



MINI REVIEW

Assessing the reliability of biodiversity databases: identifying evenly inventoried island parasitoid faunas (Hymenoptera: Ichneumonoidea) worldwide

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Abstract. 1. Taxonomic and geographic biases are common in biodiversity inventories, especially in hyperdiverse taxa, such as the Ichneumonoidea. Despite these problems, biodiversity databases could be a valuable source of information if their reliability is carefully assessed.

2. One major problem of using these data for large-scale analyses is the unevenness of data quality from different areas, which makes them difficult to compare. One way of surpassing such problem would be to identify sets of areas that are evenly inventoried.

3. Here, we propose a scoring protocol for the identification of sets of evenly inventoried areas from taxonomic databases, based on three criteria: (i) completeness at high taxonomic levels, (ii) congruence with well-established ecological relationships (such as species–area relationship), and (iii) publication effort received. We apply this protocol to the selection of a set of evenly inventoried islands worldwide for two Ichneumonoidea families (Braconidae and Ichneumonidae) from the data gathered in Taxapad database.

4. From the 118 islands included in Taxapad, 53 and 70 can be considered sufficiently inventoried for Braconidae and Ichneumonidae, respectively. The publication effort criterion was more restrictive than the other two criteria. The Indomalayan, Nearctic and Palearctic regions had more than half of their islands identified as evenly inventoried, for both families.

5. We discuss the generality of the biases and incompleteness of most biodiversity data, and also how the basic principles of the protocol proposed here can be applied to taxonomic databases devoted to other taxa. Also, the islands identified here can serve as the basis for large-scale analyses of the poorly known biogeography of the Ichneumonoidea.

Key words. Biodiversity databases, biogeography, Braconidae, Ichneumonidae, islands, sampling effort, species–area relationship, survey biases, taxonomic inventories.

Introduction

The number of studies on large-scale diversity patterns has rapidly increased in the last two decades, in part due to the compilation of extensive databases on the distribution of biodiversity (herein, biodiversity databases) and, lately, due to

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the development of biodiversity information networks, such as the Global Biodiversity Information Facility (GBIF, <http://www.gbif.org/>) (see, e.g. Soberón & Peterson, 2004; Guralnick *et al.*, 2007). Although there are numerous approaches to the creation of biodiversity databases, most of them aim to gather the scattered information available from museums and herbaria, private collections and the literature. Thus, in practice, these databases include data from a heterogeneous range of different inventories, which have been developed either with or without standardised surveys, and with varying amounts of effort (e.g. Soberón *et al.*, 1996, 2000; Hortal *et al.*, 2007).

It is well known that our knowledge of the geographical distribution of biodiversity is, in general, taxonomically and geographically biased (the so-called Linnaean and Wallacean Shortfalls; Brown & Lomolino, 1998; Lomolino, 2004; Whittaker *et al.*, 2005). If these shortfalls have a direct effect on the data included in the databases, then the description of biodiversity patterns will be compromised (Prendergast *et al.*, 1993; Stockwell & Peterson, 2002; Hortal *et al.*, 2007). Unfortunately, distributional data of outstanding quality (e.g. some of the data available for the British Isles; Griffiths *et al.*, 1999) are the exception and not the rule. Rather, the information gathered in biodiversity databases is usually biased, scarce or otherwise of poor quality (see Hortal *et al.*, 2007, 2008; Lobo *et al.*, 2007; D. Rocchini, J. Hortal, S. Lengyel, J.M. Lobo, A. Jiménez-Valverde, C. Ricotta, G. Bacaro & A. Chiarucci, unpubl., and references therein).

Although limited data quality can affect all taxa, these problems are paramount for hyperdiverse groups, such as insects (see, e.g. Gaston, 1994; Godfray *et al.*, 1999; Martín-Piera & Lobo, 2000; Baselga *et al.*, 2010). This is certainly the case in the Ichneumonoidea (Hymenoptera), a superfamily that includes two of the largest families of Hymenoptera, the Braconidae and the Ichneumonidae. These families mainly include parasitoid species that develop as larvae by feeding on or in the bodies of other arthropods, usually killing their host (Godfray, 1994; Quicke, 1997). Although approximately 17 000 braconid species and 23 000 ichneumonid species have been described so far (Yu *et al.*, 2005), these two families are still taxonomically poorly known (Quicke, 1997). Recent estimates suggest that less than one-half of the total number of species of braconids and ichneumonids have been formally described (Dolphin & Quicke, 2001; Jones *et al.*, 2009). Furthermore, taxonomical work on these families is biased against the description of tropical and small bodied species (Gaston, 1993; Jones *et al.*, 2009). These biases result in an uneven description of the parasitoid faunas in different regions of the world; while the faunas of some areas are poorly known (i.e. underdescription due to poor sampling), others are so extensively studied that they cannot be readily compared with most of the less well-inventoried areas (i.e. taxonomic inflation or overdescription; see, e.g. Lobo & Martín-Piera, 2002).

Despite their collection biases and lack of completeness, natural history collections and taxonomic works are a highly valuable resource, often providing the only essential biological information for ecological, conservation and biogeographical studies. Databases compiling data from these sources contain massive amounts of distributional information gathered over

decades or even centuries of survey work. Discarding such information because of perceived quality data issues would mean failing to take advantage of the work of several generations of naturalists. Instead, an assessment of the data quality of biodiversity databases could bridge the gap between the need for data on the distribution of biodiversity and limited investment in taxonomic and inventory work (Soberón *et al.*, 2000, 2007; Hortal *et al.*, 2007, 2008; Lobo, 2008). Where these databases provide exhaustive data on the distributional information gathered from field records and natural history collections, comprehensive sampling effort assessments can indicate which areas have been surveyed sufficiently well for their inventories to be reliable (e.g. Garcillán *et al.*, 2003; Hortal & Lobo, 2005). However, many biodiversity databases only include partial compilations of survey effort (see Hortal *et al.*, 2007), or are reduced to the output of these efforts, the inventories of particular areas (i.e. checklists). This is the case for a particular type of biodiversity databases, those that compile the information that has traditionally featured in taxonomic monographs, henceforth termed taxonomic databases. Like monographs, taxonomic databases are usually based on extensive revisionary work (i.e. beta taxonomy; see Baselga *et al.*, 2010). Despite being taxonomically exhaustive, taxonomic databases lack comprehensive information on survey effort, making it difficult to determine which territories have reliable species inventories.

In this paper, we develop a protocol for the identification of evenly inventoried areas from taxonomic databases. We describe the practical application of this conceptual protocol to determine, as an example, the islands that host comparable (but not necessarily well sampled) Braconidae and Ichneumonidae inventories, based on a database on the taxonomy and worldwide distribution of Ichneumonoidea (Yu *et al.*, 2005). The method we propose is a simple scoring protocol based on three criteria: (i) the completeness of the inventory of higher taxa (subfamily level); (ii) congruence with a realistic species–area relationship (SAR); and (iii) an indirect measurement of survey effort (measured as the number of published pages). Although we apply this protocol to the diversity of parasitoids on islands, we discuss the potential advantages and limitations of the application of these three criteria in other areas. Our goal is to provide the basis for similar assessments of other taxonomic databases, which will eventually help workers to use the taxonomic and distributional information stored within them, while minimising problems caused by variable data quality.

Data and methods

Data on Braconidae and Ichneumonidae species distribution on islands worldwide were obtained from Taxapad (Yu *et al.*, 2005). Taxapad is an interactive digital catalogue that includes information from all literature published on these two families until 2004 (see <http://www.taxapad.com/> for more information). The distribution of island species in Taxapad is organised by archipelagos, single island nations or other administrative units. Given that archipelagos usually follow the same SAR as their constituent islands (Santos *et al.*, 2010), both archipelagos and islands were considered to be comparable units. Thus, we used

both types of data together in our analyses, referring them all as *islands* for simplicity. In addition, islands or archipelagos that are divided into political subregions and that are not true islands (e.g. Haiti and Dominican Republic, Brunei, Indonesia and Malaysia, and Papua New Guinea and Indonesia), were combined to give single data points, by considering the species list and island area as the sum of those of the territories included in the island (e.g. Hispaniola, Borneo, New Guinea). Introduced species, subspecies and synonyms were excluded.

Up-to-date data on the area and location of all islands were obtained from several sources, including the UNEP Island Directory (<http://islands.unep.ch/isldir.htm>), Wikipedia (<http://en.wikipedia.org/>), GPS visualizer (<http://www.gpsvisualizer.com/geocode>) and a number of literature sources (e.g. Heaney, 1978, 1986; Lawlor, 1986; Juste & Perez del Val, 1995; Millien-Parra & Jaeger, 1999; Michaux *et al.*, 2002; Borges & Wunderlich, 2008; for more details see Appendices S1 and S2). The total land area of archipelagos was defined as the sum of the areas of their constituent islands.

Determining which island inventories are relatively complete using commonly used methodologies such as collector's curves (e.g. Hortal & Lobo, 2005) is not possible due to the lack of information on sampling effort in Taxapad. However, we argue that these data can still be used to identify those islands which harbour sufficiently reliable (and thus comparable) inventories according to three criteria: (i) completeness at higher taxonomic levels; (ii) congruence with the SAR (i.e. which islands follow a realistic SAR); and (iii) publication effort (i.e. the amount of published information). Although some of the islands might not have complete or nearly complete checklists, we assume that their observed inventories will be sufficiently complete when most or all the former criteria are met.

Criterion 1: completeness at higher taxonomic levels

Two obvious characteristics of sufficiently inventoried areas are that at least some species from most higher level taxa that are present have been recorded, and that there is no obvious bias towards recording (or not recording) any particular higher taxa. This could be assessed by determining whether the inventories include a realistic range of higher taxa. We selected subfamilies as the adequate higher level taxon because they have broad geographic distributions and are thus present on many islands. Tribe was not used because not every Ichneumonoidea species recorded in Taxapad have been assigned to this taxonomic level. We also dismissed genera because, for the Ichneumonoidea, their distributions are often geographically restricted.

Given that the number of subfamilies that are present on each island is unknown, we require an indicator of the completeness of the inventory at higher taxonomic levels that does not involve knowing their true number. So, we opted to determine if the islands host a realistic number of the most geographically widespread subfamilies within each biogeographic region. We first identified the most ubiquitous subfamilies on the islands of each biogeographic region (as defined by Moss & Wilson, 1998 and Cox, 2001), by counting the islands where each subfamily was found. Subfamilies in the upper quartiles of this distribution

were considered widespread, and hence likely to be present in most island faunas. In a second step, we identified the minimum number of subfamilies that an inventory should host to be considered potentially reliable. We plotted the accumulated number of islands in relation to the number of widespread subfamilies that were recorded there. This plot includes information from two kinds of islands; those where the observed number of subfamilies is underestimated as a direct consequence of the lack of survey effort, and those where the number recorded accurately reflects the real number of existent subfamilies (Fig. 1). It seems logical to assume that the number of poorly inventoried islands that host progressively more widespread subfamilies decreases steeply, and that this relationship is substantially shallower in well-inventoried islands. Hence, the slope of the plot of accumulated number of widespread subfamilies will show a significant change (i.e. an inflection point). We thus selected the threshold from which the effect of undersampling on the number of widespread subfamilies would be negligible as the point at which this distribution curve changes its slope (see Fig. 1). This point can be identified visually as the last point on this relationship where the number of subfamilies stops decreasing steeply. Islands with a total number of widespread subfamilies equal or higher than this value were considered to fulfil this criterion.

Criterion 2: congruence with established SAR patterns

The departure of the observed richness values from well-established ecological and/or inventory effort models can be used to determine which inventories might be reliable (e.g. Hortal *et al.*, 2001, 2007; Lobo & Martin-Piera, 2002; Garcillán *et al.*, 2003; Soberón *et al.*, 2007). The increase in species richness with increasing area (i.e. SAR) is one of the most studied patterns in ecology (Schoener, 1976; Rosenzweig, 1995, 2003; Lawton, 1996, 1999). Its generality makes it appropriate to

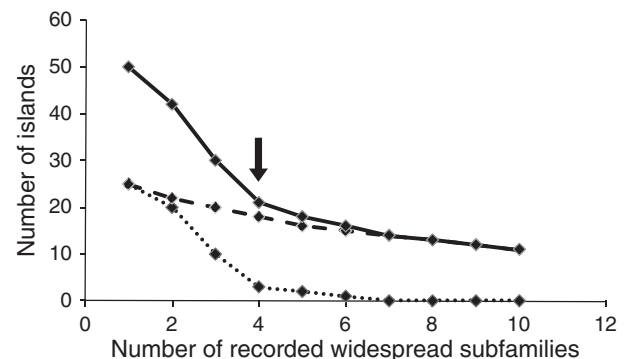


Fig. 1. The hypothetical relationship between the number of widespread subfamilies and the accumulated number of islands where these subfamilies can be found. The dotted line represents the hypothetical case of all islands being poorly inventoried, whereas the dashed line represents only well-inventoried islands. The unbroken line depicts a case where both poorly- and well-inventoried islands are present. The arrow indicates the threshold value that establishes the number of widespread subfamilies that the inventory of a well-studied island should include.

identify areas with abnormally low-recorded numbers of species (see Garcillán *et al.*, 2003).

The slopes of the SAR for islands within archipelagos (herein, ISAR) are usually between 0.25 and 0.35, although values between 0.2 and 0.45 are not uncommon (see reviews in, e.g. Rosenzweig, 1995; Whittaker & Fernández-Palacios, 2007). However, the slopes of the ISARs vary depending on the dispersal abilities and life histories of each particular group (e.g. Ricklefs & Lovette, 1999). ISARs recently reported for parasitoid faunas show slopes ranging from 0.3 to 0.6 (see Table 1 in Santos *et al.*, 2010). Based on these results and the review by Rosenzweig (1995), we assumed that the inventory from any island with a SAR ratio (log species richness/log island area) lower than 0.2 is evidently incomplete and does not pass this criterion. Given that the range of ISAR slopes reported in the literature has also an upper limit, we also used SAR ratios to identify which islands might have been so intensively inventoried that could be unsuitable for comparison with the rest of the studied areas (i.e. oversampled *sensu* Lobo & Martín-Piera, 2002). All islands with a SAR ratio greater than 0.65 were thus regarded as being potentially oversampled.

Criterion 3: publication effort

Detailed descriptions of the sampling effort, including direct (e.g. number of traps or field days) and indirect measures (e.g. accumulated number of records or captured specimens) are often used to determine the completeness of inventories (see, e.g. Garcillán *et al.*, 2003; Hortal & Lobo, 2005; Lobo, 2008). Like most taxonomic databases, Taxapad does not include information on the number of times each species has been recorded. A proxy measure for sampling effort could be the number of taxonomic publications devoted to the inventory of each area, under the assumption that it is correlated with sampling effort. We evaluated the capacity of the total number of pages of the publications to represent the sampling effort devoted to each island. We represented this measure against species richness in a log–log plot to identify whether the rate of accumulation of new species in the inventory with additional published pages shows a decreasing trend, similar to species accumulation curves (Soberón & Llorente, 1993; Hortal & Lobo, 2005). When the accumulation of new published pages does not relate with an increase in the number of species inventoried, we will assume that the completeness of the inventory is high (see Hortal *et al.*, 2007). To avoid the spurious effects due to the disparity in size of the islands, we standardised all variables by area. We chose not to use the number of publications alone because short notes would contribute just as much as detailed monographs, thereby inflating the effort estimates. In contrast, using the number of pages provides a natural weighting in favour of more exhaustive works.

Categorisation of inventories according to different criteria

Islands were assigned a score of 0, 1, 2 or 3, depending on how many of the aforementioned criteria were fulfilled. Islands

that passed all criteria were given the maximum score of 3. Similarly, islands that fulfilled any two, only one or none of the criteria were given scores of 2, 1 or 0, respectively. Only islands assigned with the two highest scores (2 and 3) were considered to be evenly inventoried, and therefore suitable for future large-scale analyses of their parasitoid faunas. Data from islands with lower scores (1) could be suitable for these analyses too, but should be discarded if they appear as outliers. Islands with a score of zero should be discarded from any future analyses.

All analyses were carried out using Statistica version 6.1 (StatSoft, Inc., 2001). Maps were drawn using IDRISI Kilimanjaro GIS software (Clark Labs, 2004).

Results

Braconidae

Of the 118 islands represented in Taxapad, 105 include records of braconid species. A total of 41 subfamilies and 5255 species have been recorded for these islands. The number of common subfamilies used in the first criterion varied according to the biogeographic region, ranging from eight in both Indomalaya and the Neotropics, to 11 in the Palearctic, with the Agathidinae, Cheloninae and Microgastrinae being the only widespread subfamilies present in every biogeographic region. The threshold used in Criterion 1 to establish the minimum number of common subfamilies that a sufficiently inventoried island should include in each region ranged from three to eight (see Figs. 2c and 2f). In total, 48 islands fulfilled this criterion: 3 from the Afrotropics (30% of all islands in this region), 8 from Australasia (30%), 13 from Indomalaya (62%), 2 from the Nearctic (67%), 8 from the Neotropics (33%) and 14 from the Palearctic (70%).

Regarding the second criterion, 14 out of the 105 islands were excluded *a priori* because only one species was recorded from them. From the rest, 18 had a SAR ratio lower than the threshold of 0.2 (dashed line in Fig. 3a) and 4 (Bermuda, Grenada, Saint Vincent and Singapore) higher than the upper threshold of 0.65 (dotted line in Fig. 3a), leaving 69 that were neither insufficiently inventoried, nor oversampled. The number of published pages was highly positively correlated with the number of species inventoried (Spearman $R = 0.91$, $P < 0.001$). However, the plots show no consistent pattern of decrease in the rate of accumulation of new species with new published pages, except for a small number of islands (Fig. 4a). Only 13 islands complied with the publication effort criterion (see Appendix S1).

After applying the three criteria only 53 islands (50% of the islands with records of braconid species) were scored with the two highest levels (Fig. 5a) (see Appendix S1). While the Indomalayan, Nearctic and Palearctic regions had more than half of their islands scored with one of these two high levels (62%, 67% and 70%, respectively), the other three regions only had around 40% of their islands ranked within these levels. Twenty-two islands were scored as level 1, and 30 failed to pass any of the criteria (Fig. 5a; see also Appendix S1).

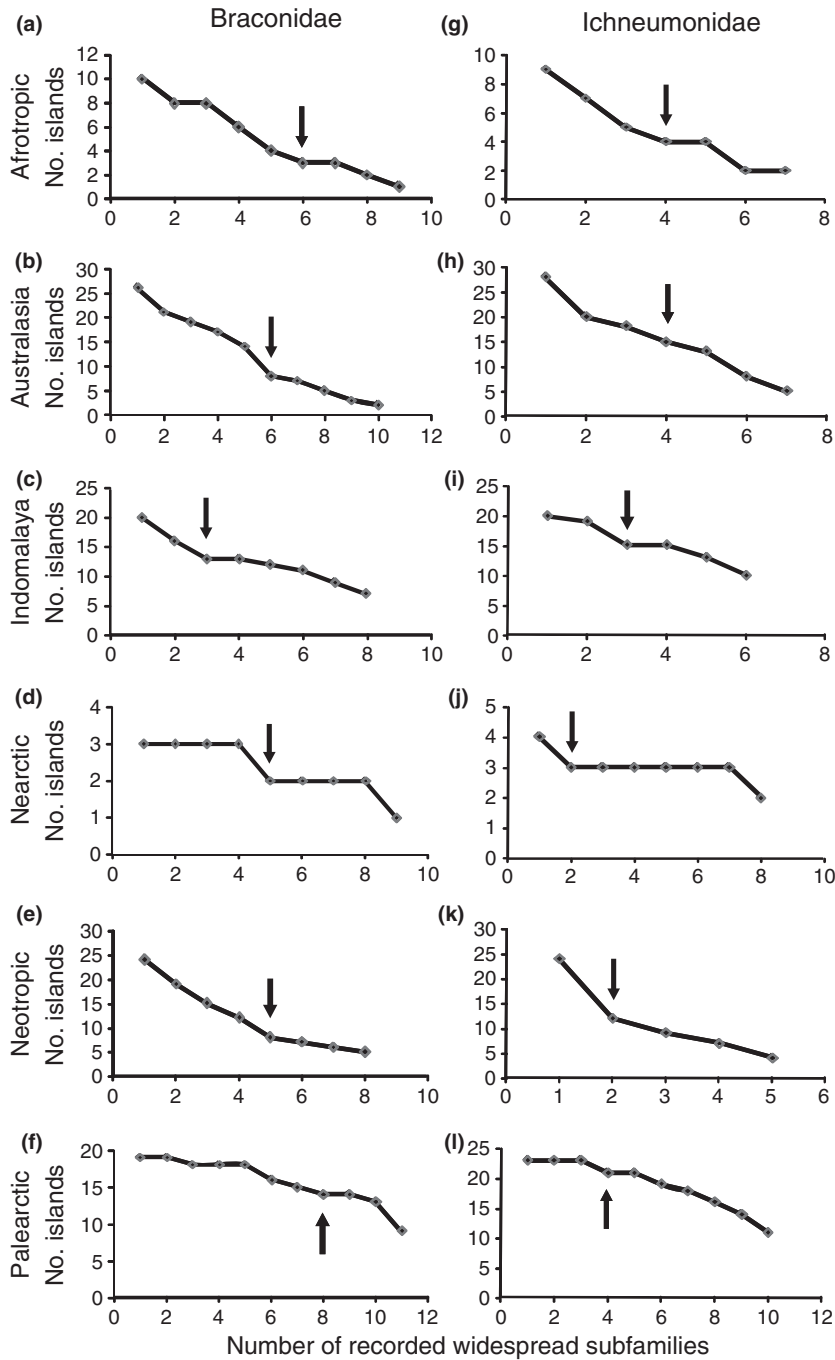


Fig. 2. The number of widespread subfamilies per accumulated number of islands. The arrow indicates the threshold value used to establish the minimum number of widespread subfamilies an island should harbour to pass the completeness at higher taxonomic levels criterion.

Ichneumonidae

One hundred and ten islands have records of ichneumonids, comprising 36 subfamilies and 7406 species. The number of widespread subfamilies in each biogeographic region ranged from 5 (in the Neotropics) to 10 (in the Palearctic) and Campopleginae and Pimplinae were the only subfamilies present in every biogeographic region. Figures 2g and 2l show the decline

in the number of islands that host progressively more widespread subfamilies. The thresholds identified here to determine the minimum number of widespread subfamilies that an evenly inventoried island should include varied from two to four. However, the threshold was not always easily established, because the slope of the relationship between the number of accumulated widespread subfamilies and the number of islands did not always reach an evident plateau (e.g. for Australasia and Pale-

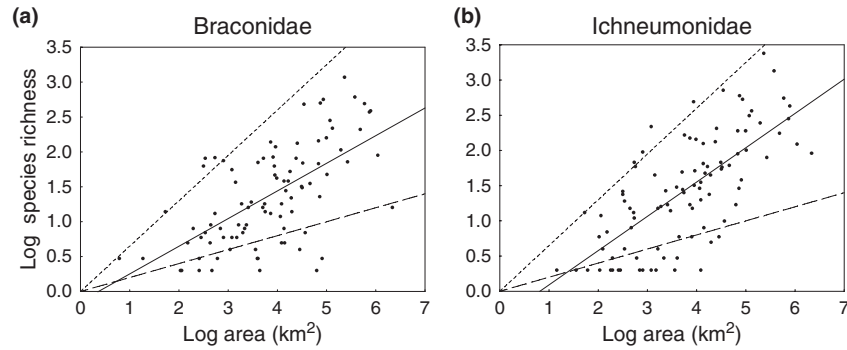


Fig. 3. Observed (continuous line) and theoretical (dotted and dashed lines) species–area relationships for (a) the Braconidae and (b) the Ichneumonidae inventories of islands worldwide. Each black point represents an island. The dotted line has a slope of 0.65, whereas the dashed line has a slope of 0.2. Islands over the lower line are considered sufficiently inventoried, and those over the upper threshold as potentially oversampled (see text).

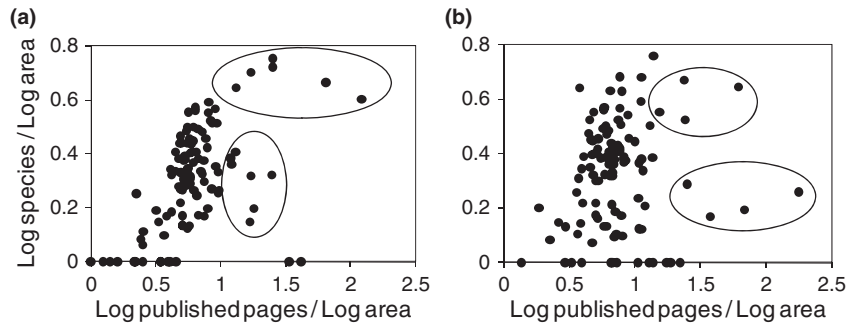


Fig. 4. The relationship between the observed number of species and the number of published pages from each island on a log–log scale standardised by island area, for (a) the Braconidae and (b) the Ichneumonidae. The circles indicate those islands that have received an important amount of effort in relation to their area.

arctic regions; see Figs 2h and 2l). Nevertheless, 70 islands fulfilled this criterion: 4 from the Afrotropics (40% of all islands in this region), 15 from Australasia (52%), 15 from the Indomalayan region (75%), 3 from the Nearctic (100%), 12 from the Neotropics (50%) and 21 from the Palearctic (91%).

Thirteen islands were discarded because only one ichneumonid species had been recorded there. Twenty of the remaining 97 islands had SAR ratios that fell below the 0.2 criterion (dashed line in Fig. 3b), and were thus discarded. In total, 77 islands fulfilled the SAR criterion, from which Corsica, Madeira, Okinawa and Singapore fell above the 0.65 SAR ratio threshold (dotted line in Fig. 3b), indicating that they might be outliers due to oversampling. As with the braconids, the number of published pages was highly positively correlated with the number of species inventoried (Spearman $R = 0.85$, $P < 0.001$). Again, except for a small subset of islands (Fig. 4b), the plots show no consistent decrease in the rate of new species accumulation with new published pages. Only eight islands complied with the publication effort criterion (see Appendix S2).

Considering all criteria, 70 islands (64% of the total number of islands with ichneumonid species) were scored with the two highest levels, and were considered evenly inventoried, and thus comparable as a group (see Fig. 5b and Appendix S2). All

regions except the Afrotropics and the Neotropics (50% and 42%, respectively) had more than half of their islands scored with one of these two levels (Australasia, 55%; Indomalaya, 68%; Nearctic, 75%; Palearctic, 91%). Eleven islands were scored as level 1 and 29 did not pass any criteria (see Appendix S2; Fig. 5b).

Discussion

Bias and incompleteness in biodiversity inventories

Although parasitic wasps are key components of nearly all terrestrial ecosystems (LaSalle & Gauld, 1993), their macroecological and evolutionary patterns have been scarcely studied outside of a few temperate and tropical areas, mainly because of the inherent difficulty of working with an hyperdiverse group with complex biological interactions and whose taxonomy is far from complete. Further, it is likely that unevenness in the effort devoted to their inventory and systematics (see, e.g. Gaston, 1993; Jones *et al.*, 2009; Baselga *et al.*, 2010) has prevented from developing large-scale analyses of their diversity patterns (but see, e.g. Hawkins, 1994 and references therein).

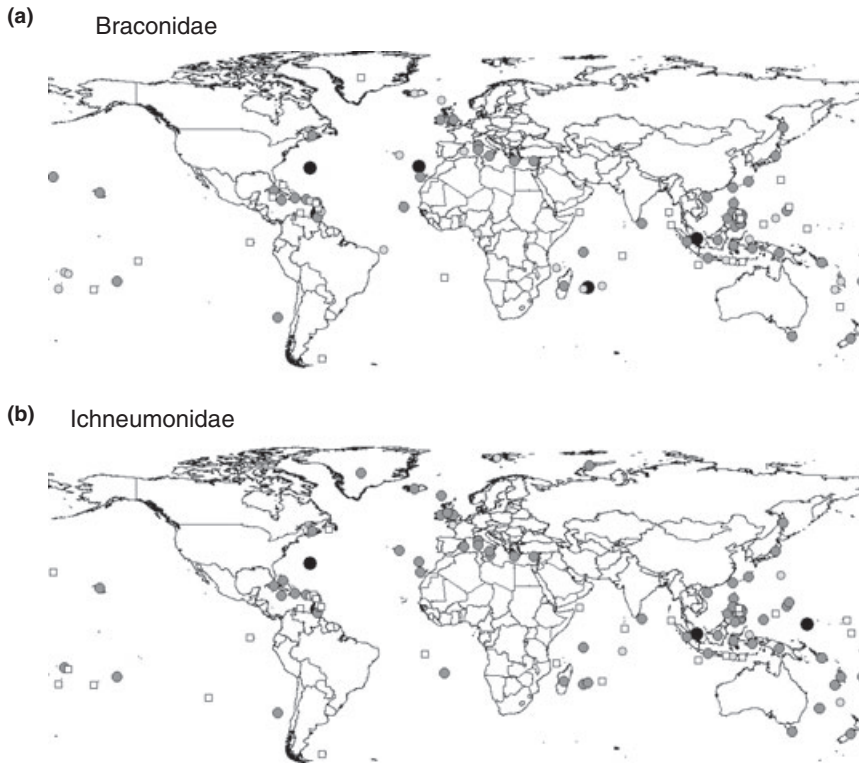


Fig. 5. The geographical distribution and scoring level of the islands that have (a) braconid species (Braconidae) and (b) ichneumonid species (Ichneumonidae). Each point represents an island, and the symbols and colours indicate the scoring value. These are as follows: white squares = islands with no score; small light grey circles = islands with score 1; medium grey circles = islands with score 2; black circles = islands with score 3. Islands with scores 2 and 3 can be considered sufficiently inventoried.

Many factors can affect the process of inventorying and describing species, and therefore the quality of taxonomic databases. The characteristics of the species affect their probability of being inventoried. For example, the body size, abundance, geographical range and ecological requirements (e.g. trophic and habitat ranges) are all known to influence species discovery (Gaston, 1991, 1993; Gaston & Blackburn, 1994; Patterson, 1994; Blackburn & Gaston, 1995; Gaston *et al.*, 1995; Cabrero-Sañudo & Lobo, 2003; Collen *et al.*, 2004; Adamowicz & Purvis, 2005; Baselga *et al.*, 2007, 2010; Guil & Cabrero-Sañudo, 2007; Jiménez-Valverde & Ortuño, 2007; Jones *et al.*, 2009). In addition, geographical biases in survey effort are the rule rather than the exception (see, e.g. Dennis *et al.*, 1999; Dennis & Thomas, 2000; Hortal *et al.*, 2007, 2008; Lobo *et al.*, 2007; Baselga *et al.*, 2010). In general, northern temperate areas have been more thoroughly studied than the tropics or south temperate regions (Gaston, 1994; Allsop, 1997; Medellín & Soberón, 1999; Cabrero-Sañudo & Lobo, 2003; Collen *et al.*, 2004; Adamowicz & Purvis, 2005; Gibbons *et al.*, 2005; Baselga *et al.*, 2007; Guil & Cabrero-Sañudo, 2007). This bias also seems to be common to the parasitoids (e.g. Gaston, 1993; Jones *et al.*, 2009; Baselga *et al.*, 2010), and is further confirmed by our results (see Fig. 5 and Appendices S1 and S2). Surveys may also be biased at smaller spatial scales. Survey effort is usually higher near recorders' home ranges, work centres, roads and railway stations or simply in more accessible natural areas (Prendergast *et al.*, 1993; Allsop, 1997; Dennis *et al.*, 1999; Dennis & Thomas, 2000; Kadmon *et al.*, 2004; Diniz-Filho *et al.*, 2005; Jiménez-Valverde & Ortuño, 2007; Sánchez-Fernández *et al.*, 2008; Baselga *et al.*, 2010). These biases seriously compromise the description of

species distributions, as well as the representation of their environmental responses (Lobo *et al.*, 2007; Hortal *et al.*, 2008; Jiménez-Valverde *et al.*, 2008; D. Rocchini, J. Hortal, S. Lengyel, J.M. Lobo, A. Jiménez-Valverde, C. Ricotta, G. Bacaro & A. Chiarucci, unpubl.).

Identifying evenly inventoried areas

Several methods have already been developed to identify and account for different types of bias and limitations of biodiversity data. The most developed ones make use of several measures of sampling effort, such as the number of survey records, individuals or traps, in combination with species accumulation curves (e.g. Soberón & Llorente, 1993; Lobo & Martín-Piera, 2002; Hortal *et al.*, 2004, 2008; Hortal & Lobo, 2005), or other relationships with survey effort (Hortal *et al.*, 2001, 2007; Lobo & Martín-Piera, 2002; Garcillán *et al.*, 2003), including species richness estimators (Petersen *et al.*, 2003; Soberón *et al.*, 2007; Lobo, 2008). However, these methodologies usually involve the use of detailed data on the surveys, which is not always accessible, especially in taxonomic databases, such as in the case study presented here. This hampers analyses of survey completeness, thereby limiting the reliability and usefulness of some databases for macroecological studies. In such cases, it is necessary to develop new methods that allow meaningful comparisons of species inventories from different areas without the need for detailed information on the recording process.

Here, we presented a protocol based in three criteria, covering the three main aspects that we believe that, ideally, characterise a

reliable inventory: (i) lack of evident biases towards particular taxa, (ii) congruence with well-established ecological relationships, and (iii) origination from works involving enough sampling effort to be potentially complete. The criterion of completeness at higher taxonomic levels accounts for the effort made in describing and inventorying species from different high-level taxa (in this case, subfamilies), taking into consideration that each region has its own colonisation and evolutionary history, and therefore its own taxonomic composition (see, e.g. Ricklefs, 2007). The most important drawback in the use of this criterion relates to how we determine which particular components an inventory must have to be considered reliable. Our sequential approach of first determining how many subfamilies are widespread in the island faunas of the region, and then establishing the minimum number of widespread subfamilies an island should have to be considered as evenly inventoried from the decay in their recorded numbers (see Fig. 1) is a plausible and easy-to-implement approach. However, identifying the point at which this decay pattern changes from being the outcome of biogeographical processes to being a consequence of undersampling can prove difficult sometimes (as evidenced by, e.g. the case of the ichneumonids from Australasia and Palearctic, Figs 2h and 2l). This has the unfortunate effect of adding some undesired subjectivity to this criterion. Also, exceptionally, some islands might truly host less widespread subfamilies due to other causes than being poorly inventoried (e.g. biogeographical factors), and therefore fail to comply with this criterion despite being, in fact, well-inventoried. Nevertheless, we believe these cases are uncommon; the consistency with the islands selected with the SAR criterion provides some support to the adequacy of the choices made.

The rationale for our second criterion comes from the assumption that obvious outliers in well-established ecological relationships are unlikely to have been completely inventoried or nearly so. Perhaps, the most adequate of these relationships is the SAR, due to its generality. Several authors have used the SAR to determine the reliability of the observed species richness from a territory by comparing it with the general relationship found for other areas or well-sampled territories (e.g. Garcillán *et al.*, 2003; Petersen *et al.*, 2003; Roos *et al.*, 2004; Adamowicz & Purvis, 2005; Nikolić *et al.*, 2008). This seems especially appropriate for islands, where land area is known to be one of the most important, although not universal, determinants of species richness (reviewed in, e.g. Whittaker & Fernández-Palacios, 2007). However, this method requires that observed species richness is compared with the extrapolation from the SAR of a well-studied area. Since, in our case study, there was no *a priori* knowledge of which areas are well sampled, it was not possible to extrapolate the number of species that might be *missing* from a particular island. Given the large body of knowledge on ISARs, our alternative solution is to use theoretical thresholds (e.g. lower and upper SAR ratio thresholds of 0.2 and 0.65, respectively) to determine when the inventory from any island is poorer, or richer, than should be expected given its area. We use an upper threshold to give cautionary advice about oversampled areas, which might not be comparable to the rest of the less-well (but sufficiently) inventoried ones (see Lobo & Martín-Piera, 2002). Thus, although we recommend discarding data from

areas with a SAR ratio of <0.2 , we also flag those that have a SAR ratio of >0.65 and would recommend that, rather than omitting them entirely, they should only be discarded if they appear as outliers in other analyses. Islands that are truly species poor could be incorrectly excluded by this criterion. However, since parasitoids typically show ISAR slopes higher than 0.3 (see, e.g. Santos *et al.*, 2010), such incorrect exclusions should be rare or non-existent.

The publication effort criterion is intended to act as a proxy for sampling effort (see, e.g. Hortal *et al.*, 2007; Soberón *et al.*, 2007). However, implementing this kind of criterion using taxonomic databases can be more difficult than expected. In our case, Taxapad only provides information on the total number of pages per publication, but no detailed record on the specific number of pages that refer to a particular island or territory. This could explain why we were unable to identify any patterns of decreasing rate of species accumulation with increasing number of published pages, except for a few islands that have received an important amount of effort in relation to their area. These problems are probably common to many databases and evidence that the implementation of a criterion based on the intensity of inventory effort needs more detailed information on the surveys than that available in most taxonomic databases (see Discussion in Hortal *et al.*, 2007).

Although we have specifically applied our protocol to islands, the generality of its principles may make it easy to adapt to mainland areas, such as countries or biogeographical provinces, and/or to other taxa. Its importance lies in the fact that only requires information on the species inventory and a few general characteristics of the areas, allowing the use of checklists that normally would be considered unsuitable for macroecological studies. Furthermore, by scoring areas instead of simply discarding some of them, this protocol can be useful for identifying different levels of uncertainty, that could be used to weight the areas in regressions or other analyses. Such scoring could also be used to allocate field and taxonomic resources. Of course, our method, like any other, has its limitations. It only allows the identification of which inventories are comparable in terms of taxonomic effort, rather than identifying well-surveyed areas. Therefore, its use within large-scale conservation assessments should be discarded (or used with caution), because these analyses need detailed and accurate results if they are to be used for decision-making. Nevertheless, we believe this protocol might be adequate as a previous step for many analyses of macroecological patterns, as evenly inventoried areas identified this way can be reliably used for large-scale analyses.

Acknowledgements

We want to thank Kostas Triantis for his suggestions on early stages of this work and to Paulo Borges, Jorge Lobo and two anonymous reviewers for valuable comments on previous versions of the manuscript. A.M.C.S. was supported by a Portuguese FCT grant (SFRH/BD/21496/2005), O.R.J. was supported by the grant NE/C519583 from the Natural Environment Research Council and J.H. by the UK Natural Environment Research Council.

Supporting Information

Additional Supporting Information may be found in the online version of this article under the DOI reference: 10.1111/j.1752-4598.2010.00079.x

Appendix S1. Islands and variables for the Braconidae.

Appendix S2. Islands and variables for the Ichneumonidae.

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Accepted 24 December 2009
First published online 27 January 2010

Editor: Yves Basset
Associate editor: Bradford Hawkins