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# FUTURE PERSPECTIVES

> "*Your time is limited, so don't waste it living someone else's life. Don't be trapped by dogma - which is living with the results of other people's thinking. Don't let the noise of others' opinions drown out your own inner voice. And most important, have the courage to follow your heart and intuition*"
>
> S. Jobs

The results presented here hopefully shed some fresh light on the origin and diversification of the Pantepui biota, tending to reconcile geological hypotheses with molecular phylogenies. However, the molecular results should be considered as still incomplete (and to some extent speculative in Chapter 11) since they are based on a fraction of Pantepui only. Sampling in the western part of Pantepui is highly needed, and the elucidation of the phylogenetic position of some groups like *Metaphryniscus* and *Cryptobatrachus* are necessary to have a complete picture of the situation. Unfortunately the current political situation in Venezuela, and associated bureaucratic obstruction, make life of scientists (local and foreign) very hard, rendering sampling in the western Pantepui extremely challenging.

Phylogenetic and morphological analyses performed during the course of this work revealed several taxonomic issues that will be soon assessed in more details. The major ones being:

- Composition of the current species groups in *Stefania* is not congruent with the phylogenetic relationships of the species themselves (species of the *evansi* and *goini* groups are polyphyletic)
- *Stefania ackawaio* MacCulloch and Lathrop, 2002 should be synonymised with *S. roraimae* Duellman and Hoogmoed, 1984
- The occurrence of *Stefania scalae* in Guyana is not confirmed since specimens identified as *S. scalae* have been confused with *S. evansi*. The distribution of *S. scalae* is therefore still restricted to the eastern part of the Gran Sabana in Venezuela.
- Several new Pantepui taxa, at least in the genera *Anomaloglossus*, *Stefania* and *Pristimantis*, await description
- *Anomaloglossus verbeeksnyderorum* Barrio-Amorós, Santos, and Jovanovic, 2010 should be synonymised with *A. wothuja* (Barrio-Amorós, Fuentes-Ramos, and Rivas-Fuenmayor, 2004)
- *Oreophrynella dendronastes* Lathrop and MacCulloch, 2007 should be synonymised with *O. macconnelli* Boulenger, 1900
- The genus *Oreophrynella* needs to be thoroughly revised
- *Tepuihyla galani* Ayarzagüena, Señaris, and Gorzula, 1993 and *T. talbergae* Duellman and Yoshpa, 1996 should be synonymised with *T. rodriguezi* (Rivero, 1968)
- *Tepuihyla edelcae* is not monophyletic, specimens previously identified as *T. edelcae* from the Chimantá Massif (Bolívar, Venezuela) belong to a distinct, undescribed species
- *Osteocephalus exophthalmus* Smith and Noonan, 2001 and "*Hyla*" *warreni* Duellman and Hoogmoed, 1992 should be transferred to the genus *Tepuihyla*

- *Neusticurus rudis* is not monophyletic
- Close genetic relationship between *Arthrosaura guianensis* and *A. hoogmoedi* suggests reconsideration of the taxonomic status of the latter, but is in strong conflict with morphology-based analyses

Historical processes behind the isolation of Pantepui from the surrounding areas remain puzzling, and the possible role of marine incursions in the isolation of Pantepui endemics remains to be assessed. This should be done by using meta-analyses involving multiple unrelated groups.

While I was working on this thesis some more fundamental questions arose, like:

(1) What are the genetic adaptations to the tepui summit habitat? What is the genomic basis of adaptation to thermic (alternance of very low and very high temperatures), hypoxic, and oxidative (exerted by strong Ultra-Violet light irradiation) stress? Amphibians seem ideal models to study this since they need adaptation both in larval and adult stages. Why some lowland species seem to cope with these challenges, and is there any genomic differentiation between lowland and tepui top populations within a same species? Since a few taxa are found from the surrounding uplands to high tepui summits Pantepui seems the ideal region to study these exciting topics.

(2) How much of the morphological variation is truly genetic, and how much of it is merely environmentally induced?

(3) How much are patterns explained by vicariant events and how much by climate?

(4) Why do some taxa tend to actively disperse, while others remain philopatric? Does ecological plasticity have a genetic basis?