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Insects as indicators of Key Biodiversity Areas

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Abstract

1. Global change is affecting insect populations worldwide as species declines have been reported from different areas of the planet.

2. Novel approaches such as the identification of Key Biodiversity Areas (KBAs) could detect areas of high biodiversity value for insect populations. The KBA approach relies on standardised criteria to identify important sites for biodiversity persistence. The application of such criteria to large numbers of species would significantly accelerate the KBA mapping process.

3. A systematic application of KBA criteria has not been tested on insects, and very little is known about the efficiency and limits of such methodology.

4. We applied four KBA criteria in Italy to 28 species/subspecies of bumblebees and identified potential KBAs for one species and three subspecies. Potential KBAs are only partially nested within current Italian KBAs and the protected areas network. When compared with potential KBAs of vertebrate species identified with the same methodology, the degree of nesting is only 12%.

5. Our results provide evidence of a tendency of the KBA network to expand as more species are assessed, raising questions about the ability of the criteria to detect areas that truly are key for biodiversity and not just for specific taxa. We also highlight issues regarding the use of KBA criteria on insects, such as data availability and the use of subspecies. Further large-scale assessments of KBAs will reveal the true potential of application of the KBA approach for insect conservation, and whether it actually may slow down the loss of important units of their extraordinary diversity.

KEYWORDS
bumblebees, Italy, KBA criteria, large-scale assessment

INTRODUCTION

Over recent years, an increasing number of studies reported evidence of insect populations declining in different areas of the planet (Goulson, 2019; Homburg et al., 2019; Lewinsohn et al., 2022; Sánchez-Bayo & Wyckhuys, 2019; Wagner et al., 2021). Although this negative trend cannot be necessarily generalised as a global issue (Saunders et al., 2020; Simmons et al., 2019), it is likely that the documented cases reflect an alarming and widespread phenomenon with devastating consequences on Earth's ecosystems. Large-scale assessments of the global population status of insects can shed light on where and which species are currently facing a decline, as well as the severity of their extinction risk (Clausnitzer et al., 2009). However, despite their extraordinary diversity and their key ecological roles, insects are rarely

included in global assessments due to the poor knowledge of their distribution and the taxonomic/geographical biases of species records (Rocha-Ortega et al., 2021).

Conservation assessments of invertebrate species usually focus on the species level but are sometimes at higher taxonomic rank (Heino & Soininen, 2007). Taxonomy is critical in biodiversity conservation because international agreements, national environmental policies and conservation organisations rely on the assumption that species are both fixed entities and identified correctly (Garnett & Christidis, 2017; Thomson et al., 2018). However, insect systematics still represents a major challenge for conservationists, as many insect groups are poorly studied (Braby & Williams, 2016; Srivathsan et al., 2023). In fact, only 8% of the globally described insect fauna has been assessed under the criteria of the International Union for Nature Conservation (IUCN, 2022). Further, it was shown that insects listed in international conservation agreements such as the Bern Convention and the Habitats Directive, are often better known, larger and widespread (Leandro et al., 2017).

In a recent study, Chowdhury et al. (2023) estimated that a large percentage of insect species are likely inadequately represented within global protected areas. Furthermore, protected areas design and management rarely focus on insects. In the present context of wildlife decline, the use of rapid and automatized methods to identify potentially relevant areas for conservation can accelerate the inclusion of many species, which are normally left out of processes such as the identification of Key Biodiversity Areas (KBAs) (Nania et al., 2023). Such methods could also be combined with other automatized approaches. For instance, species identification from large samples of malaise traps (Wührl et al., 2022), can provide an additional layer of information on the distribution of insect taxa and consequently leading to more effective conservation planning. The KBA approach aims at identifying sites that, if protected, can preserve the biodiversity hosted within them. KBAs are identified through the application of standard criteria (IUCN, 2016). Currently, with regard to identified KBAs worldwide, only 6% of KBA trigger species are invertebrates, for which KBAs are identified only under criteria A1, B1 and B2 (https://www.keybiodiversityareas.org/kba-data). A detailed description of these criteria is provided below. This evidence reveals an important gap of knowledge on the distribution of insect KBAs. KBA assessments for insect species are key to fill this gap.

This study is the first attempt to systematically apply KBA criteria to multiple insect species over a defined geographic region. We applied selected KBA criteria (A1, B1, B2 and B3, detailed in the Materials and Methods section) to 28 European bumblebees (genus *Bombus* Latreille, Hymenoptera: Apidae) following the methodology presented in Nania et al. (2023). Although KBA criteria are supposed to be applied at least to the species rank if genetic data are unavailable, we also selected subspecies with high geographic isolation and distinct morphological features (Biella et al., 2017; Cappellari et al., 2018; Dellicour et al., 2012; Intoppa et al., 2009; Martinet et al., 2018; Rasmont et al., 2021), which represent putative separate evolving biological units of conservation interest. We assessed the presence of potential KBAs in Italy based on estimates of the global population size of each taxon inferred through the use of area of habitat (AOH) maps. We provided high-resolution AOH maps for all 28 species/subspecies analysed. Additionally, we estimated the percentage of identified potential KBAs that are already found in protected land within the administrative boundaries of Italy. Finally, we address issues in the application of KBA criteria to insect taxa and suggest possible improvements of the global KBA standards to enable them to account for the complex biology and data availability of such organisms.

MATERIALS AND METHODS

Distribution maps

We retrieved occurrence points for 28 *Bombus* species/subspecies (Table 1) from the Atlas of European bees (Rasmont et al., 2015). The species are endemic/subendemic of the European continent and their global distribution can be estimated using data from Rasmont et al. (2015), this information is crucial for the construction of AOH maps and for KBA assessments (IUCN, 2016). We did not filter occurrence points based on the date of record. Although including very old records may not represent the current distribution of the species in the most accurate way, proving the extinction of a species in a locality is not easy. The fact that a species is not recorded in recent years may depend on a lack of sampling as well as on other biological factors. As the methodology applied in this study represents the first step of the KBA identification process (IUCN, 2016), a more conservative approach is preferable. The second step, the KBA delineation process, will define the distribution of true KBAs. The atlas provides species distribution data in the form of centroids, but the original occurrence points are available upon request to the authors. Most records hold georeferenced coordinate data, although for 50% of species the occurrence data of specific geographic areas (e.g., data from Scandinavia and Britain) is only available in the form of centroid of a grid. Grid size varies but the maximum grid size is 50×50 km. For this reason, it would have been meaningless to derive a distribution range following the mapping standard procedure provided by the IUCN Red List guidelines (IUCN Standards and Petitions Committee, 2022). In order to derive a distribution range for each species from its occurrence points, we used the freely accessible map 'Admin-1 State and provinces' of the Natural Earth database (nauralearthdata.com). The map contains data on internal first-order administrative boundaries worldwide, with a resolution of 1:10 m. In order to draw the boundaries of each species' geographical distribution, we performed an intersection between the species occurrence points and the administrative boundaries map. We then retained only the regions of the map intersected by the species occurrence points (Figure 1). As for some species, the accuracy of data in certain areas of their distribution is 2500 km^2 (50×50 km), and we also retained administrative areas that were surrounded by areas touching occurrences and were ≤2500 km^2, in order to avoid biases in our estimated species distributions.

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TABLE 1 A list of the species and subspecies included in this study.

Species	IUCN status	Model performance	Triggered KBA criteria
Bombus alpinus helleri Dalla Torre 1882	VU	Positive	
Bombus argillaceus (Scopoli, 1763)	LC	Positive	
Bombus barbutellus (Kirby, 1802)	LC	Positive	
Bombus bohemicus Seidl, 1838	DD	Positive	
Bombus brodmannicus delmasi (Tkalců, 1973)	EN		A1
Bombus campestris (Panzer, 1801)	LC	Positive	
Bombus cryptarum (Fabricius, 1775)	LC	Positive	
Bombus flavidus Eversmann, 1852	LC	Positive	
Bombus gerstaeckeri Morawitz, 1882	VU	Positive	
Bombus inexspectatus (Tkalcu, 1963)	EN	Positive	
Bombus konradini Reinig, 1965	EN	Positive	A1, B1
Bombus lapidarius (Linnaeus, 1758)	LC	Positive	
Bombus lucorum aritzoensis Krüger, 1951	DD	Negative	B1
Bombus mendax Gerstaecker 1869	LC	Positive	
Bombus mesomelas Gerstaecker, 1869	LC	Positive	
Bombus monticola alpestris Vogt, 1909	DD	Positive	
Bombus monticola mathildis Martinet, Cornalba & Rasmont 2016	DD		B1
Bombus mucidus Gerstaecker, 1869	NT	Positive	
Bombus norvegicus Sparre Schneider, 1918	LC	Negative	
Bombus pratorum (Linnaeus, 1761)	LC	Positive	
Bombus pyrenaeus Pérez, 1880	LC	Positive	
Bombus quadricolor (Lepeletier, 1832)	LC	Positive	
Bombus ruderatus (Fabricius, 1775)	LC	Positive	
Bombus rupestris (Fabricius, 1793)	LC	Positive	
Bombus subterraneus (Linnaeus 1758)	LC	Positive	
Bombus sylvestris (Lepeletier, 1832)	LC	Positive	
Bombus vestalis (Geoffroi in Fourcroy, 1785)	LC	Positive	
Bombus wurflenii Radoszkowski, 1860	LC	Positive	

Note: Species concepts refer to Rasmont et al. (2021). The IUCN Red List status is provided, as well as the outcome of the model performance evaluation and the KBA criteria, which were triggered by the species.

The range maps derived from the intersection of species occurrence points and the administrative map here are considered an intermediate step to produce the AOH maps. The produced range maps can include areas where the species is not found. This is due to the fact that even if a single species record falls within a large administrative region, the whole region is retained as part of the range of the species. However, when species' habitat requirements are applied to map the available habitat within the range, these areas are significantly reduced. For instance, the subspecies *Bombus alpinus helleri* only occurs within a specific elevation range on the Alpine arch. The occurrence points of this species crossed the lower region of Bayern, which extends far north from the Alps, thus the whole region was included in the range of the species. However, when the habitat of the species was mapped according to its environmental requirements, including its elevation range, the excess area was lost completely. A scheme illustrating this process is available in Appendix S1.

Area of habitat maps

Following the procedure adopted by Nania et al. (2022), we increased the information accuracy on the global distribution of the species by producing high-resolution AOH maps for all 28 species/subspecies. AOH maps show the habitat available to a species within its distribution range; they can be produced by combining the distribution range with a land cover map and altitude data (Rondinini et al., 2011). In order to generate the AOH maps, we linked the species to their habitat using the CGLS-LC100 Copernicus Land Cover map categories as habitat surrogates. The CGLS-LC100 map was produced by the EU Earth observation program and can be accessed through the dedicated portal (Buchhorn et al., 2019; Buchhorn et al., 2020). Information about habitat preference and altitude limits of the species were retrieved from unpublished records from the Zoological Museum of the University of Rome, identified using Bumblekeys (Cappellari
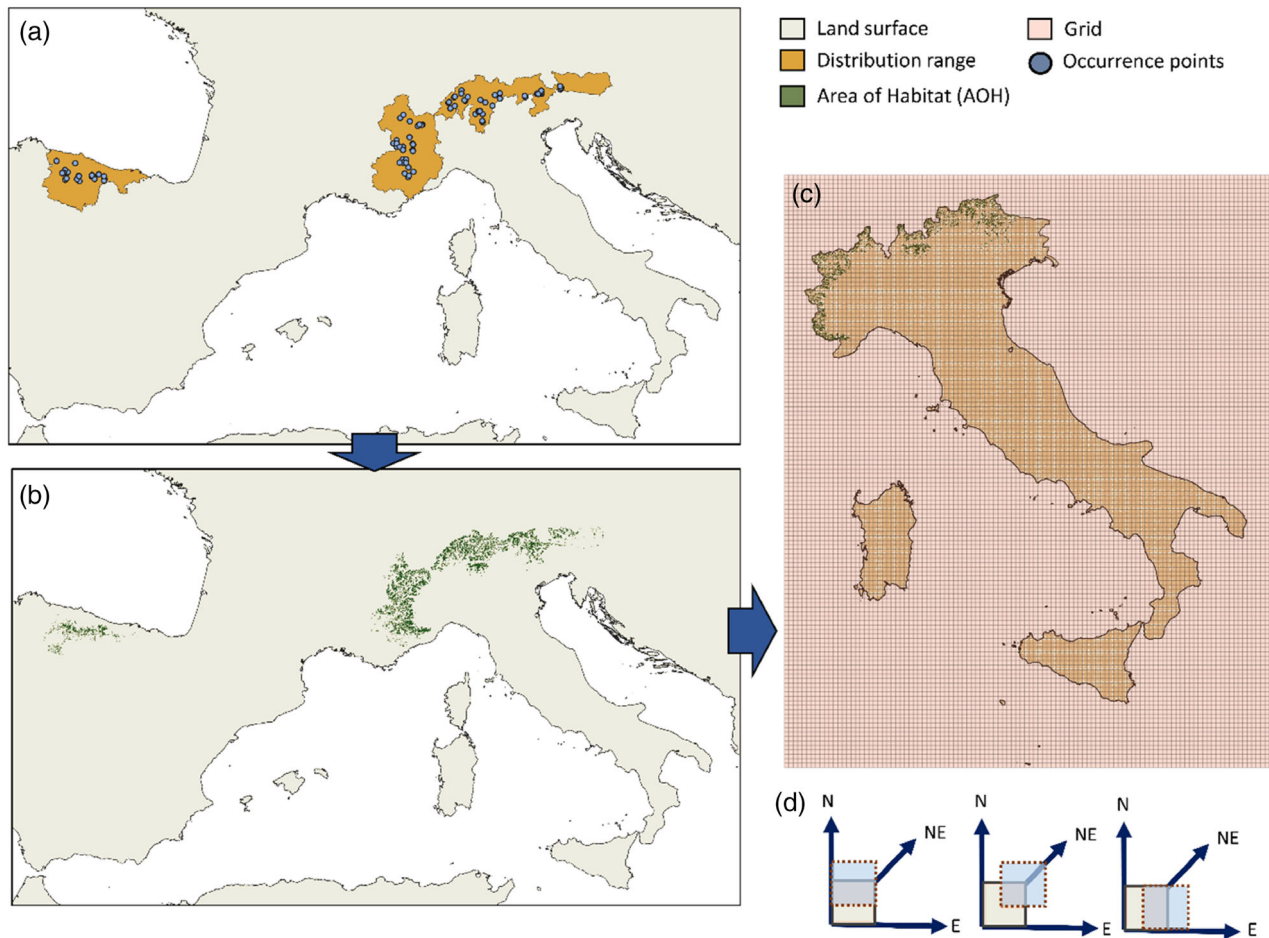
FIGURE 1 Explanatory scheme of the methodology. (a) Species occurrence points are used to delineate the range of the species. (b) The Area of Habitat map is produced by mapping the species' habitat within its distribution range. (c) A grid is positioned on the AOH map to detect potential KBAs and moved to three additional positions. The non-stationary position of the grid lowers the risk of omitting potential KBAs. (d) A representation of the cell movement in the potential KBA identification process.

et al., 2018), as well as from a monograph on the biology of the species (Rasmont et al., 2021). We selected 15 land-cover categories that are present on the land surface of Italy and compiled species-habitat association by linking the land cover categories to the habitat requirements of the species. Thus, only land-cover categories representing habitat for the species were used to build the AOH maps. Each category received a score of either 1 (if it represents habitat for the species) or 0 (if it does not represent habitat for the species). Altitudinal limits were established for each species, giving a minimum and maximum elevation at which the species can be found in the study area. A table showing which land cover categories were linked to the species habitat is available in Appendix S1. A base map containing both land cover and altitude information was built following the same procedure as Nania et al. (2023) (Figure 1). A detailed description of how the base map was produced is given in Appendix S1. The base map has a resolution of approximately 100 m at the equator, altitude data are derived from the Shuttle Radar Topography Mission (USGS EROS Archive, 2019). Finally, we reclassified the base map according to the species' habitat requirements within their distribution range. To do

this, we masked the base map with the range map of each species, keeping only land cover categories with an assigned score of 1 within the elevation limits where the species occurs. Thus, all land cover categories occurring within the distribution range but not representing habitat for the species were discarded. In order to validate our AOH maps before applying the KBA criteria, we implemented a hypergeometric distribution approach (Dahal et al., 2022), which has already been used to validate AOH maps (Nania et al., 2023). This presence-only based method describes the probability of a species' occurrence point to fall within the AOH of a species, and thus validating the map. To account for potential errors in our occurrence record dataset in the georeferencing process, as well as other imperfections of our data such as resolution limits of the AOH maps, we applied a buffer of 150 m to the occurrence points before the hypergeometric distribution test. We performed the test on the AOH maps only within the national boundaries of Italy, as species-habitat requirements were compiled according to the current knowledge on the biology of the species in Italy. Moreover, we only tested AOH maps of species for which we could retrieve at least five occurrence points in different

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localities within the species' distribution range. A detailed description of how the habitat maps were generated and validated is available in Appendix S1.

Potential KBA identification

We selected four KBA criteria that could be tested using AOH maps as an estimate of the proportion of the species' global population size, according to the global standards (IUCN, 2016). Furthermore, the four criteria were previously tested on Italian reptiles and amphibians with the same methodology (Nania et al., 2023), allowing a meaningful comparison between our results and the potential KBAs for the Italian herpetofauna. The selected criteria are the following: A1 (threatened species), B1 (individual geographically restricted species), B2 (co-occurring geographically restricted species) and B3 (geographically restricted assemblages) (IUCN, 2016; KBA Standards and Appeals Committee of IUCN SSC/WCPA, 2022). Criterion A1 refers to species that have been assessed as threatened in the IUCN Red List of Threatened Species. A site can activate A1 if it holds a significant proportion of the global population size of a threatened species. The significant proportion threshold to trigger A1 is described in the KBA standards, and it depends on the level of threat that the species is globally facing. Criterion B1 refers to species for which a significant proportion of the global population is restricted to a particular site. B1 can be activated for sites that host ≥10% of the global population of a species. Criterion B2 also refers to geographically restricted species; a site can activate B2 if it hosts ≥1% of the global population of at least two geographically restricted species. Criterion B3 can be activated if a site hosts ≥5 species that are restricted to a particular ecoregion or 10% of the species restricted to the ecoregion (IUCN, 2016; KBA Standards and Appeals Committee of IUCN SSC/WCPA, 2022).

To identify potential KBAs under the selected criteria in Italy, we produced a 10 × 10 km cell sized grid that entirely covered its administrative boundaries. This cell size was previously used to detect potential KBAs for reptiles and amphibians in Italy and was suggested to be more efficient than larger cells for this purpose (Nania et al., 2023). We then followed the procedure adopted in Nania et al. (2023) to scan the geographic surface and identify potential KBAs. Land surface scanning was performed once for each species habitat map. The grid captured the extent of species' AOH that was present within each cell. In addition to its initial position, the grid was moved by 5 km (half the size of a grid cell) along three axes: north, east and north-east. This was done in order to prevent the grid from missing potential KBAs due to its fixed position (Figure 1). The choice of how to move the grid on the map is arbitrary. This approach allows us to generate four different scans per species map, ensuring a reliable coverage of potential KBAs on the map while keeping the computational costs low. Subsequently, all cells holding a sufficient portion of the habitat global extent and, thus, able to meet the threshold of at least one of the selected KBA criteria were retained. Finally, for the species that did trigger the KBA criteria, we extracted the portion of their AOH map enclosed within the cells that met the KBA criteria threshold, regardless of the position of the grid. This last step allowed us to produce high-resolution potential KBA maps for each one of the tested criteria.

Species/subspecies for which an official IUCN Red List global or European assessment is lacking cannot be considered for the application of A1 (threatened species), as stated in the global standards (IUCN, 2016). In our case, A1 could potentially be triggered by three species, as they are currently assessed as threatened in the IUCN Red List (Table 1). However, we also included two subspecies while testing for A1: *B. alpinus helleni* and *B. brodmannicus delmasi*.

While the three species were assessed as being threatened to some degree by the IUCN Red List of Threatened Species (IUCN, 2022; Quaranta et al., 2018), the two subspecies have not been assessed. However, *B. alpinus* and *B. brodmannicus* are both listed as threatened species at either global or European level (Table 1). Thus, we assigned the same status to the subspecies as well, as the level of threat must necessarily be the same at the very least. The application of criterion B3 requires a measurement of the percentage of global population confined to single ecoregions to define assemblages (IUCN, 2016). For this purpose, we used the WWF Palaearctic Terrestrial Ecoregion map, which is freely available at the WWF portal (https://www.worldwildlife.org/publications/terrestrial-ecoregions-of-the-world, accessed on 4th June 2021).

Potential KBAs and other important sites for biodiversity

A measure of nesting was performed between the potential KBA map produced in this study using the selected criteria, and the following maps:

- National protected areas of Italy
- Natura 2000 network in Italy
- Current KBA network in Italy
- The new potential KBA for Reptiles and Amphibians in Italy (Nania et al., 2023)

The map of national protected areas was obtained from Federparchi (Italian federation for natural parks and reserves) and is available upon request, while the Natura 2000 map was retrieved from the European Environment Agency (EEA, 2021). Maps of the current KBA network within the boundaries of Italy are available from the Global Key Biodiversity Areas database upon request (https://www.keybiodiversityareas.org/kba-data/request). Currently, 99.1% of accepted KBAs in Italy are identified for avian species, no KBA was identified for insects (https://www.keybiodiversityareas.org/kba-data). The potential KBA map for Italian reptiles and amphibians was taken from Nania et al. (2023). To test the percentage of nesting between potential KBAs for different taxa, we only considered potential KBAs that were identified using cells of the same size as was adopted in this study (10 × 10 km).

RESULTS

Italian bumblebees AOH maps

We produced 28 high-resolution global AOH maps for 23 species and 5 subspecies of bumblebees occurring in Italy (Table 1). The mean extent of habitat cover within the species ranges among the validated maps is 16.4%. Maximum percentage of coverage is reached by *B. ruderatus* with available habitat covering 62.3% of its range. The lowest percentage is reached by the parasitic *B. quadricolor*, for which habitat availability corresponds to 0.09% of its range. The hypergeometric test revealed that 24 of 26 tested maps (92.3%) had a positive performance and were evaluated as being significantly better than expected from a random distribution model. Two maps were not better than expected under randomness (*B. norvegicus* and *B. lucorum aritzoensis*); however, for these two species, we had the lowest number of occurrence points, respectively, five and nine. For the rest of the tested species, the available number of occurrence points was substantially higher (Appendix S1). A detailed description of the hypergeometric distribution test is available in Appendix S1. All maps are available on the DRYAD repository: https://doi.org/10.5061/dryad.stqjq2c82.

Potential KBAs for Italian bumblebees

Of the four selected criteria, only two were triggered by at least one species (A1 and B1).

We identified potential KBAs for *B. konradini* and *B. brodmannicus delmasi* under criterion A1. One species and two subspecies were able to trigger potential KBAs under criterion B1: *B. konradini*, *B. monticola mathildis* and *B. lucorum aritzoensis*. All three of them are endemic to Italy. The total area covered by the detected potential KBAs is 1845 km^2, corresponding to 0.6% of the total surface of Italy. The majority of the new potential KBAs were identified in central Apennines and western Alps, whereas small patches were found in the island of Sardinia and northern Apennines (Figure 2).

The comparison with Italian protected areas revealed that 34.2% of the potential KBAs found in this study are nested within national protected areas, while 53.6% is included in the Natura 2000 network. With regard to the currently accepted KBAs in Italy, 47.4% of our potential KBAs for *Bombus* species are already included within these sites. Maps showing the distribution of potential KBAs compared with current KBAs, national protected areas and Natura 2000 sites are available in Appendix S1. Finally, only 12.1% of them are nested within areas that were identified as potential KBAs for reptiles and
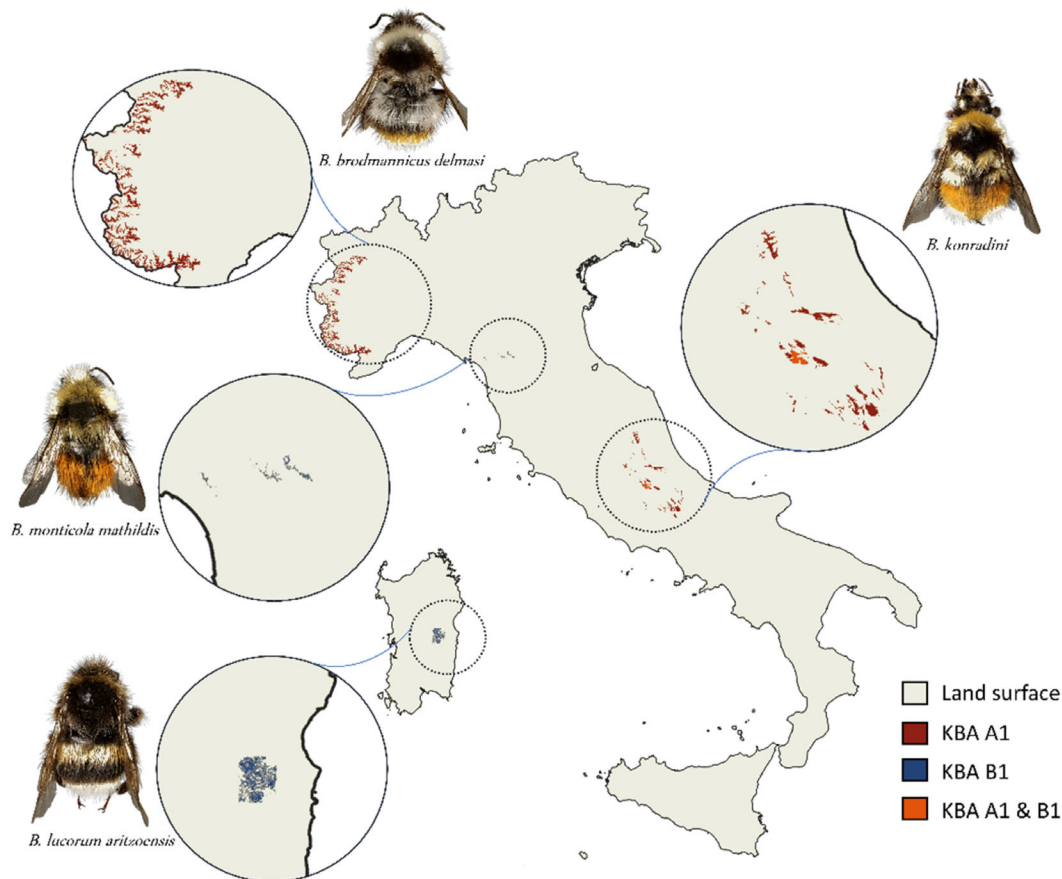

FIGURE 2 Potential KBAs for Italian bumblebees. The map shows the distribution of the potential KBAs, as well as the activated criteria and the species/subspecies that activated the KBAs.

amphibians, following the same methodology (Nania et al., 2023). Potential KBAs of both bumblebees and herpetofauna overlap mostly in the Western Alps, while small areas of overlap are also found in Sardinia.

DISCUSSION

Distribution data

The dataset of occurrence points used in this study was retrieved from what likely is one of the most complete databases revealing the global distribution of an insect group in Europe (Rasmont et al., 2015). However, part of the occurrence extent of the species was determined by centroids of a grid, sometimes as large as 50 × 50 km. This lack of accuracy can result in issues of reliability in the process of determining the true range of a species, especially when the objective is to meticulously map the availability of its habitat. Using coarse resolution range maps could lead to commission errors, taking into consideration areas where the species is thought to be present but is in fact absent (Rondinini et al., 2006; Walter et al., 2008). Thus, like the inclusion of historical records, this may lead to an overestimation of the actual range of the species and consequently its habitat availability. Despite the fact that the use of insect occurrence data has increased over the years and large datasets are becoming available (Diniz-Filho et al., 2010), for most insect species, information of occurrence is scarce and lacking accuracy (Rocha-Ortega et al., 2021). Identifying KBAs requires complete and reliable occurrence data (IUCN, 2016), as well as any macroecological analysis with conservation purpose. This evidence highlights the urgency of assembling and sharing accessible databases on the distribution of insects, as this will facilitate their inclusion in large scale conservation assessments such as the one presented in this study. Nevertheless, producing high-resolution AOH maps instead of using the whole species range proves to be efficient in reducing the total area under examination, as on average the percentage of the entire range covered by habitat was found to be 15.5%.

AOH maps are based on land cover and altitudinal limits (Brooks et al., 2019), but do not take into account the latitudinal gradient. This aspect also might influence the reliability of our maps, as altitudinal limits of the species can vary substantially along the latitude gradient. Here, we aimed at identifying potential KBAs for the species within the geographical boundaries of Italy, and thus, the altitudinal limits were set according to knowledge of the species in Italy. However, the application of KBA criteria requires an estimate of the global population size inferred through the AOH map. For this reason, the AOH maps were built across the global range of the species. Although AOH maps are built through the application of the same species' habitat requirements throughout their range, taking into consideration the variation of altitudinal range across the latitudinal gradient would allow a more reliable assessment of the species' global population.

Potential KBAs

Although we tested four different KBA criteria on our data, we found potential KBAs triggered by only two of them, A1 and B1 (Table 1). These two criteria can only be triggered by a single species, while the remaining two tested criteria (B2 and B3) need to be triggered by a higher number of species (IUCN, 2016). This evidence suggests that criteria based on single species assessments are more likely to be triggered in a multi-criteria analysis such as the one presented in this study. The same trend was observed in a previous study that systematically applied the four criteria to reptiles and amphibians in Italy (Nania et al., 2023).

As shown in our results, potential KBAs were detected for one species and four subspecies (Table 1), all of them endemic to Italy. The subject of whether or not subspecies should be considered valuable biological units in conservation biology, and how, has been discussed extensively over the years (Braby et al., 2012; Haig et al., 2006; Patten, 2015; Phillimore & Owens, 2006). For invertebrates in particular, it has been suggested how subspecies represented by isolated allopatric populations, with a distinct phenotype which is correlated with an evolutionary independence should be evaluated as significant biodiversity units for conservation (Braby et al., 2012; Ghisbain et al., 2021). The global standards for the identification of KBAs allow the detection of KBAs for subspecies solely through an assessment of their distinct genetic diversity (IUCN, 2016; KBA Standards and Appeals Committee of IUCN SSC/WCPA, 2022). Our suggestion in this regard is to allow other aspects that characterise subspecies to play a role in the identification of KBAs, such as geographical isolation, which can promote reproductive isolation and evolutionary divergence (Worsham et al., 2017). This would allow rapid assessments for many subspecies for which genetic data are still missing or not easily accessible, avoiding the loss of important biodiversity units through timely conservation actions. For instance, *B. monticola mathildis* was able to trigger potential KBAs under criterion B1 (individual geographically restricted species) in the northern Apennines (Figure 2). Previous genetic analysis using mitochondrial cytochrome oxidase subunit 1 (COI) suggested that *B. monticola mathildis* is closer to *B. konradini* than to the populations of *B. monticola* in the Alps (Martinet et al., 2018), providing evidence of some degree of isolation and divergence of this population. Including such subspecies in KBA assessments can highlight the fragility of their global population as determined by habitat availability, distinct morphological characters, and isolated and restricted distribution. Ultimately leading to rapid conservation actions if needed.

The only species that triggered both A1 and B1 is *B. konradini* (Figure 2). This species is known to be rare and of particular concern, as it is endemic to a restricted region in the central Apennines and is found almost only above 1800 m of elevation (Rasmont et al., 2021). All of the *B. konradini* habitat mapped in this study was included in potential KBAs in the central Apennines, and it represents the only potential KBAs detected in central Italy for the species tested in this study (Figure 2). This result suggests it is likely that at least part of the

potential KBAs identified for this species could reflect actual KBAs through the proposal process (KBA Standards and Appeals Committee of IUCN SSC/WCPA, 2022). However, we stress that the areas identified through our systematic approach must necessarily be considered as potential KBAs and that the actual KBA area can be smaller and differently shaped.

The nesting analysis revealed that a large portion (65.8%) of the total area found in this study is not included in national protected areas, and almost half of the area (46.4%) is left out of Natura 2000 sites. In this regard, our potential KBAs map highlights areas that are potentially important for the preservation of the species hosted by them, and for which some degree of protection may be needed. The comparison with the current KBA network in Italy suggests that, if the potential KBAs found in this study were to be confirmed, more than 30% of their total extent should be integrated as an addition to Italian KBAs. A similar trend was observed for reptiles and amphibians, for which only 18% of the potential KBAs were already included in the current KBA network (Nania et al., 2023). Moreover, only 12.1% of the potential KBAs for bumblebees were found to be nested within those for reptiles and amphibians using the same methodology. Considering the very limited number of species tested in both studies, respectively, 28 bumblebees and 59 species of reptiles and amphibians (Nania et al., 2023), if the potential new KBAs were found to be actually present, the Italian KBA network would expand significantly across the country's geographic surface. Currently, 99.1% of Italian KBAs are triggered by bird species (https://www.keybiodiversityareas.org/kba-data). It appears that, as more taxa are tested the total KBA area tends to increase. Consequently, if large numbers of both animal and plant species were tested, this phenomenon could lead to geographical over-expansion of the KBA network and a loss of relevance of these areas, as their use to inform conservation and land use planning would become more complicated.

Overall, several issues emerged regarding the implementation of insect taxa for the identification of KBAs through a systematic approach. First, the lack of accuracy of insect georeferenced data and imprecision in delineating a geographic range for the species implies assumptions that can lead to an overestimation (or underestimation) of the actual global population size of a species. We highlight the importance and necessity of assembling large-scale dataset for insect taxa avoiding approximations using low-resolution grids. These dataset should be available upon request for research purposes without loss of the original occurrence data resolution. This would lead to a progressive inclusion of insect taxa in large-scale assessments for conservation purposes as well as to an increase of consideration of such taxa when developing methodologies that serve the purpose of biodiversity conservation. We also discussed the issue of subspecies inclusion in KBA assessments. Running appropriate population genetics analysis to test for distinct genetic diversity as the only way to activate KBAs for subspecies is not a realistic approach. For most taxa, such data are not available or not easily accessible. Insect taxonomy is complex, thus the level of uncertainty of whether or not a subspecies represents an evolutionary independent unit worth of being considered for KBA assessments is high. However, insect populations are declining at a worrying rate (Goulson, 2019; Homburg et al., 2019; Lewinsohn et al., 2022; Wagner et al., 2021), and many relevant subspecies may be lost long before genetic data are finally available. Other factors such as geographic isolation can be used to include insect subspecies in KBA assessments. Finally, the observed tendency of expansion of the KBA network as more species are tested raises questions about the efficiency of the KBA approach in identifying areas that truly are key for biodiversity and not only for a limited subset of it.

AUTHOR CONTRIBUTIONS

Dario Nania: Software; conceptualization; investigation; writing – original draft; validation; methodology; data curation; formal analysis. **Maurizio Mei:** Conceptualization; data curation; investigation. **Michela Pacifici:** Writing – review and editing; methodology; visualization. **Carlo Rondinini:** Methodology; conceptualization. **Alessio De Biase:** Writing – review and editing. **Denis Michez:** Data curation. **Pierfilippo Cerretti:** Supervision; conceptualization; data curation; writing – review and editing; investigation.

CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are openly available in DRYAD at https://doi.org/10.5061/dryad.stqjq2c82.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

Appendix S1. Supporting Information.

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