



A review of mono- and bispecific genera of Amphibians worldwide

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Monospecific and bispecific genera are of particular interest in studies of taxonomic diversity and speciation evolution. Here, the distribution patterns of mono- and bispecific amphibians worldwide are investigated, with some discussion of on the conservation implications also presented. Based on an online database search (available from the American Museum of Natural History, New York), we found that the mean number of mono- and bispecific genera was similar among zoogeographic regions, with a total of 120 mono- (95 Anura, 17 Caudata, 8 Gymnophiona) and 65 bispecific (48 Anura, 10 Caudata, 7 Gymnophiona) genera. Out of 73 known amphibian families worldwide, only 35.6 % of them do not contain any mono- or bispecific genera. The frequency of mono- or bispecific genera by family was not significantly different among Anura, Caudata and Gymnophiona. There was a general tendency for the number of mono- and bispecific genera of amphibians to be positively correlated with the total number of genera in that family. In Anura, there was a preponderance of mono-specific genera in Afrotropical and Neotropical regions. Concerning bispecific genera, there was a clear preponderance in the Neotropical region for anurans. There was a positive correlation between the number of threatened genera (according to the IUCN Red List) in both the mono- and bispecific groups and the relative number of species in each taxon, thus showing that taxonomical speciosity clearly influences the frequency of occurrence of mono- and bispecific taxa in each family and order. In this regard, Anura dominated in both the number of worldwide described mono- and bispecific taxa as well as in that of the threatened ones according to IUCN Red List.

Keywords: Anura, Caudata, Gymnophiona, monospecific genera, bispecific genera, biogeography, conservation

In studies of taxonomic diversity, monospecific and bispecific genera are noteworthy compared to multispecies genera, as they may be considered either evolutionarily older (Ridley, 1993) or not-yet-diversified young lineages (Alroy et al., 2008). Furthermore, in many cases, mono- and bispecific genera are endemic to narrow areas (Ridley, 1993). Mono- and bispecific genera may be susceptible to higher extinction risk than multispecies genera, with the eventual extinction of such genera being particularly negative in evolutionary terms because it would represent the extinction of an evolutionary lineage (Cotgreave & Pagel, 1997; Purvis et al., 2000).

Recent studies have focused on the patterns of occurrence of mono- and bispecific genera of rodents, soricomorphs and chelonians, and their conservation implications (e.g. Amori et al., 2008, 2017; Amori & Luiselli, 2018). These studies revealed that the frequency of mono- and bispecific genera was significantly uneven across geographic regions, with the highest fraction of these genera associated with the Orient, followed by the Neotropical and Afrotropical regions for the chelonians (Amori & Luiselli, 2018), whereas the peaks of mono- and bispecific genera richness were observed in Neotropical, Oriental and Afrotropical regions for rodents, and in the Palearctic region for soricomorphs (Amori et al., 2008, 2017).

Despite amphibians being among the most threatened groups of animals (with 43 % of species threatened; e.g. Beebee & Griffiths, 2005; Stuart, 2008; Ceballos et al., 2010; IUCN, 2018), no previous studies have focused on their patterns of occurrence and conservation implications of their mono- and bispecific genera. Amphibians may represent ideal subjects of study because of their ancient history (Duellman & Trueb, 1994; Roelant et al., 2007; Vitt & Caldwell, 2013), limited dispersal abilities (e.g. Smith & Green, 2005; Cushman, 2006; Semlitsch, 2008), and high rates of speciation in islands (e.g., Vences & Wake, 2007; Bell et al., 2015; Schluter & Pennell, 2017). In this paper, we explore the distribution patterns of the mono- and bispecific genera of amphibians worldwide, and also present some conservation considerations.

Table 1. Synopsis of the number of mono- and bispecific genera of selected vertebrate groups, in relation to the total number of genera known from that specific taxon. Data for the number of mono- and bispecific genera were drawn from the present study (Amphibians), Amori & Luiselli, 2018 (chelonians), Amori et al., 2017 (rodents and soricomorphs). Data on the total number of genera per group were drawn from Halliday & Adler, 2002 (amphibians), Rhodin et al., 2017 (chelonians), and Wilson & Reeder, 2005 (mammals).

	Amphibians	Chelonians	Rodents	Soricomorphs
No. of monospecific genera (%)	118 (27.2 %)	28 (29.8 %)	200 (41.6 %)	18 (40 %)
No. of bispecific genera (%)	66 (15.2 %)	18 (19.1 %)	90 (18.7 %)	2 (4.4 %)
Total No. of genera	434	94	481	45

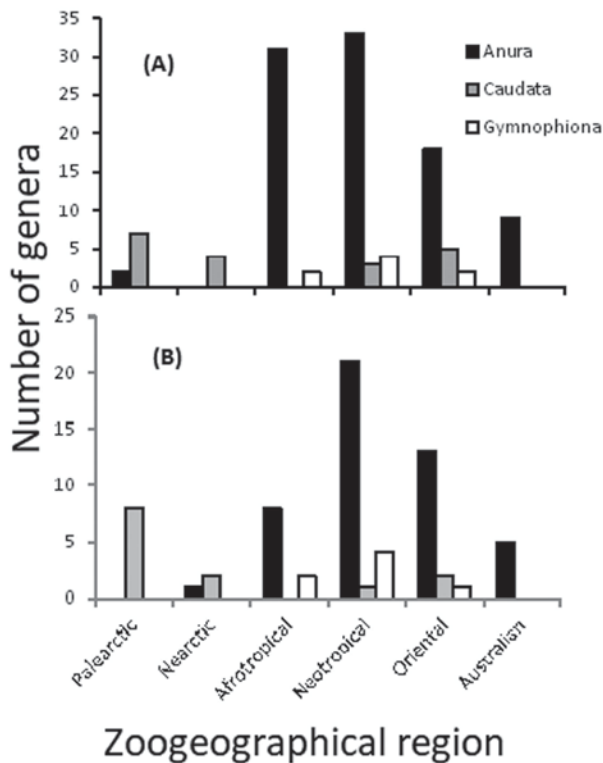


Figure 1. Frequency distribution of monospecific (A) and bispecific (B) genera of amphibians among zoogeographical regions

Data concerning the mono- and bispecific genera of amphibians were extracted from Frost (2018), and their distribution from both Frost (2018) and IUCN (2018). Their conservation status was assessed on the basis of the IUCN (2018) Red List criteria. For all analyses, fossil species were excluded. The zoogeographical region of each taxon was classified according to Wallace (1894), revised in Rueda et al. (2013). In this regard, we used the term 'Afrotropical' instead of 'Ethiopian', which was used originally by Wallace (1894). Data were obtained through the American Museum of Natural History, New York database (available at <<http://research.amnh.org/vz/herpetology/amphibia/>>) on the 9th of March 2017. For all analyses, we considered taxa occurring in more than one zoogeographical region as 'cosmopolitan'. Non-normally distributed variables were log-transformed prior to applying any statistical analyses. Non-normality of a given variable was assessed by Shapiro-Wilk W (assuming a non-normal distribution when $p < 0.05$).

We analysed the differences in the mean number of species per genus across zoogeographical regions by one-way ANOVA. For mono- and bispecific taxa, in the analyses of the mean number of species per genus across zoogeographical regions, we pooled all groups of amphibians (Anura, Caudata and Gymnophiona) given that the number of cases was too low for some groups in some zoogeographical regions (for instance: in Anura, only three families occurred in the Palearctic region). We assessed the correlation between the number of mono- or bispecific genera and the total number of genera in a given family by Pearson's correlation coefficient. We performed observed-versus-expected χ^2 test in order to compare the frequencies of; (i) mono- or bispecific genera among amphibian orders, (ii) mono- and bispecific genera among zoogeographical regions, and (iii) mono- versus bispecific genera by zoogeographical region. In order to evaluate whether the various zoogeographical regions differed in terms of relative IUCN threat level, we first determined the expected frequency of each IUCN (2018) category (Critically Endangered (CR), Endangered (EN), Vulnerable (VU), and the non-threatened Least Concern (LC) + Near Threatened (NT)) by dividing the total number of monospecific taxa listed under each category by the total number of Red List assessed monospecific taxa (% AST). Then, we multiplied the % AST of each category for the total number of taxa of the same IUCN Red List category by the number of taxa of each category in each zoogeographical region (observed; OBS) and obtained the expected (EXP) values. Then, we compared EXP and OBS using a χ^2 test. All analyses were performed by PAST 3.0 statistical software, with alpha = 0.05 and all tests were two-tailed.

The distribution of the number of species per genus is presented in Appendix 1. The mean number of species per genus did not vary significantly across zoogeographical regions (one-way ANOVA: $F_{5,63} = 0.784$, $p = 0.565$).

In total, 120 known monospecific (95 Anura, 17 Caudata, 8 Gymnophiona) (Online Appendix 2) and 65 bispecific (48 Anura, 10 Caudata, 7 Gymnophiona) (Online Appendix 3) amphibian genera are analysed.

Overall, there were 73 amphibian families, with 35.6 % without any mono- or bispecific genera. The percentage of families with no mono- or bi-specific genera was 33.3 % in Anura ($n = 54$ families in total), 44.4 % in Caudata ($n = 9$), and 40 % in Gymnophiona ($n = 10$). The frequency of mono- or bispecific genera was not significantly different among Anura, Caudata and Gymnophiona ($\chi^2 = 4.711$, $df = 2$, $P > 0.050$). In Gymnophiona, the number of monospecific genera was positively correlated with

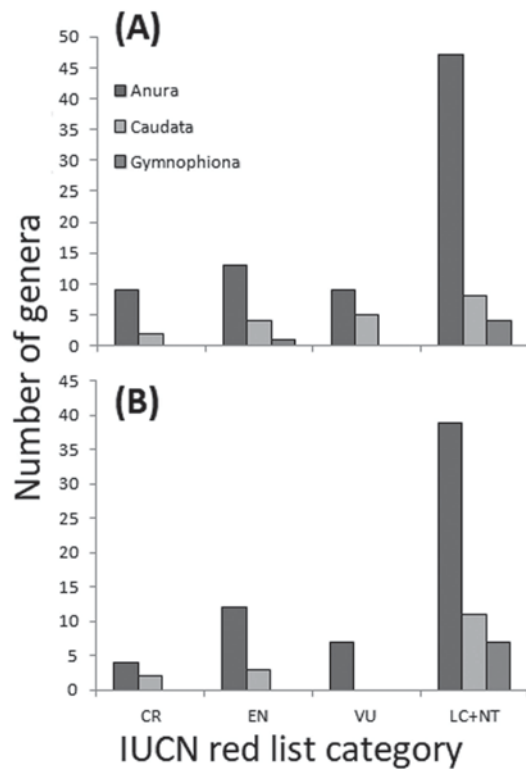


Figure 2. Frequency distribution of monospecific (A) and bispecific (B) genera of amphibians among IUCN Red List categories

the total number of genera in that family ($r = 0.873$, $P < 0.001$), whereas the same relationship was not statistically significant for the bispecific genera ($r = 0.541$, $P = 0.106$). The same relationships were found in Caudata (for monospecific taxa – $r = 0.948$, $P < 0.001$; for bispecific taxa – $r = 0.513$, $P = 0.158$), whereas in Anura there was a significant relationship for both the number of mono- and of bispecific genera (respectively, $r = 0.912$ and $r = 0.920$, all cases $P < 0.001$).

The geographical distribution of the number of species per genus is presented in Online Appendix 1. The mean number of species per genus did not vary significantly across zoogeographical regions (one-way ANOVA: $F_{5,63} = 0.784$, $p = 0.565$). In Anura, the frequency distribution of monospecific genera among zoogeographical regions differed significantly from equality ($\chi^2 = 67.210$, $df = 5$, $P < 0.001$), with a preponderance of genera in Afrotropical and Neotropical regions (Fig. 1A). In Caudata and Gymnophiona, the number of monospecific genera was too low for any statistical analyses, but the absence of the former taxon from Afrotropical region and of the latter taxon from temperate regions (Nearctic and Palearctic) are linked to the absence of the whole group from the respective zoogeographical regions. The frequency distribution of bispecific genera among zoogeographical regions was also statistically different ($\chi^2 = 29.300$, $df = 5$, $P < 0.001$), with a clear preponderance for bispecific genera in the Neotropical region (Fig. 1B). The frequency of distribution of monospecific genera did not differ significantly from that of bispecific genera across the

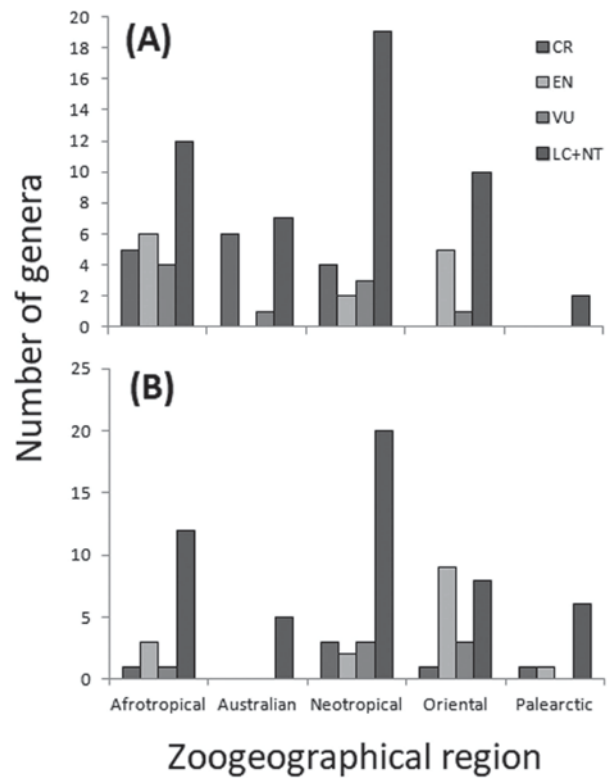


Figure 3. Frequency distribution of monospecific (A) and bispecific (B) genera of amphibians among IUCN Red List categories, by zoogeographical region

various zoogeographical regions ($\chi^2 = 4.424$, $df = 5$, $P = 0.505$).

The summary of the IUCN Red List status for the mono- and bispecific amphibian genera worldwide is presented in Figure 2. Anura clearly dominated the number of threatened mono- and bispecific genera, but this likely reflects a sampling effect as Anura also dominated the number of worldwide amphibian genera (Fig. 2). Overall, a large portion of the mono- and bispecific genera were not threatened according to the IUCN criteria. In addition, there was no significant difference between mono- and bispecific genera in terms of frequency of the various threatened categories ($\chi^2 = 2.591$, $df = 3$, $P = 0.469$). The distribution of the mono- and bispecific genera of amphibians in relation to the IUCN status by zoogeographical region is presented in Figure 3. Concerning the monospecific genera, the highest frequency of threatened taxa (especially CR) was found in the Afrotropical region (Fig. 3A); conversely, for the bispecific genera, the Oriental region supported the highest frequency of threatened taxa (Fig. 3B).

Amphibian taxonomy has undergone substantial changes over the past 20 years and still remains fluid, which is likely to also affect the number of mono- and bispecific genera. Despite this, here we show that (i) the mean number of mono- and bispecific genera was similar among zoogeographical regions, with only about 35 % of the amphibian families do not containing any mono- or bispecific genera; (ii) the number of mono- and bispecific genera depended on the total number of

genera in that family; (iii) in Anura, mono-specific genera occurred especially in Afrotropical and Neotropical regions, and bispecific genera in the Neotropical region. Whilst patterns (i) and (ii) depended merely on statistical reasons, pattern (iii) is worth of discussion in the frame of the general ecology and evolution of amphibians. Indeed, the excess of mono- and bispecific anuran genera in Afrotropical and Neotropical regions is linked to the availability of multiple niches in the tropical forest habitat, that have likely favoured speciation mechanisms for exploiting new resources and minimising interspecific competition (Duellmann, 1989; Slatyer et al., 2007; Losos, 2008). For instance, many mono- and bispecific genera are included in the family Microhylidae, which houses several ecologically highly specialised taxa with their eggs hatching into forest tree-holes or leaf axils, or with eggs developing into froglets in underground chambers (Halliday & Adler, 2002). Thus, we hypothesise that the occurrence of mono- and bispecific genera in amphibians is primarily linked to the exploitation of new micro-niches in tropical forest habitats.

Previous studies have shown that a higher diversity of mono- and bispecific genera occurred in the Oriental region in turtles (Amori & Luiselli, 2018), whereas peaks of mono- and bispecific genera richness were observed in Neotropical, Oriental and Afrotropical regions in Rodentia and in the Palearctic region in Soricomorpha (Amori et al., 2017) (Table 1). Therefore, the comparative evidence among taxonomic groups is that there is no consistent geographic pattern in these types of genera, with the frequency of mono- and bispecific genera differing remarkably by taxonomic groups in terms of “biogeographic hotspots”. We think that inter-taxa differences may reflect the evolutionary history of the various taxa rather than the relative dispersal abilities. Indeed, turtles, amphibians and small mammals are generally small to medium sized vertebrates, with relatively low dispersal potential (at least in comparison with other vertebrate groups) (Cagle, 1944; Gaines & Johnson, 1982; Ousterhout & Liebgold, 2010; Slavenko et al., 2016).

Concerning the IUCN threatened taxa, Amori et al. (2017) found that most mono- and bispecific threatened genera of rodents occurred in the Neotropical region, with no statistical pattern emerging for Soricomorpha.

For turtles, the “diversity hotspot” for threatened mono- and bispecific genera was the Oriental region (Amori & Luiselli, 2018; Rhodin et al., 2018), whereas we found an even more complicated pattern for amphibians, with Afrotropical region being the most important region for threatened monospecific genera (especially due to the contribution of Madagascar) and the Oriental region for the bispecific genera. Thus, once more our data reveal no inter-taxa consistency in the observed patterns. Also in this case, the frequency of IUCN’s (2018) threatened mono- and bispecific genera by zoogeographical region was correlated positively with the relative richness of mono- and bispecific genera in each region. The same correlation between frequency of threatened mono- and bispecific genera and of total genera richness by zoogeographical region was also observed in turtles (Amori & Luiselli, 2018) and in rodents (Amori et al.,

2017).

Pooling the mono- and bispecific genera, there was a similar percentage of occurrence among taxa (44 % in both Amphibians and Soricomorpha, and 48 % in turtles), with only rodents showing a considerably higher percentage (60 %). In addition, in all four taxa studied so far, bispecific genera were always substantially lesser than monospecific genera (representing 60-68 % in Amphibians, Chelonians and Rodents, and 90 % in Soricomorphs). Unfortunately, it is presently unknown whether this pattern was generated by chance or whether monospecific genera are really less rare than bispecific genera in the natural world. In this regard, it would be interesting to extend our approach to further taxa in order to evaluate at least the generality of the observed patterns.

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