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The sexual signals of speciation? A new sexually dimorphic *Phymaturus* species of the *patagonicus* clade from Patagonia Argentina

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Abstract

Evolution is a multivariate process which, therefore, is expected to leave multiple recognizable signals after episodes of speciation. These signals express in the genome regardless of the mechanism driving speciation, and in a few or in multiple phenotypic traits when divergent selection has been implicated. In lineages that have undergone adaptive radiations (i.e. speciation accompanied by ecological diversification), the phenotypic signals of speciation can be substantially pronounced. In contrast, within non-adaptive radiations (i.e. lineage diversification with minimal ecological diversification linked to allopatric or parapatric species distributions), phenotypic signals of speciation can be minimal. The South American lizard genus *Phymaturus* is regarded as a candidate non-adaptive radiation given the tendency for non-overlapping distributions among its phenotypically and ecologically similar (i.e. niche conservatism) species. Thus, limited phenotypic divergence has evolved among closely related species. Within the *patagonicus* clade of the genus, sexual monochromatism is highly conserved, while sexual dichromatism is rare, and mostly negligible when observed. In this paper, we provide the description of a new sexually dimorphic and dichromatic species of this clade (*Phymaturus camilae* **sp. nov.**). This species is substantially isolated spatially and phylogenetically separated from *P. ceii*, *P. delheyi* and *P. zapalensis*, the most sexually dichromatic members of the clade. In addition, the new taxon was recently identified as a ‘candidate new species’ based on molecular (nuclear) phylogenetic evidence.

Key words: Sexual dimorphism, non-adaptive radiation, lizards, *Phymaturus*, Liolaemidae, Patagonia

Introduction

Speciation driven by selection results in evolutionary signatures left on the phenotypes and niches of the newly originated species (Coyne & Orr 2004, Nosil 2012). Depending on the mechanism of selection implicated in speciation, the expression of these signatures is expected to differ across pairs of phylogenetically sister species. The evolution of phenotypic asymmetries between males and females (sexual dimorphism) has extensively been implicated with speciation in one way or another. Traditionally, divergent evolution of sexual dimorphism between species that share common ancestors has been linked to sexual selection operating in different directions on the relationship between preferences in one sex (usually females) for phenotypes expressed in the other (usually males), which results in accumulation of genetic differentiation (via emerging reproductive isolation) and ultimately in speciation (Barraclough *et al.* 1995, Panhuis *et al.* 2001, Ritchie 2007, Kraaijeveld *et al.* 2011). Under this scenario, sexually selected dimorphisms are expected to differ between species (e.g. Panhuis *et al.* 2001). On the other hand, theory suggests that natural selection-driven sexual dimorphisms can prevent speciation events from occurring. Given that disruptive natural selection is the common driving force behind both ecological dimorphisms and ecological speciation (Slatkin 1984), the first of these outcomes to express is predicted to eliminate the diverging impetus of selection needed to drive the other (Bolnick & Doebeli 2003, Butler *et al.* 2007). The expectation in these cases is that sexual dimorphisms are significantly greater in allopatric sister species