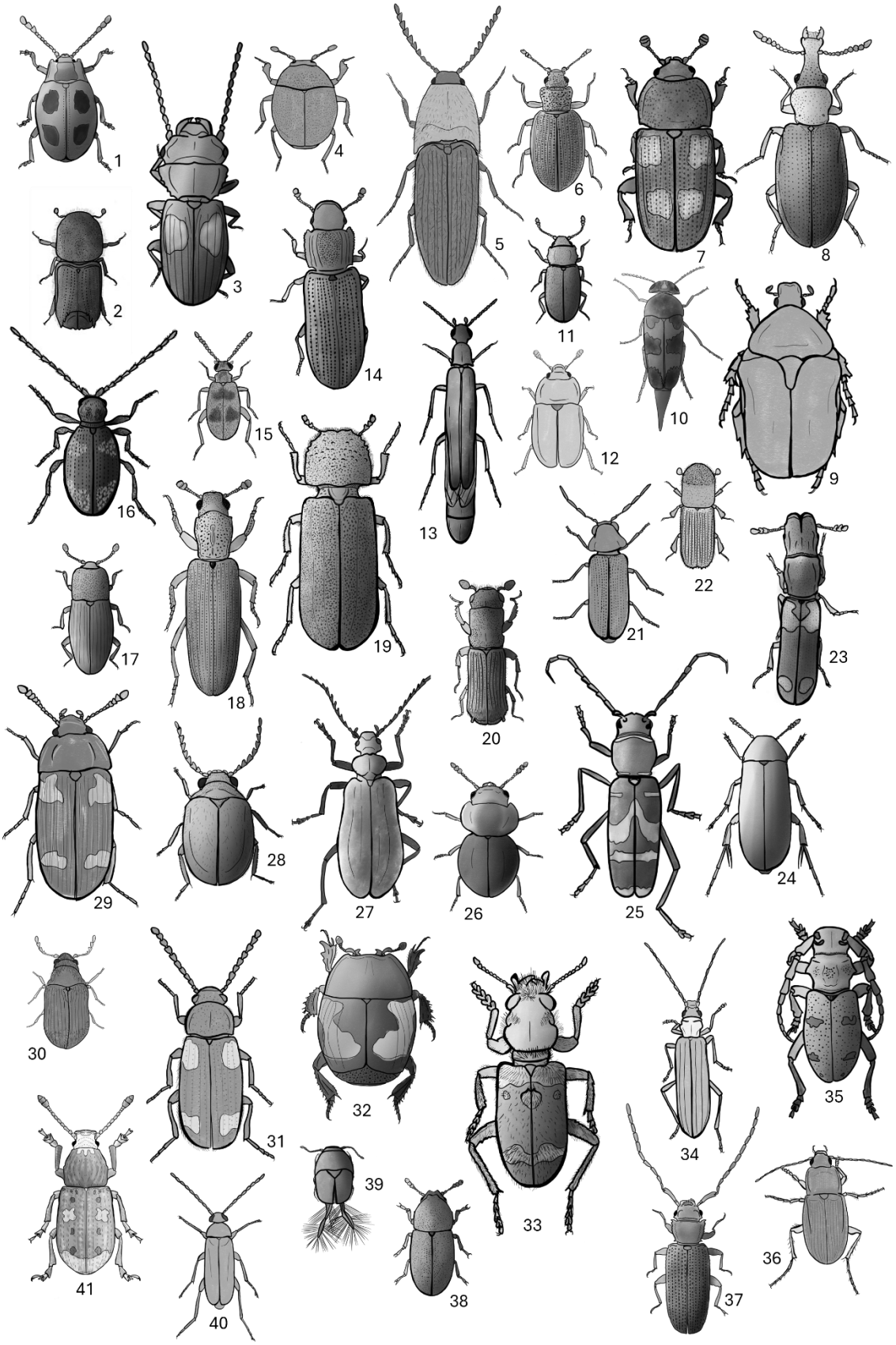


Figure 1. Representation of some families of saproxylic beetles: Endomychidae (1), Curculionidae Scolytinae (2, 22), Laemophloeidae (3), Histeridae (4, 32), Elateridae (5), Latridiidae (6), Nitidulidae (7,12), Salpingidae (8), Scarabaeidae (9), Mordellidae (10), Cryptophagidae (11), Lymexylidae (13), Zopheridae (14), Aderidae (15), Ptinidae (16, 21, 30), Cerylonidae (17), Bothrideridae (18), Bostrichidae (19), Curculionidae Platypodinae (20), Trogossitidae (23), Melandryidae (24), Cerambycidae (25, 35), Leiodidae (26), Pyrochroidae (27), Scirtidae (28), Mycetophagidae (29, Tenebrionidae (31), Cleridae (33), Oedemeridae (34), Carabidae (36), Silvanidae (37), Ciidae (38), Ptiliidae (39), Scraptiidae (40), Anthribidae (41)

Chapter 1 – Citizen Science for saproxylic beetle monitoring and conservation

Summary

Species occurrence data are essential for understanding population dynamics and informing conservation planning, and citizen science (CS) has become an increasingly important approach for collecting large-scale biodiversity information, particularly for charismatic and protected insect taxa. The present chapter provides results from the Italian long-term citizen science initiative MIPP/InNat (2014–2024), aimed at improving distributional knowledge of protected insects in Italy, through the direct involvement of citizens. Investigations were performed in order to: i. report the general results obtained by the project, ii. evaluate the increase of knowledge of target species distribution, iii. assessed the potential of volunteer-generated photographic records for ethological investigations with a focus on *Lucanus cervus* images, and iv. examine participation dynamics and drivers of long-term engagement through a dedicated sociological survey of project volunteers. After 11 years of activities, the project generated 5,968 validated records (6,292 individuals) submitted by 1,180 participants. Validated occurrence data of nine target species (i.e., five coleopterans, three lepidopterans and one orthopteran) collected between 2014 and 2021 were analysed. By combining spatial analyses of 10 × 10 km UTM grid coverage, temporal trends and distribution range estimates we assessed an increase in distributional data over time, also confirming by changes in the shape and density of *alpha hulls* polygons. Considering, eco-ethological insights, despite not being collected for behavioural purposes, a substantial subset of *L. cervus* photographs enabled the detection of sex-specific differences in behaviour, substrate use and activity, in line with what is known from the literature. The validity of such projects is therefore confirmed, also in terms of providing further information on the ecology and ethological traits of the target species. and confirmed known phenological patterns. Finally, the social survey revealed two distinct participant profiles based on reporting regularity and showed that motivation related to nature interest, social interaction and communication strategies strongly influenced sustained participation.

Overall, our results demonstrate that long-term citizen science initiatives can substantially enhance distributional knowledge of protected insects, provide complementary information on species ecology, and represent an effective framework for engaging and retaining volunteers in biodiversity monitoring.

Introduction

In a changing world, exacerbated by the climate crises, environmental degradation and biodiversity loss (Pereira et al., 2012, 2024), occurrence data are a valuable source of information that improves our knowledge on species distribution and population dynamics (Isaac and Pocock, 2015), providing a reliable baseline for conservation planning (Powney and Isaac, 2015). Concerning insects, their taxonomic diversity, species distribution, local conservation status and population trends are still poorly known (Mora et al., 2011; Wilson, 2017), despite proofs of their decline in diversity and abundance (Hallmann et al., 2017, 2021, Wagner et al., 2021b). This can be apply not only to hyper-diverse and little-studied groups, but also to more charismatic and easily detectable taxa, including those protected at national or international level and/or flagship/umbrella species (Bowen-Jones and Entwistle, 2002; Caro et al, 2004). Importantly, these taxa are often employed as proxies for a rich community and as indicators for habitat conservation status (Lindenmayer and Westgate, 2020), resulting in often being targeted by conservation programmes and initiatives. In addition, the European Commission requires Member States to monitor biodiversity through constant surveillance (Art. 11 of Habitats Directive 92/43/ECC) of protected species and habitats (i.e. listed in Annexes I, II and IV of the Habitats Directive 92/43/ECC) and to report the results every 6 years (ex Art. 17 of Habitats Directive 92/43/ECC). In order to comply with these obligations, a large number of spatially and temporally distributed records are needed, activity that requires energy- and time-consuming efforts for data collection and analysis.

Since the late twentieth century, an engaging and promising approach for collecting a consistent number of records has been represented by the citizen science (CS). This term refers to an approach based on the involvement of volunteers from the general public in scientific processes under the coordination of experts (ECSA, 2015, Eitzel et al., 2017; Shanley et al., 2019). Such initiatives find applications in many scientific fields (Bonney et al., 2009; Kullenberg and Kasperowski, 2016, Chandler et al., 2017; Pocock et al., 2018), with a remarkable number of emerging projects (most are accessible through European or global repositories, such as eu-citizen.science[7] and SciStarter[8]). A part of them is dedicated to the study of insects, often focusing on charismatic groups (van Tongeren et al., 2023; Sheard et al., 2024) which are easily detectable and identifiable also by non-experts after specific training, such as pollinators (e.g. bees, bumblebees and butterflies) (van Swaay et

[7] https://citizenscience.eu/
[8] https://scistarter.org/

al., 2008; Dennis et al., 2017; Barahona-Segovia et al., 2023) and some large-sized and conspicuous Coleoptera (Percy et al., 2000; Losey et al., 2012; Mason et al., 2015; Campanaro et al., 2017; Thomaes et al., 2021; Bardiani et al., 2022; Lenzi et al., 2023). Considering these groups, many studies have shown that the involvement of volunteers in collecting occurrence data of observed individuals provides important information on the distribution of species as well as their habitat requirements (Lucky et al., 2014;Campanaro et al., 2017; Soroye et al., 2018; Brown and Williams, 2018; Matutini et al., 2021; Lenzi et al., 2022; Redolfi De Zan et al., 2023). Conversely, within ethological studies, few CS initiatives explicitly focus on this topic from the beginning, especially if targeting invertebrates. Notable exceptions are limited to groups such as Asilidae flies (Barahona-Segovia and Pañinao-Monsálvez, 2020) or hornets (e.g. *Vespa crabro*, Pusceddu et al., 2022), where citizens' observations provided insights into prey capture or territorial behaviours. However, CS would represent a valuable tool for the ethological studies, as demonstrated by already active ethological CS projects targeting non-insect species (e.g. Hecht and Rice, 2015; Goodenough et al., 2017; Frigerio et al., 2018; Fukimoto et al., 2023). Concerning the reliability of the recorded data (Kosmala et al., 2016), this is commonly ensured by two different ways: verification of species identification carried out by the community of volunteers, advanced technologies (e.g. artificial intelligence) (Leibovici et al., 2017; Aristeidou et al., 2017; López-Guillén et al., 2024), or by a team of experts (Tulloch et al., 2013; Flaminio et al., 2021). In addition, training activities result to be crucial for generating a group of volunteers prepared, aware and therefore also highly motivated (Crall et al., 2012; Turrini et al., 2018).

Finally, the social dimension of citizen science initiatives cannot be overlooked. Indeed, citizen science has been shown to generate a wide range of impacts on participants, influencing not only the scientific sphere but also the social one (Bonney et al., 2021; Wehn et al., 2021). It generates knowledge, creates learning opportunities, improves awareness about biodiversity and nature conservation, enables civic participation and bridges the gap between specialists and non-experts (Strasser et al., 2018). Moreover, participation in CS initiatives can also increase sense of ownership and responsibility towards environmental issues, empowering citizens in decision-making processes and supporting conservation actions (Schade et al., 2021; Walker et al., 2021).

In this context, three relevant challenges concerning the application of CS to environmental monitoring and biodiversity conservation have been identified: *i.* the standardisation and validation of the gathered data, *ii.* the public awareness on biodiversity-related topics, *iii.* the long-term commitment of the participants (Frigerio et al., 2018; Richter et al., 2018). The

way these three challenges are addressed can severely affect the success or the failure and termination of a CS project (Morais et a., 2013).

In Italy, among a number of citizen science initiative dedicated to insects a long-term example is given by the first European LIFE project targeting protected insect species: the Project "Monitoring of insects with public participation" (LIFE11 NAT/IT/000252, from now on MIPP). It started in 2012 and in 2014 developed a web-app and an app for smartphone for enabling the public to collect distributional data of a selection of target species, then it ended in 2017 (Mason et al., 2015; Campanaro et al., 2017; Carpaneto et al., 2017). LIFE MIPP was continued and implemented by InNat project which started in 2017 under fundings from an agreement named START2000 and ended in 2024: the data gathered in both projects converged in the same database ("MIPP/InNat project" from now on). From its beginning to its end, the project covered a total of 40 protected species species (Campanaro et al., 2025), including five saproxylic beetle species: the cerambycids *Cerambyx cerdo* Linnaeus, 1758, *Morimus asper* (Sulzer, 1776) and *Rosalia alpina* Linnaeus, 1758, the scarabaeid *Osmoderma eremita* (Scopoli, 1763), and the lucanid *Lucanus cervus* Linnaeus, 1758. The latter, known as the "stag beetle" is a highly charismatic and the largest saproxylic beetle in Europe. It is mainly associated with mature deciduous forests, particularly lowland and mid-altitude oak woodlands, where it depends on rotten deadwood at ground level (Bardiani et al. 2017; Kuźmiński et al. 2020). The species is widely distributed across Europe (Franciscolo 1997; Bartolozzi and Sprecher-Uebersax 2006; Harvey et al. 2011; Bardiani et al. 2017; Méndez and Thomaes 2021) and shows marked sexual dimorphism, with males being larger and bearing highly variable, elongated mandibles (Harvey and Gange 2006; Hardersen et al. 2011; Romiti et al. 2015). Because of its conservation status (Annex II of the Habitats Directive, 92/43/EEC; Calix et al., 2018), several monitoring methods have been developed, including interception traps, transect surveys and collection of remains (Campanaro et al. 2011, 2016; Harvey et al. 2011; Bardiani et al. 2017; Thomaes et al. 2021). Owing to its distinctive morphology and public appeal, citizen science approaches have also been applied (Méndez et al. 2017; Thomaes et al. 2021; Bardiani et al. 2022; Giannetti et al. 2023). In contrast, behavioural ecology remains comparatively poorly investigated, with only limited information on reproduction, males fightings, feeding and dispersal derived from direct observations and telemetry studies (Kawano 1997; Tini et al. 2017, 2018; Thomaes et al. 2018; Giannetti et al. 2024).

This chapter presents the main scientific results obtained within the MIPP/InNat initiative, with a particular focus on the project's effectiveness in improving knowledge of species distributions in Italy, as well as on the additional insights that the collected data can provide

for ethological and ecological investigations, using *L. cervus* as a case study. An overview of MIPP/InNat participants is also provided, with particular attention to the factors characterising volunteer participation and retention.

It should be noted that the analyses presented in this chapter are based on data collected during different periods of the project; therefore, slight discrepancies may occur among some of the total values reported.

1. Protected insect species in Italy: occurrence data from a 10-year citizen science initiative

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Materials and methods

General information and fundings

MIPP/InNat initiative engaged volunteers in collecting occurrence data of protected insects, data records started in 2014 and concluded in 2024, covering all Italian territory.

The MIPP/InNat initiative has been developed under the funds by different projects:

• the LIFE project MIPP (LIFE11 NAT/IT/000252), “Monitoring of insects with public participation,” co-funded by the European Commission [2012–2017];

• the national agreement entitled InNat "Promozione della Rete Natura 2000 e il Monitoraggio a scala nazionale di specie di insetti protetti" funded by the former Direzione Generale per la Protezione della Natura e del Mare – Ministero dell'Ambiente e della Tutela del Territorio e del Mare and the Comando Unità Forestali, Ambientali e Agroalimentari Carabinieri – Comando Carabinieri per la Tutela Della Biodiversità e dei Parchi [2017–2018];

• the national agreement entitled START2000 "Sviluppo di strumenti di coordinamento finalizzati all'attuazione degli obiettivi e delle misure di conservazione nei siti Natura 2000 compresi nelle Riserve ed altre Aree demaniali gestiti dall'Arma dei Carabinieri" funded by the former Direzione Generale per la Protezione della Natura e del Mare – Ministero dell'Ambiente e della Tutela del Territorio e del Mare and the Comando Unità Forestali, Ambientali e Agroalimentari Carabinieri – Comando Carabinieri per la Tutela Della Biodiversità e dei Parchi [2019–2022];

• the National Recovery and Resilience Plan (NRRP), Mission 4 Component 2 Investment 1.4 – Call for tender № 3138 of 16 December 2021, rectified by Decree № 3175 of 18 December 2021 of Italian Ministry of University and Research funded by the European

Union – NextGenerationEU; Award Number: Project code CN_00000033, Concession Decree № 1034 of 17 June 2022 adopted by the Italian Ministry of University and Research, CUP B83D21014060006, Project title “National Biodiversity Future Center – NBFC” [2022–2024].

Data sampling and processing

Volunteers were asked to use the project websites of the two projects or a specific app for Android and iOS (called “MIPP” and then “InNat”) to upload pictures of observed target insects. The volunteers were free as to where or when to perform the observations. The following information was required during the uploading process: 1) tentative identification (species or genus level); 2) date and hour of the sighting; 3) geografic coordinates (WGS84, decimal); 4) location; 5) additional notes.

The geographic coordinates were collected using the GPS sensor of the smartphone, manually by using Google Maps (which was accessible through the platforms) or by entering coordinates by hand. These precise coordinates were thus stored in the InNat database and were downloadable upon request during the project. Finally, the volunteers provided their e-mail addresses and a nicknames (no sensitive data were collected), to receive any feedback about their record.

The platform was developed using MySQL and was accessible with credentials by the project staff. Once a record was uploaded, it entered the project database with the initial status "pending". Subsequently, the experts validated the associated images and the information provided. If the record was "confirmed", it became visible on the project website to everyone. When no images were provided, the volunteers were contacted by the project team and were asked to provide further details on the record. Data without images were classified as valid only after careful consideration. This strict approach resulted in approximately 3% of records without images being confirmed. Moreover, even if the volunteers had not been asked to provide the number of observed individuals during data submission, an additional column about the number of the individuals observed for each record is added and this was obtained by the project staff by counting the number of specimens portrayed in each image recorded.

In order to aid the volunteers in recognising and finding the various insects, fact sheets were provided, which included information on the morphology and ecology of the target insects. Validated and confirmed records were analysed and published as a dataset in the GBIF repository (Campanaro et al., 2024)

Results

At the beginning, LIFE MIPP covered nine target species. Subsequently, during the projects InNat and START2000, additional taxa were included, reaching gradually a total of 31 protected species listed in the Annexes II and IV of the Habitats Directive, belonging to Coleoptera, Lepidoptera, Odonata and Orthoptera (Table 3). Such later additions concern also species that are rather rare, with limited and scattered distribution and whose detection requires a somewhat higher level of volunteer training and experience (e.g. *Brachytrupes megacephalus* (Lefèvre, 1827), *Papilio alexanor* Esper, 1800 and *Phengaris teleius* (Bergsträsser, 1779)). Despite the fact that fewer records were expected, these species were nevertheless included in the initiative as even the addition of a few occurrence data would be valuable for increasing the knowledge of their distribution. In general, the names of target species were based on those adopted by the Habitats Directive.

Table 3. List of target insect species of MIPP/InNat project

Target taxon	Order	Family	Annex HD
1. *Brachytrupes megacephalus* (Lefèvre, 1827)	Orthoptera	Gryllidae	II, IV
2. *Cerambyx cerdo* Linnaeus, 1758	Coleoptera	Cerambycidae	II, IV
3. *Coenagrion mercuriale* (Charpentier, 1840)	Odonata	Coenagrionidae	II
4. *Coenonympha oedippus* (Fabricius, 1787)	Lepidoptera	Nymphalidae	II, IV
5. *Cordulegaster trinacriae* Waterstone, 1976	Odonata	Cordulegastridae	II, IV
6. *Euphydryas aurinia* (Rottemburg, 1775)	Lepidoptera	Nymphalidae	II
7. *Euphydryas maturna* (Linnaeus, 1758)	Lepidoptera	Nymphalidae	II, IV
8. *Euplagia quadripunctaria* (Poda, 1761)	Lepidoptera	Erebidae	II
9. *Gomphus flavipes* (Charpentier, 1825)	Odonata	Gomphidae	IV
10. *Leucorrhinia pectoralis* (Charpentier, 1825)	Odonata	Libellulidae	IV
11. *Lopinga achine* (Scopoli, 1763)	Lepidoptera	Nymphalidae	IV
12. *Lucanus cervus* (Linnaeus, 1758)	Coleoptera	Lucanidae	II
13. *Lycaena dispar* (Haworth, 1802)	Lepidoptera	Lycaenidae	II, IV
14. *Melanargia arge* (Sulzer, 1776)	Lepidoptera	Nymphalidae	II, IV
15. *Morimus asper* (Sulzer, 1776)	Coleoptera	Cerambycidae	II
16. *Ophiogomphus cecilia* (Fourcroy, 1785)	Odonata	Gomphidae	II, IV
17. *Osmoderma eremita* (Scopoli, 1763)	Coleoptera	Scarabaeidae	II, IV
18. *Osmoderma cristinae* Sparacio, 1994	Coleoptera	Scarabaeidae	II, IV
19. *Oxygastra curtisii* (Dale, 1834)	Odonata	Corduliidae	II, IV
20. *Papilio alexanor* Esper, 1800	Lepidoptera	Papilionidae	IV
21. *Papilio hospiton* Géné, 1839	Lepidoptera	Papilionidae	II, IV
22. *Parnassius apollo* (Linnaeus, 1758)	Lepidoptera	Papilionidae	IV
23. *Parnassius mnemosyne* (Linnaeus, 1758)	Lepidoptera	Papilionidae	IV
24. *Phengaris arion* (Linnaeus, 1758)	Lepidoptera	Lycaenidae	IV
25. *Phengaris teleius* (Bergsträsser, 1779)	Lepidoptera	Lycaenidae	II, IV

26. *Proserpinus proserpina* (Pallas, 1772)	Lepidoptera	Sphingidae	IV
27. *Rosalia alpina* (Linnaeus, 1758)	Coleoptera	Cerambycidae	II, IV
28. *Saga pedo* (Pallas, 1771)	Orthoptera	Tettigoniidae	IV
29. *Sympecma paedisca* (Brauer, 1877)	Odonata	Lestidae	IV
30. *Zerynthia cassandra* Geyer, 1828	Lepidoptera	Papilionidae	IV
31. *Zerynthia polyxena* (Denis and Schiffermüller, 1775)	Lepidoptera	Papilionidae	IV

The dataset contains 5,968 occurrence records for a total of 6,292 specimens (numbers of individuals were counted, based on the images sent by the volunteers) (Figure 2): 4,577 Coleoptera, 1,568 Lepidoptera, 108 Odonata and 39 Orthoptera. Even if commonly lepidopterans are the most recorded taxa in CS projects, our result, highlighting a majority of coleopteran records, was quite expected. In fact, the LIFE MIPP was originally mostly focused on six saproxylic beetle species that had benefitted from further dissemination and scientific activity unlike the four butterflies and the one bush cricket. In addition to this, butterflies listed in the Habitats Directive Annexes are often rarer and with a more limited and/or scattered distribution in respect to coleopterans.

Approximately 97% of the records are associated with an image portraying the reported insect.

Data were collected by more than 1,800 volunteers between 2014 and 2024 during different citizen-science projects, even if the dataset contains records from 1973 to 2024 (Figure 3), as volunteers also provided occurrence data recorded previously. These data are considered useful and interesting for the purposes of the project and have been retained analysed as well. The highest number of records was collected in the years 2018, 2019 and 2020, with a total of 781, 725 and 780 records, respectively (Figure 2).

The pattern of the records collected during a year mainly reflects the months when adults of the 31 target species are usually most active, with the bulk of records having been collected in mid-July. This may be due to the fact that the majority of records are on *Lucanus cervus* (Figure 2), which has its peak of adult activity in those weeks (Figure 4).

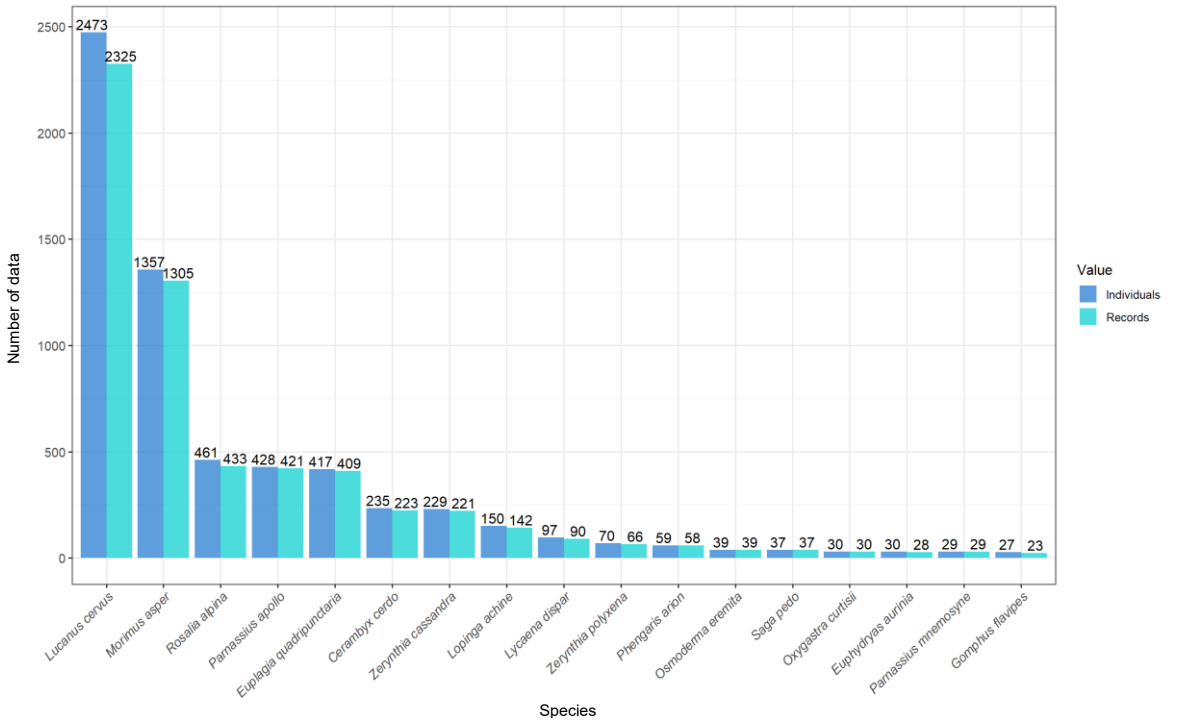
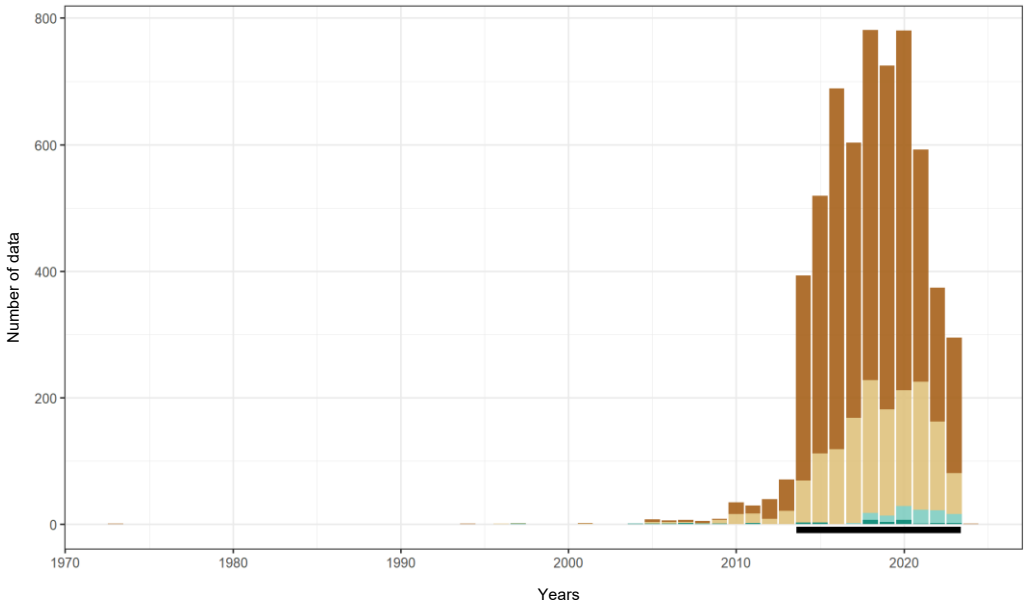


Figure 2. Barplot representing the total number of individuals and records for each insect taxon collected by the project. Only taxa with more than 20 records are plotted here.



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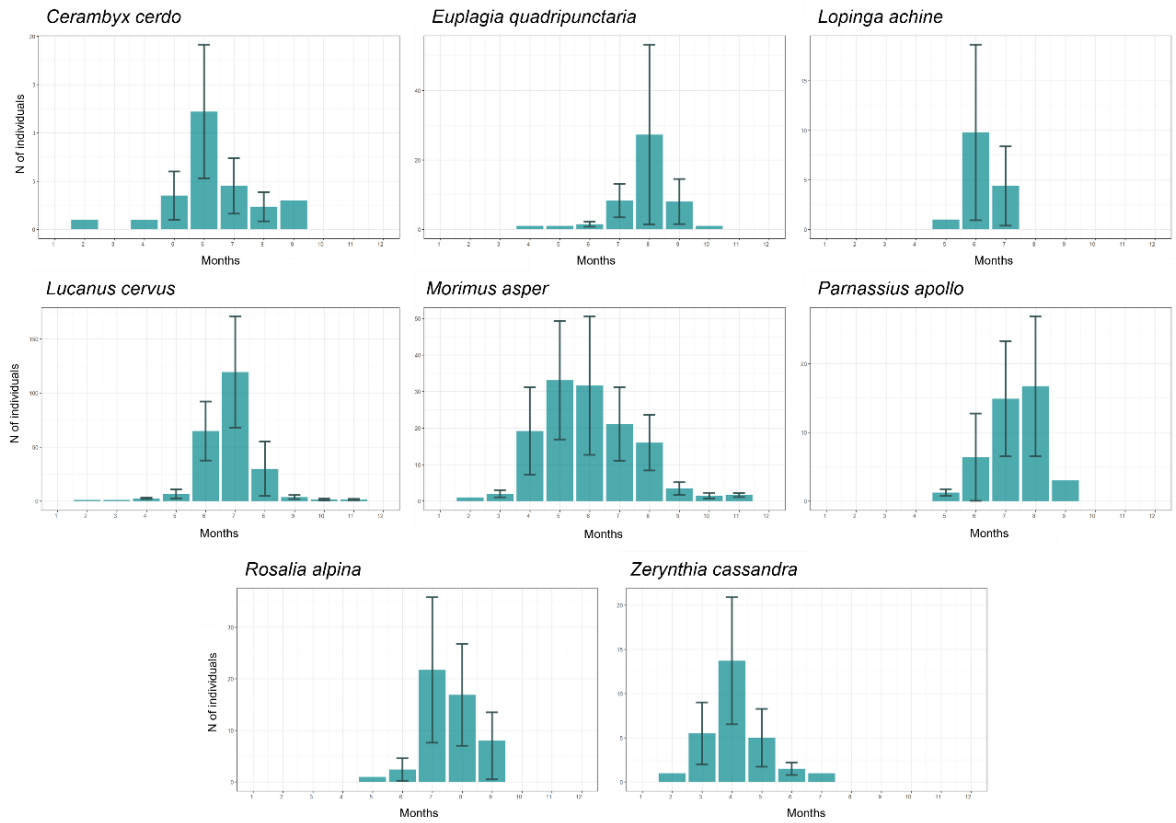


Figure 4. Barplot representing the mean montly distribution of the number of the recorded individuals , with the related standard error (grey bars). Only records from 2014 to 2023 were considered.

The dataset contains records from all the Italian territory (Figure 5). The majority of these records was collected in Central-Northern Italy possibly due to the fact that, amongst the ten most recorded species, three (i.e. *Lucanus cervus*, *Lopinga achine* and *Lycaena dispar*) are distributed exclusively in north-central regions. Moreover, five "hotspots" (Figure 5) can be observed, corresponding to protected and mountain areas in which the target species are present with quite abundant populations. The altitudes at which the target insects were recorded (Figure 6) are consistent with the species ecology. The lowest altitude recorded was 0 m a.s.l. (*Cerambyx cerdo*) and the highest altitude was 2,958 m a.s.l. (*Parnassius apollo*).

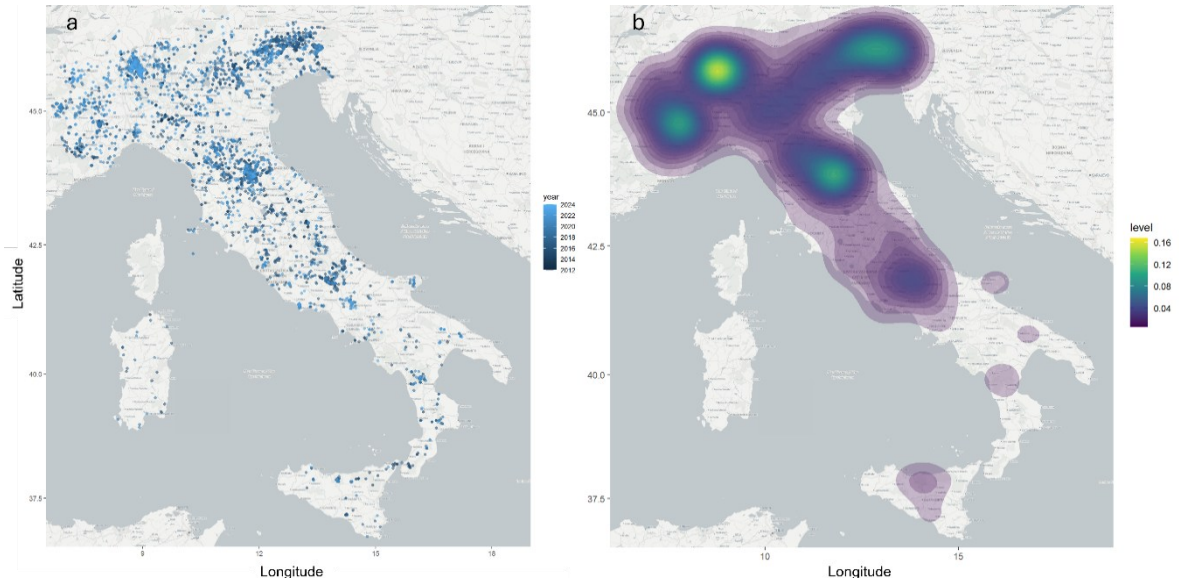


Figure 5. Geographic coverage of records. A The colour scale of the data points indicates the year of the sightings; a lighter colour indicates a more recent sighting, while a darker colour denotes older records; B Heatmap representing the concentration of records in Italy from the the lowest (in purple) to the highest (in yellow). The regions with the majority of data correspond to protected areas: Parchi Regionali dell'area Torinese (1), Parco Nazionale della Val Grande (2), Parco Regionale delle Prealpi Giulie e Parco Nazionale delle Dolomiti Bellunesi (3), Parco Nazionale delle Foreste Casentinesi (4), Parco Nazionale d'Abruzzo, Lazio e Molise (5), Parco Nazionale del Gargano (6), Parco Nazionale dell'Alta Murgia (7), Parco Nazionale del Pollino (8), Parco Regionale delle Madonie (9).

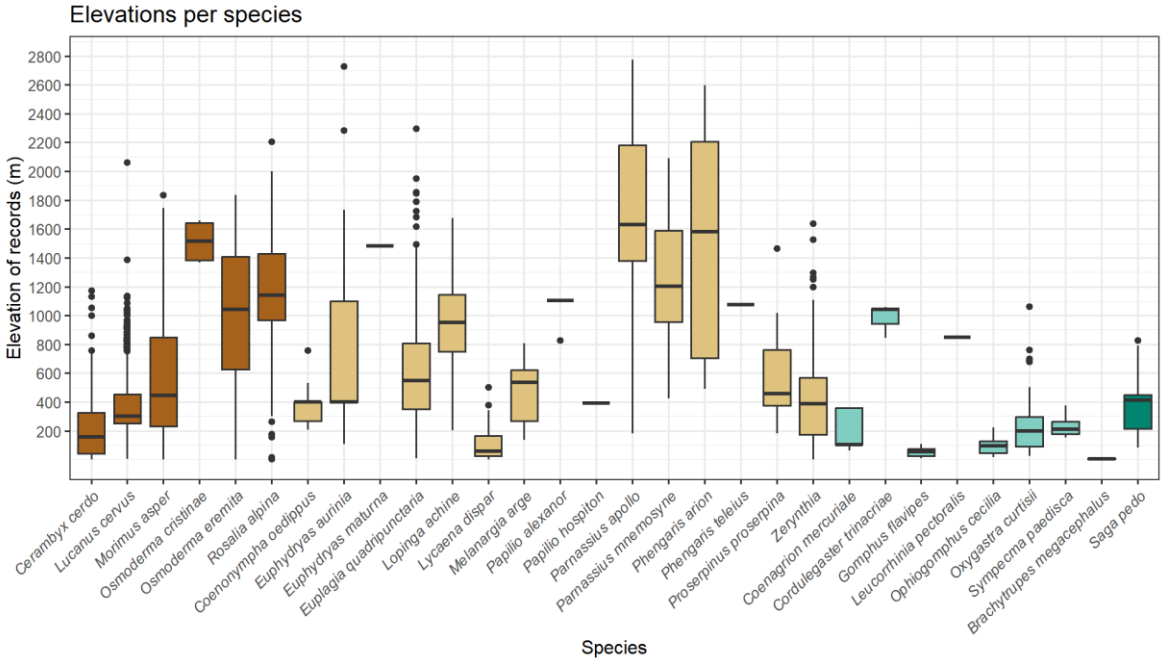


Figure 6. Boxplot showing the span of elevations at which target taxa were recorded. Orders are identified by different colours: Coleoptera in brown, Lepidoptera in light brown, Odonata in turquoise and Orthoptera in teal.

2. The longer, the better? Assessing the results of an eight-year citizen science initiative targeting protected insect species

https://doi.org/10.3389/fenvs.2025.1566160

Materials and methods

Data description

For the present analysis, the dataset updated to 14th January 2022, which comprises the validated records from 1st January 2014 to 31st December 2021, has been used. Analyses employ the same dataset for 2014 and 2015 as well as the same methods used in Zapponi et al. (2017) to guarantee comparable results. General results (e.g., number of records and correct identification rate) of the projects have been calculated. The validated records collected during the entire MIPP/InNat project duration (i.e. records from 2014 to 2024) are visible and downloadable on the platform GBIF[9] (35) and on the official Italian repository of biodiversity data (National Biodiversity Network[10]).

Although the complete dataset would include 40 targets, analyses were performed considering only the records of the nine insect species included in the project from the beginning and falling inside Italian National territory. The geographic location of records is expressed using the ETRS89 datum and the EPSG 4258 reference system. In order to compare the advances in data coverage, the dataset was divided in two blocks: data block 1 (n = 1,113) partially overlaps the dataset from Zapponi et al. (2017) and comprises the data recorded from 1st January 2014 to 31st December 2015, corresponding to part of the MIPP project, whereas data block 2 (n = 5,017) includes the data recorded from 1st January 2016 to 31st December 2021, corresponding to the second part of MIPP and the InNat project. These two data blocks were analysed using R 4.1.1 (R Core Team, 2021), and species distributions were assessed following the methods of Zapponi et al. (2017). Geographical information was used to assess how many species records were collected in protected areas (i.e., Natura 2000 sites and protected areas listed in "Elenco Ufficiale delle Aree Protette VI" - EUAP VI (EUAP, 2023), (published in Gazzetta Ufficiale n. 125 del 31.05.2010[11]). and geospatial vector data downloadable at http://www.pcn.minambiente.it/viewer/index.php?services=progetto_natura).

[9] https://cloud.gbif.org/eca/resource?r=protected_insects_of_italy&v=1.5
[10] https://www.nnb.isprambiente.it/
[11] geospatial vector data downloadable at http://www.pcn.minambiente.it/viewer/index.php?services=progetto_natura.

UTM grid

For each species, records were plotted on the UTM 10 × 10 km grid and the yearly number of cells with presence data was calculated using QGIS 3.16.11 (QGIS Development Team, 2022). A Chi Square test (degree of freedom = 1) was employed to assess statistical differences between the number of cells with presence data for the two data blocks, without taking into account records shared between the two data blocks.

UTM curves

The annual increment in species presence was analysed by plotting the number of UTM cells occupied by records of the nine target species against time expressed as years from 2014 (start of MIPP data collection) to 2021. Linear regression models, estimating the trend of the record (i.e., UTM cells) over time, were separately fitted to each species using lm() function in R 4.1.1. For each species, the slopes of the two linear models calculated for the two data blocks (i.e., 2014–2015 and 2016–2021), indicating the rate of accumulation of UTM cells over time, were compared employing a *Chi Square* test (degree of freedom = 1) to assess the differences in the rate of data increment between the first two years and the complete eight years of data collection. Species-specific results were analysed to estimate the distance from their asymptote, intended as a plateau, using this parameter as a proxy for 'project saturation' (i.e., the calculated maximum number of cells reachable with CS). This plateau was thus calculated on the basis of the increment of the records per year. Specifically, each species-specific result was fitted to an asymptotic model, using the SelfStart function "SSasympOrig" implemented in the function nls() in the R 4.1.1 package *stats* ver. 3.6.2 (36), forcing each curve to start from the origin. The number of UTM cells expected at the asymptote was estimated and a *Chi Square* test (degree of freedom = 1) was applied to compare this number with the number of actually recorded cells.

α-hulls

To assess changes in the geographic range of the nine target species recorded in the years 2016–2021, *α-hulls* were calculated for data block 1 (2014–2015) as well as for data block 2 (2016–2021), following Zapponi et al. (2017). *α hulls* were chosen compared to traditional convex hulls, because they provide an explicit mean for excluding discontinuities within a species range, allowing more robust estimates (Burgman and Fox., 2003). For each species, all duplicate coordinates were removed from the dataset using the "distinct" function in the R 4.1.1 package *dplyr*. The high density of records as well as their proximity prevented the calculation of the *α-hull* area for *L. cervus*: thus, only in this case, the distribution of the records was simplified using the gridify() function in the MMQGIS plugin ver. 2021.9.10 in

QGIS 3.16.11 (QGIS Development Team., 2022). Records were ordered on a regular grid of 0.01 latitudinal degrees, and the redundant points were removed. Species-specific areas, expressed as km2, were calculated using R 4.1.1 package *alphahull* (Pateiro-López and Rodríguez-Casal, 2010). As in Zapponi et al. (2017) and also suggested by the IUCN Standards and Petitions Subcommittee (IUCN Standards and Subcommittee, 2014), we set parameter $\alpha = 2$, and a *Chi Square* test (degree of freedom = 1) was employed to assess statistical differences between the *α hulls* results from the two blocks.

Results

UTM cells

The spatial increment of occupied cells of the UTM 10x10 km grid for each of the target species are reported in Figure 7 and corresponding results from the *Chi Square* test are reported in Table 4. Differences between the number of records from the two data blocks are statistically significant for all target species (p-value < 0.018) except for *Saga pedo* (p-value = 0.593).

UTM curves

Species-specific annual incremental curves of the occupied area are reported in Figure 8. Slopes, as well as the results of the *Chi Square* tests, are reported in Table 5. According to these analyses, despite the visible drop of the slope from the first two years versus the complete eight years of data collection for some species, this difference is not statistically significant for almost all the evaluated species (p-value > 0.1). The only significant difference (p-value = 0.016) is represented by *L. cervus*. However, for all species did the slope decrease and thus the rate of increment of occupied cells decreased over the years.

Moreover, almost all species show a statistical difference between the actual number of recorded 10x10 km UTM cells and their given mathematical plateau (p-value < 0.05) (Table 6). This suggests that almost all of the species investigated in our project are still far from reaching ‘saturation’ in distribution knowledge, intended as the maximum number of possible grid cells with records. The only two exceptions concern *Osmoderma eremita* complex (p-value = 0.137) and *Rosalia alpina* Linnaeus, 1758 (p-value = 0.055) which do not result statically significant. This suggests that these are closer to reaching ‘saturation’ in distribution knowledge.

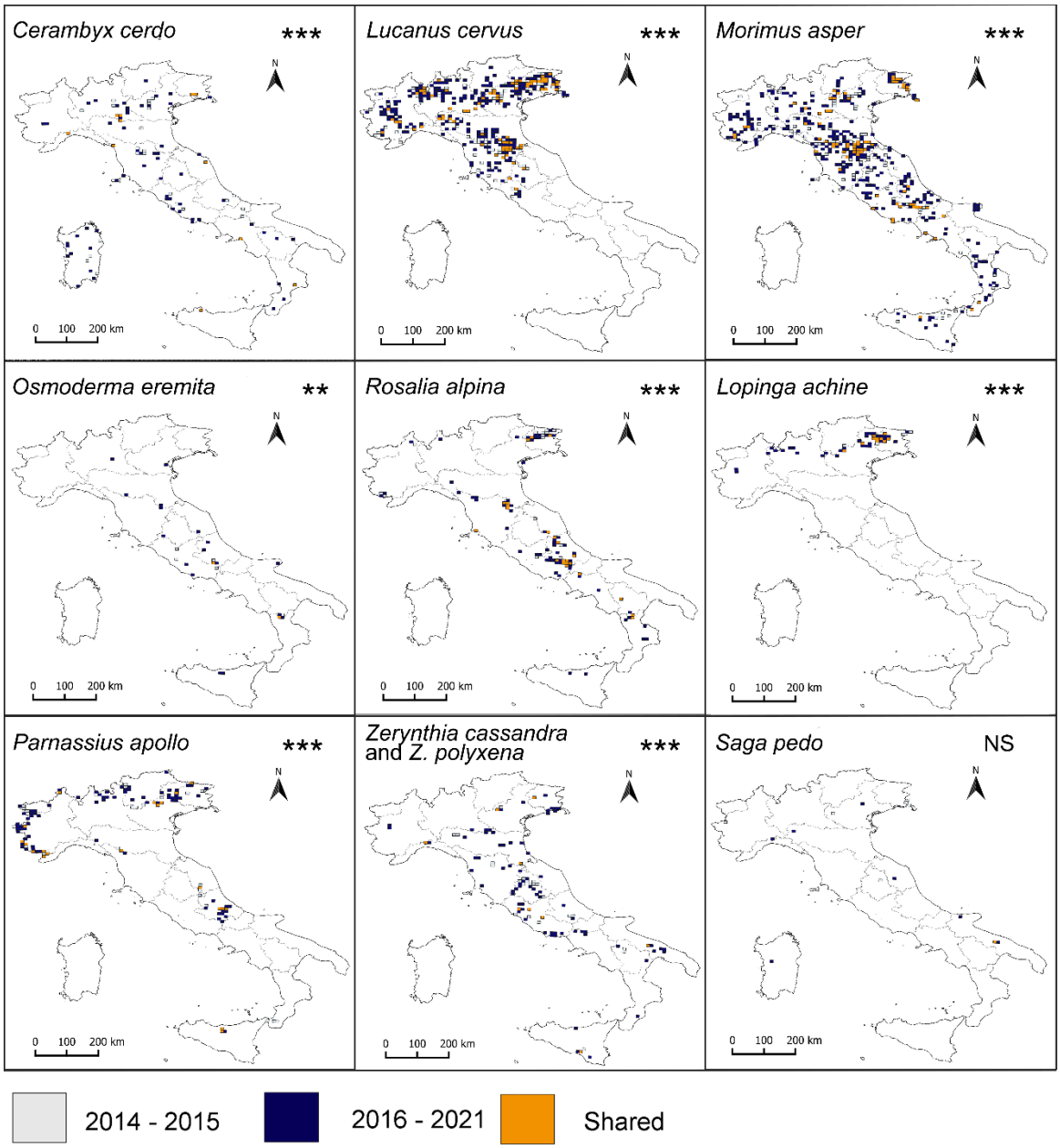


Figure 7. Maps showing the distribution of 10x10 km UTM cells occupied by the nine investigated species. Grey cells: records from data block 1 (2014–2015); blue cells: records from data block 2 (2016–2021); orange: cells shared in the two data blocks.

Table 4. Analysis of the differences in the distribution of the nine investigated species between the two data blocks: 2014–2015 vs. 2016–2021. Results from the Chi Square tests assessing statistical differences among the UTM cells of the involved species over the two given time periods (data block 1 and data block 2). In particular, the Chi Square value (χ2) and the p-value *are reported, as well as the statistical significance level (*** = high statistical significance, ** = medium statistical significance, NS = non-significant). The number of shared cells is given for full reporting, but it was not included in the analyses of the present work.*

Species	Data block 1 (2014–2015)	Data block 2 (2016–2021)	Shared cells	χ2	p-value	Statistical significance
Cerambyx cerdo	36	70	11	10.906	< 2.2e-16	***
Lucanus cervus	135	299	78	61.972	< 2.2e-16	***
Morimus asper	143	356	74	90.920	< 2.2e-16	***
Osmoderma eremita complex	7	19	2	5.538	0.018	**
Rosalia alpina	39	82	23	15.281	< 2.2e-16	***
Lopinga achine	14	41	10	13.255	< 2.2e-16	***
Parnassius apollo	43	96	20	20.209	< 2.2e-16	***
Zerynthia cassandra and *Z. polyxena*	31	80	9	21.631	< 2.2e-16	***
Saga pedo	6	8	1	0.285	0.593	NS

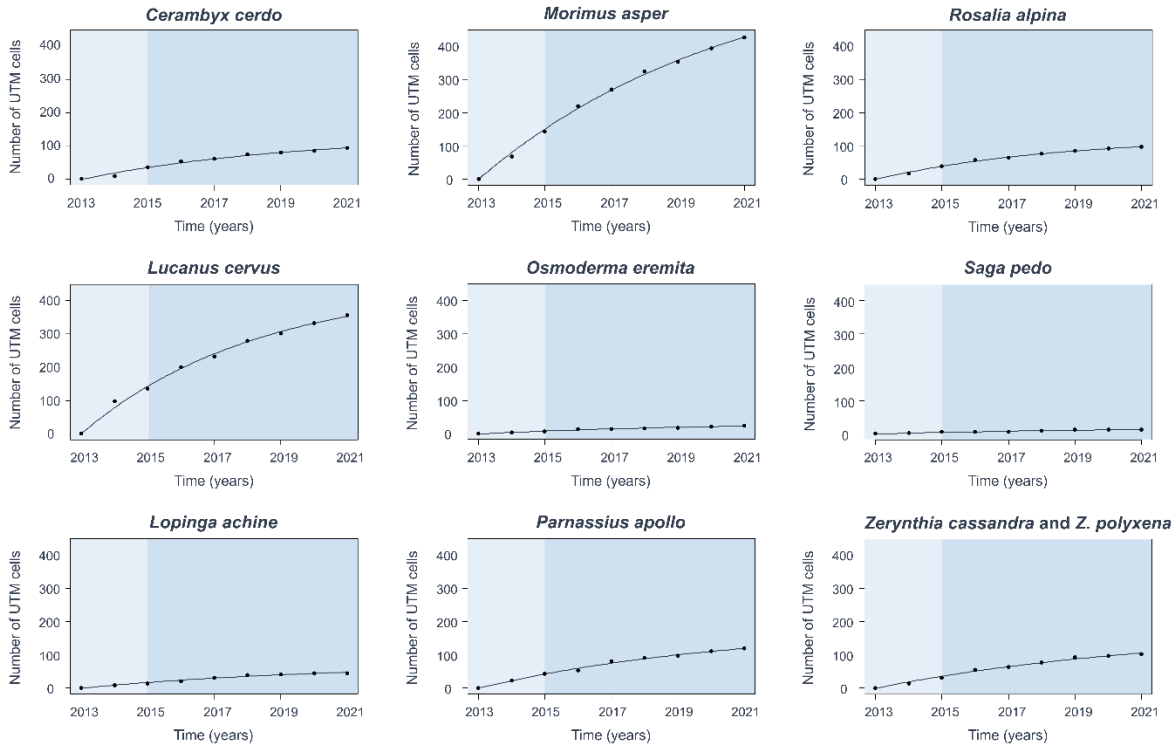


Figure 8. Annual incremental curves calculated on the 10x10 km UTM cells collected each year for the nine selected species. Light blue represents data block 1 (2014–2015), dark blue represents data block 2 (2016–2021).

Table 5. Analysis of the differences in the slopes of the incremental curves of the nine investigated species between the two data blocks: 2014–2015 vs 2016–2021.Results from the Chi Square tests assessing statistical differences among the species-specific slopes of the linear models fitted for years 2014–2015 versus years 2014–2021. In particular, the Chi Square value (χ2) and the p-value *are reported, as well as the statistical significance level (** = medium statistical significance, NS = non-significant).*

Species	Slope of the linear model fitted for years 2014–2015	Slope of the linear model fitted for years 2014–2021	χ^2	p-value	Statistical significance
Cerambyx cerdo	18.0	12.0	1.200	0.273	NS
Lucanus cervus	67.5	42.3	5.783	0.016	**
Morimus asper	71.5	53.3	2.654	0.103	NS
Osmoderma eremita complex	3.5	2.8	0.077	0.78	NS
Rosalia alpina	19.5	12.1	1.732	0.188	NS
Lopinga achine	7.0	5.9	0.093	0.759	NS
Parnassius apollo	21.5	14.7	1.277	0.258	NS
Zerynthia cassandra and Z. *polyxena*	15.5	13.3	0.168	0.681	NS
Saga pedo	3.0	1.6	0.426	0.513	NS

Table 6. Differences between the mathematically calculated asymptote and the number of cells recorded for the nine investigated species until December 2021. Species-specific mathematical plateaus (i.e., maximum number of UTM cells possibly covered by each species). The relative results from the Chi Square tests assess statistical differences among the asymptote and the number of cells recorded until December 2021. In particular, the Chi Square value (χ2) and the p-value *are reported, as well as the statistical significance level (*** = high statistical significance, ** = medium statistical significance, * = low statistical significance, NS = non-significant).*

Species	Asymptote (number of UTM cells)	SD	Natural logarithm of rate change (LRT)	SD (LRT)	Number of cells recorded until December 2021	$\chi 2$	p-value	Statistical significance
Cerambyx cerdo	132.590	18.720	-1.850	0.228	95	6.208	0.0127	**
Lucanus cervus	450.694	26.908	-1.662	0.105	356	11.116	0.000856	***
Morimus asper	661.148	43.437	-2.043	0.098	425	51.343	7.76E-13	***
Osmoderma eremita complex	35.465	7.465	-2.015	0.317	24	2.210	0.137	NS
Rosalia alpina	126.645	6.969	-1.679	0.096	98	3.652	0.055	NS
Lopinga achine	70.959	14.190	-1967	0.307	45	5.811	0.015	**
Parnassius apollo	181.977	18.750	-2.014	0.155	119	13.177	0.0002833	***
Zerynthia cassandra and *Z. polyxena*	176.844	30.035	-2.174	0.241	102	20.089	7.39E-06	***
Saga pedo	25.560	12.610	-2.369	0.661	13	4.091	0.043	*

α-hulls

Results from the α-hulls analyses are reported in Fig 9. These *α-hulls* reveal that the area covered by CS records (expressed in as km^2) has sharply increased from data block 1 (2014–2015) to data block 2 (2016–2021) for all target species, with *Saga pedo* (Pallas, 1771) as the only exception. However, this is an artefact created by the parameters imposed; when data points are too far apart they are not joined. For *Cerambyx cerdo* Linnaeus, 1758, *Morimus asper*, *O. eremita* complex, *R. alpina*, *Lopinga achine* (Scopoli, 1763) and *Zerynthia cassandra* and *Z. polyxena*, the increase in the area covered by the records results in a change of the relative shape of the area. In contrast for *L. cervus* and *Parnassius apollo* (Linnaeus, 1758), the increase in the area covered by the records results in an increased density within the same outline. *S. pedo* is the only species not showing an increase in the area covered by the records: this can be explained with the disjunct distribution of its records, also due to setting the parameter α=2, as reported in Zapponi et al. (2017) and by the IUCN Standards and Petitions Subcommittee (IUCN Standards and Subcommittee., 2014). This resulted in a low threshold for the inclusion of distant data points in the *α-hull*.

Chi Square test highlighted that all differences result highly statistically significant (p-value < 0.0001) (Table 7). Differences in the area covered by records of *S. pedo* were statistically significant but they have not been considered in the following discussion due to the above-mentioned limits of the α-hulls analysis for this sparse distributional data.

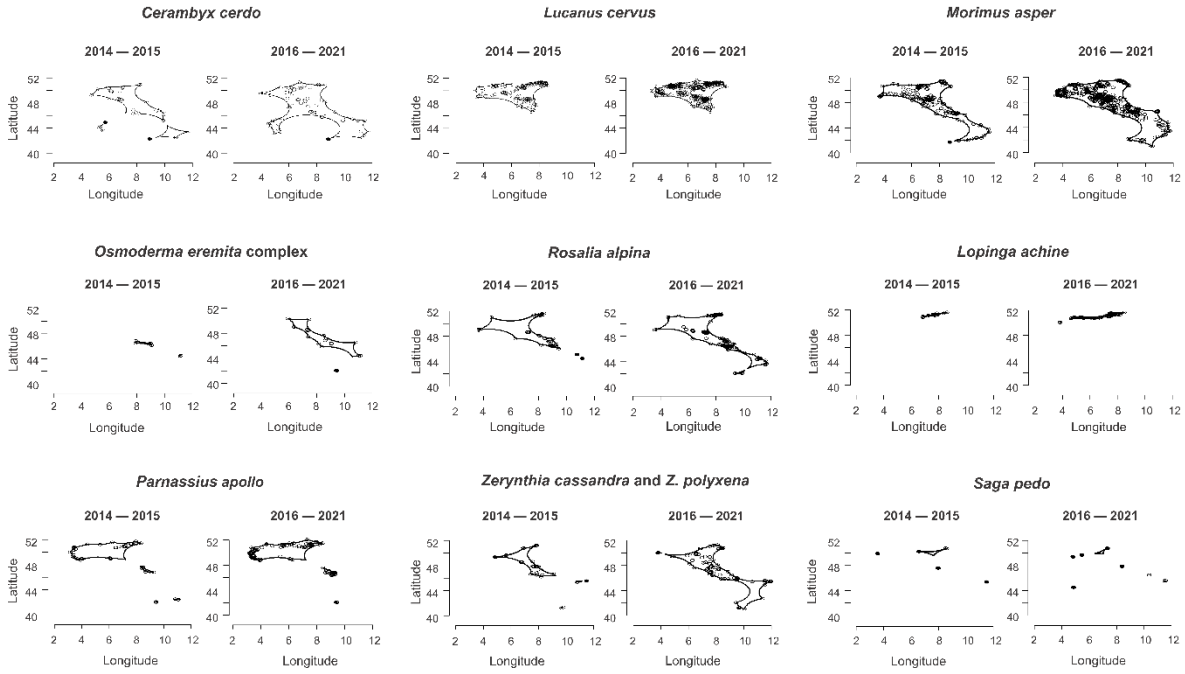


Figure 9. Graphic outputs of α-hulls analyses. Geographic distributions of the two data blocks are compared for the nine selected species

Table 7. Results from the Chi Square tests assessing statistical differences among species-specific α-hulls from the two data blocks: 2014-2015 vs. 2016-2021. The Chi Square value (χ2) and the p-value *are reported, as well as the statistical significance level (*** = high statistical significance).*

Species	Data block 1 (2014–2015) (km2)	Data block 2 (2016–2021) (km2)	χ2	p-value	Statistical significance
Cerambyx cerdo	123,501.300	233,725.400	34,010.000	< 2.2e-16	***
Lucanus cervus	123,222.000	129,938.900	178.210	< 2.2e-16	***
Morimus asper	182,511.000	276,333.400	19,184.000	< 2.2e-16	***
Osmoderma eremita complex	2,330.455	63,091.300	56,432.000	< 2.2e-16	***
Rosalia alpina	97,233.700	134,982.300	6,136.300	< 2.2e-16	***
Lopinga achine	2,456.260	9,403.167	4,069.300	< 2.2e-16	***
Parnassius apollo	93,131.150	103,391.900	535.730	< 2.2e-16	***
Zerynthia cassandra and *Z. polyxena*	45,660.960	137,290.100	45,892.000	< 2.2e-16	***
Saga pedo	4,026.352	1,682.898	961.910	< 2.2e-16	***

Discussion

Our results highlight that a CS project, which investigates the presence of protected insect species, benefits from collecting data for a long time as data coverage continuously increased during eight years of the project and none of the investigated species has already reached a plateau of grid cells covered. Similarly, Méndez and Cortés-Fossati (2021) showed that 15 years of citizen science were unable to yield a complete view of the distribution of the stag beetle in Spain. Thus, the time necessary to complete information about coverage is important and should be considered in similar future CS projects.

Results on the most and least recorded species are rather easy to interpret: the coleopteran *Lucanus cervus* is widely distributed in Central and Northern Italy and easily detectable during its summer flights (Bardiani et al., 2017). In contrast, the lepidopterans *Phengaris teleius* and *Papilio hospiton* have a very limited distribution in Italy (Stock and Genovesi, 2016) and detectability of these butterflies is presumably much lower (e.g., difficulty in observing the target closely and long enough for identification, need for specific entomological skills, dedicated photographic equipment, etc.). Similarly, results on the most mis-recorded species can be justified by the distribution of these targets; in fact, *Argynnis* (*Fabriciana*) *elisa*, *Euphydryas maturna, Leucorrhinia pectoralis* and *Papilio alexanor*

share a very limited distribution (Stock and Genovesi, 2016) and can easily be confused with similar species.

The high number of records provided by volunteers in Northern Italy, as also highlighted in Redolfi de Zan et al. (2023), suggests that this area played a leading role in our project. This may be explained by two main reasons: a greater involvement of the public in our CS project and a different attitude to this kind of initiatives. Moreover, it must also be stressed that among the northern regions in Italy, Lombardy alone accounts for approximately one sixth of the whole Italian population, leading to a strong bias towards northern regions in the results of any volunteer-based research over national territory.

Another important result concerns the high percentage (ca. 61%) of records that were collected outside protected areas indicating that many of the populations of these species, listed in the Annexes of the Habitats Directive, are currently inhabiting also outside of these dedicated areas. This result is particularly meaningful considering that many of the target species (e.g. *L. cervus*, *R. alpina*, *C. cerdo*, *O. eremita*) are listed in Annex II of the Habitats Directive and therefore require the designation of special areas of conservation. It would be interesting to better understand the relationship between citizen scientists and protected areas and the reasons why the majority of records of MIPP/InNat project fall outside protected areas. Among the possible explanations for this, it could be that volunteers do not commonly frequent protected areas and that they might collect data on the target species during routine activities (e.g., traveling from home to work route, walking the dog, etc.). Information aimed at profiling the volunteers involved in our project have been collected through a sociological survey and will be the target in an upcoming paper. Indeed, it must be noted that the protected target species of our project can be found outside protected areas. These results stress the ecological importance of the areas between the Natura 2000 network areas in the context of biodiversity, species conservation and ecological connectivity (D'Amen et al., 2013).

From a European point of view, results from the MIPP/InNat project tend to be comparable with other similar European CS projects. For example, the Vadonleso project (https://xn--vadonles-8sb.hu/) (Bagolyné Geng et al., 2018), a Hungarian CS project targeting species protected under the Habitats Directive, shares *L. cervus* with MIPP/InNat, and the data from 2021 are comparable. In fact, *L. cervus* reached 156 records in 2021 in the Vadonleso project and this species was the most recorded insect target. In our project 214 records of this species were collected in the year 2021, and this species was the most recorded target in our project as well. Moreover, in 2021, also the percentage of validated (hence correct) records are comparable in the two projects: 95% and 89% for Vadonleso and InNat projects respectively.

UTM grid

Differences in the number of records from the two analyzed data blocks (2014-15 vs. 2016-21) resulted statistically significant for all target species except for *S. pedo*. This means that our project contributed to improving the knowledge on the distribution of our targets. Similarly, a number of other studies have found that knowledge on the distribution of insects has been greatly improved thanks to CS (Smyth et al., 2013; Zapponi et al., 2017; Méndez and Cortés-Fossati, 2021). The fact that the differences between the number of records from the two data blocks were not statistically significant for *S. pedo* was most probably caused by the paucity of the data available for the analysis (i.e., 22 validated records and 13 UTM cells for *S. pedo* compared to an average of 500 validated records and 142 UTM cells for the other species, respectively). However, even if the number of occupied cells increased also for *S. pedo* (Table 5), we cannot base our evaluation of the effectiveness of the project with regard to this species.

UTM curves

Concerning the annual incremental curves of the occupied areas for our target species, a drop of the slope from the first two years versus the complete eight years of data collection for some species was observed, possibly due to natural customisation to the project. In particular, the slowdown is remarkable – and statistically significant - for *L. cervus* with a higher recording rate in the first two years in respect to the following ones. This could be explained by the charisma of the species, used as a flagship for the project promotion, especially in the first years. On the other hand, this slowdown in the accumulation curve is not statistically significant for all the other the evaluated species (p-value > 0.1): in fact, data for new cells is continuously being added for all target species

The increase of the occupied areas found with CS data underlies the high effort needed over many years in order to map the distribution of the target species. These findings highlight the need of long-term initiatives at country level, thus encouraging the continuation of similar projects, to completely map the areas occupied by the species.

None of the evaluated species approached the estimated asymptote and this means that eight years of recording are not sufficient to map the distribution of the target species within our CS project and according to Méndez and Cortés-Fossati (2021) even 15 years of citizen science were not sufficient to complete the distribution of the stag beetle in Spain. Only *O. eremita* complex and *R. alpina* seem to be approaching the mathematically calculated asymptote. Even though these results could reflect the paucity of the data available for these analyses, there could be some ecological factors affecting the results, especially considering that the plateau is mathematically calculated on the basis of yearly data collection rate. On

one hand, *O. eremita* in Italy suffers from detectability issues: in fact, it can usually be found at very low densities, possibly due to the reduced number and volume of three hollows in our national territory, thus fortuitous occasional observations are quite rare. For monitoring, the use of attractive traps is recommended (Maurizi et al., 2017). Therefore, in the case of *O. eremita*, it seems likely that the species is present in other suitable areas and might be detected only with appropriate monitoring techniques (e.g., as in Lenzi et al. (2022)). On the other hand, *R. alpina* is characterized by a patchy distribution due to its close association with an extremely specific microhabitat (i.e., mature, dead or moribund and sun-exposed trees of *Fagus* spp.), where the species is highly visible. This often results in the multiple records being collected by citizen scientists from the same grid cells which limits the increase in additional cells. These different issues influence the calculation of the mathematical plateaus for the two species, and the calculated increase of the distribution was more modest for these targets. However, for these very reasons, any newly discovered grid cell for the two above-mentioned species is highly relevant at national level. Again, as for the other analyses, results for *S. pedo* should be interpreted with caution due to the low number of records collected.

The annual incremental curves of the occupied areas highlight how our project increased the known area occupied for the target species, but our knowledge on the true distribution of these species is still far from complete. It is obvious that time is an important factor for such projects and thus this kind of initiatives should be set up as long-term monitoring programmes since an increase in their duration results in an increase in useful data recording. Additionally, climate change is a key driver of insect distributional changes which results in directional range shifts (Hassal, 2015; Engelhardt et al., 2022). Thus, our current knowledge on the distributional ranges of protected species needs to be investigated continuously.

α-hulls

α-hulls reveal that the area covered by CS records (expressed in as km^2) has sharply increased from data block 1 (2014–2015) to data block 2 (2016–2021) for all target species, with *Saga pedo* (Pallas, 1771) as the only exception. Therefore, two main species categories are identified by our analysis: easily detectable and relatively well-known species (i.e., *L. cervus* and *Parnassius apollo*) and the less easily detectable and relatively neglected species (i.e., *Cerambyx cerdo*, *Morimus asper*, *O. eremita* complex, *R. alpina*, *Lopinga achine* and *Zerynthia cassandra* and *Z. polyxena*). The first category did not experience a change in the shape of the α-hulls and differences among the two analysed data blocks can be found mainly in a greater density of data within the same α-hull shapes. In contrast, for the less easily detectable target species we found a drastic change in the shape of their α-hulls. Interestingly,

both species categories did not show changes in the position of their α-hull core over the years. This result might mean that the very first two years of data recording already defined the core of the species' distribution and the last six years dramatically impacted the α-hulls shapes with the collection of records from the edges of the distributional area. Thus, for most of our species CS records greatly enlarged the known distribution and similar results have been found by Zapponi et al. (2017) and Méndez and Cortés-Fossati (2021) and thus CS records can provide records vital for the identification of new areas of importance for the conservation of protected species.

Conclusions

The present paper analyses data from a CS project targeting species protected under the Habitats Directive. Comparison between the two data blocks, first two years of the project (2014 – 2015) vs. last six (2016 – 2021), revealed a significant and encouraging increase in distributional data coverage. Moreover, it is interesting to highlight the differences with previous analyses performed by Zapponi et al., (2017) which, in turn, compared cells records exclusively provided by citizens with the ones provided by professional scientists involved in CKMap i.e., Stoch (2005).

The MIPP/InNat project significantly contributed to increasing knowledge on the distribution of species protected under the Habitats Directive. These data not only prove to be essential information for the scientific community, but they are also of paramount importance in meeting the demands of the European Commission (i.e., Article 11 and 17 of the Habitats Directive (92/43/EEC)) and in fostering a more conscious management and design of protected areas. In light of these results on species distribution, CS projects therefore prove to be extremely beneficial for their impacts on protected areas managers, conservation executives and policy makers (Redolfi de Zan et al, 2023). New opportunities for the MIPP/InNat project concern increasing project targets. Up to date, for the newly added targets, records do not reach the same numbers of the previously included ones (i.e., from MIPP on). This result is important in highlighting the limits of CS approach with insect species that are not easy to identify and to detect due to their size and or habitat preferences (e.g., *Cucujus cinnaberinus*, *Rhysodes sulcatus*). In fact, good data and statistically robust trends require a serious investment of time and money and the chosen methods need to be scientifically sound (Schmidt and Van der Sluis, 2021). CS has a great potential, also for recording distributional data of protected insects, as shown above. However, it is also important to recognize the limits and biases of this approach (e.g., Kallimanis et al., 2017;

Deacon et al., 2023) and to identify the targets that are best investigated by professionals. For example, targeted monitoring of specific species with the aim of getting population trends are usually carried out by professionals (Schmidt and Van der Sluis 2021). Thus, methods can be validly selected from volunteer-based and professional-based solutions and these choices depend also on the culture of a specific country as well as on the availability of resources (Schmidt and Van der Sluis 2021).

Eventually, two of the major challenges related to all CS projects concerns project promotion and attractiveness towards non-professional volunteers (i.e., not biologists/naturalists or similar) so that the largest possible part of the public can be involved in the proposed activities. Analysis of InNat volunteer profiling will be reported in an upcoming paper which, as mentioned above, will be based on a sociological survey submitted to all our volunteers.

3. Recycle and reuse: an ethological perspective for citizen science data on *Lucanus cervus* (Coleoptera: Lucanidae)

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Materials and methods

Dataset Building

The original InNat dataset comprised 2,090 photographic records of *L. cervus* from Italian national territory. These data were collected by 418 volunteers over a very large time span, with the oldest record reported from 1994 and the newest one from 2023. Each record consisted of a photograph, eight descriptive parameters, and a "note" field that was not mandatory for the volunteers (see Table 8 for list and definitions). Once each field was filled in, records proceeded to expert taxonomical ID validation for the final data check and acceptance. The selection of records suitable for ethological analysis was conducted by applying three filtering criteria. First, we deleted images where only parts of the insect were visible, not the whole specimen (filter: "Parts"). Next, we excluded images with clearly or probably dead insects (e.g. antennas touching the substrate, legs gathered near the body or notes explicitly indicating this condition; filter: "Dead"). Finally, we removed images where insects were clearly being manipulated by observers (i.e. the observer's hand was visible; filter: "Manipulation"). All images of the eligible records (i.e. portraying alive and non-manipulated specimens of *L. cervus*) were processed to extract a series of parameters needed

for behavioural analyses: no. of specimens, sex, substrate, and behaviour (see Table 9 for list and definitions).

Table 8. List of descriptive parameters requested upon uploading of the record on InNat.

Parameter	Description
Volunteer ID	Volunteer NickName
Latitude	Decimal degrees, either self- or automatically compiled
Longitude	Decimal degrees, either self- or automatically compiled
Date	dd/mm/yyyy
Time	HH:MM
Location	Free input field
Province	Free input field
Region	Free input field
Notes	Free input field, not mandatory for volunteers

Table 9. Parameters used in this article for behavioral analyses and their definitions

Parameter name	Parameter description	Field	Field description
Specimens	N° of specimens in the image	1	Image representing one single specimen
		2	Image representing 2 specimens
		> 2	Image representing more than 2 specimens.
Sex	Sex of the specimen/s in the image	M	Male specimen
		F	Female specimen
		MF	A couple made by a male and a female specimens
		MM	A couple made by two male specimens
		FF	A couple made by two female specimens
Substrate	Substrate where the specimens were recorded	Air	Specimens were photographed while hovering in the air
		Artificial	Any surface of clearly anthropogenic origin
		Bare ground	Soil with no vegetation or dead leaves
		Grass	Soil with herbaceous vegetation
		Leaves	One or more leaves are visible, no possible discrimination between leaves on branches and leaves on the ground
		Natural wood	Portion of natural wood for which it is not possible discriminating between tree trunks or branches and/or between dead or living wood
		Stone	Natural aggregate of solid minerals, excluded sands (i.e., clastic sediment where fragments are not joined together)
		Tree branches	Branches of alive trees in which leaves or flowers are clearly visible

Behaviour	Behaviour identified from the image	Aggressive	Two specimens showing threatening or fighting behaviour. • Threatening: both individuals facing and both or one of the two erecting its body and head, with its mandibles wide open and legs raised; • Fighting: both individuals with mandibles touching and crossed or one grasping the body of the other with its mandibles.
		Feeding	One specimen. The head of the insect is in contact with the sap of the trees or with mature fruits.
		Couple Feeding	Two specimens. The heads of both the individuals are in contact with the sap of the trees or with mature fruits.
		Flying	One specimen. The specimen is seen hovering in the air or the specimen has its wings exposed, meaning that it is about to fly or has just landed.
		Reproductive	Two specimens, a female and a male. The male being on top of the female. Extruded male copulatory organ not always visible.
		Standing/Walking	One specimen. None of the previous behaviours therefore we assume that it is standing still or walking.
		Couple Standing/Walking	Two specimens. None of the previous behaviours therefore we assume that they are standing still or walking.

Behavioural Analyses

In each analysis, data were first organized into contingency tables to compare observed and expected frequencies (no. of records). A *Chi Square* test was then performed, followed by a standardized residuals analysis. Photographs containing more than two specimens were excluded due to their paucity (i.e., only 7). Additionally, couples consisting of only one sex (male + male or female + female) were aggregated (NN = same-sex couple).

The following analyses aimed at comparing frequencies between:

1. "Individuals and annual phenology": the relationship between the specimen(s) in the picture (number of specimens and sex) and the month in which the picture was taken was examined. Photographs taken in September, October, and November were excluded from the analysis due to their paucity (i.e. only six).
2. "Individuals and substrates": this analysis examined the relationship between the specimen(s) (number of specimens and sex) and the substrate in which the specimens were photographed. Records with air and leaves as substrates were excluded from the analysis due to their paucity (air: eight records; leaves: 12 records).
3. "Individuals and behaviours (single specimen)": this analysis focused on the relationship between a single specimen (sex: M or F) and the expressed behaviour. For the most represented behaviour (standing/walking), the relationship between sex and substrate was also investigated. As in the previous analysis, records with air and leaves as substrates were excluded due to their scarcity.
4. "Individuals and behaviours (couples)": this analysis explored the relationship between the couple (sex: MF or NN) and the expressed behaviour.

Results

After a preliminary filtering process, a total of 821 valid records were classified as "Eligible" and thus retained, while the rest was discarded through the following procedure: 376 records were excluded according to the filter "Parts," then 179 records were excluded due to the filter "Dead," and finally 714 records were excluded due to filter "Manipulation" (Figure 10). The same operation conducted separately for records with one specimen (N = 2001) and with two specimens (N = 76) showed that the percentage of excluded data was lower in the case of two specimens (14.47%) compared to one single specimen (62.57%) (Figure 10). Within the resulting ethologically valid dataset, 749 pictures portrayed a single specimen, whereas 65 portrayed two specimens. Valid photographs portraying more than two specimens were only seven, and thus they were excluded from the analyses. Among the one-specimen records, the ratio between males and females is almost 2:1, with 511 records for males and 238 for females. Considering the valid records of two specimens, the most represented couple is male + female (MF; N = 47), followed by single-sex couples (NN: male + male or female + female; N = 18). In Figure 11, examples of validated pictures used for the analysis are provided.

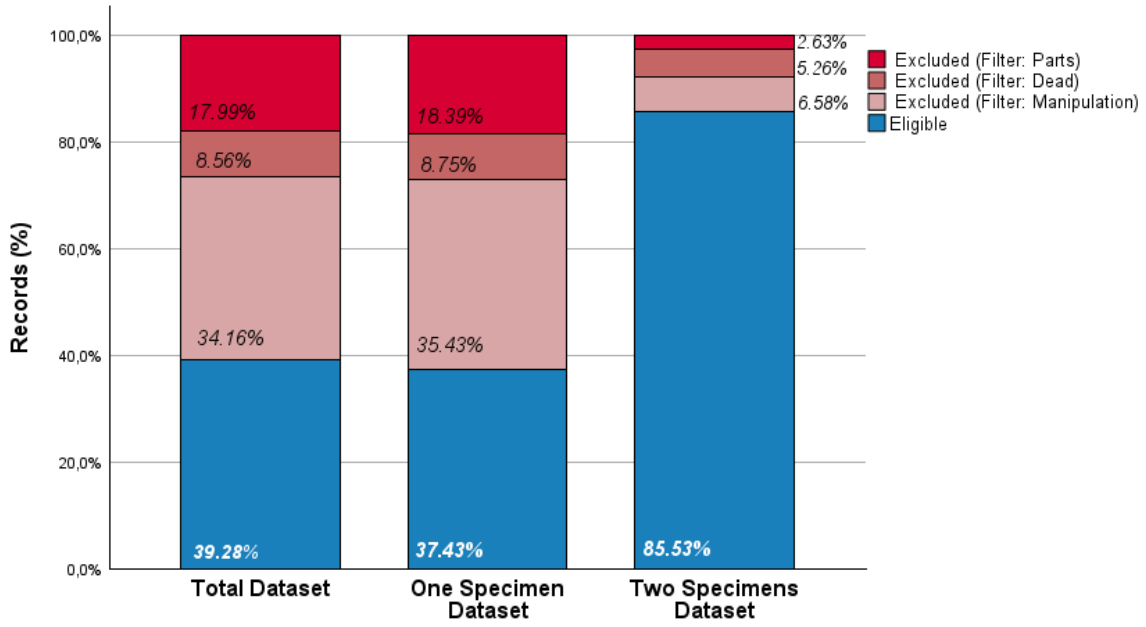


Figure 10. Distribution of records (%) of Lucanus cervus (L.) after the preliminary filtering process. The three bars represent, respectively: the entire InNat dataset (N = 2,090), the dataset of images with only one specimen (N = 2,001), and the dataset of images with two specimens (N = 76).

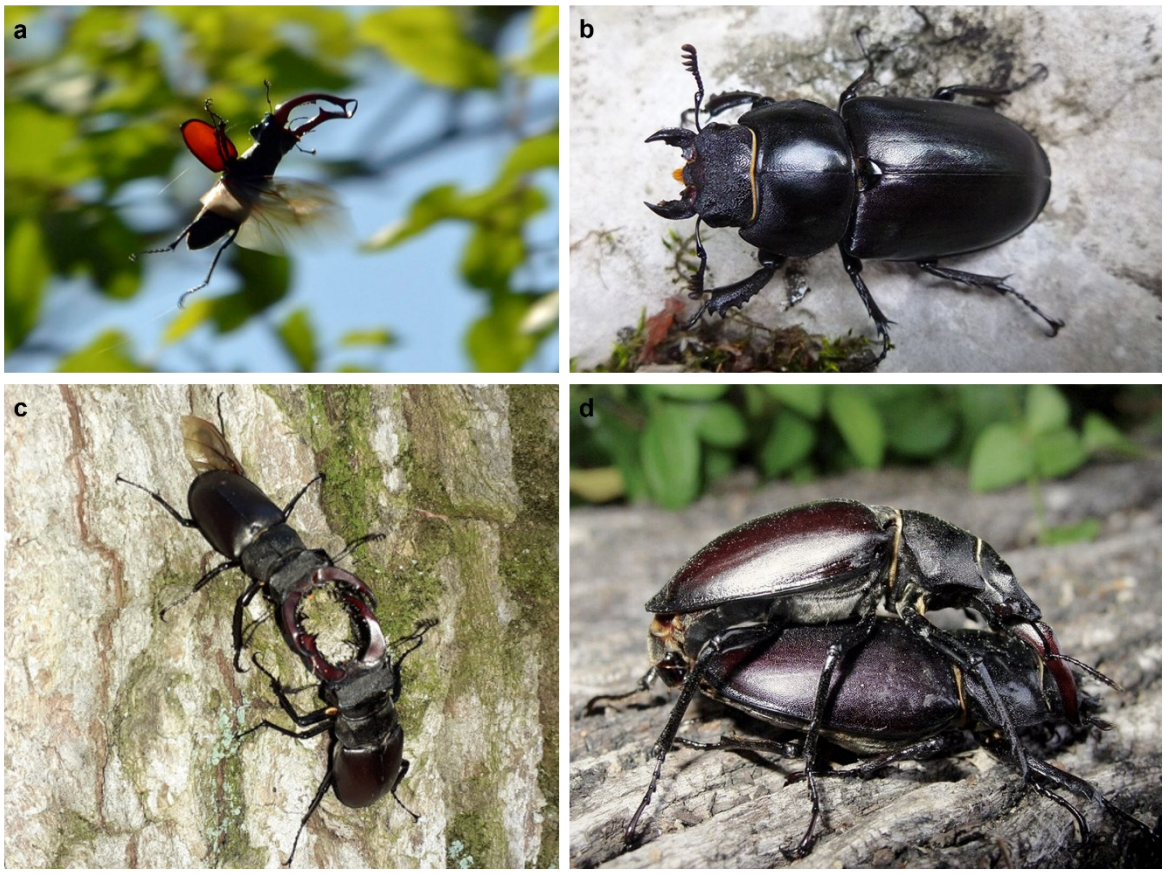


Figure 11. Examples of behavioural traits extrapolated from the recorded images of Lucanus cervus (L.). A) male flying, B) female standing/walking, C) males fighting, and D) male and female mating. Photos belong to the database of the citizen science project InNat and were taken by the participants who have conceded their copyright.

Individuals and Annual Phenology

The analysis of the distribution of the records according to the month of the year shows that the most populated month is July with a total of 427 records, followed by June (262 records), August (82 records), and May (37 records). In May, June, and July, the most represented category is single male (M) with 59.5%, 71.8%, and 66.0% of the total monthly pictures, respectively, followed by single female (F) with 16.2%, 16.4%, and 28.3% records, respectively. On the other hand, in August, single female (F) is the most represented category (79.3%), followed by single male (M, 19.5%) (Figure 12a and Table 10).

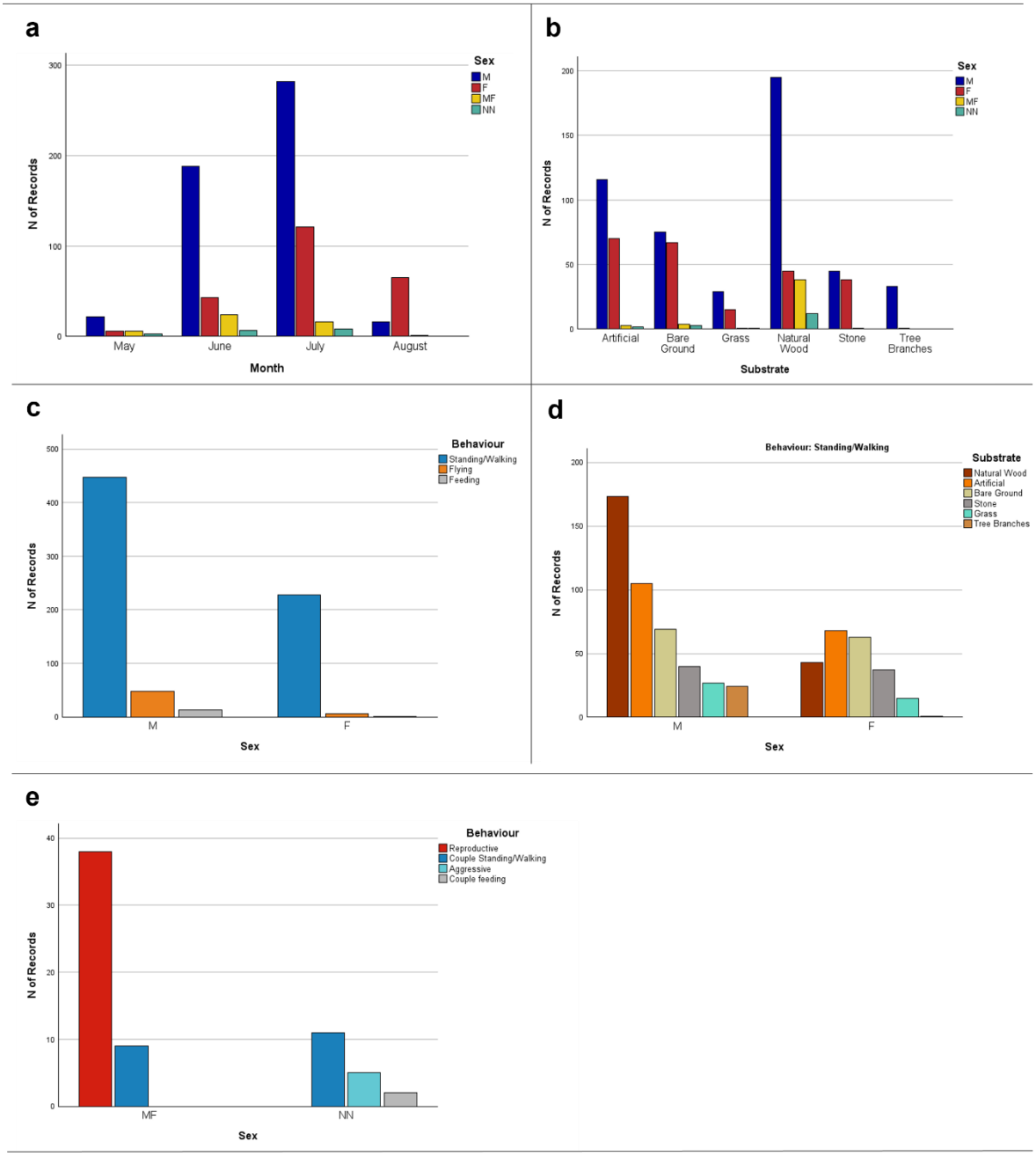


Figure 12. Main behavioral patterns of Lucanus cervus recorded by volunteers. Frequencies were compared a) between individuals and annual phenology; b) between individuals and substrates; c) between individuals and behaviors (single specimen); d) between individuals and behaviors (single specimen) for standing/walking behavior; e) between individuals and behaviors (couples). M, single male; F, single female; MF, male and female pair; NN, 2 specimens not categorized as MF. See Table 9 for the description of substrates and behaviors.

Table 10. Contingency table for the comparison of the frequencies between specimens and annual occurrence (Month vs Sex). Asterisks indicate the probability associated with the value of the standardized residual: * p-value ≤ *0.05 (value exceeds ±1.96);* ** p-value ≤ *0.01 (value exceeds ±2.58);* *** p-value ≤ *0.001 (value exceeds ±3.29).*

			Sex				
			M	F	MF	NN	Total
Month	May	Count	22	6	6	3	37
		Expected Count	23.3	10.8	2.2	.8	37.0
		% within Month	59.5%	16.2%	16.2%	8.1%	100.0%
		% within Sex	4.3%	2.6%	12.8%	16.7%	4.6%
		% of Total	2.7%	0.7%	0.7%	0.4%	4.6%
		Standardized Residual	-.3	-1.5	2.6**	2.4*	
	June	Count	188	43	24	7	262
		Expected Count	164.7	76.2	15.2	5.8	262.0
		% within Month	71.8%	16.4%	9.2%	2.7%	100.0%
		% within Sex	37.0%	18.3%	51.1%	38.9%	32.4%
		% of Total	23.3%	5.3%	3.0%	0.9%	32.4%
		Standardized Residual	1.8	-3.8***	2.2*	.5	
	July	Count	282	121	16	8	427
		Expected Count	268.5	124.2	24.8	9.5	427.0
		% within Month	66.0%	28.3%	3.7%	1.9%	100.0%
		% within Sex	55.5%	51.5%	34.0%	44.4%	52.8%
		% of Total	34.9%	15.0%	2.0%	1.0%	52.8%
		Standardized Residual	.8	-.3	-1.8	-.5	
	August	Count	16	65	1	0	82
		Expected Count	51.6	23.8	4.8	1.8	82.0
		% within Month	19.5%	79.3%	1.2%	0.0%	100.0%
		% within Sex	3.1%	27.7%	2.1%	0.0%	10.1%
		% of Total	2.0%	8.0%	0.1%	0.0%	10.1%
		Standardized Residual	-5.0***	8.4***	-1.7	-1.4	
Total		Count	508	235	47	18	808
		Expected Count	508.0	235.0	47.0	18.0	808.0
		% within Month	62.9%	29.1%	5.8%	2.2%	100.0%
		% within Sex	100.0%	100.0%	100.0%	100.0%	100.0%
		% of Total	62.9%	29.1%	5.8%	2.2%	100.0%

The statistical analysis using crosstabs shows a significant relationship between the month of data collection (month) and the sex of the specimens (M, F, MF, NN) (*Chi Square* = 142.30, p-value < 0.001). The analysis of standardized residuals suggests that, in May, there are more MF and NN couples than expected; in June, there are more MF couples and fewer single female specimens (F) than expected; and in August, there are more single female (F) and fewer male specimens than expected (Table 10, Table 11).

*Table 11. Summary of the chi-square tests performed to assess relationships between specimen traits (sex, couple type) and contextual parameters (month, substrate, behaviour). For each analysis, degrees of freedom (df), test statistic (χ^2), and significance level (*p-value*) are reported. Notable patterns based on standardized residuals are indicated, highlighting categories with observed frequencies significantly higher (↑) or lower (↓) than expected.*

Analysis	Variables	χ^2 (df)	P-value	Notable residuals
Individuals and annual phenology	Sex × Month	142.30 (9)	< 0.001	May: MF↑, ↑NN June: MF↑,F↓ August: F↑, M↓
Individuals and substrates	Sex × Substrate	110.60 (15)	< 0.001	Natural wood: F↓, MF↑, NN↑ Tree branches: M↑, F↓ Bare ground: F↑ Stone: F↑ Artificial sub.: MF↓
Individuals and behaviours (single specimen)	Sex × Behaviour	15.84 (2)	< 0.001	Flying: F↓
Individuals and behaviours (single specimen)	Sex × Substrate (Standing/Walking)	49.13 (5)	< 0.001	Natural wood: M↑, F↓ Tree branches: F↓ Bare ground: F↑ Stone: F↑
Individuals and behaviours (couples)	Sex × Behaviour	40.28 (3)	< 0.001	Reproductive: MF↑ Aggressive: NN↑ Walking/Standing: NN↑

Individuals and Substrates

The analysis of the distribution of the specimens according to the substrate shows that, generally, the preferred substrate is Natural wood with a total of 290 records, followed by Artificial substrate (191 records), Bare ground (149 records), Stone (84 records), Grass (46 records), and Tree branches (34 records). For every substrate, single male specimen (M) is the most represented category followed by single female specimen (F), but for Natural wood and Tree branches, the differences are more evident (Natural wood: M = 67.2%, F = 15.5%; Tree branches: M = 97.1%, F = 2.9%) (Figure 12b and Table 12).

The statistical analysis using crosstabs shows a significant relationship between the sex of the specimens and the substrate where the specimens were recorded ($\chi 2(15) = 110.60$, $P < 0.001$). The analysis of standardized residuals showed that males were found on tree branches more than expected, females were found more on bare ground and stone and less on natural wood and tree branches, MF couples were found more on natural wood and less on artificial substrate, and, finally, the other couples (NN) were found more in natural wood (Table 11 and Table 12).

Table 12. Contingency table for the comparison of the frequencies between specimens and substrates (Substrate vs Sex). Asterisks indicate the probability associated with the value of the standardized residual: *p-value ≤ *0.05 (exceeds ±1.96);* ** p-value ≤ *0.01 (exceeds ±2.58);* *** p-value ≤ *0.001 (exceeds ±3.29).*

			Sex				Total
			M	F	MF	NN	
Substrate	Artificial	Count	116	70	3	2	191
		Expected Count	118.6	56.8	11.3	4.3	191.0
		% within Substrate	60.7%	36.6%	1.6%	1.0%	100.0%
		% within Sex	23.5%	29.7%	6.4%	11.1%	24.1%
		% of Total	14.6%	8.8%	0.4%	0.3%	24.1%
		Standardized Residual	-.2	1.8	-2.5*	-1.1	
	Bare Ground	Count	75	67	4	3	149
		Expected Count	92.5	44.3	8.8	3.4	149.0
		% within Substrate	50.3%	45.0%	2.7%	2.0%	100.0%
		% within Sex	15.2%	28.4%	8.5%	16.7%	18.8%
		% of Total	9.4%	8.4%	0.5%	0.4%	18.8%
		Standardized Residual	-1.8	3.4***	-1.6	-.2	
	Grass	Count	29	15	1	1	46
		Expected Count	28.6	13.7	2.7	1.0	46.0
		% within Substrate	63.0%	32.6%	2.2%	2.2%	100.0%
		% within Sex	5.9%	6.4%	2.1%	5.6%	5.8%
		% of Total	3.7%	1.9%	0.1%	0.1%	5.8%
		Standardized Residual	.1	.4	-1.0	.0	

			Sex				Total
			M	F	MF	NN	
	Natural Wood	Count	195	45	38	12	290
		Expected Count	180.1	86.2	17.2	6.6	290.0
		% within Substrate	67.2%	15.5%	13.1%	4.1%	100.0%
		% within Sex	39.6%	19.1%	80.9%	66.7%	36.5%
		% of Total	24.6%	5.7%	4.8%	1.5%	36.5%
		Standardized Residual	1.1	-4.4***	5.0***	2.1*	
	Stone	Count	45	38	1	0	84
		Expected Count	52.2	25.0	5.0	1.9	84.0
		% within Substrate	53.6%	45.2%	1.2%	0.0%	100.0%
		% within Sex	9.1%	16.1%	2.1%	0.0%	10.6%
		% of Total	5.7%	4.8%	0.1%	0.0%	10.6%
		Standardized Residual	-1.0	2.6**	-1.8	-1.4	
	Tree Branches	Count	33	1	0	0	34
		Expected Count	21.1	10.1	2.0	.8	34.0
		% within Substrate	97.1%	2.9%	0.0%	0.0%	100.0%
		% within Sex	6.7%	0.4%	0.0%	0.0%	4.3%
		% of Total	4.2%	0.1%	0.0%	0.0%	4.3%
		Standardized Residual	2.6**	-2.9**	-1.4	-.9	
		Count	493	236	47	18	794
		Expected Count	493.0	236.0	47.0	18.0	794.0
Total		% within Substrate	62.1%	29.7%	5.9%	2.3%	100.0%
		% within Sex	100.0%	100.0%	100.0%	100.0%	100.0%
		% of Total	62.1%	29.7%	5.9%	2.3%	100.0%

Individuals and Behaviours (Single Specimen)

Among the one-specimen records (*N* = 743), three behaviours were identified: standing/walking (675 records), flying (54 records), and feeding (14 records). For both single male (M) and female (F) specimens, the most expressed behaviour is standing/walking (M: 88.0% and F: 97.0%), followed by flying (M: 9.4% and F: 2.6%) and feeding (M: 2.6% and F: 0.4%) (Figure 12c and Table 13).

The statistical analysis using crosstabs shows a significant relationship between the sex of the specimen and the behaviour (*Chi Square* = 15.84, p-value < 0.001). The analysis of standardized residuals shows that single female specimens tend to fly less than expected (Table 11 and Table 13).

Table 13. Contingency table for comparison of the frequencies between specimens and behaviours of single specimen (Sex vs Behaviour). Asterisks indicate the probability associated with the value of the standardized residual: * p-value ≤ *0.05 (value exceeds ±1.96);* ** p-value ≤ *0.01 (value exceeds ±2.58);* *** p-value ≤ *0.001 (value exceeds ±3.29).*

			Behaviour - One Specimen			Total
			Feeding	Flying	Standing/ Walking	
Sex	M	Count	13	48	447	508
		Expected Count	9.6	36.9	461.5	508.0
		% within Sex	2.6%	9.4%	88.0%	100.0%
		% within Behavior	92.9%	88.9%	66.2%	68.4%
		% of Total	1.7%	6.5%	60.2%	68.4%
		Standardized Residual	1.1	1.8	-.7	
	F	Count	1	6	228	235
		Expected Count	4.4	17.1	213.5	235.0
		% within Sex	0.4%	2.6%	97.0%	100.0%
		% within Behavior	7.1%	11.1%	33.8%	31.6%
		% of Total	0.1%	0.8%	30.7%	31.6%
		Standardized Residual	-1.6	-2.7**	1.0	
Total		Count	14	54	675	743
		Expected Count	14.0	54.0	675.0	743.0
		% within Sex	1.9%	7.3%	90.8%	100.0%
		% within Behavior	100.0%	100.0%	100.0%	100.0%
		% of Total	1.9%	7.3%	90.8%	100.0%

Considering only the most recorded behaviour (standing/walking), the analysis of the distribution of the two sexes shows that the preferred substrate is Natural wood (216 total records) as well, followed by Artificial substrate (173 records), Bare ground (132 records), Stone (77 records), Grass (42 records), and Tree branches (25 records), although there are some differences between sexes (Figure 12d and Table 14).

The statistical analysis using crosstabs shows a significant relationship between the sex of specimens and the substrate (*Chi Square* = 49.13, p-value < 0.001). The analysis of standardized residuals shows that single male specimens (M) are found more frequently than expected in Natural wood, whereas single female specimens (F) are found more frequently in Bare ground and Stone and less frequently in Natural wood and Tree branches (Table 11 and Table 14).

Table 14. Contingency table for the comparison of the frequencies between specimens and substrate for the most represented behaviour (Standing/Walking) of single specimen (Sex vs Substrate). Asterisks indicate the probability associated with the value of the standardized residual: * p-value ≤ *0.05 (exceeds ±1.96);* ** p-value ≤ *0.01 (exceeds ±2.58);* *** p-value ≤ *0.001 (exceeds ±3.29).*

			Substrate						Total
			Artificial	Bare Ground	Grass	Natural Wood	Stone	Tree Branches	
Sex	M	Count	105_{a}	69_{a}	$27_{a.\ b}$	$173_{b.\ c}$	40_{a}	24_{c}	438
		Expected Count	113.9	86.9	27.7	142.3	50.7	16.5	438.0
		% within Sex	24.0%	15.8%	6.2%	39.5%	9.1%	5.5%	100.0%
		% within Substrate	60.7%	52.3%	64.3%	80.1%	51.9%	96.0%	65.9%
		% of Total	15.8%	10.4%	4.1%	26.0%	6.0%	3.6%	65.9%
		Standardized Residual	-.8	-1.9	-.1	2.6**	-1.5	1.9	
	F	Count	68_{a}	63_{a}	$15_{a.\ b}$	$43_{b.\ c}$	37_{a}	1_{c}	227
		Expected Count	59.1	45.1	14.3	73.7	26.3	8.5	227.0
		% within Sex	30.0%	27.8%	6.6%	18.9%	16.3%	0.4%	100.0%
		% within Substrate	39.3%	47.7%	35.7%	19.9%	48.1%	4.0%	34.1%
		% of Total	10.2%	9.5%	2.3%	6.5%	5.6%	0.2%	34.1%
		Standardized Residual	1.2	2.7**	.2	-3.6***	2.1*	-2.6**	
Total		Count	173	132	42	216	77	25	665
		Expected Count	173.0	132.0	42.0	216.0	77.0	25.0	665.0
		% within Sex	26.0%	19.8%	6.3%	32.5%	11.6%	3.8%	100.0%
		% within Substrate	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
		% of Total	26.0%	19.8%	6.3%	32.5%	11.6%	3.8%	100.0%

Individuals and Behaviours (Couples)

Among the two-specimen records (N = 64), four behaviours have been identified: reproductive behaviour (38 records), standing/walking (20 records), aggressive behaviour (five records), and feeding (two records) (Figure 12e and Table 15).

The statistical analysis using crosstabs shows a significant relationship between the couple type (MF or NN) and the behaviour (*Chi Square* = 40.28, p-value < 0.001). The standardized residuals analysis shows that MF couples perform the reproductive behaviour more frequently than expected, whereas NN couples show aggressive and walking/standing behaviours more frequently than expected (Table 11 and Table 15).

Table 15. Contingency table for the comparison of the frequencies between specimens and behaviours of couples (Sex vs Behaviour). Asterisks indicate the probability associated with the value of the standardized residual: * p-value ≤ *0.05 (exceeds ±1.96);* ** p-value ≤ *0.01 (exceeds ±2.58);* *** p-value ≤ *0.001 (exceeds ±3.29).*

			Behaviour - Couples				Total
			Aggressive	Couple feeding	Reproductive	Couple Standing/Walking	
Sex	MF	Count	0	0	38	9	47
		Expected Count	3.6	1.4	27.5	14.5	47.0
		% within Sex	0.0%	0.0%	80.9%	19.1%	100.0%
		% within Behavior	0.0%	0.0%	100.0%	45.0%	72.3%
		% of Total	0.0%	0.0%	58.5%	13.8%	72.3%
		Standardized Residual	-1.9	-1.2	2.0*	-1.4	
	NN	Count	5	2	0	11	18
		Expected Count	1.4	.6	10.5	5.5	18.0
		% within Sex	27.8%	11.1%	0.0%	61.1%	100.0%
		% within Behavior	100.0%	100.0%	0.0%	55.0%	27.7%
		% of Total	7.7%	3.1%	0.0%	16.9%	27.7%
		Standardized Residual	3.1**	1.9	-3.2**	2.3*	
Total		Count	5	2	38	20	65
		Expected Count	5.0	2.0	38.0	20.0	65.0
		% within Sex	7.7%	3.1%	58.5%	30.8%	100.0%
		% within Behavior	100.0%	100.0%	100.0%	100.0%	100.0%
		% of Total	7.7%	3.1%	58.5%	30.8%	100.0%

Discussion

The aim of the present paper was to analyse data collected by InNat volunteers, originally intended for monitoring the species' presence and distribution, in order to explore the possibility of reusing them for ethological purposes. *Lucanus cervus* was taken as an example due to its ethological relevance and thanks to the high number of records collected over the years by InNat volunteers. Of all *L. cervus* records, the ones deemed valid for ethological purposes represent more than one-third of the total (39.0%), with photographs of single specimens having the highest share. This result is impressive given that these photographs were aimed differently, i.e. study of the distribution of this species over Italian national territory, and no specific guidelines have been given to the volunteers on how to take the pictures. Moreover, the overall highest share of single specimen photographs suggests that this species tends to lead a solitary life, as already reported in Tini et al. (2017), up until mating.

It must be highlighted that, in the case of single specimen photographs, most of the records would have been useful for ethological analyses, though many (35.0%) had to be discarded due to the presence of human disturbance or manipulation. The same does not apply in the case of images portraying two specimens, whose discard rate was much lower (only ca. 7.0%). This, as well, suggests a difference in the attitude of volunteers who appear more respectful in the case of beetle interactions than in the case of single specimens, though always considering the sound difference in the numbers of single-specimen versus two-specimen images (ca. 26:1). A possible explanation could be that, in the case of couples, volunteers are less intrusive because they develop interest in the observed behaviour. This given, notwithstanding the highest number of single-specimen photographs, the most ethologically informative ones are images portraying two specimens.

Considering the sex ratio, it soundly leans toward males: males are more than double in respect to females (i.e., 511 and 238, respectively). This finding is not unexpected due to the much more elusive habits of females, which make them less easily visible and findable (Tini et al., 2017, 2018), as well as the preference and fascination for the large-jawed males who are more attractive to the public.

Concerning seasonal variations, the analyses conducted for the entire dataset follow what is already known about the stag beetle phenology in Italy (Campanaro et al., 2011; Bardiani et al., 2017) and Europe (Thomaes et al., 2021), having July as the month with the highest number of records, followed by June, August, and May. If males and females are considered separately, single male and single female specimens were increasingly recorded from May to July, then increasingly dropped in August, near the end of the stag beetle phenological

season; on the other hand, the highest number of male–female couple records can be found in June, then records slightly decreased in July until being almost absent in August. These results are in line with previous research (Harvey et al., 2011), highlighting the habits of the species: single specimens are abundant in the first part of the season, and couples tend to be established quite early; after copulation, females oviposit (July), and specimens start decreasing (August).

Regarding the substrate analyses, males are found preferentially on natural wood and artificial substrate, while females mainly on artificial substrate and bare ground and secondarily natural wood. These results are in line with previous research as well (Tini et al., 2017, 2018), demonstrating that male stag beetles tend to lead more spatially dispersed lives in respect to females, which are more terricolous. However, during the breeding season, males tend to use tree branches as fighting arenas where females are also lured to for mating purposes (Tini et al., 2017, 2018). Females, on the other hand, except for the breeding season in which they tend to attend tree branches as well, exhibit more terricolous habits, which relate to the need to bury themselves or their eggs under the ground for protection (Harvey et al., 2011; Bardiani et al., 2017; Tini et al., 2017). In the case of the substrate category, natural wood, it was not possible to discriminate whether the trunks or the branches were dead or alive, on the ground or standing: such information would have been interesting in order to relate it with the life stages of *L. cervus*, since dead and rotting wood constitutes the most important part of the diet for its larvae. The results of the analysis focused on the substrate employed during the standing/walking behaviour (i.e., the most recorded one) do not deviate from the above-mentioned results.

The most common substrate on which couples were recorded has been natural wood: given the ecology of the species, it is not unexpected to observe male–female and male–male couples on this substrate, especially during the breeding season, with different purposes, either mating or fighting, respectively. On the other hand, in the case of female–female couples, the few evaluated records do not allow for further discussion.

In the case of the sex vs. behaviour analyses, especially for single-specimen photographs, it is hard to grasp the exhibited behaviour. In fact, the behavioural categories are only three, with the “standing/walking” category having the highest share. This result highlights the difficulty in deciphering the observed behaviours due to the lack of many environmental and specific cues, such as the presence of other sexes, specimens, or animals nearby and the state of the specimen (e.g. just landed, about to soar, exploring the space with the antennae). The lack of a “scenario” description by the volunteers results in substantial data loss, which could

be avoided just by requesting volunteers for a short and simple description. As an example, the presence of exposed wings was registered as flight even though it does not guarantee a totally correct interpretation of borderline cases of flight behaviour (i.e., cases where the specimens are not seen hovering in the air) precisely due to the lack of specific description. The same applies for the "standing/walking" category, where, with the available data, it is not possible to discern whether the animal was standing still or moving, and thus, without any further descriptive comment from the volunteers, an important piece of information, useful for defining the activity cycle of the insect, is lacking. The only clearly detectable behaviours are feeding and flight, and these were almost exclusively performed by males, with the crosstabs analysis suggesting that females tend to fly less than expected: this could be due to the fact that males do disperse more than females, and thus they need energy (Tini et al., 2018).

Furthermore, in the case of two-specimen photographs, four behaviours are observed, with the reproductive one having the highest share, followed by standing/walking, aggression, and feeding. Given the high number of male–female couples, it is not surprising to state that the most common observed behaviour is reproduction, even though it is not possible to discriminate between an effective copula and a mate-guarding event (i.e. no additional information is available regarding whether the genitalia of the two individuals are actually in contact or what happened before and/or after the observed behaviour). This lack in the behaviour interpretation, as already mentioned above for single-specimen behaviours, could be easily solved by requiring a brief specific description of the scenario in which the behaviour is observed: one of the major factors enabling the discrimination of a reproductive copula from a mate-guarding copula is, for example, the presence of other males in the area. Some volunteers did state the presence of other stag beetles nearby, but they did not state the number, the sex, and the distance from the couples, all of these being essential elements for a correct interpretation of a behaviour.

In conclusion, using the above-mentioned CS initiative as a proxy, we here suggest a series of good practices (Table 16): if implemented in ongoing or future CS projects, these good practices will make data collected by volunteers suitable and valuable for both distributional studies and ethological analyses. First of all, any disturbance must be avoided: the specimen must not be too closely observed in order to record a behaviour that is not influenced by the presence and disturbance of volunteers. Once the performed behaviour reaches the end, the sex (and the species, if needed) of the specimen needs to be registered: this can be done by taking close-up (or zoomed) pictures of the specimen or by reporting the sex (and species)

in the note section of the record. Then, the attention needs to be focused on the nearby environment: are there any other specimens nearby? How distant are they from the observed specimen(s)? Moreover, a short description of the substrate must be given. All this information will help researchers to correctly interpret doubtful behaviours (e.g. copula and mate-guarding) and to discriminate between similar substrates (e.g. dead or rotting wood vs. alive wood). The last suggestion concerns the size of the observed specimens: this information is usually hard to report due to the stochasticity of such records, but it would be a good practice to always give some clues on the dimensions of the recorded specimens. In order not to disturb the individuals, a comparison can be made (and reported) with a commonly known object or, in the case of couples, a comparison between the two specimens can be recorded (i.e. one is clearly bigger than the other; one is half the size of the other). This information could be used as a reference to get an indication of the specimen(s) size (although having a measuring instrument, e.g. a ruler, would be recommended if the measurement does not harm, disturb, or request manipulation of the observed specimens). Due to the unprecedented spread of internet-based solutions and apps for smartphones, it would not be too time-consuming for volunteers to fill in all the requested information. Results from the present paper could be used to develop new CS-based ethological studies, but they could also serve as best practices for ongoing CS projects due to the easy inclusion of the above-mentioned suggestion in already existing species recording apps.

Table 16. List of challenging issues highlighted by the present study and the related good practices proposed for projects aimed at studying insects ethological traits through citizen science

Experienced issue	Proposed good practice	Details
Disturbance during observation	Implement strict observation protocols	• Do not manipulate individuals • Maintain a safe distance • Avoid noticeable gestures or noises • Record required information once the observation ends
Data misinterpretation	Provide detailed identification guidance	• Specify details like species, sex, and count of individuals • Use close-up or macro photography • Include comprehensive notes on observations • Provide a simplified list of behavior
Lack of environmental context	Provide detailed description of the surrounding environment	• Describe the immediate surroundings and substrate • Include weather conditions • Note proximity of other individuals or species • Indicate the distance between observed individuals and other individuals or species
Inadequate morphological data	Standardize morphological data reporting	• Provide the size of the individuals by comparing them to commonly known objects (single specimens) or comparing them with one another (i.e., one is half the size of the other) • If it does not cause disturb, harm or request manipulation, measure individuals using a specific tool (e.g., a ruler)
Inconsistent data reporting	Standardize protocols for data reporting	• Provide clear instructions for recording observations • Develop web interface system or mobile app in which data entry forms are standardized

4. Engaging me softly: comparing social drivers for continuative citizens' participation in a long-term citizen science initiative on protected species monitoring

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Materials and methods

An online questionnaire, administered online through Limesurvey[12], was proposed to the volunteers who took part in the MIPP/InNat initiative in the period 2014−2021 and registered to the InNat portal. Participants received personalised contact emails, inviting them to take part in the survey. The web survey incorporated the subject heading "Survey InNat" in the email. Participants were informed that participation was voluntary and provided instructions to contact the research team for any inquiries or additional information. They were also informed that those interested would receive a brief summary of the study results. The confidentiality of responses was guaranteed. The response rate was calculated by dividing the number of returned questionnaires by the total number of questionnaires that reached potential respondents. The questionnaire comprised six sections and a total of 36 questions (see supplementary materials S1). The survey collected socio-demographic data about volunteers (section 1) and opinions on their role as volunteers in a citizen science project (section 2). In the latter section, two more elements have been added, namely those related to the historical contingency in which data was collected and a specific slant related to communication. Regarding the former element, it should be noted that data was collected in February 2022: at that time there were still many restrictions on personal mobility in Italy due to the Covid-19 pandemic and, at best, some restrictions were gradually being lessened (WHS, 2023). For this reason, we included some questions on the extent of the lockdown. Then, the latter element about communication channels was investigated testing the impact of a) MIPP/InNat's initiative promotion tools (e.g., public events; open lectures; web advertising); b) users' preferred mode of uploading records. Subsequently, the survey collected information about any possible previous CS experience (section 3), it performed a test on the acquired skills on the monitored insect species (section 4), and it recorded opinions concerning the ecological crisis, the level of awareness of humankind-environment ecological relationship, and the trust in the ability of humankind to rule the nature and even

[12] http://www.limesurvey.org

to solve environmental issues, respectively (section 5): in the last section, ecocentric and promethean values were measured using the New Ecological
Paradigm (NEP) scale (Dunlap et al., 2000). A reduced NEP scale was employed, with eight statements out of the original 15, to which respondents are asked to express their level of agreement on a four-degree scale. The eight statements are roughly divided in two subgroups: one group reverbs ecocentric values (i.e., awareness of ecological crisis, its relevance and human responsibility) and the second group gathers items for promethean values (i.e., trust in human progress, technological solutionism). Finally, each respondent was asked to agree to being further contacted for possible interviews (section 6). The questionnaire as well as the anonymized responses are publicly available on Zenodo repository (Lenzi et al., 2024).

The survey respondents contributed a total of 3,709 reports, constituting 47.9% of the total reports submitted to the MIPP/InNat. As reported in Table 17, the data show that survey respondents exhibit, on average, a higher level of engagement compared to the overall cohort of volunteers who submitted at least one report to the MIPP/InNat project. The former cohort exhibited a mean of 10 submissions per participant, in contrast to 4 for the latter. Furthermore, the data reveal that a minimum of 25% of survey respondents contributed no fewer than 6 reports, suggesting a notably higher level of participation.

Table 17. Comparison between total MIPP/InNat Volunteers (until 2021) and survey respondents: descriptive statistics about reports submitted

	MIPP/InNat	Survey respondents
Volunteers	1632	364
Reports per volunteer		
Mean	4	10
Dev Std	21	36
Min	1	1
1st quartile	1	1
Median	1	2
3rd quartile	3	6
Max	572	437
Tot	7738	3709

In order to perform the analysis, we identified two classes of participants according to their "continuity" in the activity of reporting species. In the remainder of this paper, we will name the two classes as CV (Consistent Volunteers) and NVC (Non-consistent Volunteers). To split the volunteers in the two classes, we defined a Regularity Index (RI). The index considers both seniority and the number of reports sent from the first year of reporting up to

2021. Seniority is the number of years since the first confirmed record reported by a participant. The RI is defined as follows:

$$RI = i/max_i$$

where "i" is defined as follows:

i = (total number of records sent per participant)/ (seniority in years)

The value of "i" is normalised using max_i, i.e., the maximum value of i computed over all the volunteers. The basic idea underlying the index is to consider a combination of these two elements, i.e., "seniority" and "total number of reports". The allocation of responding volunteers into the classes was based on the value of the Regularity Index (RI) and a threshold. The selection of the threshold was performed in order to include in Class CV those volunteers that provided at least two reports per year, looking at the average of all the years. However, we did not want to consider only this criterion to divide the volunteers in the two classes. In fact, our intent was to put in Class CV those volunteers: (a) engaged for a high number of years; (b) with at least a certain average of reports per year (approximately 2); (c) with a high number of reports. Therefore, we manually labelled all the 364 volunteers either as "consistent" or "not consistent" according to (b). Then we varied the value of the threshold from 0.001 to 1 and looked that the capability of the threshold in terms of maximizing the F1 measure, the number of years and the total number of reports. The F1 measure was computed as

$$F1 = TP/(TP + (FP + FN)/2)$$

where:

- TP is the number of volunteers labelled as consistent and correctly allocated in Class CV
- FP is the number of volunteers labelled as non-consistent but allocated in Class CV
- FN is the number of volunteers labelled as consistent but allocated in Class NCV

As shown in Table 18, the highest value of F1 was obtained with a threshold value of 0.016; however, we were not only interested in "maximizing" F1, but we also wanted to consider the high number of years (seniority) and the high number of reports. All of these led to the selection of 0.018 as a threshold. In fact, in our case, the "optimal" threshold is not the one that maximizes only criterion (b) – used for manual labelling – but the one that satisfies all the three criteria (a-c) as much as possible. We carried out the same analysis by labelling as "non-consistent" the volunteers who satisfied the criterion of the average number of reports per year (b), but who also provided their records in a short time span (e.g., 1 year). The procedure led to the same threshold value. We opted to use the threshold to have the possibility to automatically process a high number of participants, if necessary for future

works. This given, Consistent Volunteers (CV) class comprises volunteers with RI>=0.018, while Non-Consistent Volunteers (NCV) class comprises volunteers with RI < 0.018.

Results were analysed using Jamovi Version 2.3 (The Jamovi project, 2022), a free and open software based on a statistical spreadsheet built on top of the R statistical language (R Core Team, 2021). To explore the relationship between variables, we performed a Principal Component Analysis (PCA, varimax rotation) (see supplementary materials). The variables are connected along eight factors that partially align with potential enablers recorded in literature. It should be noted that PCA has shown the connection between variables: this offered further robustness for the construction of the thematic areas in our analysis. We tested a binomial regression model considering the CV and NCV classes as dependent variable: the model proved to be inefficient ($R^2McF = 0.146$, Confidence Interval 95%) and most of the variables resulted not relevant in predicting the belonging to a class of consistent or to a class of non-consistent volunteers (see supplementary materials S2). Consequently, data have been analysed using contingency analysis taking into consideration five areas encompassing the 15 variables reported in the literature as crucial to predict engagement into CS projects (Table 19). Given that most of the variable are ordinal we largely used Kendall's Tau-b; it is a correlation coefficient that measures the strength and direction of association that exists between two variables measured on at least an ordinal scale. A risk analysis was also performed to assess differences in the sociability between the two identified classes and a selection of subgroups (e.g., age, gender). The risk analysis is based on a squared table 2x2. Odds ratio (OR) serves as a metric to gauge the relationship between a specific variable and its subsequent effect on two different groups: it essentially quantifies the likelihood of the occurrence of an outcome based on a given factor, relative to the likelihood of the occurrence of the same outcome in the absence of that factor. Relative Risk (RR) is a measure of the risk of a certain event happening in one group compared to the risk of the same event happening in another group.

Results

Out of a total of 1632 volunteers, 364 completed the questionnaire, resulting in a success rate of 22.3%. Responding volunteers were divided in two classes based on the above defined regularity index (RI) and the identified threshold value (RI = 0.018): Consistent Volunteers (CV) class comprises 94 volunteers, while Non-Consistent Volunteers (NCV) class comprises 270 volunteers.

Since the RI might not fully capture some phenomena, such as an initial peak in engagement and a significant decrease over time, for volunteers in Class CV we visually inspected the

presence of a possible decrease of engagement over time; in this case the engagement was measured in terms of reports per year. Within volunteers engaged for at least three years (60/94), 26.6% showed a negative slope in the regression line; however, only 15% contributed with one report in the last year of activity. Results from the two classes were compared along potential enablers of engagement recorded through variables selected from literature (see Table 18). Results will be commented throughout this section checking sets of variables related to the following potential enablers: i) Socio-demographic features of participants, ii) Interest in scientific topics, iii) Ecocentrism and conservation, iv) Leisure time, and v) Communication and use of digital technologies

Table 18. Performance of RI's values in classifying respondents. The first column reports the value of the threshold, the second column reports the F1 value, the third column represents the average number of years in Class CV, and the fourth column refers to the average number of total reports computed over all the volunteers in Class CV. The underlined values show the thresholds established.

RI	F1	Average years	Average number of reports
0.010	0.69	3.67	18.96
0.011	0.89	4.47	27.41
0.012	0.89	4.47	27.41
0.013	0.92	4.48	28.79
0.014	0.94	4.48	29.64
0.015	0.94	4.45	29.83
0.016	1.00	4.56	32.95
0.017	0.98	4.53	34.02
0.018	0.94	4.46	35.77
0.019	0.94	4.46	35.77
0.020	0.94	4.46	35.77
0.021	0.85	4.94	42.57
0.022	0.83	4.87	43.36
0.023	0.82	4.86	43.85
0.024	0.81	4.86	44.86
0.025	0.81	4.86	44.86

Table 19. The five areas summarizing potential enablers recorded through 15 variables considered for the present paper. A general overview of the results is provided, as well as the main differences identified between the two classes of participants (n = 364), i.e., class CV – Consistent Volunteers (n = 94) and class NCV – Non-Consistent Volunteers (n = 270).

Potential enablers	Variables	General overview	Differences between Classes
1 - Socio-demographic features of participants	Age	Mainly mature participants: age average: 48.2 y.o.	No statistically significant differences between classes
	Gender	Male: 61.5% Female: 37.9% Other: 0.6%	No statistically significant differences between classes
	Education	High level of education (degree or more): 58%	No statistically significant differences between classes
	Working condition	Occupied: 60% high school teachers: 8.2% researchers or academics: 4.1%	No statistically significant differences between classes
	Residency	Urban area: 52%	No statistically significant differences between classes
2 - Interest in scientific topic	Passion for entomology	Passionate for bugs: 31.5%	No statistically significant differences between classes
	Fascination in natural science	Fascinated by natural sciences: 31.8%	No statistically significant differences between classes
	Usage of data for research reason	Use data from the LIFE MIPP/InNat initiative for research purposes: 31%	No statistically significant differences between classes
3 - Ecocentrism and conservation	Ecocentrism/ prometheanism	Ecocentric values: 56% Promethean values: 12.3%	Similar values between classes but index associated differently between them
	Feeling useful to nature conservation	Feel useful to nature conservation: 87.6%	Class CV: 90% are more likely to feel useful to nature conservation; class NCV participant: 86% are more likely to feel useful to nature conservation
	Feeling closer to nature	Feel closer to nature in taking part to the project: 85%	No statistically significant differences between classes

4 - Leisure time	Where and when people signal	During their free time: 82.1% During dedicated events: 5.9%	Class CV participants: 66.7% collect data in dedicated excursions Class NCV participant: 56.7% collect data in dedicated excursions
	Sociability	Inviting other people to MIPP/InNat activities: 66%	Class CV participants tend to involve other people, mostly male aged 31–45 years
	Covid Effect	Having suffered for not collecting data during the Covid-19 pandemic lockdown: 47.5%	Class CV participants: 66.6% Class NCV participants: 41.1%
5 - Communication and use of digital technologies	Preferred channel for sharing data	Preferential use of the app: 66.8%	No statistically significant differences between classes
	How participants learned about the project	Meeting the project leaders: 36% Querying on web: 26% By word of mouth: 26.6%	Class CV participants: 33.3% learned about the project autonomously (e.g. querying) on the web.

Socio-demographic features

A first set of potential enablers consists of socio-demographic features such as age, educational attainment, gender, residency and working condition. Respondents were quite homogeneous considering the different variables we recorded (Table 19). MIPP/InNat involved mature people (average = 48 years old), predominantly male (61% of the total), with a high level of education: 44% own a university degree and this percentage is about 20% higher compared to the share of Italian population holding a degree (23.1% on population between 25 and 64 years old). Within this context, Class NCV results to be slightly younger than Class CV, but the difference is not statistically significant (p-value = 0.809). The two Classes confirm the same general composition in terms of working conditions: volunteers are predominantly made up of employees (77% of the total of respondents) with a few researchers or university teachers (11.6%). From a territorial point of view, the distribution of volunteers results to be similar throughout the country, with a clear predominance of volunteers living in small and medium-sized towns (more than 60% of the total) and in Northern or Central Italy. These data are in line with national statistics. We noticed that there is a slight over-representation (+ 4%) of respondents living in rural

areas: 44% vs the 48% recorded nationally by official data. This proportion does not change significantly between the two classes

Interest in scientific topics

Considering the interest in scientific topics as the second potential enabler for engagement, the two classes show a general interest in scientific topics and more specifically entomology: 31.5% of respondents admit being passionate about insects while 31.8% declare to be interested in natural sciences. Given this, 31.1% of the respondents are considering using the project data for research purposes and 33.0% consider MIPP/InNat data as a useful tool to identify suitable sites where they may observe or photograph the target species (instrumental interest) with a barely significant difference between classes, respectively 27.7% for CV and 34.8% for NCV ($X2 = 7.40$; p-value = 0.060) and a weak association between classes and instrumental interest (Tau-b = 0.120; p-value = 0.013). Previous experience in CS projects does not seem to be decisive, and no significant differences can be found in the two classes ($X2 = 0.172$; p-value = 0.678). However, 42.9% of respondents stated to have already had experience in CS projects before getting involved in MIPP/InNat initiative.

Ecocentrism and conservation

The two classes share the attitude concerning outdoor activities: 84.4% of volunteers feel to be closer to nature when collecting data for MIPP/InNat and 87.7% feel that their involvement in MIPP/InNat is useful for nature conservation. Then, these feelings match with volunteers sharing a strong feeling on the urgency of ecological crisis: the majority of respondents reports strong agreement concerning statements outlining awareness of the ecological crisis and the relative human responsibility (Fig 13).

Looking at the distribution of responses, we can notice high level of agreement for items that can be easily interpreted as Ecocentric (NEP 1; NEP 3; NEP 5; NEP 7). However, we also noticed some trust attributed to human ability in mitigating ecological crisis (NEP 4) and in extracting resources from the environment (NEP 6). We used the items of the NEP scale to build two indices and make comparisons between the two classes to measure the inclination of respondents both towards prometheanism and another towards ecocentrism. A joint analysis of the classes of indices' score derived from these items (Table 20) shows that ecocentric values are negatively associated with promethean values (Kendall's Tau-b: -0.236; $p < 0.001$). Nonetheless, there are different intensities between the two Classes: Kendall's Taub = -0.443 and -0.157 for Class CV and NCV, respectively. This result

suggests that volunteers from Class NCV share a less negative opinion concerning the potential impact of humans on the ecological crisis in respect to their counterparts.

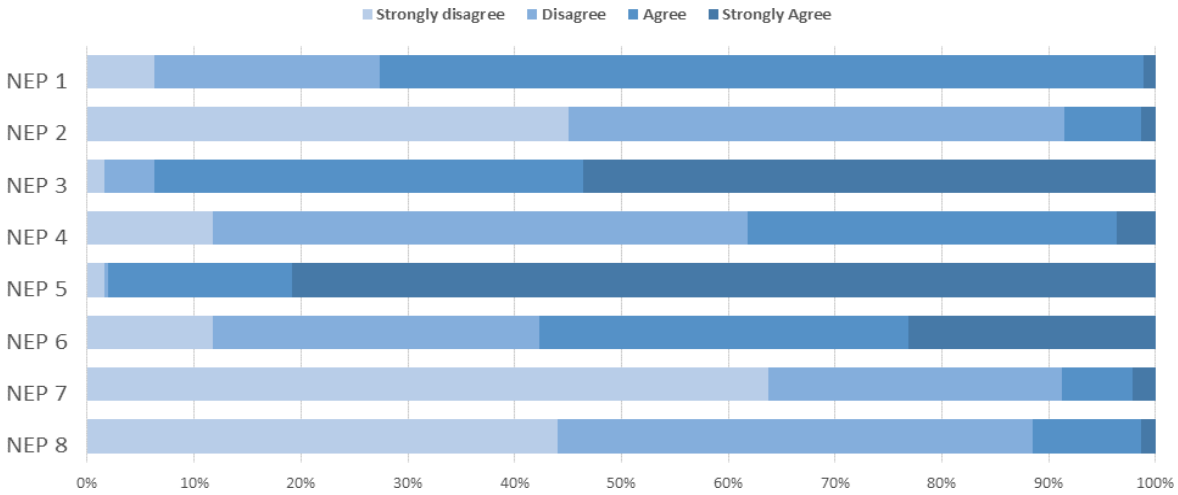


Figure 13. New Ecological Paradigm (NEP) Scale analysis: agreement and disagreement levels (i.e., strongly disagree, disagree, agree and strongly agree) about eight selected NEP Items. NEP1: we are approaching the limit of the number of people the earth can support (Ecocentrism); NEP2: humans have the right to modify the natural environment to suit their needs (Prometheanism); NEP3: if humans interfere with nature it often produces disastrous consequences (Ecocentrism); NEP4: human ingenuity will insure that we do not make the Earth unlivable (Prometheanism); NEP5: humans are seriously abusing the environment (Ecocentrism); NEP6: the Earth has plenty of natural resources if we just learn how to use them (Prometheanism); NEP7: the so-called "ecological crisis" facing humankind has been greatly exaggerated (Prometheanism); NEP8: humans will eventually learn enough about how nature works to be able to control it (Prometheanism).

Table 20. Contingency analysis of promethean and ecocentric attitudes in classes: comparison between participants.

			Ecocentrism classes				
Participant Classes	Kendall's Tau-b	p-value	Prom. classes	Low	Average	High	Total
Class CV - Consistent participants (n=94)	-0.443	< 0.001	Low	1.06%	4.26%	26.60%	31.91%
			Average	11.70%	14.89%	30.85%	57.45%
			High	6.38%	4.26%	0.00%	10.64%
			Total	19.15%	23.40%	57.45%	100.00%
Class NCV – Non consistent participants (n=270)	-0.157	0.005	Low	1.48%	4.81%	16.67%	22.96%
			Average	12.96%	18.52%	32.59%	64.07%
			High	2.22%	4.44%	6.30%	12.96%
			Total	16.67%	27.78%	55.56%	100.00%
Total (n=364)	-0.236	< 0.001	Low	1.37%	4.67%	19.23%	25.27%
			Average	12.64%	17.58%	32.14%	62.36%
			High	3.30%	4.40%	4.67%	12.36%
			Total	17.31%	26.65%	56.04%	100.00%

Leisure time

About 85% of volunteers state that the pleasure of feeling closer to nature represents a positive feature of participating in the MIPP/InNat initiative, and almost all volunteers (97%) list the promoted activity among their hobbies. Recording insect data appears to be a "social" activity (i.e., carried out with other people): ca. 66% of respondents (240 individuals) state that they involved other people in the activities proposed by MIPP/InNat: among them, siblings have the most relevant share (76%), followed by friends (ca. 55%) and other people (e.g., colleagues) (ca. 49%). In this regard, volunteers from Class CV tend to be keener to engage other people compared to the ones from Class NCV: indeed, the difference between the two classes concerning the tendency to invite other people, despite being very small (ca. 66% vs. 63% for Classes CV and NCV, respectively), results statistically significant (p-value = 0.024). According to the performed risk analysis (Table 21), in respect to Class NCV, Class CV participants tend to invite others to take part to MIPP/InNat more as highlighted by the odds ratio = 1.715. However, there are no significant differences in inviting siblings or acquaintances whereas there is significant evidence when it comes to inviting friends (odds ratio = 1.642). Moreover, even if the relative risk may not always be clear-cut for inviting people in general and friends in particular (1.182 and 1.355 respectively), Class CV participants result to involve their own network of relations to a greater extent in respect to Class NCV. Additionally, even though values are just above the significance threshold (χ^2 = 3.80), they increase when Classes are stratified by age and gender. More specifically, Class CV participants are keener to invite their families, especially when considering males (χ^2 = 23.97; Odds ratio = 5.52) between 31 and 45 years old (χ^2 = 4.64; Odds ratio = 7.35).

*Table 21. Risk analysis on the variable "sociability":comparison of OR and RR between Class CV and Class NCV participants concerning the involvement of other people in the activities proposed by MIPP/InNat. * = significant value for χ^2, above critical value 3.80, and valid confidence interval, minimum extreme above 1.*

		Odds ratio		Relative risk
Type of invited people	Value	Confidence Interval	Value	Confidence Interval
general* (χ^2 = 4.11)	1.715	1.01 - 3.37	1.182	1.005 - 2.326
siblings (χ^2 = 3.43)	1.564	0.97 - 3.21	1.234	0.988 - 2.538
friends* (χ^2 = 4.15)	1.642	1.01 - 3.22	1.355	1.011 - 2.658
other, e.g. colleagues (χ^2 = 0.289)	1.123	0.68 - 5.93	1.081	0.773 - 5.709

Furthermore, two out of three volunteers (74.5%) from Class CV tend to collect data during dedicated excursions, while such activity is performed by 56% of the Class NCV. In general, 5.8% of volunteers report attending events organised by MIPP/InNat researchers.
As far as Covid-19 related restrictions are concerned (Table 22), 66% of Class CV express to having (at least "Fairly") suffered from not reporting during the pandemic, while this suffering was experienced by 41% Class NCV.

Table 22. Contingent analysis between participants Classes about their affective commitment to the project during Covid-19-related restrictions ($\chi^2 = 16.01$, p-value *= 0.001; Kendall's Tau-b = −0.186, p < 0.001).*

	Did you suffer from not reporting for the MIPP/InNat project during Covid-19-related restrictions?				
	Not at all	Slightly	Fairly	Very	Total
Class CV – Consistent participants (n=94)	12.77%	21.28%	39.36%	26.60%	100.00%
Class NCV – Non-Consistent participants (n=270)	22.59%	36.30%	30.37%	10.74%	100.00%
Total (n=364)	20.05%	32.42%	32.69%	14.84%	100.00%

Project's communication strategies and use of digital technologies

A relevant potential set of enablers for engagement are communication strategies which often rely on digital technologies. Volunteers appear to mostly use the mobile applications: 50% of them affirm to use it very often. Then, volunteers were asked to state how they first knew about MIPP/InNat (Table 23). Most of the volunteers could not remember and were therefore excluded from the analysis, leading to responses only from ca. 25% of the volunteers who took part in the survey, equally distributed between the two classes: 23 out of 94 (24.5%) from Class CV and 68 out of 270 (25.2%) from Class NCV. The most relevant access point to be engaged in MIPP/InNat was the direct face-to-face interaction: 39.6% of volunteers declared to have started gathering insect records after meeting the MIPP/InNat staff. The second most relevant access point to the project was the web (e.g., social networks, webpages, etc.) from which about 29% of volunteers received information, while 18.3% have been engaged by friends and 12.8% read about the project in the press or found some announcements in an attended protected area (data merged into the category "Other"). Considering the two classes of volunteers, a similar pattern to the one described above was found in Class NCV, with face-to-face meetings playing a crucial role in the engagement (ca 41.6%) whereas for Class CV the situation was different. In fact, 33.8% of volunteers from

Class CV state to have been engaged after a meeting with MIPP/InNat staff and another 33.8% after having found information online.

Although the significance of this analysis is weak (p-value = 0.082) it shows that the web is not the most relevant first contact channel for the volunteers to be engaged but it marks a difference between well the two Classes. Indeed, the web plays a sound role for Class CV, as declared by the 33.8% of respondents, though its role decreases when considering Class NCV (27.72%).

Table 23. Mode of first contact with MIPP/InNat initiative for the two classes of participants ($\chi^2 = 6.69$, p-value = *0.082; Kendall's Tau-b = −0.116,* p-value = *0.038).*

Participants Classes	Direct contact with researchers	Personal contact with friends	Information on the Web	Other	Total
Class CV (n=71)	33,80%	12,68%	33,80%	19,72%	100.00%
Class NCV (n=202)	41.58%	20.30%	27.72%	10.40%	100.00%
Total (n=273)	39.56%	18.32%	29.30%	12.82%	100.00%

Discussion

The above-reported analyses elaborated data collected through a dedicated web survey whose response rate (22.3%) was satisfactory; as a recent review confirmed that online surveys based on invitation can reach about 44% of response rate on average (Wu et al., 2022). In this context, our response rate is lower, but it should be assessed according to two factors, namely the efficiency and the engagement of participants. Firstly, a fully completed questionnaire every four e-mail contacts, calling for voluntary-based participation to the survey, with no reward system, proved quite high efficiency. Secondly, the full list of potential respondents included volunteers that reported a single observation once in ten years; bearing these elements in mind, we can consider our response rate as satisfactory, although to be improved for future research attempts.

Sociodemographic features

Results from the two classes are quite homogeneous, profiling the typical MIPP/InNat volunteer as a mature male with a high level of education, living in a small or medium-sized town in Northern or Central Italy and working as an employee (cf. Pateman et al., 2021). A similar result on the age, sex ratio and education level of the participants has been obtained by Larson et al. (2020) studying the participants of the Audubon's Christmas Count, the world's oldest citizen science project. Even though our data agree with Martellos et al.

(2021), stating that higher retention rates are evident in older age cases, this pattern does not result statistically significant in our case. The general composition concerning the type of employment accounts only for a few researchers or university professors which is perhaps relatively unexpected, given the efforts made by the project to reach out to schools and universities, especially during the first years. Our analyses detected the existence of a self-selection process which is in line with the discussion on the real potential of citizen science for the democratisation of science (Strasser et al., 2018): indeed MIPP/InNat mainly attracted and kept engaged participants falling under the demographic of mature male individuals with higher educational attainment (Jönsson et al., 2023). However, literature itself confirms that a recurring element characterising the profile of participants in CS activities is a high level of education, occupation and age (cf. Füchslin et al., 2019; West et al., 2021). Moreover, as will be further discussed in section 4.2, literature also shows the importance of a rather strong interest in scientific issues, with a high level of cultural consumption of information and entertainment related to scientific research: whether it is simple curiosity or a real passion linked to a hobby, volunteers tend to invest their free time in scientifically meaningful activities. Eventually, literature reports that in many cases there may be a drive to participate in CS projects linked to personal interests in the proposed topic. In the case of projects on biodiversity and nature conservation (Dunkley et al., 2021; Lucrezi et al., 2022), as the case of MIPP/InNat itself, the driving factor to contribute to the protection of the environment in its various forms must be considered. Given this context, sociodemographic variables and features have been proven to play an indirect crucial role in volunteer engagement (Nov et al., 2014): personal values, norms, interest in scientific topics and trust in scientific institutions (Bedessem et al., 2023) are also relevant and should be regarded as key factors fostering participants' engagement.

Interest in scientific topics

It has been proven that environmental CS projects usually attract and engage volunteers who already have a predisposition and curiosity towards nature, as well as enthusiasm in learning new insights about biodiversity and in taking part in nature conservation activities (Shirk et al., 2012; Bonney et al., 2016; Domroese et al., 2017; Phillips et al., 2018; Phillips et al., 2019; Greving et al., 2023). No great differences have been found in the two classes concerning interest in scientific topics. In fact, MIPP/InNat volunteers from both classes seem to be truly passionate and fascinated by natural science and entomology and less interested in any utilitaristic perspective on the collected data (e.g., scientific research, photographic interest). This given, we can assume that volunteers from both classes have

been engaged by the project because they are genuinely motivated to do so. In other studies, such as Larson et al. (2020), these personal motivations are clearly overcome by the more general ones concerning the importance of supporting species conservation. Thus, our results are in contrast with other studies in which the motivation of participants vary considerably with the acquisition of experience during the project (i.e., from non-consistent to consistent participants): Asingizwe et al., (2020) found that initial motivation is connected to curiosity and desire of learning, while it changes, switching to the use of collected data and researchers support with the continuous participation to the project. In this context, Larson et al. (2020) found that advancing science and contributing to conservation are two themes that grow accordingly with project participation. The demonstrated interest in biodiversity conservation and monitoring, as well as the one for natural sciences more in general, perfectly fits with the ecocentric values investigated by the survey. In fact, it is no surprise to see a match between the general interest for the environment and the awareness of the ecological crisis and human responsibility, as confirmed in other studies (e.g., Bruckermann et al., 2021; West et al., 2021; Kaplan et al., 2022).

Ecocentrism and conservation

Being part of an environmental CS project often provides the possibility of acting in close contact with the natural environment thus developing a consequent feeling of attachment and responsibility towards nature and the studied species (or ecosystems) (Halliwell et al., 2021; Pocock et al., 2023). Collecting data for MIPP/InNat seems to enhance such a feeling of being closer to nature and mainly useful for nature conservation. This attitude is well represented in participants belonging to both Classes and it perfectly reflects attitudes largely dominated by ecocentric values. Thus, the observed scenario is one of awareness of the path of the ecological crisis and human responsibility. Although promethean values are less present, this aspect is a clear discriminant between the two Classes and seems to grasp a specific feature of who did participate more constantly across time. In fact, it seems that Class CV volunteers have a more pessimistic view on the human role on the ecological crisis whereas it seems that Class NCV volunteers share a strong belief in the positive impacts of humans on the ongoing ecological and biodiversity crisis. A negative association between promethean and ecocentric values is observed. This can be expected also theoretically (Inglehart et al., 1995; Pittaway et al., 2018): indeed, the relevance of values that see humans having a great capacity to solve self-generated environmental problems may appear incompatible with the presence of values related to the ecological crisis, such as ecocentric values, but they still may coexist. While noting these differences, it seems unlikely that the

attachment to ecocentric values and the sense of perceived usefulness for environmental protection are decisive elements in ensuring greater consistency across time in participation for reporting activities within the project.

Leisure time

Most volunteers from both Classes list insects recording among their hobbies and state that one of the positive features of participating in MIPP/InNat is the pleasure of feeling closer to nature. This suggests that volunteers probably perceived MIPP/InNat as a good motivation to go for walks and spend time in natural areas. Currently, we suppose that what is observed with the variables connected to leisure time is more probably an effect rather than an element that can explain constancy. Indeed, the link between the affective sphere and reporting constancy becomes clearer when examining the opinion on the period of COVID19 restrictions. While Class CV volunteers suffered from not reporting during the pandemic and are also positively associated with an affective relationship with the project, Class NCV volunteers state a minor suffering and result negatively associated with an affective relationship with the project. Results from Class CV combined with their engagement in open-air leisure activities, in respect to Class NCV, portrays highly committed volunteers who dedicate their free time to reporting contributions. Moreover, we explored sociability, checking if MIPP/InNat provided an opportunity for the engagement of others (e.g., siblings, friends, colleagues): it did in the case of Class CV participants who result to engage their networks more than Class NCV. Although we spotted some statistically significant differences between Class CV and Class NCV (gender and age), it must be taken into account that these are both very similar (see section 4.1) and it is reasonable to think that they do not comprise such different people in terms of world-views (see section 4.2 and 4.3). These are hints that can be explored further by either replicating the survey by applying it to another project, or deepening those hints as hypotheses to be explored in a qualitative way.

Communication and use of digital technologies

The issue of engaging non-professionals or amateurs is very critical in nature monitoring (Chandler et al., 2017) and it gained renovated momentum in the last ten years using Information Communication Technologies (ICTs). In fact, ICTs have played a relevant role in the development and increase of projects and participants worldwide (Newman et al., 2012; Haklay et al., 2015; Giardullo et al., 2023a). Indeed, much hope has been placed on the application of ICTs to CS projects in terms of increasing participation (Triezenberg et al., 2012); these expectations are reflected in a widespread investment in apps for smartphones and social media between both newer and longer active projects (Giardullo et

al., 2023b). For example, thanks to ICTs, CS initiatives can encompass small teams or millions of individuals working together towards a shared objective, such as gathering data, analysing it or reporting on findings ("contributory and collaborative projects", Follett et al., 2015). Moreover, social media and other digital platforms or apps are to date some of the most common strategies to inform and engage potential volunteers: the proliferation of digital technologies is considered a key driver for project success and rise in participation rates (Newman et al., 2012; Wynn et al., 2017; Richter et al., 2018). On the other hand, it has been demonstrated that direct contacts, such as face-to-face interactions, is essential to enhance participants' motivation (Cappa et al., 2016, Richter et al., 2018). Motivating the volunteers through direct personal contacts appears important for keeping them involved: professional researchers involved in public engagement meetings can contribute to promote the CS activity and to create a favourable environment for the development of a constant long-lasting collaboration and network of volunteers. Moreover, a direct engagement through public promotion/workshops can contribute to building commitment in the case of long-lasting projects.

This given, analyses on this dimension only considered volunteers who clearly stated how they first learned about the project. Results partially disconfirm the above-mentioned research results by Cappa et al. (2016): face to face interaction turns out to be relevant but it may need to be supported by online recruiting, or by activities that allow maintaining a constant relationship with the volunteer, which are easier and more rapid if performed online. However, one of the major risks of online communication is that, even though it seems to be effective in recruiting highly motivated volunteers, it also increases the opportunity for self-selection of people already highly engaged in CS or extremely interested in scientific and environmental topics such as biodiversity monitoring. This could be due either to individual motivation (i.e., motivated individuals actively looking for projects to for volunteer) or to algorithmic technologies of search engines and social networks (i.e., algorithms used by any given platform aimed at accommodating user preferences, Gillespie 2014). Even though providing greater inclusiveness by reaching more people who will tend to be highly motivated to stay active in the project, all of this could also result in a challenge that is difficult to address, namely a selective inclusiveness: in the present study case, we have detected a self-selection bias that restricts the project ability to attract volunteers outside the demographic of mature individuals with higher qualifications, as highlighted by Jönsson et al. (2023). Nevertheless, any online platform of a project (primarily social media) aids the recruitment process by engaging volunteers who exhibit a heightened sense of motivation

even prior to encountering the project, whether in person or not. In fact, at least theoretically, an online recruiting approach might ensure a consistent and reliable pool of volunteers. Research on recommendation systems in computer sciences consider how to develop new algorithms to increase recruitment rate for projects (Ben Zaken et al., 2022). As an example, SciStarter (https://scistarter.org/), a portal that matches volunteers with projects, relies on this approach. Given this, algorithmic technologies connected to search and social platforms are certainly a valuable tool for project sustainability, though individual motivation still plays a significant role when compared to other recruitment methods. However, this strategy may address the biases about the age class of participants but it can hardly avoid self-selection biases which seem to dramatically affect participants' profiles. Considering the two classes of volunteers, these differ on the type of access point stated (i.e., web or face-to-face interactions) and we can interpret such differences as a proxy of the motivational drivers between respondents: it seems plausible to affirm that Class CV volunteers, whose responses were well-balanced between the two main types of access point, have more actively followed and looked for biodiversity contents (e.g., biodiversity monitoring, ecological issues, CS project) compared to volunteers from Class NCV. Notwithstanding the low significance of the contingency analysis reported in Table 22, results from Table 23 may suggest such a relationship and, perhaps, a further research path to be explored in the future.

Conclusion

A key issue in CS projects is to keep participants actively engaged for a long period. This is particularly relevant in biodiversity projects aimed at the assessment of species conservation status that require a high number of data, ideally largely distributed and covering several years. This given, the present paper explored potential enablers that might keep volunteers active in a project. Based on the long-lasting MIPP/InNat initiative, the analyses explored five areas resuming potential enablers that, according to the literature, are relevant in keeping participants engaged in a biodiversity monitoring project. The survey proposed in 2022 to MIPP/InNat volunteers highlighted the presence of two Classes of volunteers: those most active and "loyal" (Class CV) and those less (Class NCV). As discussed above, the two classes are homogenous, differing significantly only on a few parameters.

Class CV accounts for mature people, predominantly male, with a high level of education. These volunteers are more emotionally committed to MIPP/InNat and show a stronger ecocentric view compared to promethean values. They tend to collect data during dedicated excursions and express more suffering from not reporting during the pandemic.

Class CV participants have been involved equally through face-to-face interactions with researchers and online communication.

Class NCV accounts for slightly younger people (thus no statistical significance have been found) in respect to Class CV. They appear to be less emotionally attached to the project, also showing a less ecocentric view and a stronger belief in promethean values. Volunteers from Class NCV tend to collect data during daily routes and felt less regretful about not reporting during the pandemic. They have been mainly involved by face-to-face interactions, with online communication playing a less relevant role.

In general, although MIPP/InNat did not directly involved participants in practices aimed at proactively support biodiversity and the species investigated by the project, as other conservation CS projects may do, e.g., (Phillips et al., 2019; Wibowo et al., 2017), it must be noted that volunteers result to be very committed (e.g., they consider the activities promoted by the project as a hobby): this could be possibly due to the self-selection process. Although such a process guarantees a core of motivated volunteers, in turn it can become a bias: as many researchers report, in general CS volunteers tend to be more highly educated and already interested in the topics proposed by a project. This is not negative *per se*, but it represents the outcome of a self-selection process that is difficult to overcome. Also, MIPP/InNat has a limited ability to attract participants outside the above-outlined demographic. Coherently, the study highlights the importance of personal networks of volunteers as potential trigger for volunteer recruitment. Class CV participants are more prone to invite other people to join the project compared to Class NCV participants: they invite people with whom they are in close relationship (siblings and friends), that perhaps share the same interests (e.g., open air activities, biology or even insects). In conclusion, the present study provides a detailed account of MIPP/InNat volunteers, also prompting a re-evaluation of the position of online recruitment. The above-mentioned results are to be considered a preliminary approach to the sociological aspects concerning MIPP/InNat as a case study: further examination employing other research methods, such as in-depth interviews, is thus required to gain more detailed insights into additional factors that could facilitate more comprehensive and successful campaigns for CS project, especially in terms of volunteer retention.

Chapter 2: Temperature drives trait-dependent responses in insect phenology

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Summary

Shifts in insect phenology represent a critical and understudied concern, even as we gather more evidence about the effects of climate change on insect communities. This is particularly true for saproxylic beetles, where a lack of long-term data hinders research. Here, we explored interannual changes in a saproxylic beetle community in Mediterranean woodlands by comparing two one-year sampling events conducted 11 years apart. We analysed trends in air temperature and relative humidity over the past 22 years and explored if differences in phenological patterns were detectable between the two sampling periods, also considering functional traits (i.e., trophic guild and body size). Our key findings reveal significant shifts in the community's activity patterns, with different climatic variables influencing them each year. This suggests a potential adaptive phenological response to the warming trend in the area. Our analysis also showed differential responses among trophic guilds and body size classes, reinforcing the importance of functional approaches in climate change studies. Overall, our research highlights that species activity periods may become increasingly unpredictable, underscoring the critical need for continued long-term research.

Introduction

In the present global warming and climate change scenario, natural environments are facing severe transformations which affect the animal and plant populations inhabiting them (Cowie et al., 2022; Pereira et al., 2012, 2024). Evidence of insect decline has been accumulating on a planetary scale. But the nature and the magnitude of these changes remain poorly understood (Herrera et al., 2019; Crossley et al., 2020; van Klink et al., 2020; Sallé et al., 2020; Andersson et al. 2022).

It is known that insect community changes concern not only species richness, composition, and abundances (Hallmann et al., 2017; Lister and Garcia, 2018; Didham et al., 2020; Montgomery et al., 2020; Pilotto et al., 2020; Wagner et al., 2021b), but also shifts in phenological patterns (Sinervo et al., 2010; García-Robledo et al., 2016; Pecl et al., 2017; Schleuning et al., 2020; Harvey et al., 2023). The ongoing variability and thus unpredictability of temperatures and humidity levels may induce instability, or even shifts, in species phenological patterns (Gordo and Sanz, 2005; Forrest, 2016; Abarca and Spahn, 2021; Buckley, 2022), because insect development is, to some extent, connected to such environmental variables (Ahas et al., 2000; Both et al., 2004; Gordo and Sanz, 2005). Phenological mismatches represent a pivotal topic concerning insects' response to climate change because of the possible decoupling of activity among insect communities and the interacting taxa they rely on (Forrest et al., 2016; Pincebourde et al., 2017; Abarca and Spahn, 2021; Rajagopalan et al., 2024). For example, a decoupling of the activity in both insect-insect and insect-plant interactions could increase the whole community's vulnerability. The latter can produce relevant consequences at an ecosystem level, especially when key ecological interactions are involved, such as predation (population control) and pollination (van Dis et al., 2023; Vázquez et al., 2023). On the other hand, at a species level, the synchronisation of adults of the same population plays a key role, as many species have narrow time windows for sexual reproduction (Bjørnstad et al., 2016). Therefore, mismatches in adult outbreaks could lead to increased vulnerability in local population (Sugio et al., 2020). Analysing interannual changes in phenology and the abiotic factors driving insect responses is thus of great importance for understanding how insect communities may compensate climate change impacts (Sverdrup-Thygeson et al., 2014; Gutiérrez and Wilson 2021). Furthermore, exploring differential responses across trophic guilds or functional traits (i.e., body size) can provide a deeper understanding on ecological forces behind the changes.

Saproxylic insects (those depending during at least one part of their life cycle on dead or decaying wood, or on the presence of other saproxylic organisms (Speight, 1989; Stokland et al., 2012), and beetles in particular, represent an appropriate target group to delve into insect responses to environmental changes (Martikainen and Kaila, 2004; Harris et al., 2019; Sánchez-Bayo and Wyckhuys, 2019; Basile et al., 2023; Quinto et al., 2023). Saproxylic beetles represent the most abundant and diverse insect group across forest ecosystems in terms of species richness, functional roles (i.e., nutrient recycling, species population control, and pollination) and microhabitat occupancy (Müller et al., 2013; Ulyshen and Šobotník, 2018; Micó et al., 2020). Tree hollows constitute an important microhabitat for a large number saproxylic species (Micó, 2018). Because of their strong dependence on these stable micro-conditions and microsite availability, this group is ultimately rather vulnerable to environmental changes (Seibold et al., 2015). In fact, several species are considered worthy of protection or at risk of extinction (Nieto et al., 2010). However, despite this known vulnerability, little is known about how these saproxylic communities may be responding to climate change.

Studying the effects of climate change on saproxylic beetle's population inhabiting tree hollows is challenging. This is because they are prone to natural interannual fluctuations in abundance, a common trait among insects, which are not necessarily indicative of actual population increases or declines (Wolda, 1978, Martikainen and Kaila, 2004). To fully understand interannual patterns, robust multi-temporal datasets are required. However, such data are quite rare in saproxylic communities, both due to the considerable effort needed to collect and identify species or the alarming scarcity of freely available datasets for comparative purposes (Campanaro and Parisi, 2021, Rocha-Ortega et al., 2021). Consequently, despite their immense ecological importance, saproxylic beetle communities, as many other insect communities, remain largely understudied from a temporal perspective (Sverdrup-Thygeson et al., 2014).

The objective of this study was to further explore the nature of interannual changes in the saproxylic beetle community inhabiting tree hollows in a Mediterranean woodland within a protected area in Spain. Motivated by previous research revealing marked changes in saproxylic beetle diversity and interaction patterns after an 11-year period (Quinto et al., 2023), our specific focus was to analyse the phenological shifts within this community and their relationship with abiotic factors. To achieve this, we compared data collected during two one-year sampling events conducted 11 years apart. First, the 2000 to 2022 climate series of the studied area were analysed to provide a climatic framework for our two

sampling events. Specifically, we investigated whether significant climate change was indeed occurring over the last 22 years. Next, we explored whether tree hollow saproxylic community face any interannual changes, related to trophic guilds or body size. This approach, by working with a large number of species clustered, allowed us to avoid the noise caused by natural fluctuations in certain species and provided a clearer picture of the interannual changes occurring within the saproxylic community. Subsequently, we delved into changes in phenological patterns, considering the whole community, taking also into account trophic guild and body size, and single species. Finally, we evaluated how climate variables (i.e., temperature and relative humidity) may shape phenology. The attainment of these objectives represents a starting point for understanding temporal dynamics of biological traits across tree hollow saproxylic communities, with some insights on potential adaptative responses to environmental changes. As phenological shifts are a key response to temperature variations (Buckley 2022), we predicted that the mentioned community would exhibit significant and contrasting interannual phenological shifts. We hypothesized that the magnitude of such changes, in both phenology and abundance, is driven by abiotic factors and biological traits such as trophic guild and body size traits (Chichorro et al., 2019, 2022).

Materials and Methods

Study area

The field research was conducted at the Cabañeros National Park (central Spain), a protected natural area of 40,856 hectares characterised by a Mediterranean climate. Three Mediterranean woodland types were considered: deciduous oak Quercus pyrenaica Willd. woodland, deciduous riparian ash Fraxinus angustifolia Vahl. woodland, and sclerophyllous oak Quercus ilex Lam woodland. These woodlands are mature (mean number and standard error for trunk diameter (cm) of woodland types were: 66.37 ± 2.34 in deciduous oak, 69 ± 2.61 in deciduous riparian ash and 49.35 ± 1.58 in sclerophyllous oak) and were managed in the past. Therefore, to some extent, the current distribution of tree hollows resulted from ancient traditional practices in each woodland type (Quinto et al., 2014; 2023).

Beetle sampling and species processing

Saproxylic beetles were collected over two, one-year sampling campaigns: from March 2009 to February 2010 (referred to as T1), and from March 2021 to February 2022 (referred to as T2). Fifteen to sixteen tree hollows were selected in each woodland type for each period. To avoid potential effects deriving from fauna extraction during the first sampling, neighbouring woodland patches were considered. Selected patches had the same forest

structure. Moreover, at T2 an effort was made to select a pool of tree hollows with similar characteristics to those in T1 (see Quinto et al., 2023 for more details). Emergence traps covering tree hollows were used as a sampling method (Figure 14), which is the most effective method to survey saproxylic communities that inhabit tree hollows (Quinto et al., 2013). This trap consists of a black acrylic mesh that fits each hollow opening and is sealed with staples. This is an absolute method that, from the exact moment of installation, is capable of capturing virtually all species emerging from the hollows. Emerging specimens come into white collecting pots containing propylene glycol as preservative, thus ensuring passive sampling. In total, 48 and 47 traps were selected in T1 and T2, respectively. Samples were collected monthly over the course of a year both in T1 and T2. The two sampling periods represent two single "temporal windows" but this sampling design with standard and easily controlled conditions —including a protected area, an absolute and systematic sampling method, and the selection of patches and tree hollows that ensured no significant changes between years—allowed for a reliable comparison of the two events. All the collected specimens were stored in 70% ethanol. The nomenclature mostly follows Fauna Europaea (de Jong et al., 2014) and Bouchard et al. (2011). The identified material was deposited at the Entomological Collection of the University of Alicante (CEUA-CIBIO).



Figure 14. Emergence traps used for the sampling, placed at the entrance of the tree hollows

Climatic variables

Climatic trends in the study area

The annual historical evolution of the monthly average temperatures and humidity from 2000 to 2022 was obtained from the Porzuna (CR03) weather station in Ciudad Real (Castilla-La Mancha, Spain). The station is located near the study area. The minimum and maximum distances to the nearest and furthest sampling points for beetles were 17.04 km and 37.30 km, respectively. This observatory belongs to the Agroclimatic Information System for Irrigation (SIAR) of the Ministry of Agriculture, Fisheries and Food of Spain.

To verify the homogeneity of the climatic series before the analysis, the von Neumann test (absolute homogenisation) based on the randomness of the series under study was applied, without the need for a homogeneous reference series (Martín Vide 2003). The test consisted in calculating:

$$\delta^2 = \left(\frac{1}{n} - 1\right) \sum (X_{i+1} - X_i)^2$$

The resulting value was divided by the series variance. In this case, the result obtained was 1.85, and since the quotient was close to 2, the series was considered random, and therefore, homogeneous.

The non-parametric Mann-Kendall test was applied to analyse whether the temperature and humidity evolution presented any statistical significance. To perform this calculation, we used the Makesens macro developed by the Finnish Meteorological Institute in 2002. This allowed obtaining the statistical test Z for trend detection and the Sen's slope estimate of the trend (Salmi et al., 2002).

Climatic variables of sampled years

Monthly temperature and humidity of the 12 sampled months of T1 and T2 used as predictive climatic variables of the phenology changes were registered using hobo data-loggers (HOBO U23 Pro v2 Temperature/Relative Humidity Data Loggers with U23-001 sensor). Two to three data loggers were attached to the trunk of the trapped trees in each sampled forest. They were programmed to record temperature and relative humidity values every 4 hours throughout each sampling year. To analyse the phenological changes, we considered the monthly values of mean, maximum and minimum temperature as well as relative humidity for each year (T1 and T2).

Data analysis

Temporal variation in saproxylic communities was assessed at the National Park scale, thereby encompassing the natural variation in species traits that can occur among forest types. Community changes were first explored by comparing data collected in 2009-2010 (T1) with those collected in 2021-2022 (T2). The General Linear Model (GLM) was applied to explore the interactive effects of time (i.e., year) on trophic guild and body length (abundance as response variable).

Species were assigned to the following trophic guilds: Mycetophagous (M), Predators (P), Saprophagous (S), Saproxylophagous (SX) and Xylophagous (X). For these, we consulted Audisio et al. (2014), Bouget et al. (2019) and Micó et al. (2021), and we also relied on expert advice. On the other hand, body length data came from an existing database (Micó et al., 2020, Pérez-Sánchez et al., 2021, Martínez-Pérez et al., in prep). Values for this functional trait were divided into four size classes (Q), identified based on distribution quartiles within our sample, with Q1: $x < 3.16$ mm, Q2: 3.16 mm $< x <$ 4.5 mm, Q3: 4.5 mm $< x <$ 10 mm, Q4: $x > 10$ mm. The implementation of these functional traits allowed detecting potential changes as well as the interaction between these variables, highlighting even the mildest signals. GLM was fitted using a Poisson distribution for data count. GLM was first performed with each predictor variable separately, and later in combination with all of them, in order to compare the goodness of fit of the model. To analyse the statistical inference over the fitted GLM, we used the deviance function from the stats package, specifically Type II Wald *Chi Square* tests. We performed Tukey's HSD pairwise post hoc comparisons to determine significant differences between significant treatments.

Data was processed using RStudio 2023.12.0+369 (R Core Team, 2023).

Changes in phenological patterns

The "activity period" of the adults of a given species was defined as the months in which each species was collected. Thus, the phenological pattern refers to the set of months in which a given species was found, considering the relative abundances of the collected individuals.

In order to investigate possible changes in the phenological patterns at a community level, and due to the need for a statistically significant number of yearly observations for each species (i.e., at least 20), the analyses were performed exclusively considering the species clusters described above, i.e., trophic guild (TG) classes (M, P, S, SX and X) and body length (BL) classes (Q1, Q2, Q3 and Q4).

To explore the phenological distribution of the TG/BL class abundances, a Principal Component Analysis (PCA) was performed on the monthly normalised abundance values of TG/BL for T1 and T2, separately. Then, a Generalised Procrustes Analysis (GPA) was conducted between the observation scores of the first three PC axes of T1 and of T2 to test whether the ordination spaces of the two years were superimposable (i.e., similar), and which month showed the biggest difference. Procrustes superimposition (Gower, 1971, 1975) is a morphometric analysis aimed at minimising the sum-of-squared distances between corresponding objects in a Euclidean space (Podani, 2000; Peres-Neto and Jackson, 2001). GPA is a comparison of the 'shapes' of two ordinations with the same dimensionality (i.e., the same number of axes) by superimposition methods: if all objects are influenced in a similar manner by the underlying sets of variables, the shapes of both ordinations will resemble one another. By contrast, if both sets of variables are independent from each other, then the corresponding object configurations in ordination space will be only weakly related (Bajocco et al., 2010). Though relatively well-known in the framework of morphometric analysis (e.g. Rohlf and Slice, 1990; Bookstein, 1996), the use of Procrustes methods to interpret datasets with different attributes (e.g. phenological features) is limited (but see Olden et al., 2001; Peres-Neto and Jackson, 2001; Bajocco et al., 2010). In order to find an optimal superimposition that maximises their fit, configurations are warped by centring, linear scaling, and rotation. The residual sum-of-squared distance (d2) between the corresponding objects in their best fit (i.e., consensus configuration) represents an inverse measure of their degree of association (Gower, 1971). We tested the statistical significance of the Procrustean fit with a Monte Carlo simulation technique to yield a reference distribution (see Podani, 2000): 1000 pairs of random ordinations were generated by permuting the original objects and compared using a GPA. The p-values (one-tailed test) were computed as the proportion of randomly derived distance values that were as low or lower than the actual distance value.

To assess the role of the climatic variables, we first performed a Redundancy analysis (RDA) to quantify the predictive role of the weather variables on TG and BL classes, for T1 and T2, separately. The RDA method was developed by Rao (1964) and introduced to ecological data analysis by Ter Braak and Prentice (1988). It consists of an asymmetric canonical ordination technique that measures redundancy (sensu Gittins, 1979). Accordingly, the ordination of the dependent variables is forced to be explained by the configuration of the independent variables such that the RDA axes represent the percentage of the variance of the response variables explained by the predictors (van den Brink and ter Braak, 1999). In

our case, while TG/BL class abundance represented the response variables, the predictor variables were as follow: mean, maximum and minimum temperatures (meanTemp, maxTemp and minTemp, respectively) and mean, maximum and minimum relative humidity (meanRH, maxRH and minRh, respectively).

The multivariate procedures mentioned above were also performed at the species level, for T1 and T2 separately. In this case, only species with more than 20 individuals/year were included, i.e., *Calathus granatensis* Vuillefroy, 1866, *Cetonia carthami aurataeformis* Curti, 1913, *Epuraea fuscicollis* (Stephens, 1835), *Ischnomera xanthoderes* (Mulsant, 1858), *Mycetochara quadrimaculata* (Latreille, 1804), *Mycetophagous. Quadriguttatus* Müller in Germar, 1821, *Prionocyphon* sp. (P.W.J. Müller, 1821), *Ptinus timidus* Brisout de Barneville, 1866, *Rhamna semen* Peyerimhoff de Fontenelle, 1913, *Soronia oblonga* C. Brisout de Barneville, 1863, *Xyleborus monographus* Fabricius, 1792 . First, a PCA was performed on monthly normalised abundance values of the selected species; then, a GPA was performed on the observation scores for the first three PC axes for each species. Finally, an RDA was led to quantify the predictive role of the weather variables (temperature and relative humidity) on species abundance.

In addition, a linear regression analysis between selected species abundance in T1 vs T2 was performed to determine which species showed a significant relation between the two time periods and which months differed the most. We then performed, for T1 and T2 separately, a stepwise regression analysis ($p<0.05$ as entrance threshold) between temperature as well as relative humidity data and abundance of all species together, to check whether the weather variables contributed differently.

Results

Climatic trends in the study area

Concerning the climatic framework of our sampling events, based on the temperature variables, the annual average maximum temperature ($\alpha = 0.05$) increased significantly between 2000 and 2022, specifically with a mean of +0.07°C/year, and a total increase of 1.3º C (mean temperature), 1.4º C (maximum temperature and), 0.4º C (minimum temperature) (Figure 15). The increase in the annual average maximum temperature was also confirmed in July, October, and December. An annual increase of 0.1°C/year ($\alpha = 0.1$) was encountered in July, and the maximum average temperature increased by 2.3°C. The October and December months showed an annual increase of 0.13°C/year and 0.075°C/year,

respectively (α = 0.05). For this period, it was estimated that maximum temperature increased by 3°C in October and 1.73°C in December.

Regarding relative humidity, the annual average as well as the average maximum and minimum humidity did not show a significant increasing trend: less than 90% significance (α > 0.1) (Figure 15).

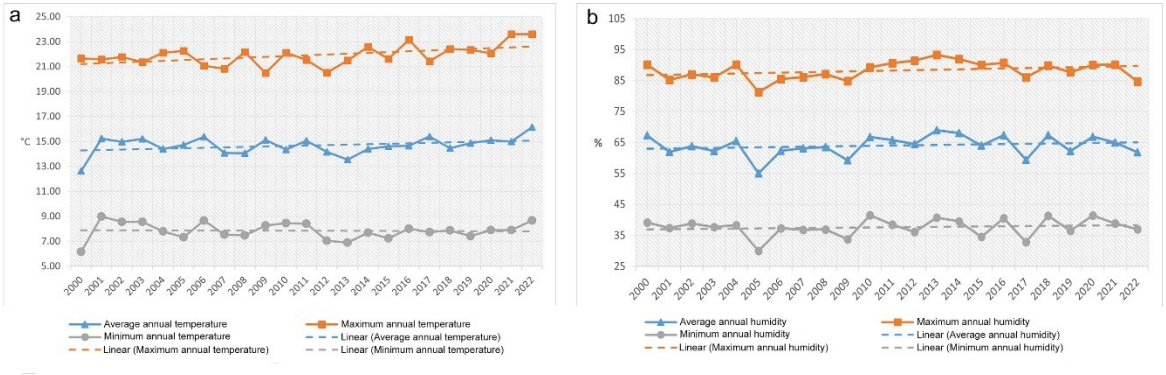


Figure 15. Historical interannual evolution of mean temperatures and their linear trend (a), and the mean relative humidities and their linear trends (b) in Cabañeros National Park. Source: SIAR.

Interannual differences in abundances

A total of 4,080 beetles were collected over the two sampling years, and they belonged to 156 species and 35 coleopteran families. About 77 species occurred only in one single sampling period, in a balanced way: 38 were collected only in T1, and 39 only in T2. A total of 2,369 individuals were collected in T1, and 1,711 in T2, (28% less than in the first sample). This difference was statistically significant (p-value < 0.001) and it turned out to be strongly influenced by trophic guild and body length (Table 24). Moreover, the most striking result was the interaction Time*Trophic guild*Body length (Table 24, Figure 16). While P and SX classes in T2 are less than in T1, the direction of change varies in S and M according to body length class.

Table 24. Analysis of deviance (Type II Wald Chi-square tests) in the fitted models for the abundance. The R2 = 0.975. * = p-value ≤ *0.05,* ** = p-value ≤ *0.01,* *** = p-value ≤ *0.001.*

Explanatory variables	*df*	*Chisq*	p-value
Time	1	96.64	<0.001***
Trophic guild	4	9.65	0.05*
Body length	3	3.58	0.311
Time*Trophic guild	4	107.11	<0.001***
Time*Body length	3	162.95	<0.001***
Trophic guild*Body length	9	5.23	0.814
Time*Trophic guild*Body length	9	108.05	<0.001***

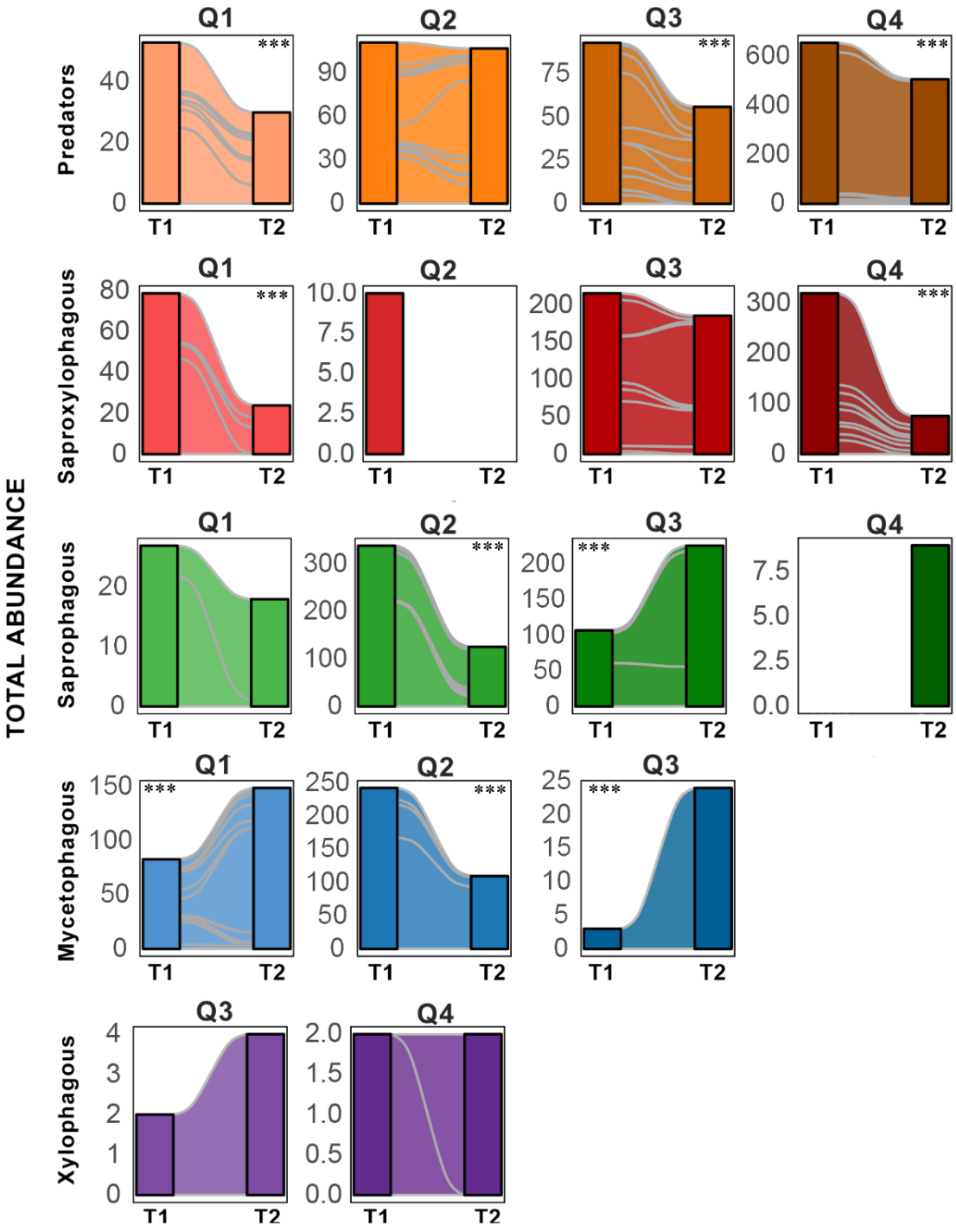


Figure 16. Interactive effects between Trophic Guild and Body Length over time tested using Tukey HSD pairwise comparison. Trophic Guild: P: predators; SX: saproxylophagous, S: saprophagous; M: mycetophagous; X: xylophagous. Body size: Q1: x < 3.16 mm, Q2: 3.16 mm < x < 4.5 mm, Q3: 4.5 mm < x < 10 mm, Q4: x > 10 mm. Time: T1: from March 2009 to February 2010, T2: from March 2021 to February 2022. *** = p-value ≤ *0.001.*

Interannual differences in phenological patterns

At a community level, the PCA biplots presented ordination space differences between T1 and T2, both for the Trophic Guild (TG) and for the Body Length (BL) classes, the explained variance between the years falling sharply in both cases (Figure 17). The general observed pattern in T1 (89% of explained variance) changes considerably in T2 (77% of explained variance for all classes), both for TG and BL groups. For example, the species of X, which are mostly abundant in July and August in T1, seem to anticipate their phenology in T2 with a major influence by June, May and July. In addition, the abundances of S, SX, M and P, which are concentrated in May and June in T1, are rearranged in T2: S and SX anticipate their phenology with greater abundances in March and May, while M and S postpone their peaks to July/May and June/July, respectively. When considering the BL group, the overall phenological pattern changes from T1 (91% of explained variance) to T2 (88% of explained variance). The smallest species (Q1) mainly influenced by June and May in T1 postpone their abundance peak to July in T2, as well as the little-medium sized species (Q2), which appear abundant mainly in March and June in T1, and then postpone their phenology with abundance peaks mainly to May and June in T2. Similarly, in T1, the medium-large species (Q3) are clearly related to May, and then postpone their abundance peak to June in T2. Conversely, the larger species (Q4) is more influenced by July and May in T1, and largely influenced by March in T2.

In general, the GPA shows that the T1 phenological configuration differs significantly from that of T2, both for TG and BL classes. In fact, for TG, the correlation coefficients (Table 25) of the first three PCA axes of T1 and T2 are mainly below 0.5 as absolute value, except for the correlation between the first T1 and T2 axes ($r = 0.802$). For BL, they are mainly below 0.5 in terms of absolute value, except for the first T1 axis with the second and third T2 axes ($r = 0.699$ and -0.525, respectively), and for the second T1 axis with the third T2 axis ($r = 0.676$). Moreover, the residuals of the monthly abundance distribution within the TG and BL ordination spaces (Figure 18) highlight that the major abundance distribution differences occurred during the summer months.

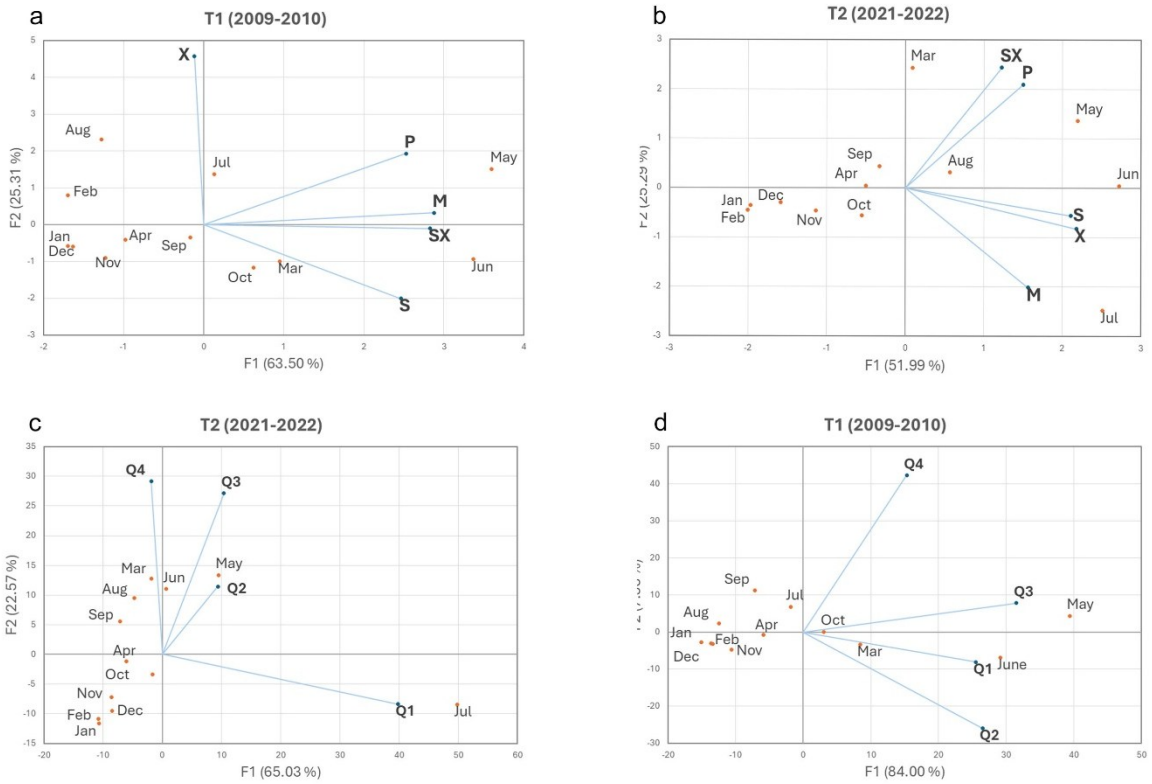


Figure 17. PCA biplots on the distribution of the community abundances within the year. Blue vectors represent the trophic guilds (a and b) and the body length classes (c and d); red dots represent the phenological observations. Trophic Guild: P: predators; SX: saproxylophagous, S: saprophagous; M: mycetophagous; X: xylophagous. Body size: Q1: x < 3.16 mm, Q2: 3.16 mm < x < 4.5 mm, Q3: 4.5 mm < x < 10 mm, Q4: x > 10 mm. Time: T1: from March 2009 to February 2010, T2: from March 2021 to February 2022. *** = p-value ≤ *0.001.*

Table 25. Correlation coefficients (r) among the first three PCA axes of 2009 vs 2021, for TG and BL. In bold: values larger than 0.5 as absolute value.

	TG			BL		
PCA axes	F1_2009	F2_2009	F3_2009	F1_2009	F2_2009	F3_2009
F1_2021	0.802	0.365	0.005	0.290	0.441	-0.376
F2_2021	0.356	-0.133	0.085	0.699	0.168	0.129
F3_2021	-0.025	-0.103	-0.185	-0.525	0.676	0.283

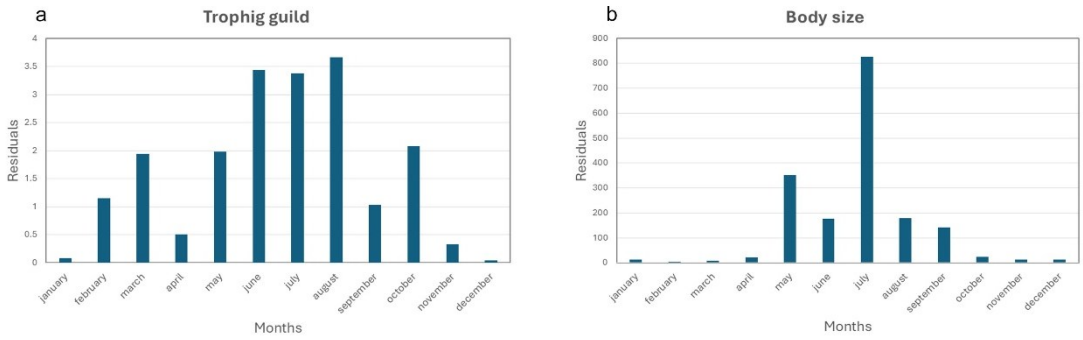


Figure 18. Residuals for trophic guild (a) and body length (b) with respect to the consensus configuration after GPA scaling, rotation and translation.

Considering the role of the selected environmental variables (i.e., temperatures (minimum: MinTemp, mean: MeanTemp, maximum: MaxTemp) and relative humidities (minimum: MinRH, mean: MeanRH, maximum: MaxRH), the stepwise variable selection method shows that in T1, MinRH plays a relevant role in influencing specific phenological patterns. In fact, it is the retained variable in the model with 44% of explained variability (p-value = 0.026). On the other hand, in T2, the most important variable is the MaxTemp since it is retained in the model with 69% of the explained variability (p-value = 0.001). Such results are also confirmed by the RDA: in T1, MinRH represents the most contributing driving factor (94% of explained variance), almost coinciding with the first RDA axis, and it negatively influences the community abundances distribution, except for the X class for which MaxRH represents the main driving factor. Conversely, in T2, MaxTemp and MinTemp are the driving factors that contribute the most (90% of explained variance) (Figure 19).

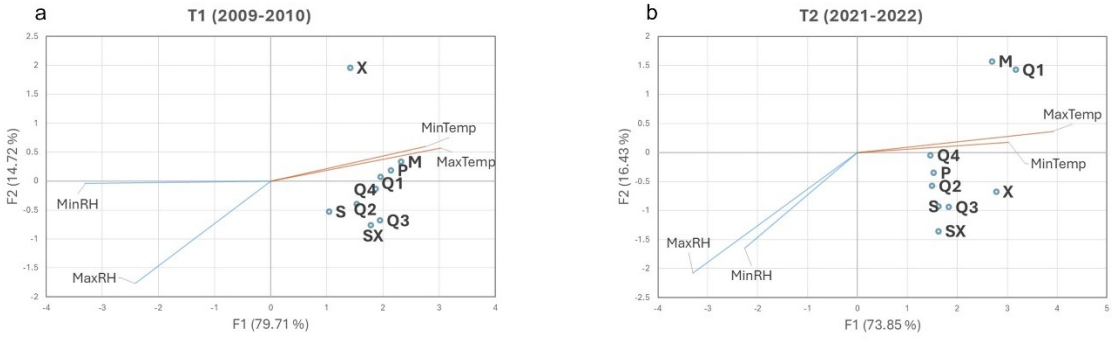


Figure 19. RDA plots for T1 (a) and T2 (b). Red vectors: explanatory variables (MinTemp and MaxTemp: minimum and maximum temperatures, MinRH and MaxRH: minimum and maximum relative humidity); blue dots: response variables (TG and BL). Trophic Guild: P: predators; SX: saproxylophagous, S: saprophagous; M: mycetophagous; X: xylophagous. Body size: Q1: x < 3.16 mm, Q2: 3.16 mm < x < 4.5 mm, Q3: 4.5 mm < x < 10 mm, Q4: x > 10 mm. Time: T1: from March 2009 to February 2010, T2: from March 2021 to February 2022.

Regarding the species level, the linear regression analysis among the phenological patterns of the 11 selected species in T1 and in T2 highlights a lack of significant correlations (i.e., specific phenological patterns in T1 and T2 are statistically different) for *C. granatensis* (r2 = 0.153), *C. aurataeformis* (r2 = 0.31), *M. quadriguttatus* (r2 = 0.093), *P. timidus* (r2 = 0.078) and *X. monographus* (r2 = 0.004) (Table 26). Considering these five species, the months presenting the highest dissimilarity values between the two years are that of late spring/summer: from May to September, with a peak in August for *C. granatensis* and *C. aurataeformis*, in June and April for *M. quadriguttatus*, in May for *P. timidus*, and in July for *X. monographus* (Figure 20).

Table 26. Pearson determination coefficients (r2) between species abundance in 2009 and 2021. In bold: p > 0.05, representing the species for which the phenological pattern in T2 does not show a significant correlation with the one in T1.

Species	r2
1. *Calathus granatensis* Vuillefroy, 1866	0.153
2. *Cetonia carthami aurataeformis* Curti, 1913	0.31
3. *Epuraea fuscicollis* (Stephens, 1835)	0.52
4. *Ischnomera xanthoderes* (Mulsant, 1858)	0.988
5. *Mycetochara quadrimaculata* (Latreille, 1804)	0.877
6. *Mycetophagus quadriguttatus* Müller, 1821	0.093
7. *Prionocyphon* sp.	0.597
8. *Ptinus timidus* Brisout de Barneville, 1866	0.078
9. *Rhamna semen* Peyerimhoff de Fontenelle, 1913	0.994
10. *Soronia oblonga* Brisout de Barneville, 1863	0.509
11. *Xyleborus monographus* Fabricius, 1792	0.004

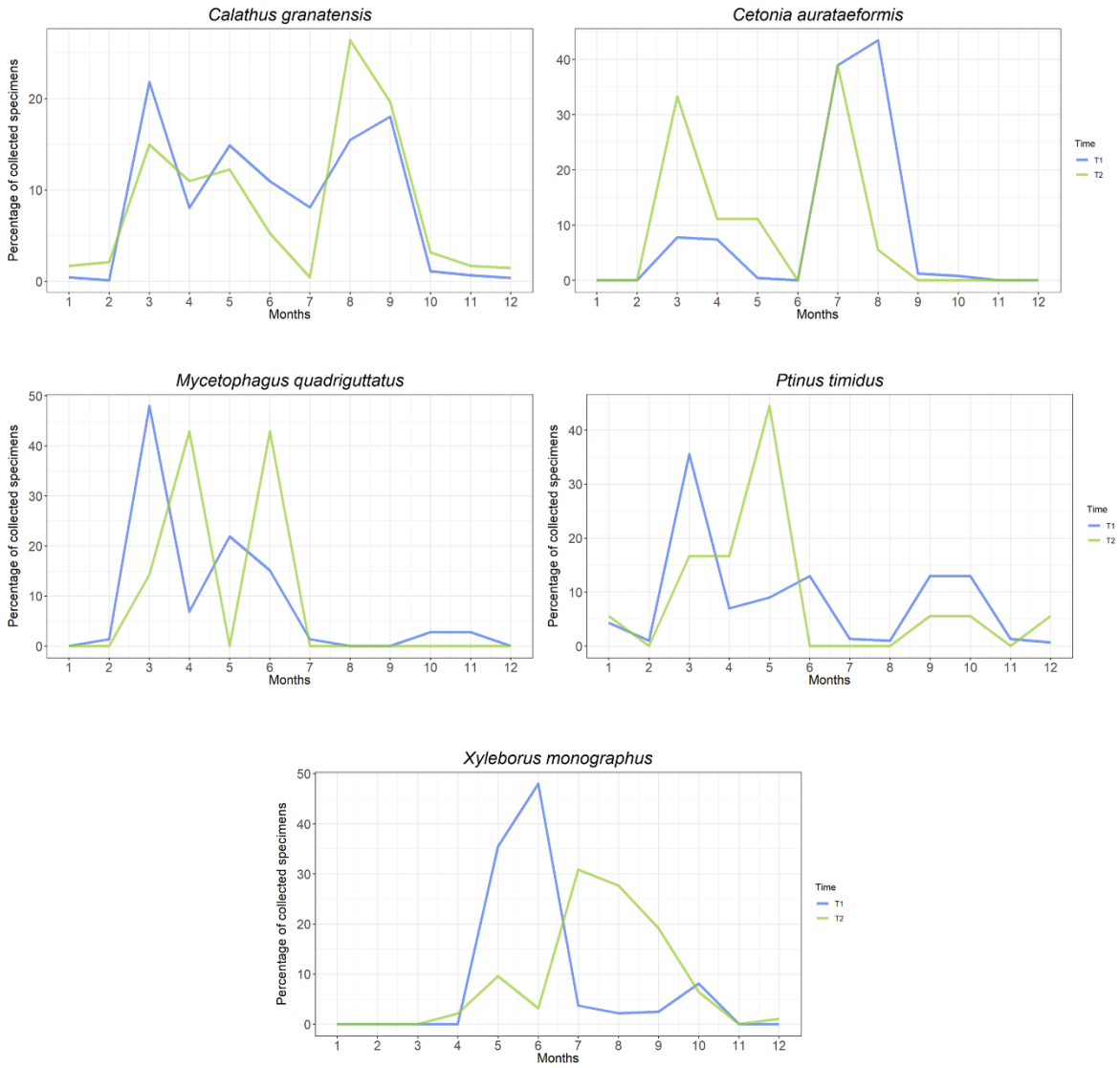


Figure 20. Temporal distribution within the year of the abundances of the five species whose phenological pattern of T2 (green line) significantly differ from the one of T1 (blue line)

The PCA biplots estimated on the 11 selected species show a clear difference between the ordination space in T1 and T2, with a reduction from 62% to 47% of the explained variance between the sampling periods (Figure 21). Moreover, it confirms the phenological pattern changes of the five above-mentioned species. C. granatensis is mostly influenced by May in T1, whereas it postpones its abundance peak to late summer in T2, June having a major influence. *C. c. aurataeformis* presents an abundance peak in October in T1, while it is also influenced by July in T2. *M. quadriguttatus* shows an abundance peak in March in T1, which is ultimately the most influential month, while in T2, it postpones its pattern, undergoing the major influence of March, April and June. Similarly, *P. timidus* shows a greater abundance in March in T1, and then it postpones its flight period peak to May in T2. Finally, *X.*

monographus show a phenological advance as well, May/June being the most influential months in T1, and July, August and September in T2.

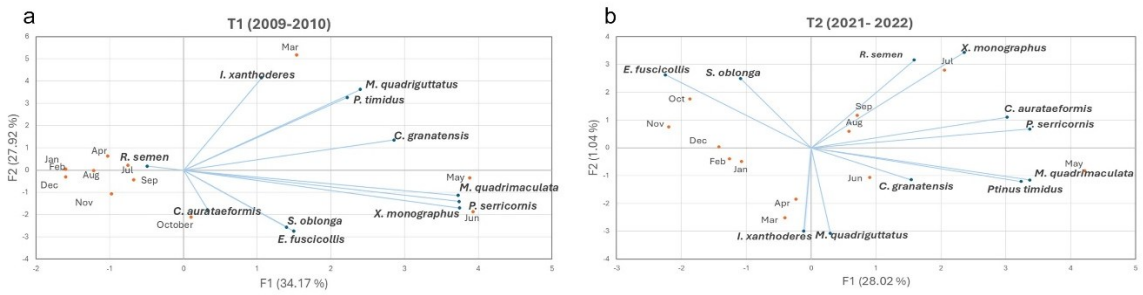


Figure 21. PCA biplots for T1 (a) and T2 (b) for the selected species. Blue vectors: species; red dots: phenological observations. Time: T1: from March 2009 to February 2010, T2: from March 2021 to February 2022.

Focusing on the general patterns of the five species, the GPA reveals that the T2 phenological pattern differs significantly from that of T1. The correlation coefficients among the first three PCA T1 and T2 axes are mainly below 0.5 in terms of absolute value (Table 27), with the following exceptions: the first T1 and T2 axes (r = 0.607), the second T1 and T2 axes (r = -0.541), the third T1 axis and the first T2 axis (r = -0.710). Specifically, June retains the greatest difference between the T1 and T2 abundance distributions (Figure 22).

Table 27. Correlation coefficients (r) among the first three PCA axes of T1 vs T2, for the selected species. In bold: values larger than 0.5 as absolute value.

PCA axes	F1_2009	F2_2009	F3_2009
F1_2021	0.607	0.038	-0.710
F2_2021	-0.361	-0.541	-0.124
F3_2021	0.156	0.031	0.457

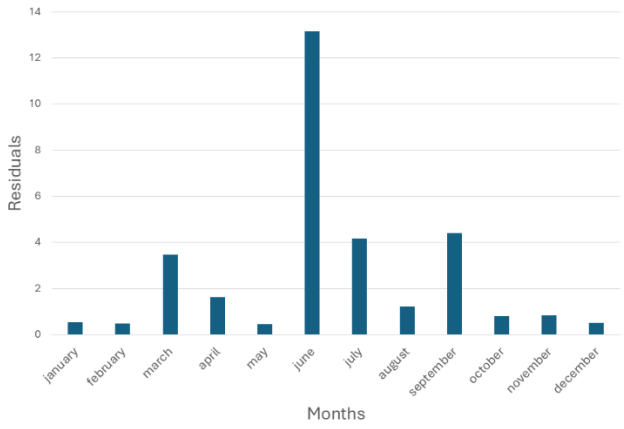


Figure 22. Residuals for the selected species with respect to the consensus configuration after GPA scaling, rotation, and translation.

In addition, the RDA confirms the influence of MinRH in T1 (75% of variance explained) which negatively affects species abundances, while MinTemp and MaxTemp-values affect it positively. It is worth noting that, also at a community level, even if MinRH represents the most Contributing driving factor in T1 (almost coinciding with the first RDA axis), it loses importance in T2, in favour of MaxTemp which remains the main contributing variable (Figure 23).

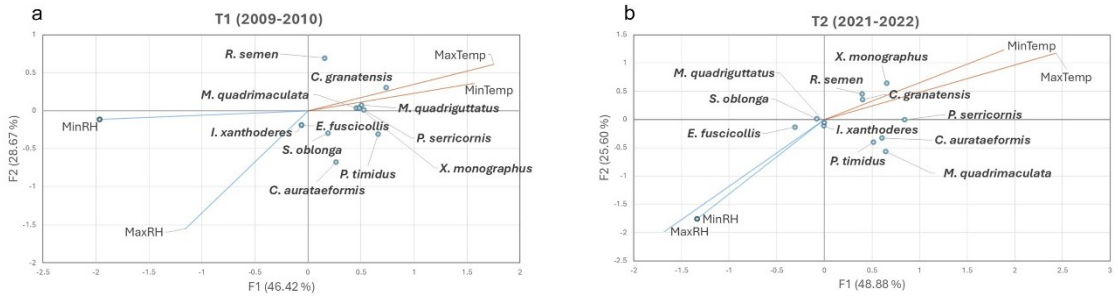


Figure 23. RDA plots of the selected species for T1 (a) and T2 (b). Red vectors: explanatory climatic variables (MinTemp and MaxTemp: minimum and maximum temperatures, MinRH and MaxRH: minimum and maximum relative humidity); blue dots: response variables (species). Time: T1: from March 2009 to February 2010, T2: from March 2021 to February 2022.

Discussion

Our key findings reveal significant changes in activity patterns between the two sampled years in Cabañeros National Park, driven by different climatic variables. These results suggest a potential adaptive response to the warming trend in the area.

Climatic trends: a worrying scenario

The analyses of climate trends in the study area provide a necessary framework to justify the relevance of this work. The analyses of the temperature trends from 2000 to 2022 displayed significant values for the annual average maximum temperature with a total increase of 1.51°C, and this is in line with general global temperature trends (NOAA 2023; NASA 2024). Specifically, such a rise in maximum temperature values is mainly observable in July, October and December with 2.30°C, 3.00°C and 1.73°C increases, respectively. Our results confirm that global warming is pronounced in Mediterranean forests (Lindhe et al. 2010; Lozano-García et al. 2017). The saproxylic community in European and Mediterranean forests seems to benefit from an increase in mean and minimum temperatures in terms of species richness and abundance (Kamboyi 2019; Micó et al. 2022;). But the observed maximum temperature increase of 0.07°C/year is concerning. Indeed, projections for Mediterranean forests show that maximum temperature increases of merely 1.00°C imply a

decrease in the taxonomic, ecological, and functional diversity of the saproxylic beetle community (Buckley 2022; Micó et al. 2022). This is, therefore, a worrying scenario, especially regarding the summer and autumn months which represent key activity periods for most forest beetle species.

Abundance changes are not independent of functional classes

Trophic guild and body length were determining factors of community interannual changes but led to contrasting responses when broken down into functional clusters (Figure 16). Almost all body length classes of predators and saproxylophagous show a lower number of individuals in T2 than those in T1, whereas the responses of saprophagous and mycetophagous varied, with lower or higher abundances, according to the body classes. This finding is of utmost importance from a functional perspective, given that larger species exert a more pronounced influence on ecosystem processes. Larger predators, for instance, are capable of preying on larger prey, and larger saproxylophagous play a greater role in wood decomposition (Micó et al. 2020). It should be noted that, only ~51% of taxa were collected in both sampling events, with five and three species statistically "unique" to T1 and T2, respectively, suggesting a rearrangement of species composition between T1 and T2 due to the different or even contrasting specific responses.

Phenological patterns: towards less predictable insect activity

Species phenology is also a relevant factor to consider when analysing temporal changes at both a community and species levels, as not all months have undergone the same temperature rise trend over the last 20 years. Phenological pattern variations between T1 and T2 were detected both at a community and a species levels. These results confirm how insect phenology is one of the traits most influenced by temperature variations (Scott and Epstein 1987; Gordo and Sanz 2005; Cohen et al. 2018; Rebaudo and Rabhi 2018) and therefore also highly sensitive to today's climate change (Forrest 2016; Abarca and Spahn 2021; Buckley 2022). This scenario is, moreover, remarkable, because even single modifications in species annual phenology can have serious impacts on species conservation. This is especially true in the case of taxa with a short activity time-window, as any phenological pattern decoupling can also affect intra and interspecific dynamics (Forrest et al. 2016; Larson et al. 2019; Wilson et al. 2021; Rajagopalan et al. 2024). Regarding the functional classes, they all presented a different phenology in T1 and T2, with a sound reassessment of the general pattern between the years. Specifically, inconsistent responses were detected: the abundance peaks of xylophagous, saproxylophagous and predators, as well as the larger species, were anticipated, while the peaks of mycetophagous and saprophagous, together with the smaller

and medium-sized species, were postponed. The earlier peaks of xylophagous, saproxylophagous, and predatory species could be the result of an earlier emergence of adults induced by higher temperatures, that are known to accelerate metabolic rates and shorten developmental time in many insects (Damos and Savopoulou-Soultani 2012; Forrest 2016). Conversely, the delayed peaks of mycetophagous and saprophagous species may be in addition influenced by microclimatic characteristics and lower humidity rates (Kauserud et al. 2008; Boddy et al. 2014). For example, Mediterranean macro fungi assemblages may delay their autumnal emergence likely in response to a delayed rewetting of litter and woody debris after extended summer drought (Vogt-Schilb et al. 2022). Even if such specific relationships are not truly investigated in the present work, the diversity of the observed responses certainly shows the complexity of adaptations to environmental variations raising concerns about a possible trophic and/or functional guild decoupling within the entire ecological network (Tylianakis et al. 2008; Thomsen et al. 2016; Pellissier and Rasmann 2018).

Considering the species level, out of the 11 selected taxa, five showed a discrepancy in the adult flight period between the two sampling events. In general, the species flight period span did not change, but abundance peaks of individuals varied between T1 and T2. Specifically, four species postponed their abundance peaks from early spring to late spring/early summer. However, *C. c. aurataeformis* presented a single peak in its phenological pattern in T1, while it displayed a multimodal curve with a second peak in March in T2. Of note, the change from a unimodal to a bimodal phenology in insects can signal a change in the annual number of generations within a species; moreover, voltinism changes have been related to increasing temperatures (Danks 2007; Altermatt 2010; Sampaio et al. 2021, 2022). *C. c. aurataeformis* is a key species characterising Mediterranean tree hollows and, as in many Mediterranean cetoniid species, the presence of active adults in Autumn has been explained by a second generation of adults that can emerge in the same year due to favourable climatic conditions. Here, we found a marked peak in early spring, which was found neither in T1 nor in the literature. The latter suggests two different scenarios that need to be tested: whether both peaks (spring and summer) are from the same generation or whether a part of the second peak (summer) can belong to a second generation. Special attention should be paid to the possible adult activity decoupling both between species belonging to different guilds and within the same species, possibly resulting in the disruption of important ecological dynamics with unpredictable consequences (Heard et al. 2012; Marshall et al. 2020; Rajagopalan et al. 2024).

By relating phenological pattern changes to environmental variables, it was found that minimum humidity values played a fairly important role in T1, while the driving factors in T2 were maximum and minimum temperature values. The interannual increase in maximum temperatures across the last 22 years (mainly in July, October and December) seems to be promoting major but different phenological shifts within the community, probably affecting diversity patterns and flight activity in saproxylic beetles. Nevertheless, it is necessary to conduct further studies in this regard.

Conclusion

In the current climate change framework, it is particularly important to explore phenological changes in insect communities, as species activity periods may become increasingly unpredictable, with largely unknown consequences. Furthermore, the varying responses we observed across trophic guilds and body sizes reinforce the importance of a functional approach to understanding how saproxylic communities are responding to climate change. Finally, given the paucity of long-term datasets for saproxylic beetles, there is a clear need to expand monitoring efforts, as every additional contribution will enhance our understanding of how these ecologically important communities respond to environmental changes over time.

Chapter 3: Responses of saproxylic beetle assemblages to silvicultural practices

Summary

Saproxylic beetles are among the most species-rich and functionally important components of forest biodiversity and, due to their strong dependence on specific substrates and microclimatic condition, they are sensitive to environmental changes. This given, we investigated beetle assemblages in temperate beech forest that historically underwent a coppice-with-standards regime but, over recent decades, has been subjected to different management options, such as natural evolution (NE), and the conversion to high forest through periodic thinning (PT) and anticipated seed cutting (AC). With this purpose, beetle sampling was conducted in 2023-2024 across the three forest stands, and structural forest variables were measured in each plot to explore their influence on saproxylic assemblages. A total of 11,494 individuals belonging to 116 saproxylic species were collected in one-year sampling. The assemblages were numerically dominated by few taxa, with about 40% of species recorded only once, but they also included "Threatened" and "Data Deficient" species, confirming the conservation value of the studied forest despite its long history of exploitation. Although species richness and total abundance did not differ among stands, significant differences emerged in diversity metrics and community composition across silvicultural options, with the stand subject to natural evolution showing higher diversity values for the whole community and mycophagous species, while the stand subject to anticipated seed-cutting supported a more diverse saproxylophagous assemblage and the highest number of exclusive species. Finally, diversity patterns were significantly related to forest structure and canopy features, with contrasting responses among trophic guilds to tree size, stump volume and canopy cover.

Overall, our findings show that different silvicultural strategies support distinct saproxylic beetle assemblages, but that currently observed patterns are strongly mediated by the long-lasting legacy of past coppice management. Passive abandonment alone appears insufficient to promote the full range of saproxylic niches, as transitional stand structures still constrain community development. Thid given, the present work underscores the importance of adaptive forest management strategies that explicitly consider historical management legacies when aiming to support saproxylic biodiversity in Mediterranean beech forests.

Introduction

Forests are historically exploited by humans through intensive forestry activities: to date, more than 95% of European forests are under management and temperate forests are considered the most influenced by human activities (Schmitt et al., 2009EEA, 2016). Nevertheless, European woodlands host c.a. 80% of terrestrial biodiversity, covering a wide variety of taxa, from microorganisms and fungi to vertebrates and arthropods. Beech (*Fagus sylvatica* L.) woodlands are among the most widespread broadleaved forest types in Europe and play a central role in forest biodiversity, providing multiple ecosystem services (Marchesini et al., 2023). Beech forest stands have traditionally been managed under even-aged systems aimed at timber production, resulting in simplified stand structures and decreased plant diversity, causing the loss of old-growth attributes such as large senescent trees, a multi-layered vertical structure and high amounts of deadwood (Paletto et al., 2014; Schulze, 2018; Bujoczek and Bujoczek, 2022). As a consequence, structurally complex and unmanaged beech forests are now uncommon and largely confined to small areas (Kucbel et al., 2012; Neudam et al., 2023). Conversely, since the second half of the twentieth century, a combination of socio-economic drivers, such as rural depopulation, reduced demand for traditional forest products and declining profitability of forestry in marginal or mountainous areas, has contributed to a gradual abandonment of some historically managed forest stands (Navarro and Pereira, 2012; Kuemmerle et al., 2015; Plieninger et al., 2016). At the same time, the adoption of new close-to-nature forest management approaches, aimed at enhancing biodiversity through increased structural and age diversity (Brang et al., 2014), is increasingly considered a promising strategy for reconciling human activities with biodiversity conservation. This resulted in the conversion of a number of intensively exploited stands towards more natural forest conditions (Nocentini et al., 2021; Stritih et al., 2026).

This heterogeneous pattern of forest stand use can be particularly observed in beech forests that are widely distributed across the Alps and the Apennines in Italy, where historically maintained or regularly harvested coppices coexist with gradually abandoned or less intensively managed forest stands (Antonucci et al., 2021; Pallotta et al., 2022). However, even in areas where active management has declined, stand structure often continues to reflect past interventions, resulting in forests that are predominantly even-aged and structurally homogeneous (Dieler et al., 2017). This significantly affects forest-dwelling species, as well as communities' structure and function (e.g., (Parisi et al., 2024; Portaccio et al., 2026).

Saproxylic species, defined as organisms depending at least in part of their life cycle on dead or decaying wood or linked organisms (Speight, 1989; Stokland et al., 2012), constitute about one-quarter of forest biodiversity (Siitonen, 2001). Among these, beetles represent the most abundant and diverse group both in terms of species richness, functional roles (i.e., nutrient recycling, species population control, and pollination) and microhabitat occupancy (Müller et al., 2013; Ulyshen and Šobotník, 2018; Micó et al., 2020;). Because of their strong dependence on micro-conditions and resource availability (Brunet et al., 2010; Bouget et al., 2013; Schall et al., 2018b; Edelmann et al., 2022), saproxylic beetles are rather vulnerable and highly responsive to environmental changes (Martikainen and Kaila, 2004; Seibold et al., 2015; Cálix et al., 2018; Sánchez-Bayo and Wyckhuys, 2019). Given this, they represents a suitable target group for investigating the effects of a forest management which shapes and influences deadwood diversity and its spatial distribution (Grove, 2002; Paletto et al., 2014; Roberge et al., 2015; Basile et al., 2023). For instance, beetle assemblages in managed forests differ markedly from those in unmanaged or strictly protected reserves (Müller et al., 2013; Roth et al., 2019), as well as distinct forestry approaches may inconsistently affect communities both in terms of species richness and functional composition (Kirby and Watkins, 2015; Schall et al., 2018a; Parisi et al., 2024).

In addition, recent studies suggest that treating saproxylic beetles as a homogeneous group may obscure important variation in the responses of different taxa, as these effects are strongly shaped by functional traits, such as trophic guilds or specific requirements for deadwood types and microhabitats (Hekkala and Roberge, 2018; Sallé et al., 2020). Accordingly, incorporating functional groups into the assessment of community responses can provide a more nuanced perspective, highlighting that guilds do not respond uniformly to management interventions or environmental changes (Vanderwel et al., 2006; Buse et al., 2016; Pérez-Sánchez et al., 2020; Lenzi et al., 2025).

The present study aims at evaluating the effect of forest management on the saproxylic beetle community inhabiting Mediterranean beech forest investigating both the entire beetle community and the single trophic guilds. We hypothesize that (a) stands under different silvicultural treatments host specialized insect communities in terms of species and trophic guilds, (b) the stand left to natural evolution host a more diverse and less homogenous beetle community, (c) stand structural characters shapes community and trophic guild structure.

Materials and Methods

Study area

Data were collected in Alpe di Catenaia (Chitignano, Arezzo, Italy), a beech forest in Central Apennines which has a consistent and well-documented history of forest management differentiated at stand level (Figure 24, Table 28). Specifically, the area host stands that were managed under a coppice with standards regime until 1972 and were subsequently converted to other management options. Currently, the forest area is characterized by (i) stands under natural evolution (NE), (ii) stands converted through periodic (every 10-15 years) thinning from below with the last intervention carried out in 2018 (PE), and (iii) stands subject to an alternative conversion approach, consisting of two periodic thinning cuts followed by an anticipated seed cutting (AC). This latter treatment occurred in 2006 (Cutini et al., 2015). The altitude ranged between 1100 and 1200 m a.s.l. (Table 28).

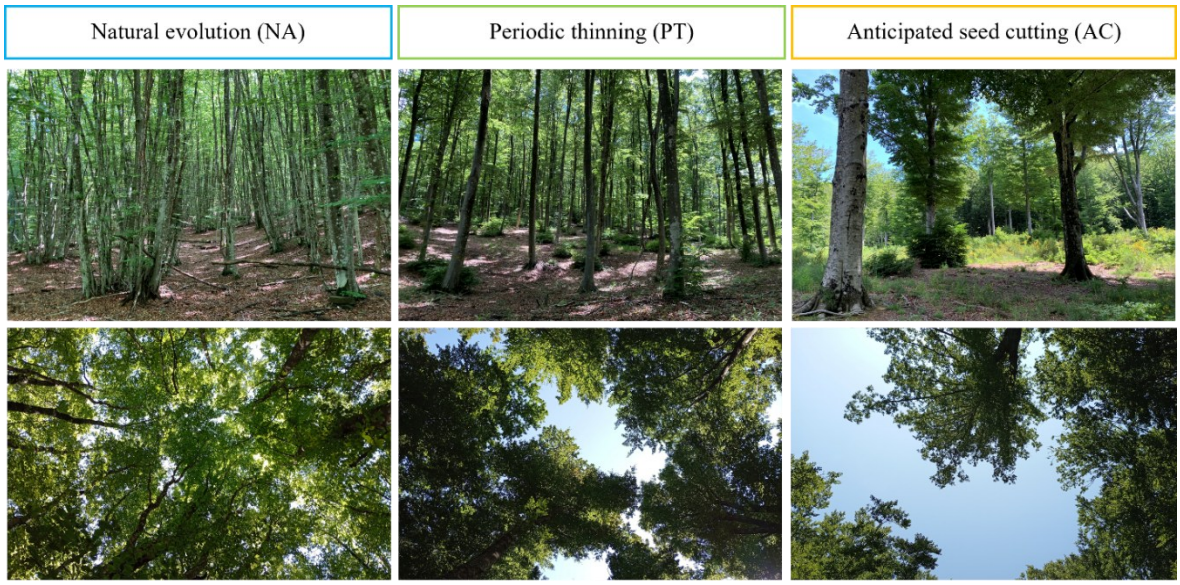


Figure 24. Representation of the investigated stands under different silvicultural options: natural evolution (NE), periodic thinning (PT), periodic thinning followed by an anticipated seed cutting (AC). The first row represents the forest structure and the second one shows the canopy cover.

Table 28. Description of the investigated stands with details on each silvicultural option, decimal coordinates (WGS84) of centroid and the mean altitude

Stand code	Silvicultural option	Latitude (WGS84)	Longitude (WGS84)	Altitude (m a.s.l)
NE	Natural evolution.	43.6497288	11.9145674	1,080.00
	Coppice with standards until 1970s, then left to natural evolution from that date onwards			
PT	Periodic thinning.	43.6500558	11.9128846	1,055.00
	Coppice with standards until 1970s. then actively converted via periodic thinning from below, carried out at 10-15 years interval, with the last thinning occurring in 2018			
AC	Anticipated seed cutting.	43.658546	11.919425	1,105.00
	Coppice with standards until 1970s, then actively converted via two periodic thinnings followed by an anticipated seed cutting in 2006			

Data collection and analysis

Data on forest structure and beetle community were collected between 2023 and 2024 in three 15 × 15 m plots per stand type according to the protocol of Burrascano et al. (2021), for a total of nine plots. Plots within each stand were spaced 60–100 m apart to ensure spatial independence and capture within-stand heterogeneity, even in stands with relatively low heterogeneity. Their number and arrangement were determined as a compromise between adequate coverage and practical constraints, such as the geomorphology, size, and configuration of forest compartments.

All data have been processed using R software (R Core Team, 2025)

Stand structure

Tree species, diameter at breast height (DBH ≥ 5 cm) and height of standing elements (snags, living and dead trees) were recorded using a tree caliper and an electronic hypsometer (Vertex IV-360 and Transponder T3). The number and volume of logs (larger diameter ≥ 10 cm) were assessed through the Line Intersect Method (Marshall et al., 2003; Van Wagner, 1968). Main stand structural parameters (i.e., mean diameter, tree density, basal area, tree volume) were calculated for living trees; deadwood volume was split into standing (snag, dead trees) and lying (logs) components. Volume of living trees and snags > 20 cm was calculated through the volume functions developed for the Italian National Forest Inventory (Tabacchi et al., 2011). Volume of snags < 20 cm was estimated according to the formula of an ellipsoid cone as in (Brunet and Isacsson, 2009); volume of log was calculated using Van

Vagner's formula (Van Wagner, 1968). The diameter variability of living trees was evaluated using the Gini index (Lexerød and Eid, 2006). The diversity of living tree species was calculated using the most common taxonomic indexes based on the proportional abundances of species (Shannon, Simpson and Pielou, (Magurran, 2013). Diversity indexes were calculated by using the *forestmangr* package (Braga et al., 2020); the Gini index was calculated using the *reldis* package (Handcock, 2023). Living and dead trees volumes were calculated using the *ForIT* package (Puletti et al., 2017a).

Canopy cover data were collected using smartphone adopting the method described and tested in (Chianucci et al., 2019). Pictures were collected once a month (at the time of beetle sampling), from the 15th of July 2022 to the 12th of April 2023. Images portraying canopy cover were processed using *coveR* (Chianucci et al., 2022). The canopy cover variables retrieved are described in Table 29.

Exploratory analyses were conducted using correlations derived from a principal component analysis (PCA; centered and standardized variables; *vegan* package) with the aim of reducing predictor dimensionality and identifying variables most strongly associated with the different silvicultural treatments. Significance tests among forest stands were then conducted only for variables identified as relevant by the PCA, namely those with high loadings on the retained principal components. After having tested data normality (shapiro.test() function) group differences were assessed by one-way ANOVA, with Tukey's HSD post hoc test (tuckeyHSD() of *vegan* package) applied when significant (p-value < 0.05).

Beetles diversity

Specimens were collected using nine Window Flight Traps (Bouget et al., 2008; Burrascano et al., 2021), each settled in the center of the plot. Traps were installed on the 20th of April 2023 and were deactivated on the 12th of April 2024, allowing for a one-year-long sampling campaign. Traps were loaded with collecting jars filled with 70% ethanol and jars were controlled and replaced monthly, for a total of 12 sampling sessions.

The collected specimens were sorted to family level using the available taxonomical key (Dal Cortivo et al., 2021) while nomenclature followed Bouchard et al. (2011) and Carpaneto et al. (2015). Species-level identification was subsequently assigned to and performed by expert taxonomists (see Acknowledgements section for details). Trophic guild, IUCN Red List Status and additional ecological information have been added for each identified species based on experts' experience and literature (Carpaneto et al., 2015).

All collected specimens are deposited in the entomological collection of CREA Research Center for Plant Protection and Certification (Florence and Rome, Italy).

To assess species accumulation over time, we constructed a temporal cumulative species accumulation curve considering observed data using *tidyverse* and *ggplot2* packages (Wickham, 2016), then estimating permutation curves employing the specaccum() function of *vegan* package (Oksanen et al., 2025). Beetle alpha diversity differences among forest stands were investigated by computing the most common diversity metrics (i.e., abundance, species richness, Pielou's evenness, Shannon, Gini-Simpson and Simpson indexes) (Hill, 1973; Magurran, 2013; Pielou, 1966), using the diversity() function of *vegan* package (Oksanen et al., 2025). Then, a one-way Analysis of Variance (ANOVA) was performed using the aov() function of basic *stat* package. Where ANOVA indicated significant differences ($p < 0.05$), we conducted Tukey's Honest Significant Difference post-hoc tests employing the tukeyHSD() function. These analyses have been performed first considering all the identified saproxylic species, and then focusing on the five most represented trophic guilds (Carpaneto et al., 2015): Mycophagous (MY), Mycetophagous (MB), Saproxylophagous (SX), Predators (PR) and Xylophagous (XY). All indexes were calculated considering data collected during the late spring / summer months, thus covering the period of greatest activity for most of the considered taxa (Gillespie et al., 2017; Stokland et al., 2012).

Beta diversity was then explored for the three stands, considering plots as repetitions. The function vegdist() of *vegan* package (Oksanen et al., 2025) was used to calculate the two dissimilarity indexes Bray-Curtis (Bray and Curtis, 1957; Legendre and Legendre, 2012), and Jaccard (Jaccard, 1901; Legendre and Legendre, 2012). Inter-stand statistically different beta diversity values were then tested with a PERMANOVA test (Anderson, 2001) using the function adonis2() of vegan package and the Post hoc pairwise permutational tests were performed using adonis2() function to identify differences among groups.

Correlation analysis and models

The forest variables investigated are described in Table 29. The correlation with saproxylic beetles' abundance and diversity were explored through correlation analyses.

The first analysis was carried out on all the identified saproxylic species, considering the already calculated diversity metrics. This given, a Pearson correlation matrix was computed using the cor() function in base R and the statistical significance of each pairwise correlation was assessed using a custom function cor.mtest() that performs two-tailed correlation tests via cor.test() across all variable combinations. Correlation matrix was then plotted

employing the *corrplot* package (Taiyun Wei, 2021), in order to reduce dataset considering the biodiversity indexes related to MY, SH and XY trophic guilds.

Table 29. Forest variables adopted in this publication with relative code and description; the prefix "can_" indicates that the variables relate to canopy characteristics, while the prefix "str_" is used for those describing forest structure of living or dead trees

Variable name	Code	Description
Canopy cover variables		
Crown Cover	can_CC	Proportion of ground covered by vertical projection of crowns, ignoring gaps
Clumping Index	can_CI	Description of deviation of foliage distribution from randomness (CI = Le/L),
Crown Porosity	can_CP	Fraction of empty spaces within tree crowns
Foliage Cover	can_FC	Proportion of ground covered by foliage including internal gaps
Leaf Area Index	can_L	Total one-sided leaf area per unit ground surface area
Effective Leaf Area Index	can_Le	Total one-sided leaf area per unit ground surface area accounting for non-random foliage distribution and canopy gaps
Dendrometric variables		
Snags	str_DT_vol	Volume of standing dead trees (m^3 ha^{-1})
Basal area per hectare	str_G_ha	Sum of the basal area of trees in a hectare (m^2 ha^{-1})
Gini index	str_gini_dbh	Index describing tree diametre distribution; a measure of structural diversity
Volume of lying deadwood	str_lyd_vol	Total volume of lying deadwood in the forest (m^3 ha^{-1})
Mean Diametre	str_MD	Average diametre at breast height (DBH) of trees (cm)
Number of trees/ha	str_N_ha	Tree density per hectare (n ha^{-1})
Quadratic Mean Diametre	str_QMD	Quadratic average diametre at breast height (DBH) of trees (cm)
Volume of stumps	str_stump_vol	Remaining parts of cut or naturally broken trees (m^3 ha^{-1})
Wood volume per hectare	str_Vol_ha	Volume of standing trees per hectare (m^3 ha^{-1})

To further investigate the influence of forest structural and compositional variables on beetle diversity, we fitted a linear mixed-effects model (LMM) using the *lme4* package (Bates et al., 2015). Alpha diversity metrics were modeled individually as response variables. Predictor variables (fixed effects) were selected among indicators of stand structure and canopy attributes, based on the correlation matrix, the PCA and ecological values. Random

intercepts were included for date and plotID to account for the repeated sampling within plots and the temporal pseudoreplication across sampling dates. Before modeling, predictor variables were checked for multicollinearity using variance inflation factors (VIF) from the *car* package (Fox et al., 2024) and highly collinear variables (VIF > 5) were excluded from the final models. The model was thus specified as:

$$\text{Div. Index} \sim can_Le + str_QMD + str_Shannon + str_stump_vol + str_DW_tot + (1 \mid date) + (1 \mid plotID)$$

In addition, the goodness-of-fit of candidate models was evaluated using the Akaike Information Criterion (AIC), the proportion of variance explained by the fixed and random components (R^2 values) calculated with the r.squaredGLMM() function from the *MuMIn* package and evaluating also ecological consistency. Model residuals were visually inspected to verify normality and homoscedasticity through residual versus fitted plots, Q–Q plots, and histograms, then Shapiro–Wilk tests were performed employing the shapiro.test() function. Autocorrelation functions were used to assess temporal autocorrelation.

To visualize the results of the mixed-effects model, we extracted the fixed and random parameters using the *lme4* package. Fixed-effect estimates, p-values, and 95% confidence intervals were computed to assess the significance of each predictor. Random-effect standard deviations were derived from the variance–covariance structure of the model. These components were then combined and plotted using *ggplot2* to display the estimated effects with their confidence intervals, alongside the random-effect variances, allowing for an intuitive comparison of predictor influence and the contribution of hierarchical random factors.

Results

Stand structure characterisation

The PCA revealed a clear separation among the three stand types along the first two axes (Figure 25). The first principal component (PC1, 53.1% of explained variance) is mainly associated with canopy cover, tree density and deadwood volume. These variables positively characterized plots under natural evolution (NE), which cluster on the positive side of PC1. The second principal component (PC2, 25.8% of explained variance) is related to other structural attributes, such as tree diameter, stump volume and tree diversity indexes. Plots

subject to anticipated seed cutting (AC) are mainly associated with higher scores along PC2, while plots subject to periodic thinning (PT) show an intermediate position, partially overlapping with both NE and AC stands. Overall, the PCA highlighted distinct gradients in structural and canopy attributes characterising the different stand types.

ANOVA test revealed significant differences among all the three stands for leaf area index, quadratic mean diameter, and total deadwood volume (Table 30). No significant differences were observed between PT and AC in either the density of living trees or the volume of standing dead trees. Notably, no standing dead trees were present in PT and AC.

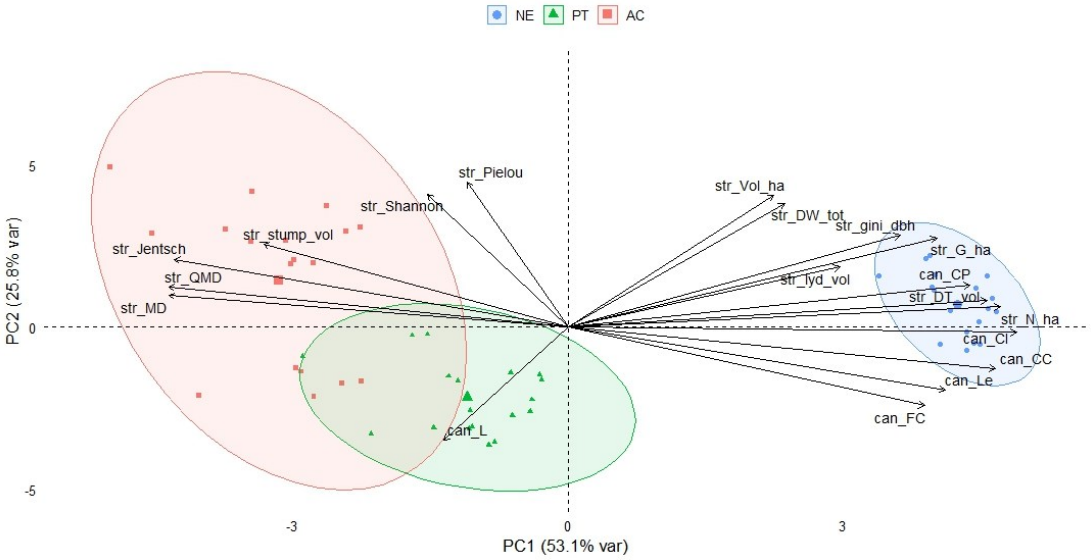


Figure 25. Principal Component Analysis (PCA) of forest structural variables across three conversion types: Natural evolution (NE), Periodic thinning (PT), Anticipated seed cutting (AC). Vectors indicate the contribution and direction of each structural variable to the principal components. The axes show the percentage of variance explained by PC1 and PC2

Table 30. Mean (± standard deviation) of the primary response variables (measuring unit) of stand structure in stands under the tree management options: natural evolution (NE), periodic thinning (PT) and anticipated seed cutting (AC). Parameters are shown with significance level. Lowercase letters highlight significant differences ($p < 0.05$) among stand types according to Tukey's post hoc test

Structural variable	Natural evolution (NE)	Periodic thinning (PT)	Anticipated seed cutting (AC)	p-value
Leaf Area Index	1.72 (±0.014) a	1.72 (±0.02) b	1.604 (±0.082) c	≤ 0.001***
Tree density (n ha $^{-1}$)	2,132.58 (±350.76) a	268.93 (±8.17) b	113.23 (±29.46) b	≤ 0.001***
Quadratic mean diameter (cm)	18.09 (±2.25) a	31.55 (±2.46) b	59.76 (±4.72) c	≤ 0.001***
Standing dead trees volume (m^3 ha^{-1})	6.312 (±1.45) a	0 b	0 b	0.003**
Total deadwood volume (m^3 ha^{-1})	18.32 (±2.704) a	7.36 (±1.04) b	14.20 (±2.68)	0.038*

Structure and diversity of saproxylic beetle community

At the end of the sampling, a total of 13,072 beetle specimens were collected. Of the overall 56 families, 30 saproxylic families were considered (Table 31), resulting in 11,494 individuals identified into 116 species. Within the identified samples, the most abundant families are Curculionidae (~ 93%), Mycetophagidae (2%), Latridiidae (1%) and Salpingidae (1%). Considering richness, Curculionidae, is the most diverse family with 21 species, followed by Cerambycidae and Ciidae (with 12 and 11 species, respectively) (Figure 26).

The investigated community results to be dominated by the presence of a few abundant species, together representing ~90% of the collected individuals within the area (Figure 26c). The most recorded species belongs to Curculionidae Scolytinae: *Xyleborinus saxesenii* (Ratzeburg, 1837) with 4,982 individuals, *Xylosandrus germanus* (Blandford, 1894) with 2,139, *Anisandrus dispar* (Fabricius, 1792) with 1,518 and *Eidophelus fagi* (Fabricius, 1798) with 1,286 individuals. Other well-represented species are *Trypodendron domesticum* (Curculionidae: Scolytinae), *Litargus connexus* (Geoffroy, 1785) (Mycetophagidae), *Trypodendron signatum* (J.C.Fabricius, 1792) (Curculionidae: Scolytinae) and *Enicmus brevicornis* (Mannerheim, 1844) (Latridiidae) with 579, 507, 182, 110 and 100 individuals respectively (Table 30). Conversely ~40% of species occur only once.

Focusing on the conservation status of the investigated beetle assemblage a total of four identified species are considered threatened by the IUCN Red List of Italian Saproxylic beetles (Carpaneto et al., 2015) (Figure 27), specifically, two Vulnerable (VU) species, such as the Elateridae *Brachygonus campadellii* Platia and Gudenzi, 2000 and *Denticollis linearis* (Linnaeus 1758), and two Critically Endangered (CR) ones, i.e., the Nitidulidae *Epuraea silacea* (Herbst, 1783) and the Elateridae *Stenagostus rhombeus* (Olivier, 1790). Moreover, four taxa turn to be Data Deficent (DD): the three Corylophidae *Arthrolips nana* (Mulsant and Rey, 1861), *Arthrolips obscura* (Sahlberg, 1833)*, Clypastrea reitteri* Bowestead, 1999, and the Latridiidae *Enicmus atriceps* Hansen, 1962. In all the stands DD and VU species have been collected, while CR species were found only in PT and AC.

Table 31. List of species collected and investigated in the present study. Details about the Italian IUCN Category and trophic guild (Carpaneto et al., 2015) are provided, as well as the total number of individuals collected

Family / Species	IUCN	Trophic guild	N of individuals	Stand
Anthribidae			18	
Dissoleucas niveirostris (Fabricius, 1798)	LC	XY	3	PT; AC
Platystomos albinus (Linnaeus, 1758)	LC	XY	15	NE; PT; AC
Biphyllidae			43	
Biphyllus frater (Aubé, 1850)	LC	SX	1	PT
Diplocoelus fagi (Chevrolat, 1837)	LC	SX	42	NE; PT; AC
Bostrichidae			3	
Scobicia chevrieri (Villa and Villa, 1835)	LC	XY	3	NE; PT; AC
Cantharidae			11	
Malthinus seriepunctatus Kiesenwetter, 1852	NA	PR	1	PT
Malthodes ganglbaueri florentinus Liberti, 2015	NA	PR	1	NE
Malthodes marginatus (Latreille, 1805)	NA	PR	1	AC
Malthodes septembrinus Liberti, 2015	NA	PR	1	PT
Malthodes sp	NA	PR	6	NE; PT; AC
Malthodes spathifer Kiesenwetter, 1852	NA	PR	1	PT
Cerambycidae			35	
Cortodera humeralis (Schaller, 1783)	LC	XY	1	AC
Leiopus femoratus Fairmaire, 1859	NT	XY	6	PT; AC
Leiopus cfr. *nebulosus* (Linnaeus, 1758)	LC	XY	5	PT
Mesosa nebulosa (Fabricius, 1781)	LC	XY	1	NE ;PT
Molorchus marmottani (Brisout de Barneville, 1863)	LC	XY	1	AC
Obrium brunneum (Fabricius, 1792)	LC	XY	1	AC
Phymatodes testaceus (Linnaeus, 1758)	LC	XY	4	NE; PT
Rutpela maculata (Poda, 1761)	LC	XY	2	AC
Saperda scalaris (Linnaeus, 1758)	LC	XY	5	PT; AC
Tetrops praestus (Linnaeus, 1758)	LC	XY	2	AC
Xylotrechus arvicola (Olivier, 1795)	LC	XY	6	NE; PT; AC
Xylotrechus stebbingi Gahan, 1906	INV	XY	1	PT
Cerylonidae			11	
Cerylon fagi Brisout, 1867	LC	MY	11	NE; PT; AC
Ciidae	LC	MB	27	
Cis boleti (Scopoli, 1763)	LC	MB	9	PT; AC
Cis festivus (Panzer, 1793)	LC	MB	1	AC
Cis micans (Fabricius, 1792)	LC	MB	2	AC
Cis rugulosus Mellié, 1849	NA	MB	1	PT
Cis sp.	NA	MB	1	AC
Cis submicans Abeille de Perrin, 1874	NA	MB	6	PT; AC
Cis villosulus (Marsham, 1802)	NA	MB	1	AC
Ennearthron cornutum (Gyllenhal, 1827)	LC	MB	1	NE
Octotemnus glabriculus (Gyllenhal, 1827)	NA	MB	1	AC

Orthocis alni (Gyllenhal, 1813)	NA	MB	2	NE
Sulcacis nitidus (Fabricius, 1792)	NA	MB	2	AC
Cleridae			5	
Opilo mollis (Linnaeus, 1758)	LC	PR	1	NE
Thanasimus formicarius (Linnaeus, 1758)	LC	PR	2	NE
Tillus elongatus (Linnaeus, 1758)	NT	PR	2	NE
Corylophidae			9	
Arthrolips nana (Mulsant and Rey, 1861	DD	MY	1	AC
Arthrolips obscura (C.R. Sahlberg, 1833)	DD	MY	1	AC
Clypastrea reitteri Bowestead, 1999	DD	MY	7	PT; AC
Cucujidae			1	
Pediacus dermestoides (Fabricius, 1792)	NT	PR	1	NE
Curculionidae			10668	
Acalles parvulus Boheman, 1837	LC	SX	1	PT
Anisandrus dispar (Fabricius, 1792)	LC	MY	1518	NE; PT; AC
Cryphalus piceae (Ratzeburg, 1837)	LC	XY	11	NE; PT
Dryocoetes villosus (Fabricius, 1792)	LC	XY	1	NE
Eidophelus fagi (Fabricius, 1792)	LC	MY	1286	NE; PT; AC
Hylastinus obscurus (Marsham, 1802)	LC	XY	1	PT
Kyklioacalles roboris (Curtis, 1834)	LC	SX	1	PT
Phloeotribus cristatus (Fauvel, 1889)	LC	XY	1	AC
*Pityokteines vorontzovi (*Jakobson, 1895)	LC	XY	1	NE
Pityophthorus pityographus (Ratzeburg, 1837)	LC	XY	2	NE; PT
Pityophthorus sp.	LC	XY	1	NE
Platypus cylindrus (Fabricius, 1792)	LC	XY	4	NE; PT; AC
Scolytus intricatus (Ratzeburg, 1837)	LC	XY	7	NE
Scolytus multistriatus (Marsham, 1802)	LC	XY	1	AC
Tomicus minor (Hartig, 1834)	LC	XY	2	PT
Trypodendron domesticum (Linnaeus, 1758)	LC	MY	507	NE; PT; AC
Trypodendron signatum (Fabricius, 1792)	LC	XY	110	NE; PT; AC
Xyleborinus saxesenii (Ratzeburg, 1837)	LC	MY	4982	NE; PT; AC
Xyleborus dryographus (Ratzeburg, 1837)	LC	MY	4	NE
Xyleborus monographus (Fabricius, 1792)	LC	MY	88	NE; PT; AC
Xylosandrus germanus (Blandford, 1894)	INV	MY	2139	NE; PT; AC
Elateridae			30	
Brachygonus campadellii Platia and Gudenzi, 2000	CR	PR	3	PT; AC
Denticollis linearis (Linnaeus, 1758)	CR	PR	1	AC
Hemicrepidius hirtus (Herbst, 1784)	NA	SX	7	NE; PT; AC
Hemicrepidius nigerrimus (Desbrochers des Loges, 1870)	NA	SX	1	AC
Melanotus villosus (Geoffroy, 1785)	LC	PR	15	NE; PT; AC
Stenagostus rhombeus (Olivier 1790)	VU	PR	3	NE; PT; AC
Endomychidae			3	
Symbiotes gibberosus (Lucas, 1849)	LC	MB	2	NE
Symbiotes latus Redtenbacher, 1849	LC	MB	1	AC

Histeridae			2	
Gnathoncus buyssoni Auzat, 1917	NA	NI	1	AC
Paromalus flavicornis (Herbst, 1791)	LC	PR	1	PT
Latridiidae			128	
Cartodere nodifer (Westwood, 1839)	LC	MY	5	PT; AC
Corticarina similata (Gyllenhal, 1827)	LC	MY	2	PT; AC
Enicmus atriceps Hansen, 1962	DD	MY	3	NE; PT
Enicmus brevicornis (Mannerheim, 1844)	LC	MY	100	NE; PT; AC
Enicmus histrio Joy and Tomlin, 1910	LC	MY	1	NE
Enicmus rugosus (Herbst, 1793)	LC	MY	5	PT; AC
Enicmus testaceus (Stephens, 1830)	LC	MY	6	NE; AC
Stephostethus alternans (Mannerheim, 1844)	LC	MY	6	NE; AC
Lymexylidae			4	
Elateroides dermestoides (Linnaeus, 1760)	NT	XY	4	NE; PT; AC
Melandryidae			19	
Abdera biflexuosa (Curtis, 1829)	LC	MY	3	NE; AC
Conopalpus testaceus (Olivier, 1790)	NT	MY	1	NE
Melandrya caraboides (Linnaeus, 1760)	NT	MY	1	AC
Orchesia micans (Panzer, 1793)	LC	MY	1	AC
Orchesia undulata Kraatz, 1853	LC	MY	3	NE; AC
Phloiotrya sp.	LC	MY	1	AC
Phloiotrya tenuis (Hampe, 1850)	NT	MY	7	NE; PT
Serropalpus barbatus (Schaller, 1783)	NT	MY	2	PT
Mordellidae			4	
Tomoxia bucephala Costa, 1854	LC	SX	4	NE; PT; AC
Mycetophagidae			274	
Litargus connexus (Geoffroy, 1785)	LC	MY	182	NE; PT; AC
Mycetophagus atomarius (Fabricius, 1787)	LC	MY	20	NE; PT; AC
Mycetophagus quadripustulatus (Linnaeus, 1761)	LC	MY	71	NE; PT; AC
Stereophilus filicornis (Reitter, 1887)	NA	MY	1	AC
Nitidulidae			3	
Cryptarcha strigata (Fabricius, 1787)	LC	SF	1	AC
Epuraea melanocephala (Marsham, 1802)	LC	MY	1	AC
Epuraea silacea (Herbst, 1783)	VU	MY	1	PT
Salpingidae			114	
Lissodema denticolle (Gyllenhal, 1813)	LC	SX	2	AC
Salpingus planirostris (Fabricius, 1787)	LC	SX	83	NE; PT; AC
Vincenzellus ruficollis (Panzer, 1794)	LC	MY	29	NE; PT; AC
Scarabeidae			1	
Cetonia aurata (Linnaeus, 1758)	LC	SX	1	PT
Scirtidae			4	
Conopalpus testaceus (Olivier, 1790)	NT	MY	1	PT
Elodes sp.	NA	HW	1	AC
Prionocyphon serricornis (Müller, 1821)	NT	HW	2	NE; PT
Scraptiidae			30	

Anaspis lurida Stephens, 1832	LC	SX	27	NE; PT; AC
Anaspis maculata (Geoffroy in Fourcroy, 1785)	NA	SX	2	AC
Anaspis nigripes Brisout de Barneville 1866	NA	SX	1	AC
Silvanidae			7	
Uleiota planatus (Linnaeus, 1760)	LC	MY	7	NE; PT
Sphindidae			1	
*Aspidiphorus orbiculatus (*Gyllenhal, 1808)	LC	MY	1	PT
Tenebrionidae			15	
Corticeus unicolor Piller and Mitterpacher, 1783	LC	CO	1	NE
Mycetochara linearis (Illiger, 1794)	LC	SX	13	NE
Palorus depressus (Fabricius, 1790)	LC	SX	1	PT
Trogossitidae			11	
Nemozoma elongatum (Linnaeus, 1760)	LC	PR	11	NE; PT; AC
Zopheridae			12	
Colydium filiforme Fabricius, 1792	NT	PR	1	NE
Coxelus pictus (Sturm, 1807)	LC	SX	2	PT
Synchita undata Guérin-Méneville, 1844	NT	SX	9	NE; PT; AC

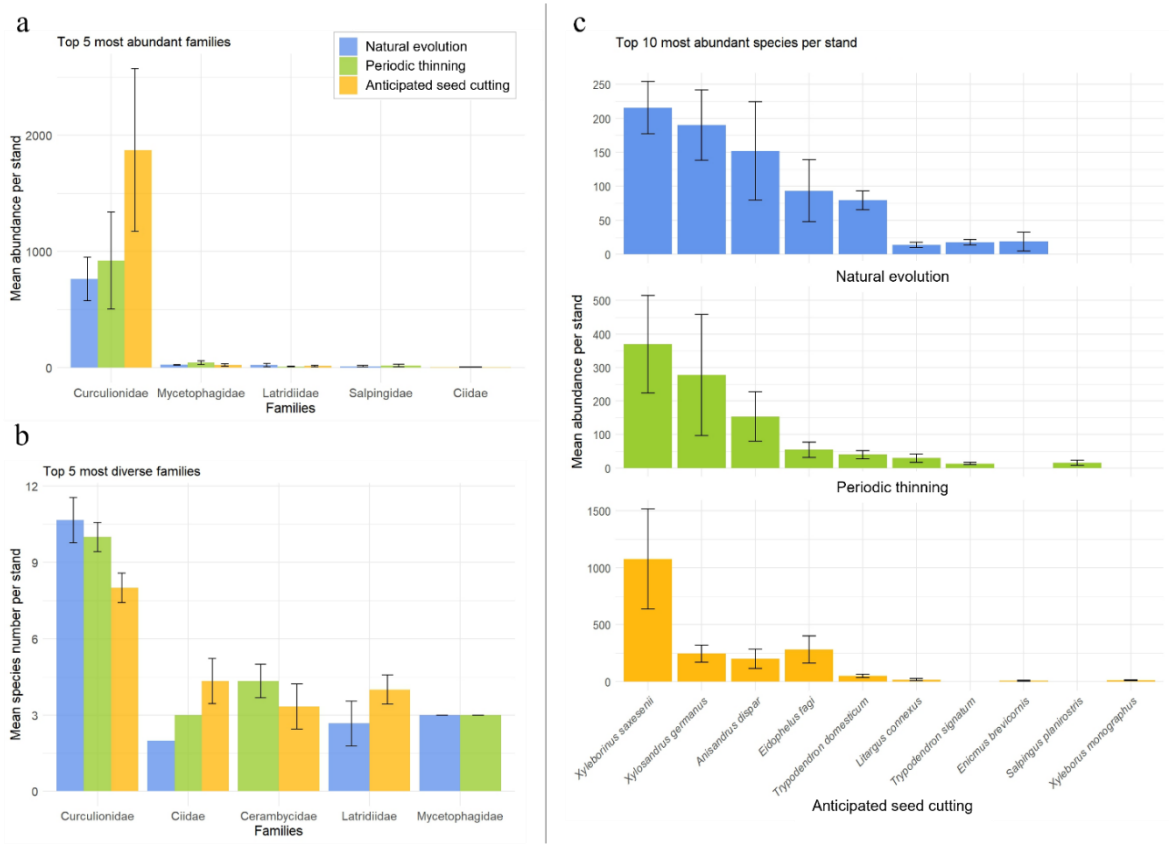


Figure 26. Bar plots representing the five most abundant families with the relative mean number of individuals (a), the five most diverse families with the relative mean number of species (b) and the detail about the 10 most abundant species with the mean number of individuals for each stand (c). Data referring to the stand under natural evolution (NE) are in blue, those referring to periodic thinning (PT) treatment are in green and those collected in the stand under anticipated seed cutting (AC) are in orange. Means are calculated as the mean of the three plots and the black bars represent the relative standard error.

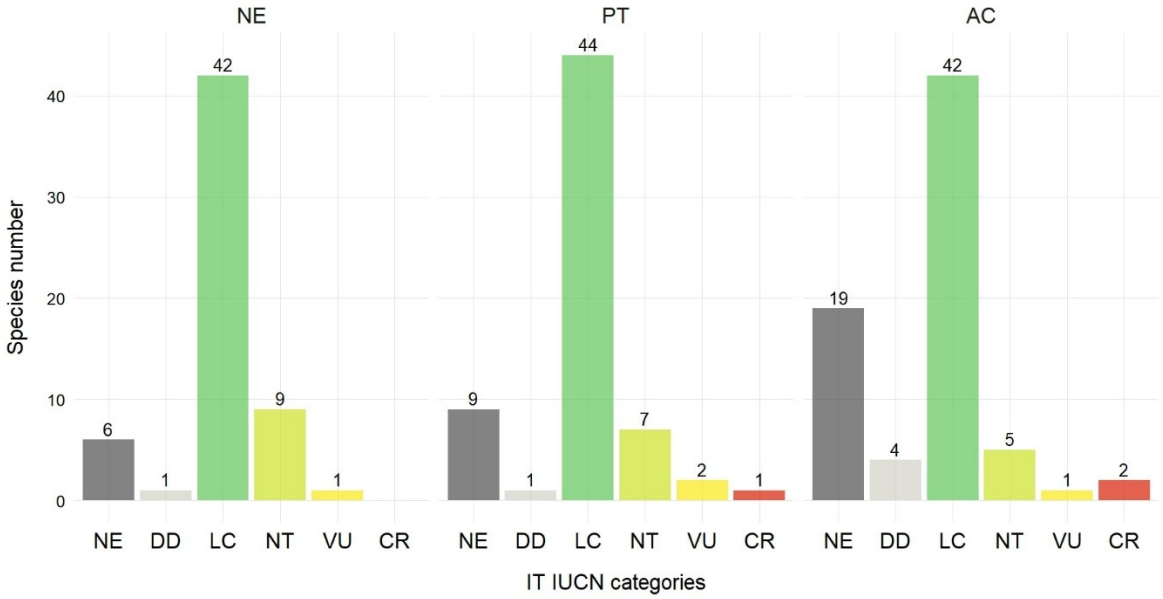


Figure 27. Bar plots representing the distribution of IUCN categories (Carpaneto et al., 2015) considering species richness, among the stands under different management options: natural evolution (NE), periodic thinning (PT) and anticipated seed cutting (AC). Acronyms and colours refer to the standards adopted by the IUCN Red List of Threatened Species (IUCN 2025): critically endangered (CR), vulnerable (VU), near threatened (NT), least concern (LC), data deficient (DD), not evaluated (NE).

Concerning trophic guilds, among the identified saproxylic species, 36 are mycophagous (MY), 27 xylophagous (XY), 18 saproxylophagous (SX), 17 predators (PR), 13 mycetophagous depending on the carpophores of large tree fungi (MB), 2 saprophagous inhabiting water-filled tree hollows (HW), 1 connected with nests of birds in tree hollows (NI) and 1 species feeding on fermenting sap exudate (Figure 28). Considering specimens number, the results are as follows: 11,005 MY, 202 XY, 199 SX, 52 PR, 31 MB, 3 HW, 1 NI and 1 SF (Table 31). All these categories are present in AC, while in NE and in PT we found MY, XY, SX, PR, MB and HW, with similar proportions.

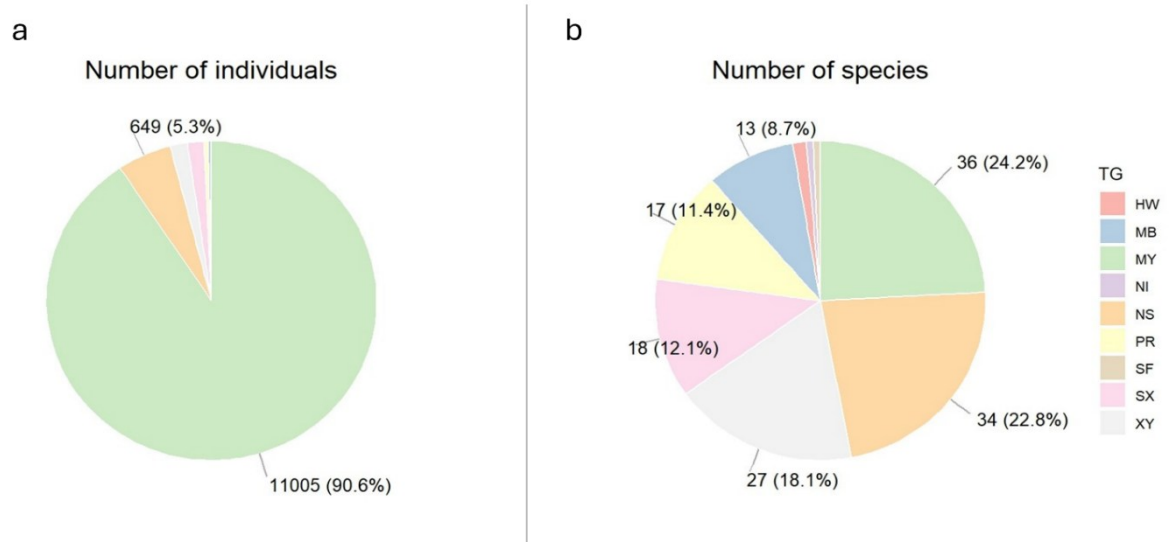


Figure 28. Pie chart representing the contribution of trophic guilds (TG) within the whole sample, with a focus on the species number (a) and on the number of individuals (b)

Alpha diversity

Considering diversity metrics (Table 32, Figure 29), evenness resulted to be lower in AC with significant differences in respect to NE (p-value=0.0002) and PT (p-value=0.0021). Gini-Simpson index turns to be higher in AC with significant differences in respect to NE (p-value=0.0007) and to PT (p-value=0.0030). Shannon index is lower in AC with significant differences in respect to NE (p-value=0.0044) and to PT (p-value=0.0072). Simpson index is lower in AC with significant differences in respect to NE (p-value=0.0007) and to PT (p-value=0.0030). Concerning richness and abundance, no significant differences are observed among the three stands.

Focusing on trophic guilds, differences among stands are observed only in MY species and in SX (Table 32, Figure 30). Specifically, in MY species, evenness statistically differs among plots (p-value: 0.00280), with lower values in AC in respect to NE (p-value: 0.00316) and PT (p-value: 0.0218893), as well as Gini-Simpson and Shannon indexes which are different among plots (p-values: 0.0279 and 0.0192, respectively), with significant differences between AC and NE (p-values: 0.02558 and 0.01840). Species richness and abundance do not differ among plots. On the other hand, in SX species, Gini-Simpson index results to be higher in AC (p-value: 0.0186), with significant differences in respect to NE (p-value: 0.0255), and a similar pattern can be observed for the Shannon index, which is higher in AC with a significant difference in respect to NE (p-value: 0.06851). No differences are observed among plots for evenness, species richness and abundance.

Table 32. Mean (± standard deviation) of the primary response variables (measuring unit) of diversity metrics in stands under the tree management options: natural evolution (NE), periodic thinning (PT) and anticipated seed cutting (AC). Data are reported for the whole saproxylic community and then focusing on single trophic guilds (i.e., mycophagous, predator, saproxylophagous and xylophagous) Parameters are shown with significance level. Lowercase letters highlight significant differences (p < 0.05) among stand types according to Tukey's post hoc test Parameters are shown with significance level. Lowercase letters highlight significant differences (p < 0.05) among stand types according to Tukey's post hoc test

Diversity metric	Natural evolution (NE)	Periodic thinning (PT)	Anticipated seed cutting (AC)	p-value
All saproxylics				
Species richness	7.267 (±1.332)	7.355 (±1.265)	7.689 (±1.298)	n.s.
Abundance	85.033 (±23.990)	99.387 (±35.362)	202.137 (±70.546)	n.s.
Shannon	0.988 (±0.128) a	0.952 (±0.127) a	0.712 (±0.103) b	< 0.004 **
Gini-Simpson	0.463 (±0.057) a	0.440 (±0.055) a	0.333 (±0.047) b	< 0.003 **
Simpson	0.537 (±0.057) a	0.560 (±0.055) a	0.667 (±0.047) b	< 0.003 **
Evenness	0.686 (±0.042) a	0.700 (±0.034)	0.508 (±0.040) b	< 0.005 **
Mycophagous				
Species richness	7.133 (±0.904)	7.467 (±0.951)	8.00 (±0.889)	n.s.
Abundance	138.267 (±41.219)	183.333 (64.773)	392.214 (±127.465)	n.s.
Shannon	1.209 (±0.085) a	1.126 (±0.081) a	0.848 (±0.107) b	< 0.023 **
Gini-Simpson	0.596 (±0.039) a	0.550 (±0.036) a	0.402 (±0.057) a	< 0.00 ***
Simpson	0.404 (±0.039) a	0.450 (±0.036) a	0.598 (±0.057) a	< 0.011*
Evenness	0.676 (±0.038) a	0.624 (±0.038) a	0.419 (±0.042) b	< 9.96e-05 ***
Predators				
Species richness	1.875 (±0.398)	1.571 (±0.202)	1.300 (±0.153)	n.s.
Abundance	1.875 (±0.398)	1.875 (±0.261)	2.00 (±0.471)	n.s.
Shannon	0.484 (±0.199)	0.388 (0.137)	0.176 (±0.091)	n.s.
Gini-Simpson	0.302 (±0.188)	0.278 (±0.098)	0.120 (±0.062)	n.s.
Simpson	0.698 (±0.118)	0.722 (±0.098)	0.881 (±0.062)	n.s.
Evenness	1.00 (±0.00)	0.980 (±0.020=	0.844 (±0.082)	n.s.
Saproxylophagous				
Species richness	1.786 (±0.408)	2.231 (±0.303)	2.636 (±0.544)	n.s.
Abundance	3.643 (±1.097)	5.923 (±1.112)	4.636 (±0.801)	n.s.
Shannon	0.276 (±0.139) a	0.595 (±0.134)	0.734 (±0.184) b	0.091 °
Gini-Simpson	0.144 (±0.069) a	0.362 (±0.078)	0.424 (±0.092) b	0.039 *
Simpson	0.856 (±0.069) a	0.638 (0.078)	0.576 (±0.092) b	0.039 *
Evenness	0.768 (±0.100)	0.868 (±0.048)	0.934 (±0.032)	n.s.
Xylophagous				
Species richness	2.700 (±0.559)	3.082 (±0.557)	2.083 (±0.358)	n.s.
Abundance	7.500 (±1.440)	6.167 (±1.709)	3.167 (±0.672)	n.s.

Shannon	0.744 (±0.197)	0.787 (±0.183)	0.522 (0.163)	n.s.
Gini-Simpson	0.427 (±0.100)	0.429 (0.090)	0.307 (±0.094)	n.s.
Simpson	0.573 (±0.100)	0.571 (±0.090)	0.693 (±0.094)	n.s.
Evenness	0.942 (±0.026)	0.868 (±0.076)	0.936 (±0.044)	n.s.

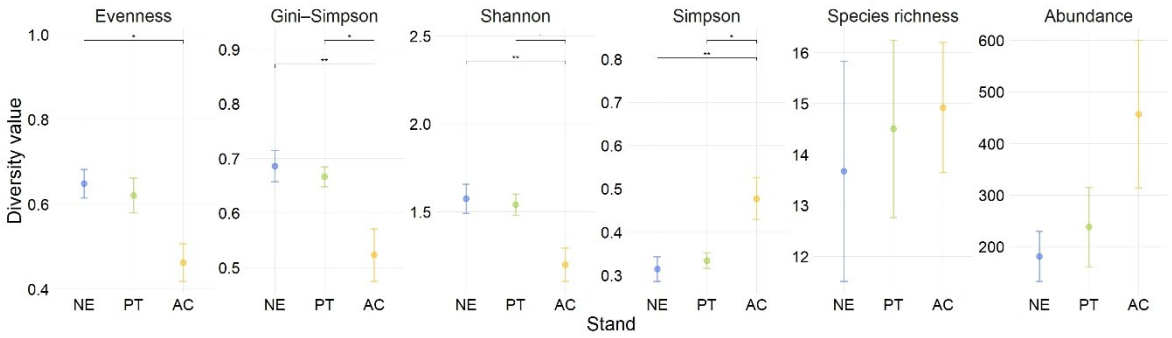


Figure 29. Chart showing variation in saproxylic beetle diversity and abundance across the three forest stands: natural evolution (NE), periodic thinning (PT), anticipated seed cutting (AC). Diversity is measured using Pielou's evenness, Gini–Simpson, Shannon, and Simpson indexes, while Species Richness and Abundance represent total community metrics. Asterisks above brackets provide information about significant differences among stands (= p-value < 0.05; ** = p-value < 0.005).*

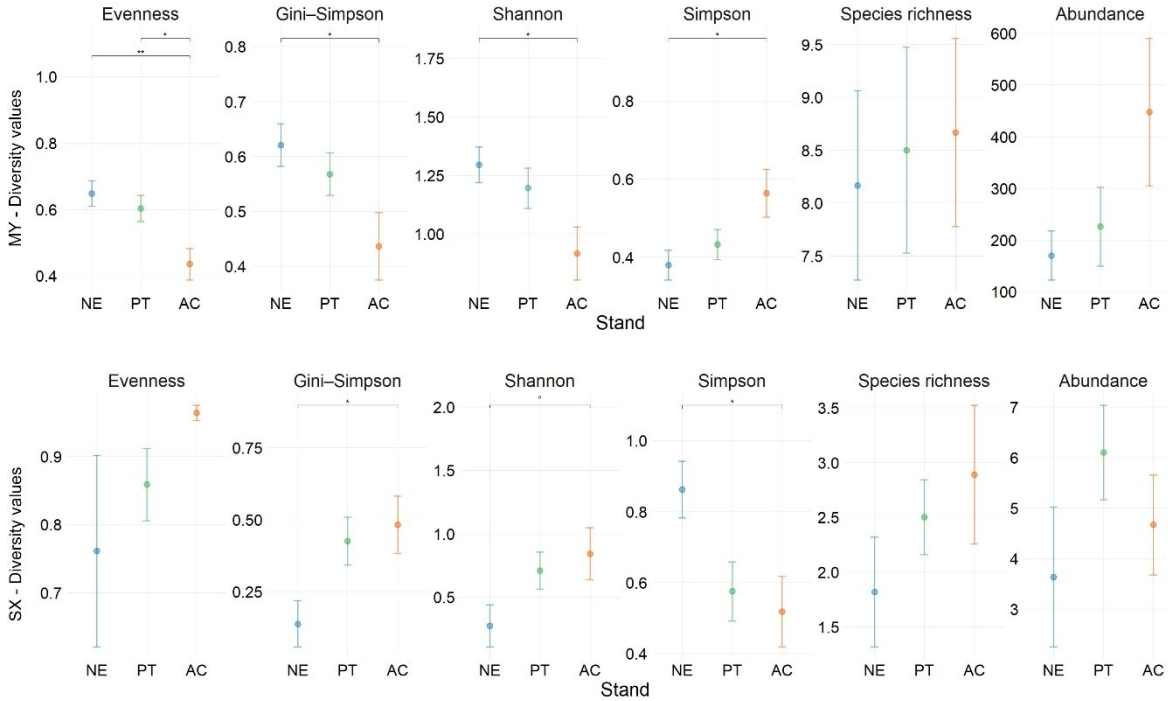


Figure 30. Chart showing variation in mycophagous (a) and saproxylophagous (b) diversity and abundance across the three forest stands: natural evolution (NE), periodic thinning (PT), anticipated seed cutting (AC). Diversity is measured using evenness, Gini–Simpson, Shannon, and Simpson indexes, while Species Richness and Number of Individuals represent total community metrics. Asterisks above brackets provide information about significant differences among stands (=p-value < 0.05; ** = p-value < 0.005).*

Beta diversity

Beta diversity showed moderate but consistent differences in species composition among management options. The NE stand shared 61% and 65% of its species with the PT and the AC stands, respectively, whereas PT and AC shared 58% of species. Despite this high proportion of shared taxa, community composition differed significantly among management options, as indicated by the PERMANOVA test (Table 33). Pairwise post-hoc comparisons, however, were not significant, likely due to the limited number of observations.

When considering species unique to each stand, NE and PT stands hosted 17 and 18 exclusive species, respectively, whereas the AC supported a higher number of unique taxa (i.e., 29).

Table 33. Results of the PERMANOVA test of differences in beta diversity among the three forest stands. Df indicates the degrees of freedom, SumOfSqs the sum of squares associated with each term, R^2 the proportion of variance explained, F the pseudo-F statistic, and Pr(>F) the permutation-based p-value*. The effect of stand on community composition was significant (pseudo-F = 1.528, R^2 = 0.337, p-value = 0.009), indicating that differences among stands explain 33.7% of the total variation in beta diversity.*

	Df	SumOfSqs	R2	F	Pr(>F)
Model	2	0.5615741	0.3374509	1.527966	0.009 **
Residual	6	1.1025913	0.6625491	*NA*	
Total	8	1.6641654	1.0000000	*NA*	

Influence of forest structure and management on beetle diversity

Correlation analysis showed statistically significant associations among alpha diversity indexes and forest structure parameters, as well as with canopy characteristics (Figure 31). In particular, Shannon and Gini-Simpson indexes, as well as the evenness, resulted to be positively correlated with the number of trees per hectare (sc_str_N_ha) and crown porosity (sc_can_CP). These indexes are negatively correlated with the volumes of stumps (sc_str_stump_vol) and the square of the average diameter of the trees (sc_str_QMD), on the contrary Simpson index and individual abundances are positively correlated.

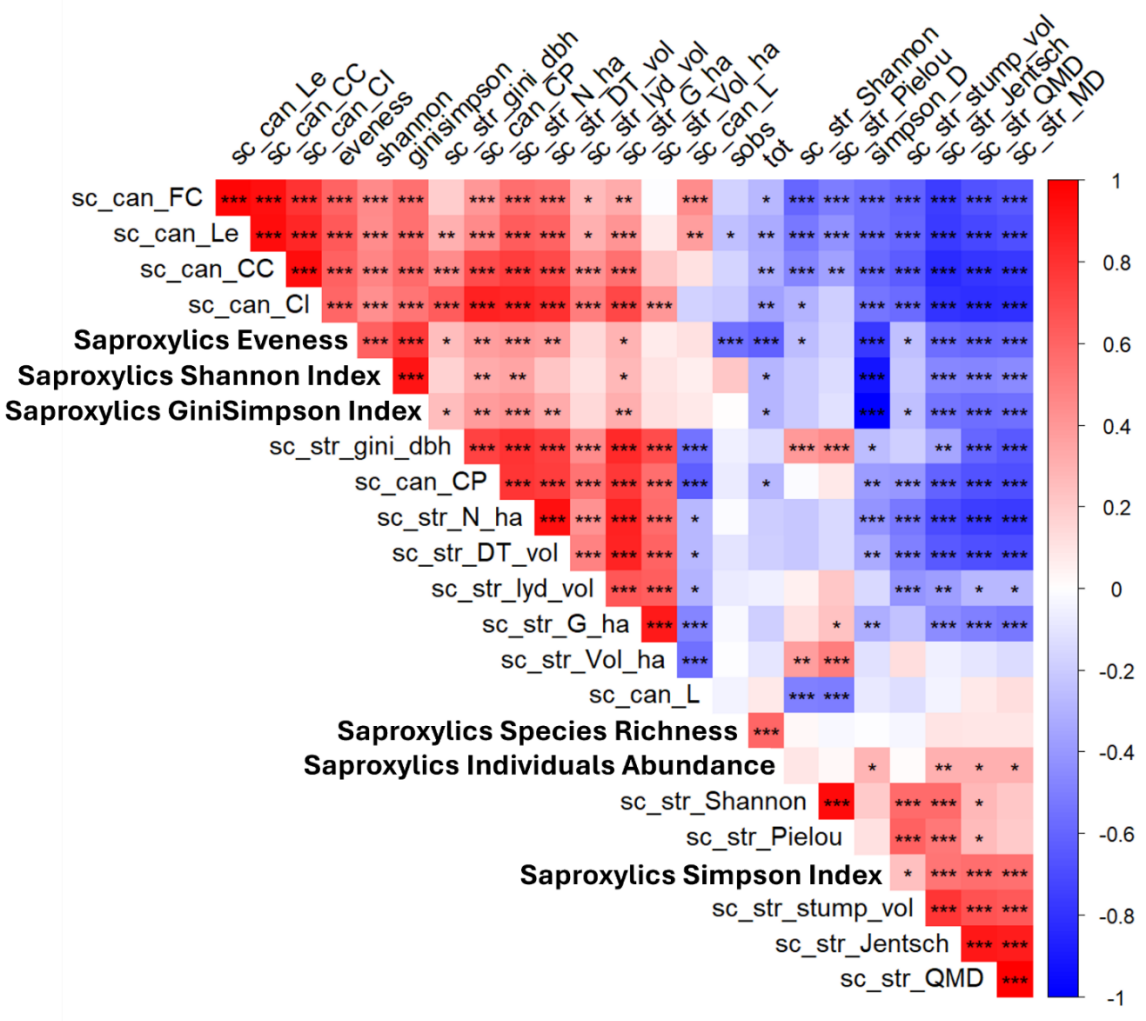


Figure 31. Corrplot representing correlations among structural variables, canopy attributes and alpha diversity indices considering the whole saproxylic community. All the values are scaled. The shades of red indicate a positive correlation, while those of purple indicate a negative one (= p-value < 0.05; ** = p-value < 0.005, *** = p-value < 0.0005).*

Linear Mixed Models (Figure 32, Table 34) showed that evenness is negatively affected by the increase in tree size (str_QMD, β: 0.455±0.002, p-value: 0.008**), and positively influenced by the volume of stumps (stump_vol, β: 0.018±0.007, p-value: 0.058), with no relevant effects played by canopy cover, even if a positive trend is observed. Gini-Simpson index is negatively influenced by the tree size (str_QMD, β: -0.006±0.001, p-value: 0.002**), and positively affected by the volume of stumps (stump_vol, β: 0.017±0.005, p-value: 0.021*), as well as by canopy cover (can_Le, β: 0.177±0.090, p-value: 0.059). Shannon index results to be negatively influenced only by tree diameters (str_QMD, β: -0.013±0.005, p-value: 0.045*). Considering species richness and individual abundances, the first seems not to depend on any of the selected factors, while the second is positively influenced by tree diameters (str_QMD, β: 15.139±4.787, p-value: 0.017*) and negatively by stumps volume (stump_vol, β: -52.524±18.816, p-value: 0.036*).

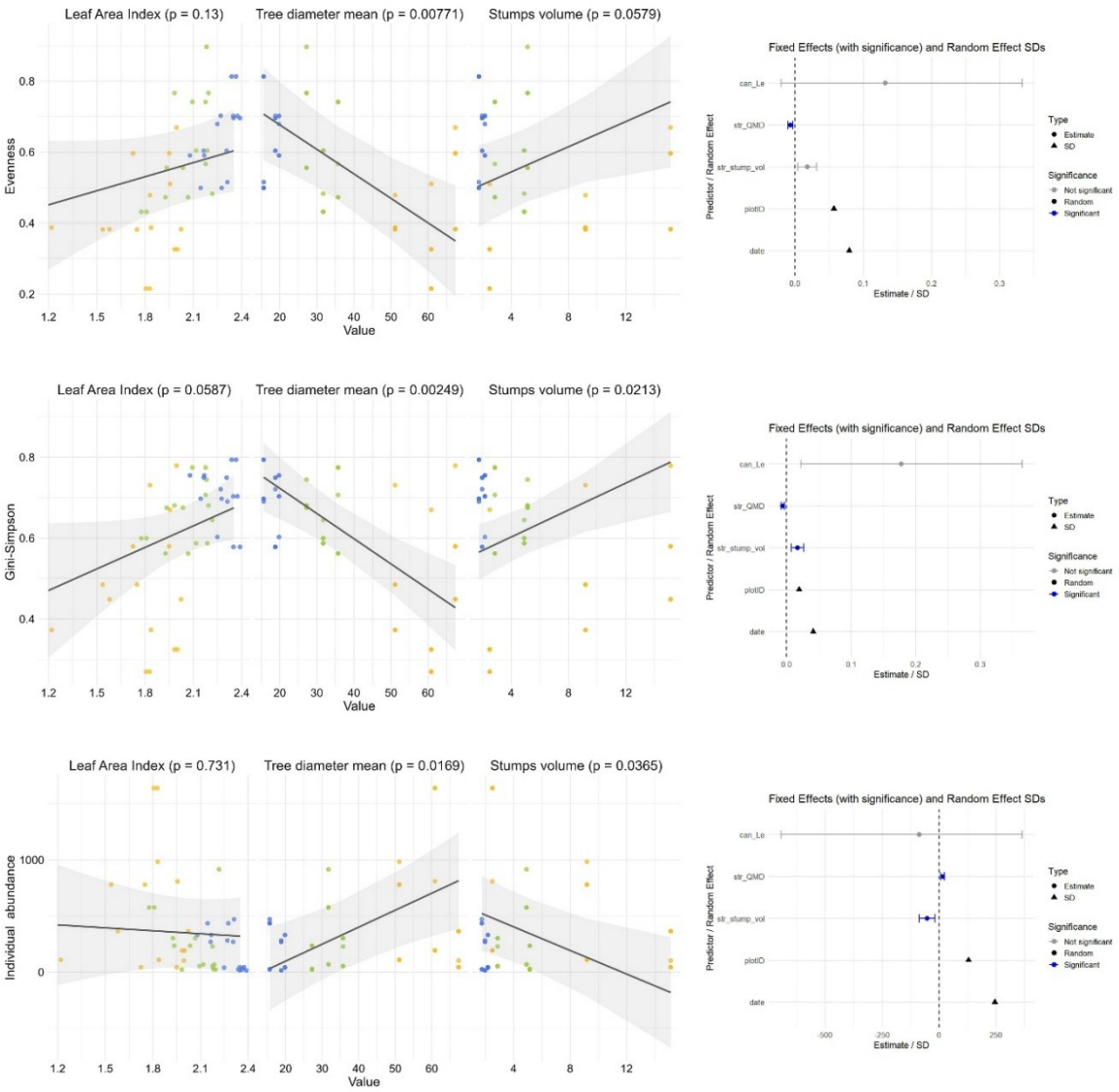


Figure 32. Conditional variation of biodiversity metrics in relation to structural forest variables. Each row shows the statistically significant responses of (i) Pielou's evenness, (ii) Gini–Simpson index and (iii) individual abundance, to the main structural predictors: leaf area index, mean tree diameter, and stump volume. Scatterplots display observed data with fitted linear trends (±95% CI) colored by forest stand: natural evolution (NE) in blue, periodic thinning (PT) in green and anticipated seed cutting (AC) in orange. Right-hand panels show parameter estimates (±SE) from the corresponding linear mixed-effects models, including fixed and random effects (date as random factor). Significant predictors ($p < 0.05$) are highlighted in blue.

Focusing on trophic guilds, the diversity of mycophagous species (MY) is mostly influenced by canopy cover and by tree dimensions (Figure 33, Table 34). Evenness is positively driven by the leaf area index (can_Le, β: -0.248±0.097, p-value= 0.015*) and negatively by tree diameter (str_QMD, β: -0.006±0.002, p-value: 0.003**). A similar relation can be observed when considering Gini-Simpson index, which is positively driven by leaf area index (can_Le, β: -0.213±0.108, p-value: 0.0531) and slightly negatively by tree diameter (str_QMD, β: -0.004±0.002, p-value: 0.079). On the other hand, abundance is positively associated with tree diameters (str_QMD, p-value: 0.0219*) and negatively with stumps volume (str_stump_vol, β: -39.503±14.596, p-value: 0.040*). Predator species (PR) result to be slightly significantly negatively influenced in terms of diversity and number of species by tree diameters, specifically considering Gini-Simpson index (str_QMD, β: -0-009±0.004, p-value: 0.09), Shannon index (str_QMD, β: -0.013±0.006, p-value: 0.08), and species richness (str_QMD, , β: -0.023±0.011, p-value: 0.094). On the other hand, PR abundance shows a slightly significant positive association with canopy cover (can_Le, β: 1.247±0.713, p-value: 0.090) and a significant one with stumps volume (str_stump_vol, β: 0.204±0.061, p-value: 0.024*). Considering Xylophagous (XY), Shannon index results to be negatively influenced by leaf area index (can_Le, β: -1.199±0.546, p-value: 0.036*), as well as species richness is (i.e., can_Le, β: -4.089±1.533, p-value: 0.012*). In addition, XY abundance seems to be negatively influenced by tree diameters (str_QMD, β: -0.069±0.026, p-value: 0.014*). Finally, no statistically significant association has been detected between Saproxylophagous (SX) diversity indexes and forest variables.

Table 34. Results of the linear mixed-effects models (LMMs) relating forest structural variables to diversity metrics. For each model, the table reports the response variable (Diversity metric), the predictor variable (Variable), the estimated regression coefficient (Estimate), its standard error (Std. error), the associated degrees of freedom (df), and the p-value *(*P-value*). Only results obtained by valid models (i.e., are reported. Only results from statistically valid models are reported (i.e. models showing successful convergence and satisfying standard model assumptions).*

Diversity metric	Variable	Estimate	Std. error	df	P-value
All saproxylics					
Evenness	(Intercept)	0.455	0.216	38.748	0.042*
	can_Le	0.132	0.086	39.918	0.130
	str_QMD	-0.007	0.002	6.977	0.008**
	str_stump_vol	0.018	0.007	5.726	0.058°
Gini-Simpson	(Intercept)	0.401	0.219	24.433	0.080°
	can_Le	0.177	0.090	25.848	0.059°
	str_QMD	-0.006	0.001	7.723	0.002**
	str_stump_vol	0.017	0.005	5.866	0.021*

Shannon	(Intercept)	0.967	0.612	38.434	0.123
	can_Le	0.378	0.250	40.294	0.138
	str_QMD	-0.013	0.005	7.385	0.045
	str_stump_vol	0.032	0.021	6.034	0.179
Abundance	(Intercept)	240.063	634.300	35.006	0.707
	can_Le	-87.436	252.274	36.605	0.731
	str_QMD	15.139	4.787	6.685	0.017*
	str_stump_vol	-52.524	18.816	5.238	0.036*
Richness	(Intercept)	21.732	11.573	39.208	0.0679
	can_Le	-3.133	4.571	40.058	0.497
	str_QMD	0.068	0.102	7.348	0.526
	str_stump_vol	-0.502	0.411	6.087	0.267
Mycophagous					
Evenness	(Intercept)	0.250	0.241	32.318	0.309
	can_Le	0.248	0.097	33.134	0.015*
	str_QMD	-0.006	0.002	8.173	0.003**
	str_stump_vol	0.009	0.006	7.382	0.189
Gini-Simpson	(Intercept)	0.216	0.277	46.759	0.439
	can_Le	0.213	0.108	48.293	0.053°
	str_QMD	-0.004	0.002	7.786	0.079°
	str_stump_vol	0.002	0.009	6.693	0.808
Shannon	(Intercept)	0.478	0.578	49.305	0.412
	can_Le	0.393	0.223	51.430	0.085°
	str_QMD	-0.007	0.005	7.586	0.202
	str_stump_vol	-0.003	0.020	6.563	0.893
Abundance	(Intercept)	165.438	514.749	37.235	0.750
	can_Le	-56.221	201.216	38.270	0.781
	str_QMD	11.143	3.675	6.248	0.022*
	str_stump_vol	-39.503	14.596	5.367	0.040*
Richness	(Intercept)	1.748	4.527	44.476	0.701
	can_Le	2.013	1.652	53.976	0.228
	str_QMD	0.069	0.042	6.943	0.147
	str_stump_vol	-0.243	0.173	6.131	0.209
Predators					
Gini-Simpson	(Intercept)	0.446	0.513	20.536	0.395
	can_Le	0.024	0.211	25.115	0.909
	str_QMD	-0.009	0.004	5.449	0.085°
	str_stump_vol	0.017	0.016	4.589	0.358
Shannon	(Intercept)	0.604	0.805	21.788	-0.960
	can_Le	0.071	0.330	25.623	1.247
	str_QMD	-0.013	0.006	5.716	-0.018*
	str_stump_vol	0.026	0.025	4.742	0.204
Abundance	(Intercept)	-0.960	1.753	26.445	0.589

	can_Le	1.247	0.713	31.595	0.090°
	str_QMD	-0.018	0.015	5.433	0.294
	str_stump_vol	0.204	0.061	4.510	0.024*
Richness	(Intercept)	1.739	1.496	22.961	0.257
	can_Le	0.244	0.612	26.161	0.694
	str_QMD	-0.023	0.011	5.940	0.094°
	str_stump_vol	0.048	0.045	4.894	0.332
Saproxylophagous					
Evenness	(Intercept)	0.548	0.231	51.540	0.022*
	can_Le	0.142	0.091	54.000	0.124
	str_QMD	0.002	0.002	6.939	0.366
	str_stump_vol	0.000	0.010	6.521	0.997
Shannon	(Intercept)	1.173	0.986	42.923	0.241
	can_Le	-0.392	0.391	43.894	0.321
	str_QMD	0.007	0.007	8.148	0.329
	str_stump_vol	-0.010	0.029	7.654	0.736
Abundance	(Intercept)	12.806	7.535	40.644	0.097°
	can_Le	-3.371	2.952	42.069	0.260
	str_QMD	0.007	0.081	7.021	0.936
	str_stump_vol	-0.211	0.340	6.572	0.556
Richness	(Intercept)	4.116	2.738	41.655	0.140
	can_Le	-1.005	1.083	42.023	0.359
	str_QMD	0.018	0.019	8.167	0.374
	str_stump_vol	-0.079	0.079	7.750	0.348
Xylophagous					
Shannon	(Intercept)	3.959	1.347	25.870	0.007**
	can_Le	-1.199	0.546	28.588	0.036*
	str_QMD	-0.018	0.008	4.727	0.093°
	str_stump_vol	-0.019	0.034	4.864	0.601
Abundance	(Intercept)	11.513	4.924	38.831	0.025*
	can_Le	-2.584	1.984	38.912	0.201
	str_QMD	-0.069	0.026	38.566	0.014*
	str_stump_vol	-0.069	0.108	37.741	0.529
Richness	(Intercept)	13.224	3.792	29.016	0.002**
	can_Le	-4.089	1.533	32.219	0.012*
	str_QMD	-0.053	0.026	4.670	0.098°
	str_stump_vol	-0.052	0.106	4.518	0.642

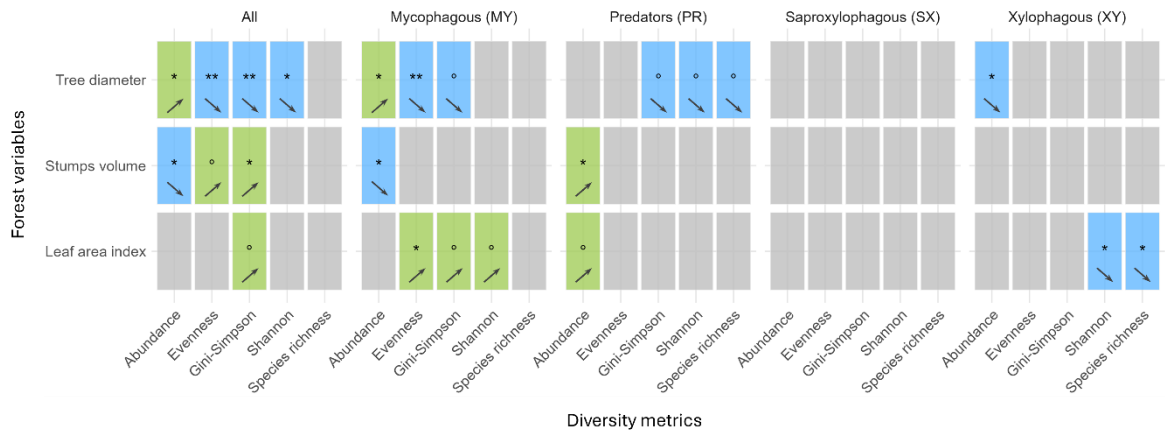


*Figure 33. Graphical representation of the direction and significance of relationships between forest structural variables (i.e., Leaf area index, Quadratic mean of tree diametres and Stumps volume) and diversity indices (i.e., Gini-Simpson index, Abundance, Pielou's evenness, Shannon index, Species richness), based on linear mixed-effects models. Colors and arrows indicate the direction of the effect (light blue with downward arrow = negative, green with upward harrow = positive), while asterisks denote significance levels (°: 0.05 < p < 0.10, *: p < 0.05, **: p < 0.01).*

Discussion

The effects of forest management on saproxylic beetle diversity and community composition have been addressed in several regional contexts (Buse et al., 2010; Edelmann et al., 2022; Uhl et al., 2025). However, few studies explicitly focus on the long-term effects of the abandonment of a particular silvicultural regime in beech woodlands (Chianucci et al, 2016; Roth et al., 2019). Specifically, the present study investigates saproxylic beetle diversity and community structure across forest stands that once shared the same management (i.e., coppice with standards) but have undergone, over recent decades, divergent conversion pathways to high forest condition, resulting in distinct management options: natural evolution, periodic thinning, and anticipated seed cutting (Cutini et al., 2015).

Structure and diversity of saproxylic beetle community

The investigated saproxylic beetle community results to be highly unbalanced and dominated by few species, among which *Xyleborinus saxesenii* represents more than 40% of the all investigated individuals. This pattern is consistent with those reported from other temperate forests, where communities are typically characterized by a strong numerical dominance of few taxa (McGeoch et al., 2007). In particular, this is a characteristic feature of *X. saxesenii*, which is a highly prolific generalist ambrosia beetle, usually subject to fluctuations and willing to predominate over all other saproxylic insect species when present (Galko et al., 2014). It is also worth noting that the high number of individuals collected for this species, as well as for other abundant Scolytinae species may be influenced by the use

of ethanol as preservative in our traps (Cavaletto et al., 2021; Chen et al., 2021; Miller, 2025). Indeed, this effect is likely enhanced in open environments, such as the anticipated seed cutting stand, where the attractant may have a greater chance of spreading and individuals have more space to fly (Bouget et al., 2009). Many species of ambrosia beetles, in fact, take advantage of the wind for their dispersal (Jones et al., 2019; Stočes et al., 2025). Among the most abundant species we also report the presence of the xylem-boring beetle *Xylosandrus germanus*, native to Southeast Asia and which is known in Italy since 1992 (Kirkendall and Faccoli, 2010), with populations in Lombardy, Piedmont and Friuli Venezia Giulia (EPPO, 2021). To our knowledge, this is the first record of the species in Tuscany (Contarini et al., 2020).

Despite the numerical dominance by a limited number of species, the occurrence of "Threatened" and "Data Deficient" species highlights the conservation relevance of the investigated stands, especially for plots under anticipated seed cutting, as also reported by Parisi et al. (2024). This finding indicates that even forest systems under high management pressure can support the conservation of threatened species (Carpaneto et al., 2015), therefore suggesting that a balance between forest productivity and the retention of key structural features may play an important role in sustaining diverse and functionally rich saproxylic insect communities (Mason and Zapponi, 2016; McGeoch et al., 2007).

Considering trophic guild composition, in terms of abundance the community is dominated by mycophagous species, largely due to the high numbers of Scolytinae, whereas the low abundance values of the other guilds suggest limited substrate diversity throughout the study area. The exception is represented by the anticipated seed cutting stand, which supports a higher number of trophic guilds, indicating that more structurally heterogeneous stands with larger isolated trees can provide a great variety of microhabitats (Ouin et al., 2015; Larrieu et al., 2018). In fact, structural heterogeneity allows for the coexistence of a broader range of functional groups compared with more uniform stands, such as those with dense or closed canopies, where limited resource availability and reduced niche diversity may constrain beetle community composition (Bouget et al., 2013; Bujoczek and Bujoczek, 2022).

Alpha and *beta* diversity offering a more nuanced perspective on community structure and heterogeneity, as well as species turnover (Whittaker, 1972; Anderson, 2001). In this study, different values of diversity indexes emerge among the different silvicultural options. In particular, Shannon index and evenness result to be significantly lower in the plots under anticipated seed cutting conversion, where higher values of dominance were observed, as measured by the Gini-Simpson index, indicating an assemblage numerically dominated by

few abundant taxa. Conversely, the plots under natural evolution show higher values of diversity and evenness, resulting in a more balanced community structure which is a relevant result as this stand had a long history of coppicing and has been left to evolve freely for about 50 years (Cutini et al., 2015). Its evolution lead to an increased canopy extension (Figure 24, Table 30), resulting in a possible reduction of community composition in terms of heliophilous species (Müllerová et al., 2015; Ambrožová et al., 2022), while enhancing species more related to shadow and humidity (Edelmann et al., 2022; Menocal et al., 2022), also thanks to the increase in standing and lying deadwood (even if of small dimensions) (Ranius and Jansson, 2000; Müller and Bütler, 2010; Della Rocca et al., 2014; Seibold and Thorn, 2018). More insights are provided when focusing on trophic guilds, with differences among silvicultural regimes in terms of evenness and diversity indexes in mycophagous and saproxylophagous species. In particular, these two guilds exhibit opposite patterns between the unmanaged and the anticipated seed cutting stands highlighting how specific silvicultural practices can selectively benefit certain functional groups over others (Gossner et al., 2013; Sallé et al., 2020). Specifically, mycophagous species are more diversified in the abandoned coppice left to natural evolution, suggesting a higher abundance and richness of wood-related fungi in these stands (Leschen, 1994; Santamaria et al., 2023). This pattern is likely promoted by the dense canopy cover and the large amounts of deadwood at various decomposition stages increasing humidity and providing abundant substrate for fungal growth, thereby supporting a richer community of fungi-dependent beetles (Yamashita and Hijii, 2007; Bässler et al., 2010;). On the other hand, saproxylophagous trophic guild result to be more diversified and balanced in the anticipated seed cutting stand, where large-sized trees are more suitable for hosting cavities and other micro-habitats which provide organic matter associated with decaying wood (Micó, 2018; Spina et al., 2023).

Overall, the three management options seem to host quite different communities, with particular reference to anticipated seed cutting stand. Such differences are mainly related to the occurrence of unique species within each stand, rather than to a complete restructuring of the assemblages (Sebek et al., 2022). This pattern is particularly relevant given the spatial proximity of the stands, suggesting that the observed differences are hardly explained by dispersal limitation alone but can rather reflect fine-scale habitat differentiation associated with contrasting silvicultural histories (Micó et al., 2013).

From a broader perspective, none of the three stands show particularly low levels of diversity, indicating that all of them are inhabited by a variety of species, likely associated with stand-specific structural and microhabitat conditions and despite the relatively small

and spatially constrained extent of each management unit. It is well established that increasing environmental heterogeneity promotes biological diversity by enlarging the range of available niches and resources (Paillet et al., 2010; Stein et al., 2014; Schall et al., 2018a). In this context, different management strategies applied to forest stands that originally shared the same silvicultural regime appear, even over a relatively short time span of a few decades, to have promoted the establishment of distinct species assemblages, ultimately contributing to higher biodiversity at the landscape scale (Roberge et al., 2015; Joelsson et al., 2018).

Influence of forest structure and management on beetle diversity

Saproxylic assemblages in temperate forests are largely driven by resource availability, habitat heterogeneity, and microclimatic conditions linked to canopy cover and forest structure (Stokland et al., 2012a; Bouget et al., 2013b; Seibold and Thorn, 2018; Edelmann et al., 2022). In our study, considering the entire saproxylic beetle assemblage, contrasting effects of forest structural variables were observed. Concerning forest structure, *alpha* diversity of the whole community results positively associated with stump volume, whereas tree diameter, commonly reported as a positive driver of saproxylic beetle diversity (Larrieu and Cabanettes, 2012; Zumr et al., 2023), emerges in our study as a negative predictor of diversity. In contrast, and in line with previous evidence (Rappa et al., 2022), tree diameter shows a positive association with total beetle abundance, suggesting a potential decoupling between patterns of diversity and numerical dominance along gradients of tree size. Conversely, we observe that canopy cover positively affect saproxylic diversity (Parisi et al., 2021), even if more open conditions are generally considered favourable for beetles assemblages (Hardersen et al., 2020; Edelmann et al., 2022; Perlík et al., 2023) due to increased light and microclimatic heterogeneity (Gossner et al., 2013; Seibold et al., 2016). Our results concerning trophic guild patterns also reflect differential sensitivity of functional groups to forest drivers. Diversity of micophagous species turns to be positively associated with canopy cover, likely reflecting the preferences of many fungivore species (Balázs et al., 2024), as well as Scolytinae, for canopy closure (Jones et al., 2019; Holuša et al., 2021; Menocal et al., 2022). In contrast, the diversity of the xylophagous species shows negative correlations with canopy closure and tree diameter, diverging from literature (Seibold et al., 2015; Nakládal et al., 2022; Zumr et al., 2023) and suggesting that this group in the study area may be more influenced by other environmental factors not considered in this study. Predators guild shows intermediate responses, with abundance increasing with stump volume and canopy cover, as reported by (Jukes et al., 2002), while diversity decreasing with

tree size. These patterns align with studies showing that predatory saproxylic beetles are more influenced by substrate availability and structural complexity than by tree size alone, being more abundant in areas with diverse deadwood, both in terms of type and decay level (Johansson et al., 2007; Bergmark et al., 2024;).

Conclusions

Our results indicate that different silvicultural approaches applied to Mediterranean beech forests with a similar management history can lead to distinct saproxylic beetle assemblages, affecting both diversity metrics and community composition. However, the observed responses also reflect the transitional structural conditions of the investigated stands and this highlights how the combined and long-lasting influence of historical management and current stand structure can shape biodiversity. Importantly, the stand left to natural evolution still exhibits both structural features and a saproxylic beetle assemblage that are far from those expected in a truly naturalised forest, with several characteristics remaining strongly constrained by the legacy of its former intensive coppice management. The still dense and continuous canopy likely limits the establishment of species requiring lighter and drier habitats, indicating that abandonment alone does not necessarily promote a broad range of saproxylic niches in the short term. By contrast, the anticipated seed cutting stand, despite its higher level of human intervention, has allowed a subset of trees to reach large dimensions and develop a higher diversity substrates, thereby supporting additional trophic guilds that were poorly represented in the other stands. However, under the current silvicultural regime, standard trees are eventually removed during regeneration cuttings to facilitate seedling establishment, and therefore the favourable conditions for saproxylic diversity observed at the moment are likely to be only temporary.

Taken together, our results indicate that maintaining patches under low-intensity management can play a key role in sustaining biodiversity, even in forest landscapes with a long history of timber exploitation. However, passive abandonment alone is seldom sufficient. Rather, these areas require targeted management actions aimed at promoting specific forest attributes that support natural ecological processes. At the same time, such measures should explicitly take into account the legacy of past management, which continues to shape current biodiversity patterns and influences the trajectories of forest succession.

Thesis discussion

This doctoral thesis explored the contribution of different approaches for investigating the conservation status of saproxylic beetles and their responses to environmental changes, both in terms of single species and community. By presenting studies with different focuses on distributional, ethological, and ecological analyses conducted at diverse spatial and temporal scales, this work offers an overview of different approaches that can be employed to collect and interpretate biodiversity data. Overall, the results highlight the value of addressing multiple issues particularly in the context of ongoing environmental change (Pereira et al., 2010, 2024), which requires constant and long-term monitoring at different scales, including taxonomic and functional levels.

Specifically, the findings of Chapter 1 demonstrate that citizen science initiatives can represent an effective opportunity for improving both scientific knowledge and the awareness of non-experts participants, particularly when data are collected over extended temporal periods. In fact, the MIPP/InNat project substantially improved knowledge on the distribution of protected insect species in Italy, providing new records at both national and local scales and highlighting the ecological importance of matrix landscapes connecting protected areas (cfr. Redolfi de Zan., 2023). Beyond distributional information, opportunistic photographic records also proved to be valuable for obtaining ecological and ethological insights, as shown by the case of *Lucanus cervus* images, indicating that CS data could have effective additional application in biological and ecological researches (Feldman et al., 2021; Campbell et al., 2023; Mason et al., 2025; Gisondi et al., 2025c), emphasising the potential of such initiatives, which go beyond merely providing attendance. We also highlight the relevant role of the social context in which citizen science initiatives operate (Tauginiene et al., 2020; Vasiliades et al., 2021), by paying attention not only to volunteer recruitment and the attractiveness of the project to broader audiences, but also, and perhaps more importantly, to long-term participant retention (Robinson et al., 2021). In this regard, the potential of digital technologies and social media can be an effective support, but this approach still strongly requires the implementation of human contact and interactions (Brouwer et al., 2019; Schumann et al., 2024). Furthermore, the outcomes of the MIPP/InNat initiative directly fostered the development of a new citizen science project specifically focused on the study of ecological and ethological traits of *L. cervus* through direct field observations in nature carried out by volunteers. This project, named BOB – Behavioural

Observation in Beetles[13], was developed by applying the experience gained during the MIPP/InNat project, particularly with regard to the definition of the scientific framework and the communication and recruitment strategies. In addition, BOB incorporates the methodological recommendations that emerged from the eco-ethological analyses of *L. cervus* photographic records, which were used to design a dedicated and standardised data-collection protocol, including the development of a dedicated smartphone application to foster a standardised data collection during field observations.

From this long-term monitoring perspective and the need to assess dynamics of insect assemblages through time, Chapter 2 shifts the focus to the effects of temporal dynamics and the effects of climatic variables on saproxylic beetle communities in a Mediterranean forest. In this region, which is recognized as climate change hotspots due to it pronounced warming trends and increasing frequency of heat extremes (Paeth et al., 2017; Lazoglou et al., 2024), even small increases in temperature can disproportionately affect population dynamics and species interactions (Uhl et al., 2022). In our study, an increase in maximum temperatures over the last two decades is documented, providing a significant environmental background for interpreting the observed patterns of saproxylic beetles inhabiting tree hollows. In fact, although the available data only covers two time periods and we cannot therefore refer to a trend, differences in terms of abundance and phenology (both at functional and taxonomic level) between samplings 10 years apart are evident, suggesting that saproxylic communities could rapidly respond to ongoing climatic shifts at different scales (Ekman et al., 2024; Hågvar and Ødegaard, 2025). In addition, the observed variability and inconsistency in abundance and phenological responses among taxa or functional groups indicates also that climate change effects are neither uniform nor easily predictable (Forrest, 2016; Jackson et al., 2022; Neupane et al., 2024), with remarkable potential ecological implications (Kellermann and van Heerwaarden, 2019; Harvey et al., 2023). For instance, anticipated activity peaks in some functional groups or species, coupled with delayed peaks in others, raise concerns about potential temporal mismatches within ecological networks (Renner and Zohner, 2018). These findings highlight the importance of adopting functional and trait-based approaches when assessing community responses to environmental change, as focusing solely on species richness or total abundance may obscure important functional reorganizations that are critical for ecosystem functioning (Li et al., 2021; Stewart et al., 2022; Scherer et al., 2023).

[13] https://www.beetleobserver.com/

In this context, it is necessary also considering a broader range of environmental changes that may influence saproxylic beetles' dynamics, especially those driven by human activities such as forest management (Schulze, 2018; Edelmann et al., 2022). Indeed, as highlighted in Chapter 3, different silvicultural practices can reshape these communities (Parisi et al., 2024), even across neighbouring stands that previously shared the same management regimes (Cutini et al., 2015; Chianucci et al., 2016). Even if no differences in terms of richness nor abundance have been detected among the silvicultural options, such changes are evident in diversity metrics, as well as in distinct species composition. Moreover, the contrasting responses observed for tree size, canopy cover and deadwood availability indicate that diversity patterns cannot be inferred from single structural proxies, and that different components of habitat complexity should be evaluated (Johansson et al., 2007; Holuša et al., 2021; Parisi et al., 2021), including constrains due to the history of the area. In this regard, the results underscore how a past management regime continues to shape present-day communities, with observed patterns arising from the interplay between past legacies and ongoing interventions. Recognizing this interaction is crucial for developing forest management strategies aimed at reconciling productive objectives with the preservation of biodiversity.

Thesis conclusions and future perspectives

The present thesis confirms the still present uncertainties in forecasting saproxylic beetle responses to environmental changes. Indeed, without a deep understanding of species' ecology and community dynamics, conservation efforts may remain greatly constrained. Conversely, the work demonstrates the potential impacts of different methods and the valuable insights they provide to researchers: citizen science offers extensive, large-scale data, as well as engaging the public and raising awareness, whereas local-scale studies conducted by specialised teams can give precise and timely ecological insights. By offering diverse results and generating distinct impacts, both within and beyond the scientific sphere, these approaches do not preclude one another. On the contrary, they should be pursued in parallel to maximize their overall effectiveness. In this context I also highlight the value of interdisciplinary collaboration, beyond its mere contribution to improving scientific outcomes: integrating entomology, forest ecology and conservation management can support a more balanced and evidence-based reconciliation between forest productivity and biodiversity conservation, while the inclusion of social perspectives and citizen involvement may contribute to increasing public awareness and, potentially, to fostering more responsible attitudes towards the use and exploitation of forest resources.

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