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Tackling the taxonomic impediment: a global assessment for the ant-nest beetle diversity (Coleoptera, Carabidae, Paussini)

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We evaluated the completeness and historical trends of the taxonomic knowledge of the myrmecophilous ground beetle tribe Paussini (Coleoptera, Carabidae, Paussinae). Species accumulation curves were modelled using a logistic function. Similar analyses were conducted for genera and subgenera. Although not all biogeographical regions have been equally explored, accumulation curves reached a plateau in all cases. Our models predict that about 96% of the world fauna has been already described. However, the asymptotes calculated for the Australian and Oriental species should be interpreted as false plateaus because of the lack of recent research. Similarly, patterns of genera accumulation indicate that a plateau has been reached. As a result of continued debate on the use and validity of Paussini subgenera, the accumulation curves of subgenera showed stepped patterns, with no evidence of plateaus. Thus, although relatively few species are expected to be described in the future, the species accumulation curves indicate that the taxonomic inventory is not yet complete. Differences in accumulation patterns among biogeographical regions can be used to highlight the areas where more species are expected, and hence where taxonomical efforts should be concentrated. © 2011 The Linnean Society of London, *Biological Journal of the Linnean Society*, 2011, ••, ••–••.

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ADDITIONAL KEYWORDS: biogeographical regions – Carabidae – Coleoptera – Paussinae – sigmoid functions – species accumulation curves – year of description.

INTRODUCTION

One of the most serious obstacles in biodiversity research and conservation is the so-called taxonomic impediment, i.e. the difficulty in identifying an enormous number of living species, most of which probably remain undescribed (Gaston, 1991; Pimm *et al.*, 1995; Lomolino *et al.*, 2010).

In order to avoid biases in our knowledge and to optimize future taxonomical efforts, the first priority is to assess the current state of biotic inventories

(Baselga *et al.*, 2007; Hortal *et al.*, 2008). Although taxonomic knowledge is essential for conservation (Sutton & Collins, 1991; Barrowclough, 1992), there is a serious crisis in taxonomical interest (Boero, 2001). Most funds are allocated to other research fields (namely molecular phylogenetics and ecology), for which taxonomical knowledge is an obvious prerequisite (Cotterill, 1995; Krell, 2000). Moreover, there is increasing pressure to adopt immediate conservation actions, even in the absence of adequate taxonomic information. As a result of these socio-economic pressures, there is an increasing use of the taxonomically well investigated groups (namely vertebrates and

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plants) to find diversity hot spots and assess conservation priorities (Fattorini, 2006, 2009; Lamoreux *et al.*, 2006; Kier *et al.*, 2009), but results are often contradictory, because the hot spots for different groups tend to have different geographical distributions (e.g. Prendergast *et al.*, 1993), and vertebrates typically perform poorly as surrogates for invertebrate richness (Fattorini, 2010).

Although arthropods as a whole are still poorly known, they include a number of taxa for which detailed and comprehensive taxonomic information is available. In fact, there is an enormous volume of taxonomic data hidden in museum collections and obscure literature that is only known by taxonomists, and is difficult to access by non-taxonomists, but which can be profitably used (Soberón, Llorente & Oñate, 2000; Meier & Dikow, 2004; Guralnick & Van Cleve, 2005). Large (ranging from countrywide to global) databases are available for vertebrates and plants, and have been repeatedly used to predict the global diversity of these groups (e.g. Medellín & Soberón, 1999; Solow & Smith, 2005), but rarely for arthropods because information is dispersed and it is difficult to evaluate the quality.

In recent times, the importance of global assessments of arthropod diversity has been repeatedly stressed (Basset *et al.*, 1996; Godfray, Lewis & Memmott, 1999; Ødegaard, 2000), yet few studies have assessed the quality of taxonomic information of arthropod groups at a global level (examples are Gaston, Scoble & Crock, 1995; Sihvonen & Siljander, 2005; Baselga *et al.*, 2010). The most basic question is how complete is the taxonomic status of a given group, i.e. whether the species list of a given group can be considered fairly complete, or if there are still many species to describe.

In this paper, we evaluated the completeness of the taxonomic knowledge about a group of myrmecophilous beetles, the tribe Paussini ('ant-nest beetles') of the family Carabidae (Coleoptera, Adephaga), at a global level. Assessing the completeness of taxonomic knowledge for the Paussini is of particular importance, because these insects belong to a clade of crucial importance for the phylogeny of the most primitive beetles (Di Giulio *et al.*, 2003). Also they are a good example of an arthropod group for which information is abundant but dispersed in specialized literature, which is a common state of affairs for many arthropod groups.

Thus, our study differs profoundly from previous works that attempted to evaluate the taxonomic knowledge of plant or animal groups for which large databases are easily available and currently used in biogeographical and conservation research.

In general, for assessing the status of the taxonomical process in a given group, the study should

be addressed to assess the growth through time of the cumulative number of valid names to estimate the number of species that remain to be discovered in a given taxonomic group, globally or regionally (Steyskal, 1965; Medellín & Soberón, 1999; Cabrero-Sanudo & Lobo, 2003; Baselga & Novoa, 2006; Hortal *et al.*, 2008). The presence of a plateau in new species described over time is considered evidence that no, or few, species remain to be described.

In our research we also used the Paussini to discuss some recurrent shortcomings in previous research that dealt with groups for which the historical accumulation of taxonomic information is reaching a plateau, and to show a possible solution based on the application of sigmoid fitting equations. We also applied similar approaches to patterns in the discovery trends of genera and subgenera, and discussed the evolutionary implications.

In particular, the aims of this paper were: (1) to assess the completeness of current taxonomic knowledge for the tribe Paussini by modelling species accumulation curves; (2) to predict the probable number of existing species, both globally and in different biogeographical regions; (3) to highlight the biogeographical regions for which more species are expected, and hence deserve more attention.

MATERIAL AND METHODS

DATA COLLECTION

This study was based on a computerized database containing information on all the putatively valid names of the Paussini species, as of spring 2010. It was basically constructed using Luna de Carvalho's (1989) monograph, then complemented, reviewed, and updated with reference to Lorenz (2005) and Nagel (2003), and finally re-checked against the personal database of W. Moore (unpubl. data). Further data were extracted from Nagel (2006, 2009), Geiselhardt, Nagel & Peschke (2007), Maruyama (2005, 2009), and Maruyama *et al.* (2008).

The following information was recorded for each species and subspecies: generic assignment, subgeneric assignment, author, year of description, type locality (and its country), biogeographical region of species distribution, and synonyms. We also recorded the authorship and year of the description of genera and subgenera.

The use of subgenera in the tribe Paussini is very controversial. For example, in the catalogue of the Palaearctic region, Nagel (2003) listed all subgenus names used for the genus *Paussus* under the genus name without providing an explicit synonymization. On the other hand, molecular data (W. Moore, pers. comm.) suggest that at least some subgenera

represent really distinct phyletic lines. For these reasons, we retained subgenera in our database as currently accepted/used by most authors (e.g. Lorenz, 2005).

As in similar previous studies (see Gaston & Hudson, 1994; Gaston, Scoble & Crock, 1995; Scoble, Gaston & Crook, 1995; Sihvonen & Siljander, 2005), we followed Wallace's scheme, with some minor modifications (see Lomolino *et al.*, 2010). The biogeographical regions are: (1) Neotropics – Central and South America, including Mexico; (2) Palaearctic – Europe, North Africa, the Middle East, the former Soviet Union (FSU), Mongolia, China, Japan, and Korea; (3) Africa – all of Africa, excluding the area mentioned in (2), but including Madagascar; (4) Oriental – from Pakistan, India, Nepal, and Bhutan through to New Guinea and the Pacific Islands, including Hawaii; (5) Australia – including Tasmania and New Zealand. In a few cases, the range of a species mainly distributed in a given biogeographical region also extended very marginally into an adjacent region, especially at transitional zones (for example, African species that reach the southern limits of the Palaearctic region in southern areas of North African countries). In these circumstances, we assigned the species to the biogeographical region that included most of its range. No extant species is known from the Nearctic region.

The database included 572 species and 17 subspecies.

HISTORICAL ACCUMULATION CURVES OF SPECIES

We extracted the year of description of all valid species and subspecies, and grouped the years into decades. Decades were established in the usual way (1770–1779, 1780–1789, and so on), starting with the decade including the year of description of the first Paussini species (1775) (cf. Gaston *et al.*, 1995; Soberón *et al.*, 2000; Sihvonen & Siljander, 2005). We plotted the number of valid taxa as well as their cumulative number against the decade of description both at the global level and for each biogeographical region separately.

To model species accumulation curves, we initially tried several models commonly used for the curves derived from sampling efforts. In particular, on the basis of recent reviews (Melo *et al.*, 2003; Thompson *et al.*, 2003; Hortal, Borges & Gaspar, 2006), we applied the following asymptotic models using non-linear fitting procedures: clench, linear, Chapman–Richards, rational, beta-P, and Weibull. However, no model gave an acceptable fit. In some cases the obtained fit deviated strongly from the observed pattern, or produced unrealistic values for the fitted parameters. In many instances, the algorithm failed

to converge. Using different starting values of parameters or different research algorithms in two different programs (STATISTICA and XLSTAT) did not improve the results. These frustrating outcomes were also noted by Thompson *et al.* (2003) and Fattorini & Fowles (2005) for the Weibull model in other contexts. The failure of these functions in modelling the accumulation of species descriptions is not new. Baselga *et al.* (2010) were also unable to find valuable fits to their species accumulation curve of described species plotted against year of description using different types of species accumulation functions. The same problem was encountered by Medellín & Soberón (1999). They found that the accumulation curve of terrestrial mammals had a sigmoid shape, and so to apply a logarithmic model they excluded the first part of the curve, fitting only the portion that followed the expected pattern. We believe that it is preferable to search for alternative models that are adequate to describe the entire data set, rather than to manipulate the data to conform to a predetermined model.

By examining scatter plots of our data set, we noticed that they follow a sigmoid distribution, and a similar trend can be observed in the accumulation curves presented by Medellín & Soberón (1999), Wilson & Costello (2005), Sihvonen & Siljander (2005), and Baselga *et al.* (2010). This sigmoid relationship is very different from the typical species accumulation curves found in ecological studies, for which the aforementioned asymptotic and logarithm models have been proposed. Species accumulation curves found in ecological samples are characterized by a steep initial increase in the number of species sampled, followed by a gradual plateauing of the curve as fewer new species are recorded with increased sampling effort. Thus, fitting with the models that are efficient for this kind of accumulation curve cannot be appropriate for the sigmoid relationships found in our study, and those observed in previous research. Wilson & Costello (2005) showed that most discovery curves have a sigmoid shape, and found that a logistic function can explain the pattern adequately.

In fact there are various versions of the logistic function. Taking advantage from recent developments in the cognate field of the species–area relationship (Tjørve, 2009; Fattorini & Fowles, 2005; Fattorini, 2007; Dengler, 2009; Williams, Lamont & Henstridge, 2009), we applied the Tjørve logistic function $y = b_0 / [1 + \exp(b_1x + b_2)]$, where b_0 , b_1 and b_2 are estimated parameters, to our data. This sigmoid model gave excellent fits, and because the first parameter (b_0) is the upper asymptote, it provides an immediate estimate of the expected number of species.

Although several explanations can be evoked to explain why species accumulation curves have a

sigmoid shape, we think that the logistic function captures two different aspects of the process of species accumulation: the upper asymptote is a biological datum (the number of species that exist), whereas the shape of the curve is a reflection of taxonomic activity (progresses in technology, exploration of new areas, increases in the number of taxonomists, etc.).

Similar analyses were conducted for genera and subgenera. Descriptions of subgenera through time were, however, much more irregular, so we do not use curve fitting to model the pattern. We analysed genus and subgenus taxonomy to investigate advances in the state of taxonomic knowledge, because the descriptions of new genera and subgenera are a rough measure of the development of beta taxonomy, i.e. the study of the relationships between the already described taxa *sensu* Mayr (1969).

RESULTS

The rate of species description per decade, when the absolute numbers are considered, is very irregular (Fig. 1A). Between 1775 (when the first species of

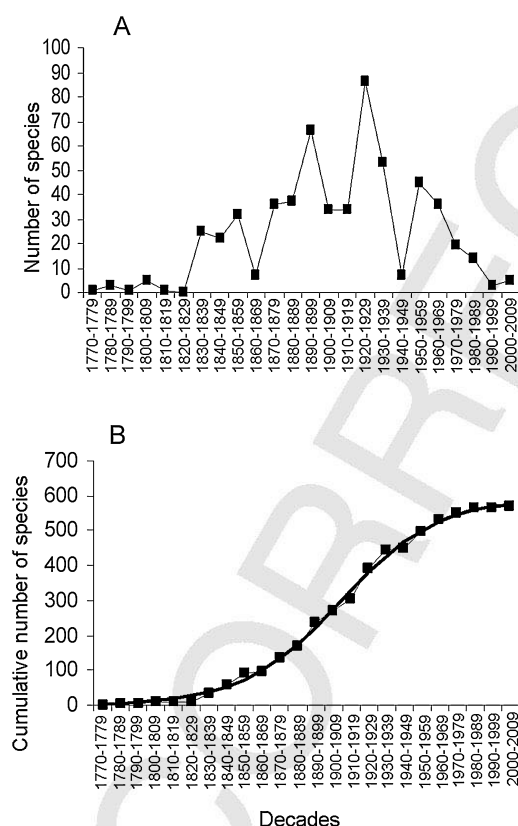


Figure 1. Numbers of described species of Paussini (A), and their cumulative numbers (B), by decade. Fitting equation: $y = 594.907/[1 + \exp(-0.362x + 5.230)]$, $R^2 = 0.998$.

Paussini was described by Linnaeus) and 1840, only 31 species were described, and no species was described in the decade 1820–1829. The first attempt to describe Paussini taxonomy was made by Westwood, mainly in the years 1830–1859. In the latter half of the 19th century species were described at an increasing rate, with two peaks in 1870–1879 and especially in 1890–1899, thanks to the intense activity of Wasmann. However, the description of species peaked in 1920–1929, mostly with the work of Wasmann, Kolbe, and Reichensperger. The low level of species descriptions in the decades 1910–1919 and 1940–1949 may be explained by the effects of the First and Second World Wars. Since the 1950s descriptions decreased progressively, with a minor peak for the period 1950–1969, mostly attributed to Reichensperger and notably to Luna de Carvalho.

When the cumulative numbers are considered, the increase per decade was low until the 1840s. The cumulative numbers of species descriptions has now reached a plateau. The estimated asymptotic value for the fitted curve is 595 species (Fig. 1B). Because the number of currently recognized valid species is 572, the model predicts the existence of 23 undescribed species, with about 96% of the world fauna having already been described.

The rate of species descriptions shows important differences among our biogeographical regions (Fig. 2). In the Palaearctic region the rate of descriptions has been erratic, and an asymptote is yet to be reached (21 expected species; 20 described species) (Fig. 2A). The same holds true for the Neotropics, where the current number of known species (15) is the same as the expected number of species (Fig. 2B).

In the other biogeographical regions there was a slow start that lasted approximately until the 1850s. In the African region the pattern was more varied. Species descriptions peaked in the decades 1880–1899 and 1920–1939, but, after a fall in 1940–1949, there was a further increase in 1950. After the 1950s, species description decreased progressively, and the current number of described species (352) is about 94% of the predicted value (374) (Fig. 2C). The Oriental region shows two peaks, in 1830–1849 and 1890–1919, with the current number of described species (111) sitting very close to the expected number of species at the asymptote (less than 115) (Fig. 2D). Finally, in the Australian region, species descriptions were concentrated in the decades 1870–1879 and 1920–1929. No further addition was recorded after 1939, and only three additional species are predicted to exist by the model (Fig. 2E).

The largest numbers of described species occur in Africa (352 species), followed by the Oriental (111 species) and Australian (65 species) regions, covering about 73% of the fauna. Africa is also the

biogeographical region for which the highest number and percentage of new descriptions are expected (22 species, which is an increase of ~6%). Species richness was not related to the area of the biogeographical regions (Spearman rank correlation coefficient, $r_s = 0.429$, $P = 0.397$). There are large differences in the number of described species between the biogeographical regions within the Northern and Southern hemispheres. Only 20 species have been described from the Palearctic region, and none have been described from the Nearctic one. In the Southern hemisphere most species have been described from the African and Oriental regions. It is worth noting that the number of described species is substantially smaller in the large biogeographical regions of the Nearctic and the Neotropics, compared with the large biogeographical regions of the same latitudes in the Old World.

Paussini species are currently allocated in 23 genera. The decade with the highest number of valid genera (four) was 1830–1839 (Fig. 3A). Patterns of genera accumulation through time indicate a good sigmoid shape (Fig. 3B).

The study of subgenera indicates a proliferation in the description of subgenera during the periods 1920–1929 and 1980–1989 (Fig. 4). Species allocation among genera is strongly dominated by the richest genus (*Paussus*), with 342 ascribed species and 25 subgenera. Species distribution among subgenera is also very uneven: the subgenus with the highest number of species is *Cochliopaussus*. The relationship between number of species and number of subgenera per genus was significantly positive ($r_s = 0.964$, $P < 0.001$); thus the genera that have the highest number of species are also more subdivided into subgenera.

DISCUSSION

Our taxonomic analyses revealed that 572 species of Paussini are currently known and placed into 23 genera. The subspecies concept has rarely been applied to Paussini, with only 17 taxa described as subspecies.

Species accumulation curves of the world Paussini fauna suggest that this tribe of carabid beetles is taxonomically stable: according to the trends analysed here, few new species are expected to be described in the future. However, not all biogeographical regions have been equally explored, and there is an indication that, at least in some cases, the apparent plateau results from a lack of adequate research. In particular, we believe that the number of Oriental species is probably underestimated because of the large number of genera/subgenera occurring in the Oriental region, and the irregular trend of species

description (see Fig. 2). Results of ongoing expeditions in the area, especially by Japanese, Swiss (cf. Maruyama *et al.*, 2008, Nagel, 2009), Chinese, and Czech collectors support this conclusion.

In general, temporal trends in species descriptions mirror dramatic events in human history. The overall trend in species descriptions shows two falls, in correspondence with the First and Second World Wars. The first peak in African species description occurred in the decade 1880–1899, which can be considered an indirect reflection of the first phase of African exploration that took place between 1840 and 1870, and is a direct effect of the German expansion in central Africa in the 1880s in particular. The second peak occurred in the decade 1920–1939, which coincides with the third phase of African colonialism, during which the most influential European states organized and stabilized their territories. The first peak (1830–1849) of species description from the Oriental region is a reflection of the increasing British control in India. Most Paussini species have been described from Africa, and it is therefore not surprising that the museums that preserve large concentrations of type material are those of countries that had wide colonies in Africa (Belgium, Germany, and France).

Recent papers on taxonomic developments based on species accumulation curves did not apply fitting equations (Gaston *et al.*, 1995; Sihvonen & Siljander, 2005), or found that current models failed to fit the data (Baselga *et al.*, 2010). In accordance with Wilson & Costello's (2005) findings, we found that our species accumulation curves were sigmoid in shape, and this is the reason why models used to fit species accumulation curves in ecological studies were inadequate. By contrast, a logistic function, proposed by Tjørve (2009) for the species–area relationship, and which has a distinctly sigmoid behaviour, fitted the data very well. As we found that a sigmoid distribution is also present in the scatter plots published by Gaston *et al.* (1995), Sihvonen & Siljander (2005), Wilson & Costello (2005), and Baselga *et al.* (2010), we believe that a sigmoid pattern is probably ubiquitous in accumulation curves of species descriptions for well-investigated taxonomic groups (cf. Wilson & Costello, 2005). The first portion of the accumulation curve is expected to have a slow increase in species descriptions, because the early taxonomists were very few, with inadequate technical tools, and were inclined to pay little attention to details. With the increase in the number of taxonomists and technical tools (e.g. use of microscopical characters), species description increases sharply. However, with the increasing number of species descriptions the probability of finding new species will decrease, so the curve will plateau. Our results support this hypothetical trend and we advocate the use of the sigmoid function to fit

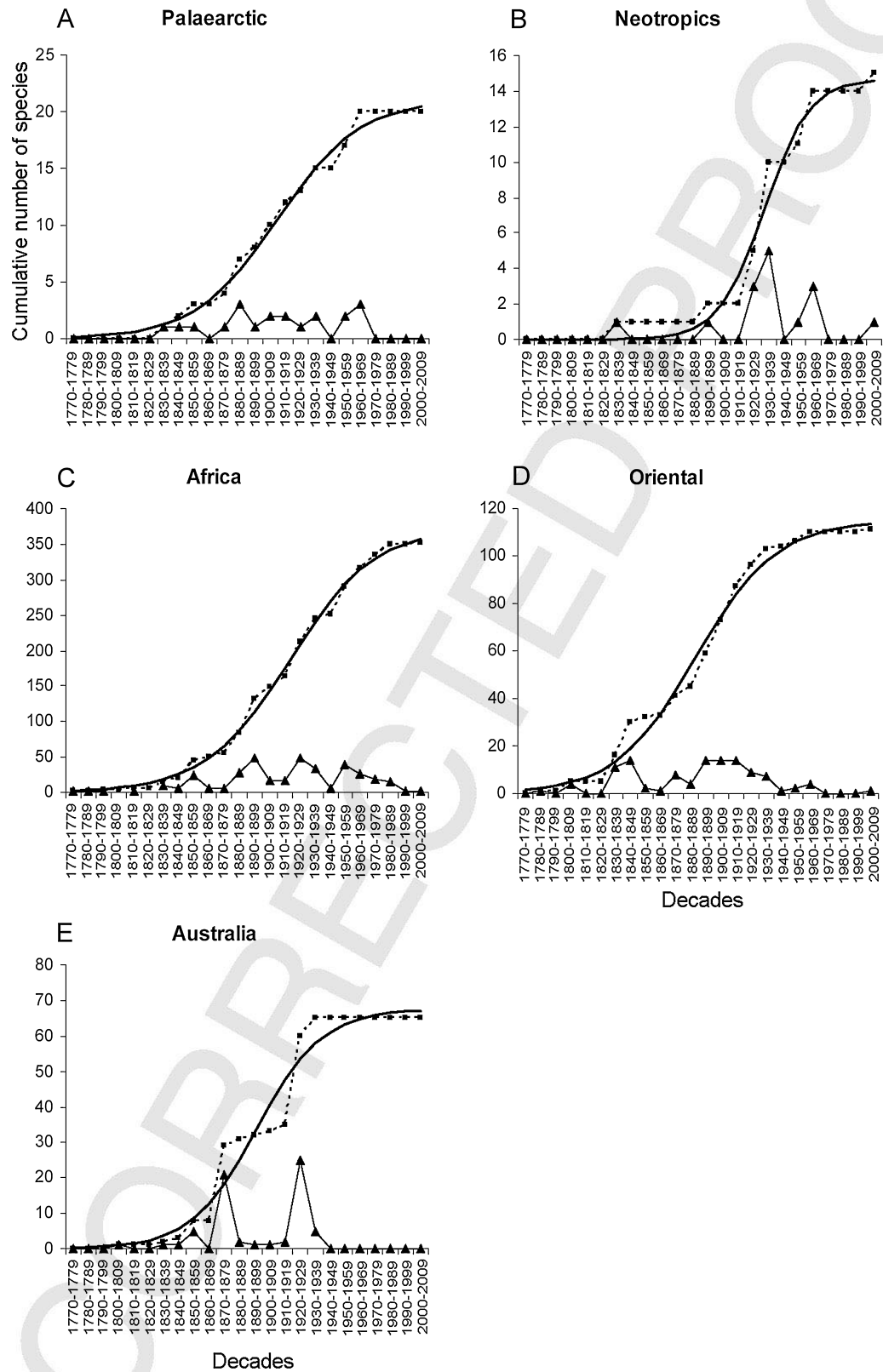


Figure 2. Number of described species of Paussini from different biogeographical regions, by decade. Both absolute (▲, solid line) and cumulative (■, dashed line) numbers are shown. The equations of the fitted curves (solid line) are as follows: A, $y = 21.017/[1 + \exp(-0.368x + 5.319)]$, $R^2 = 0.994$; B, $y = 14.694/[1 + \exp(-0.664x + 11.105)]$, $R^2 = 0.984$; C, $y = 373.846/[1 + \exp(-0.355x + 5.452)]$, $R^2 = 0.997$; D, $y = 114.742/[1 + \exp(-0.375x + 4.634)]$, $R^2 = 0.991$; E, $y = 67.543/[1 + \exp(-0.465x + 6.109)]$, $R^2 = 0.972$.

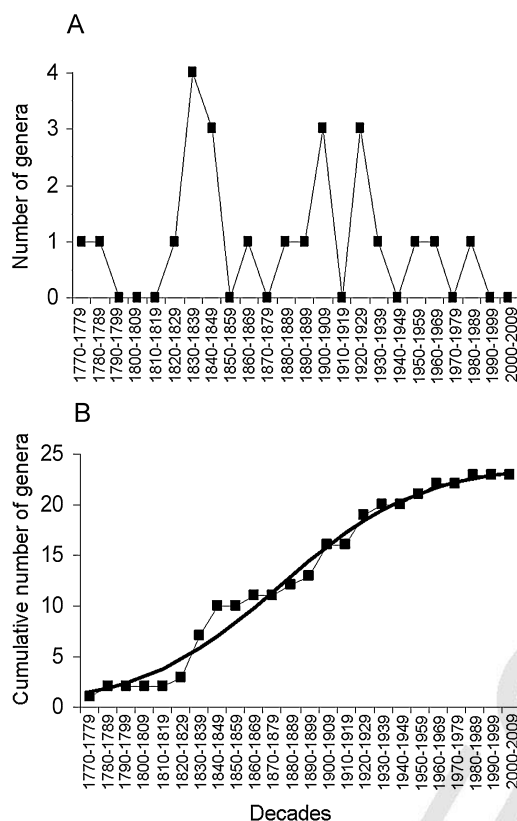


Figure 3. Numbers of described genera of Paussini (A), and their cumulative numbers (B), by decade. Fitting equation: $y = 24.030/[1 + \exp(-0.258x + 2.941)]$, $R^2 = 0.981$.

species description curves in future works to test whether or not this pattern is consistent through different taxonomic groups.

Our general model (all species) predicts the presence of 595 species of Paussini worldwide. This general model can be compared with models constructed for single biogeographical regions. The set of species used to calculate the asymptotes of the individual curves (563 species) was slightly inferior to the number used for the overall model (572 species) because we were unable to establish the biogeographical region of some species. The difference in the two sets is, however, so small that we can assume that the two analyses (overall model versus individual models) dealt with the same data set.

The sum of the expected species from curves calculated for each biogeographical region separately (indi-

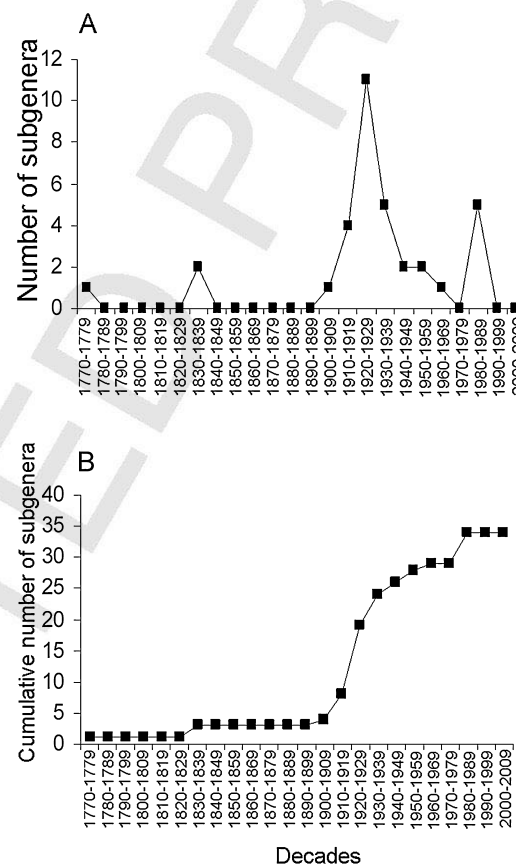


Figure 4. Numbers of described subgenera of Paussini (A), and their cumulative numbers (B), by decade.

vidual curves) gives a value of 593 species, which is very close to the total number of species predicted by the overall model. This consistency of results indicates that our fitting models performed very well in all cases: if any of the individual models used for single biogeographical regions have produced unreliable estimates, this would have produced inconsistency between the expected value obtained from the overall model and that obtained from summing the asymptotic values of the individual models. It is, however, important to recall that a sigmoid function can give reliable results only if a plateau is reached. Thus, it is important to stress that this function allows one to estimate an expected number of species only when the number of known species is not far from the expected one. Because our graphs showed

that a plateau was reached in all cases, the sigmoid model was applicable. However, it is inappropriate to model species accumulation curves that are far from the plateau. In other words, the function provides an estimated number of existing species only for well-surveyed groups.

A second important caveat is that the observed final plateau may be the result of interrupted taxonomical work. For example, no species has been described from Australia after the 1930s, so we have a well-defined plateau, and the function gave an asymptotic value identical to the known number of species. However, if this lack of new descriptions of Australian species after 1939 is simply the result of a lack of research after that period, then it is a false plateau, and thus the asymptote calculated is an inaccurate estimate of species diversity. In the Australian scarab beetles there have been many recent descriptions after what appeared to be a plateau in the 1920s (Allsopp, 1997), and similar false plateaus took place during the late 1800s in the Geometridae (Gaston *et al.*, 1995). In the case of the Australian Paussini, taxonomical progress has been hampered by the lack of revisionary work and by the phenotypical similarity of most species, which makes it difficult to assess the taxonomic status of populations of the genus *Arthropterus* (see Luna de Carvalho, 1989).

A similar situation can be recognized for the Paussine fauna of South-East Asia, as discussed above. On the other hand, the plateaus reached for the Palaearctic and African regions seem to be reliable, as these areas have been constantly explored and studied by several entomologists and paussine specialists. It is not expected that further research in these regions will modify the present number of described species significantly, and the number of species predicted to be described in the future from Africa seems reasonable. In particular, it is likely that new species will be described from areas that remain scarcely investigated, and have a high level of endemism, such as Madagascar (W. Moore, pers. comm.).

Thus, we believe that for a relatively well-known group of insects, differences in accumulation patterns among biogeographical regions can be used to highlight the areas where more species are expected, and hence where taxonomical efforts should be concentrated.

The vast majority of Paussini genera were instituted before the cladistic era, so there is no proof that the species arrangements into genera reflect true phylogenetic relationships. It is possible that some morphological characteristics have been over-emphasized and others have been overlooked, and that current genera might be strongly biased by a 'phenetic' approach. On the other hand, we believe it

to be unlikely that the species allocation into genera is completely disconnected from phylogenetic relationships. In particular, the high concentration of species in certain genera (notably in the genus *Paussus* and a few others) may reflect the hyperbolic shape of the frequency distribution of taxa with different numbers of subtaxa (Burlando, 1993). The taxonomy of subgenera is quite different because of its high instability, as shown by the diversity of taxonomic treatment among authors (Luna de Carvalho, 1989; Nagel, 2003; Lorenz, 2005). Moreover, the number of subgenera per genus is correlated with the number of species per genus. Thus, we suspect that most subgenera were created to subdivide the genera with more species into smaller units just for practical reasons. Recently it has been proposed to infer phylogenetic patterns from taxonomy in lieu of cladistic information, for example for biogeographic purposes (Porzecanski & Cracraft, 2005). We believe that it might be an acceptable choice only for groups in which the taxonomy is stable, and that therefore reflect truly distinct phyletic lineages. The instability of species allocation into subgenera indicates that subgenera cannot be used as monophyletic groups in the absence of a cladistic analysis.

It is well known that there is an enormous disparity between the number of described species and the total number of species in existence, a state of affairs known as the 'Linnean shortfall' (Lomolino *et al.*, 2010). To surpass the Linnean shortfall it is essential to effectively tackle the taxonomic impediment. This shortfall is not homogeneous among groups, because arthropods, which are the most speciose animal group, are also the taxon for which more species are still being discovered (e.g. Ladle & Whittaker, 2011). Given the current trends in the specialization and training of taxonomists, the Linnean shortfall is likely to remain problematic for many years, and many of the undiscovered species will become extinct before they are known to science (Lomolino *et al.*, 2010). Thus, it is important to evaluate the completeness of the available inventories of species, and to have some idea of how many species remain to be described. We believe that this is also possible for seemingly 'obscure' taxa, for which taxonomic activity is low and information is sparse, and we hope our study of Paussini taxonomy is a good example of the problems and perspectives involved.

To

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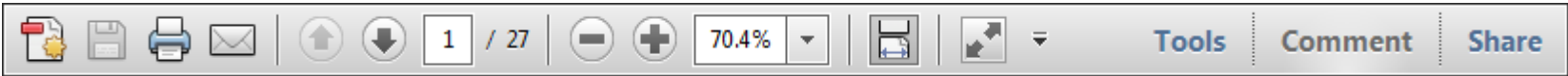
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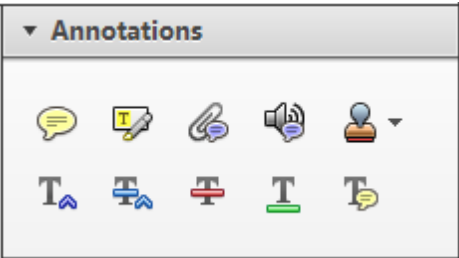
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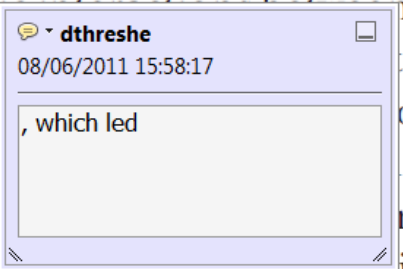


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How to use it

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- Type the replacement text into the blue box that appears.

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2. **Strikethrough (Del)** Tool – for deleting text.




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Highlights text in yellow and opens up a text box where comments can be entered.


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- Highlight the relevant section of text.
- Click on the [Add note to text](#) icon in the Annotations section.
- Type instruction on what should be changed regarding the text into the yellow box that appears.

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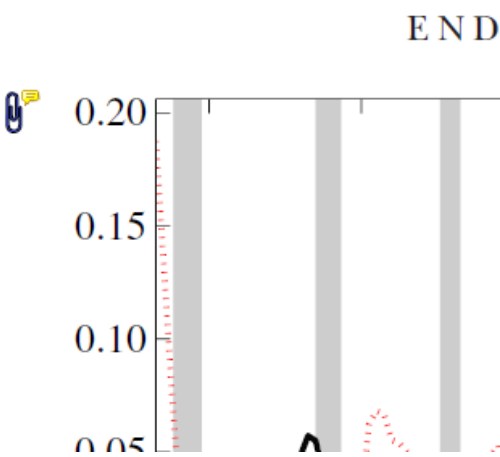


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- Click on the proof to where you'd like the attached file to be linked.
- Select the file to be attached from your computer or network.
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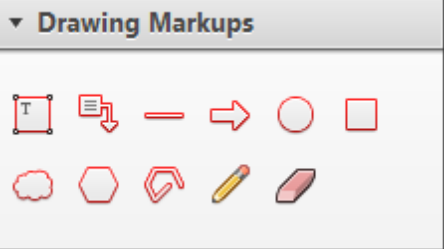
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- Click on the proof where you'd like the stamp to appear. (Where a proof is to be approved as it is, this would normally be on the first page).

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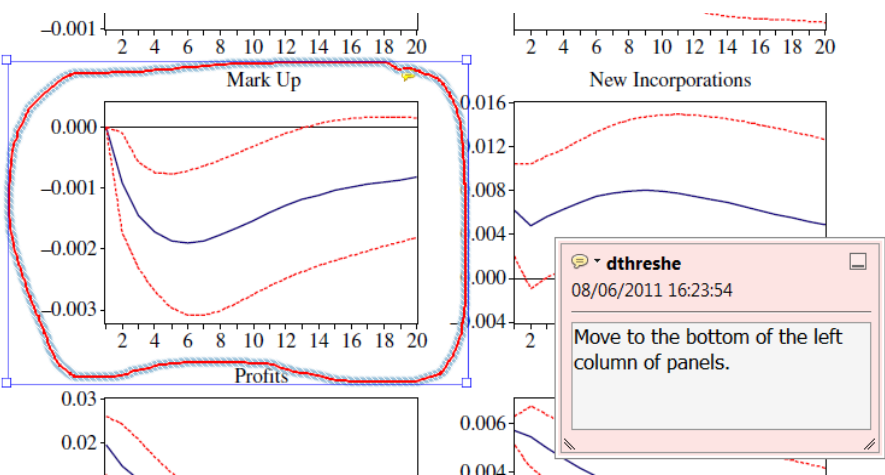


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Allows shapes, lines and freeform annotations to be drawn on proofs and for comment to be made on these marks..

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- Double click on the shape and type any text in the red box that appears.



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