

The current status of genetic exploration in amphibians: taxonomic and geographical disparities

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Abstract. We evaluated the current amount of available gene sequences in Amphibia based on public online resources and analysing the number of sequences at the level of species and genera, and according to their distribution at continental level. There are significant disparities considering the level of genetic exploration in different taxonomic groups of Amphibia as well as in different geographical units. Total number of sequences per species as well as taxonomic species coverage was highest in salamanders and lowest in caecilians, and was highest in taxa from Europe, North America and Madagascar, and lowest in Latin America.

Introduction

Today, living amphibians comprise more than 6000 known species. In the last 11 years (1992-2003) this number has increased by 26.3 % and many undiscovered species still remain in species-rich tropical countries (Köhler et al., 2005). At the same time, an evaluation according to IUCN red list criteria revealed that amphibians are suffering severe declines with about 32.5 % of the known species being globally threatened (Stuart et al., 2004).

The establishment of molecular genetics as a tool in systematics and the reconstruction of phylogenetic relationships has led to accumulation of many gene sequences of amphibians and the compilation of a complete phylogenetic tree of the Amphibia has been proposed by initiatives such as AmphibiaTree (<http://www.amphibiatree.org>). The need for a better understanding of the systematics of this highly threatened vertebrate class and the proposed goal of completion of its phylogenetic tree propelled us to draw up an interim balance of available gene sequences to detect deficits, progresses and future needs at the current stage.

Materials and methods

The number of DNA sequences of amphibians available from public resources (<http://www.ncbi.nlm.nih.gov/Genbank>) was analysed as of June 2005 at the levels of species (5758 species considered), genera, families and orders, without considering genome projects currently

underway. We compiled a database with amphibian genera currently recognised as valid, including their allocation to order and family, as well as their geographic distribution at continental level by using AmphibiaWeb (2005) and Frost (2004). We used a scheme slightly modified from geographical definitions of continents and set the geographic categories as follows: sub-Saharan Africa, Latin America (including the Caribbean), North America, Australia/New Guinea, Asia, Madagascar and Europe (including northern Africa) (Fig. 1). Genera with intercontinental distribution were split among continents according to respective species distributions. The analysis was facilitated by the fact that most amphibian genera and almost all species have distribution areas restricted to a single continent. The number of species sequenced as well as the total number of nucleotide sequences available per genus was evaluated using the GenBank taxonomy browser (June 2005). Sequences from genera not considered valid taxa anymore were transferred to the respective valid genus.

A recently published major contribution on amphibian systematics (Frost et al., 2006) provided additional gene sequences of about 500 amphibian species, many of them not sequenced before. These sequences were not included in our analysis and therefore may in part contribute to a picture different from the results presented herein. However, we argue that the identified differences among taxonomic groups and geographical regions constitute a pattern not significantly altered by the sequences accumulated by Frost et al. (2006).

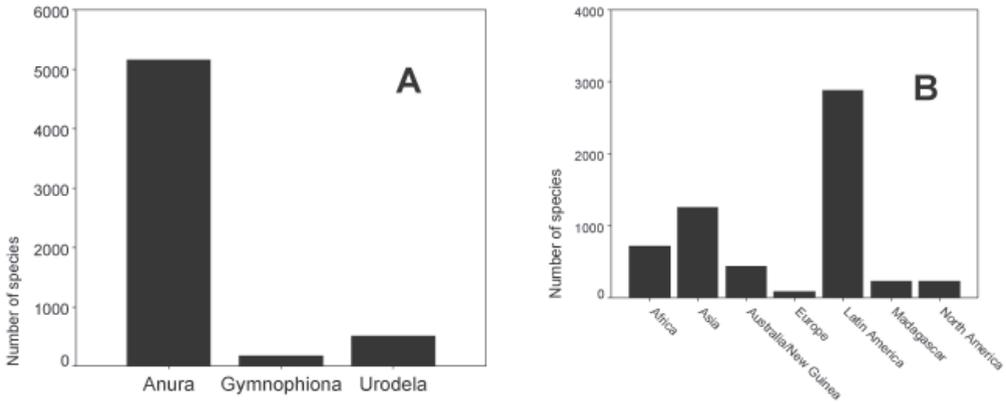
Results

Our analysis revealed that among amphibians, salamanders are best studied with respect to the number of available nucleotide sequences. At average, more than nine sequences are available per species within the Urodela. This is clearly contrasted by the respective mean value for Anura with approximately two available sequences per species and Gymnophiona with approximately one available sequence per species at average (Fig. 2). Generally, European amphibians are best studied genetically, with an average number of available sequences per species of approximately 22. With regard to this character, Europe is followed by North America (approximately 17 available sequences

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Figure 1. (A) Numbers of species recognised by order; (B) Numbers of species recognised per continent.



per species at average), and Madagascar (approximately 7 Sequences per species). Africa, Asia, Australia/New Guinea and Latin America display considerably lower mean values ranging from one to three available sequences per known species (Fig. 3). However, the Australian situation is likely to change soon due to the intensive, yet unpublished, ongoing sequencing projects by several working groups (S. Keogh, personal communication).

Referring to the number of species for which gene sequences are available, about 86 % of the known

species of Gymnophiona lack any sequence data as do approximately 76 % of the recognised anuran species, but only 29 % of species of Urodela (Fig. 4). When considering the number of species studied genetically at continental level, Latin American amphibians are the least explored ones with about 83 % of the known species lacking sequence data. This value is also comparably high in Australia/New Guinea (81 %), Africa (76 %) and to some lesser extent in Asia (68 %). In contrast, only 12 % of European species are without any sequence data (Fig 5).

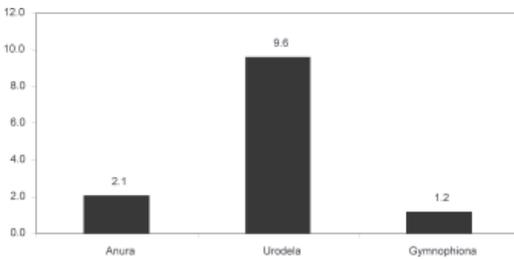


Figure 2. Average number of available sequences per species by amphibian order.

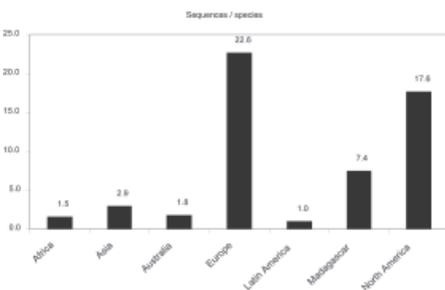


Figure 3. Average number of sequences available per species by continent.

Conclusions

In summary, there are obvious disparities in the degree of genetic exploration between certain taxonomic groups and when comparing different geographical regions. Generally, species-rich tropical regions are ‘under-represented’, as is the diverse order of Anura when compared to the less species-rich and comparably well-studied order Urodela. Among the amphibians without available sequence data are many which are indispensable for the understanding of amphibian systematics and evolution. In view of the goal to compile a complete phylogenetic tree of Amphibia and the exposed threat to this vertebrate group, the following actions are needed: (1) global coordination of sampling activities to avoid major overlap of efforts, (2) intensified field work in remote tropical regions, (3) specific search for key taxa and highly endangered species.

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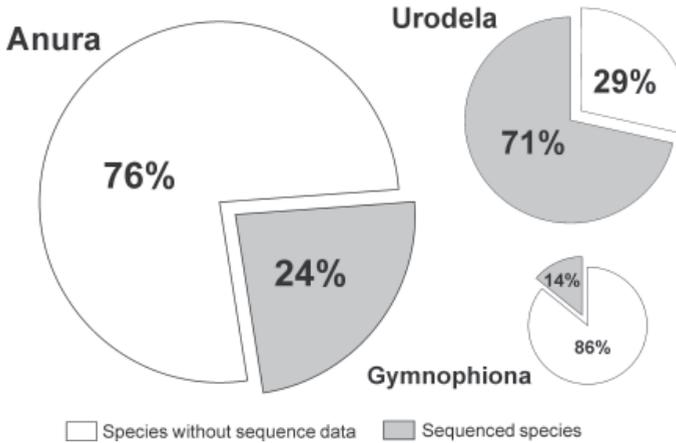


Figure 4. Portions of sequenced amphibian species by order (by June 2005).

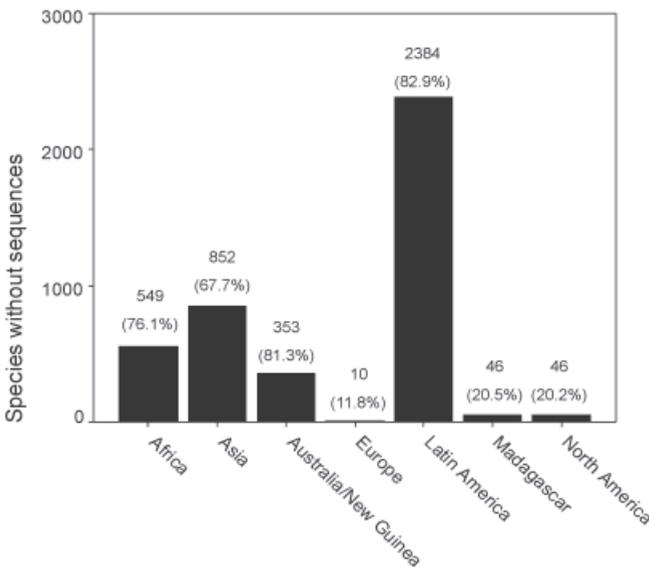


Figure 5. Number and percentage of species without sequences in Genbank by continental distribution.