Two lizard species that occur in northern Uruguay are poorly known: Stenocercus azureus and Hemidactylus mabouia. We sequenced the genes 12S and ND2 and estimated phylogenetic trees. The H. mabouia sequence found in Rivera City was unique and more closely related to a widely distributed haplotype found in Brazil, Argentina, and the Caribbean. The S. azureus from near Masoller (Salto) grouped with a sample of S. azureus from Bajada de Pena (Rivera). We encourage further sampling in order to assess the population structure of H. mabouia in Rivera City and to delineate potential conservation units of S. azureus in the region.

Keywords: DNA, phylogeny, biogeography.
Evolutionary affinities of two rare lizards from Uruguay

We estimated gene trees with BEAST 1.8.4 (Drummond et al., 2012) based on the alignments and the best substitution models selected with jModelTest2 (Darriba et al., 2012). Posterior trees were summarized with TreeAnnotator 1.8.4 (Drummond et al., 2012) and visualized with FigTree 1.4.3 (Rambaut, 2012). We also estimated a haplotype network for the *H. mabouia* dataset using TCS 1.21 (Clement et al., 2000).

We analyzed 352 base pairs of 12S for *H. mabouia* (GenBank accession number KX645627). The sample from Rivera was unique among the available sequences of *H. mabouia* in GenBank. The estimated genealogy shows that this haplotype found in Rivera is more closely related to a widely distributed haplotype found in Brazil, Argentina, and the Caribbean (Fig. 2A). However, all internal nodes within *H. mabouia* have very low support, and consequently, these relationships should be regarded as a polytomy. This lack of resolution is consistent with the very few mutational steps connecting the haplotypes (Fig. 2B). Other haplotypes of *H. mabouia* are even more widely distributed in the Americas and Africa, or are exclusive from Africa (Fig. 2B, Appendix). For *S. azureus*, we obtained 657 bp of ND2 (GenBank accession number KX663824). The sample obtained close to Masoller grouped with a sample of *S. azureus* from Bajada de Pena in Departamento de Rivera (GenBank accession number DQ080214), which is aprox. 18 km from our sample locality (Fig. 3). Despite this short geographic distance, these samples differed by four mutational steps (0.6% divergence).

Our results suggest that *H. mabouia* in Rivera dispersed most likely from a neighboring population in Brazil, instead of being directly transported from ancestral populations in subsaharan Africa. Widely distributed haplotypes separated by a few mutational steps suggest a recent range expansion of the species after colonization of the Americas. This result is consistent with the oldest known records in Paraguay (Cacciari & Motte, 2009), Argentina, and Uruguay (Baldo et al., 2008) in the mid-80s, while the species was well known and widely distributed in Brazil earlier (Kluge, 1969). It has been reported that the species was accidentally introduced via banana shipments from southern Brazil towards eastern Uruguay (Baldo et al., 2008). Therefore, it is possible that this same mechanism of human transportation has introduced the species in Rivera City that has an intense transportation activity across the international border. Additional geographic sampling and more rapidly evolving molecular markers would be necessary to further elucidate the routes of dispersal of this invasive species in Uruguay and the region.

Fig. 1. Map of northern Uruguay showing the sampling localities for *Stenocercus azureus* (A) and *Hemidactylus mabouia* (B). The yellow solid line represents the international border between Uruguay and Brazil, and the dotted yellow line indicates the limits between the Departamentos of Rivera, Tacuarembó, and Salto.
encourage further sampling in Rivera City in order to evaluate the current phase of the invasion given its high abundance as reflected in numerous sightings throughout the city.

The estimated genealogy for Stenocercus shows that the sample from near Masoller corresponds to S. azureus, but it also reveals that there is differentiation between nearby localities. This result is consistent with the assignment of these localities to different geographic basins despite the short distance separating them: our sample locality belongs to the Arapey River basin, and Bajada de...
Pena is located within the Tacuarembó River basin (Fig. 1). Given this level of differentiation at a small geographic scale and the fragmented nature of the rocky hills habitat within the distribution range, it is possible that the species harbors strong genetic structure. Because the species is of conservation concern (Carreira & Maneyro, 2015; www.icmbio.gov.br/portal/faunabrasileira/lista-de-especies), we encourage an increased sampling effort in the region (Uruguay, northeastern Argentina, and southern Brazil) to delineate potential conservation units.

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Appendix. DNA sequence alignments and phylogenetic trees in TreeBASE repository: https://treebase.org/treebase-web/search/study/summary.html?id=23594

The GenBank accession numbers of H. mabouia 12S sequences and their associated haplotypes are: (A) KC840429, DQ120374, DQ120373, DQ120372, DQ120371, DQ120370, DQ120369, DQ120368, DQ120367, DQ120366, DQ120365, DQ120364, DQ120363, DQ120362, DQ120361, DQ120359; (B) DQ120375, DQ120358, DQ120357, DQ120356, DQ120355, DQ120354, DQ120353, DQ120352, DQ120351, DQ120350, DQ120349, DQ120348, AY156909, AF324794; (C) KC818685, DQ120360; (D) DQ120377, DQ120376; (E) KX645627.

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