

Hybridization between caimans: the cherry on the (evolutionary) cake

Gualberto Pacheco-Sierra^{*1,3}, Patricia Amavet^{2,3} and Carlos Piña^{1,3}

¹Centro de Investigación Científica y de Transferencia Tecnológica a la Producción, España 149, Diamante E3105BWA, Argentina. *(chunko.pacheco@gmail.com) (cidcarlos@infoaire.com.ar)

²Laboratorio de Genética, Departamento de Ciencias Naturales (FHUC - UNL), CONICET, Ciudad Universitaria, Santa Fe S3001XAI, Argentina. (pamavet@fhuc.unl.edu.ar)

³Proyecto Yacaré – Laboratorio de Zoología Aplicada: Anexo Vertebrados (FHUC-UNL /MASPyMA), Av. Aristóbulo del Valle 8700, Santa Fe 3000, Argentina.

Abstract: In the last decades, several researches on crocodylians have been carried out with a genetic focus from a macro-evolutionary perspective that has defined the phylogenies that we know so far; or from a micro-evolutionary approach that has determined the genetic conservation status of populations of different species at the local level. However, interspecific hybridization processes have a significant influence at both evolutionary levels (e.g. reticulation, divergence, speciation, phylogeographic continuum, introgression, variable genetic diversity, etc.) and they have been greatly underestimated, which can lead to the erroneous determination of phylogenies due to semi-permeability in species boundaries. Our objective was to identify if there is a pattern of hybridization between *Caiman yacare* and *Caiman latirostris* in the southernmost distribution of crocodylians in the American continent (South America) and compare it with the hybridization processes that we have studied in Mexico (North America). Our results determined the existence of a hybridization pattern between both species (using maximum likelihood and Bayesian analysis); with a marked hybrid zone that is potentially wider due to the large distribution of both species in South America. This hybridization process is bidirectional with potentially fertile offspring. From our mtDNA analysis it is not possible to determinate if this is an ancestral hybridization process or not. This comparison of the hybridization processes between crocodylians from the north and south of the continent allows us to infer that the hybridization processes between crocodylians have great potential to expansion of hybrid zone and possible displacement of non-admixed species. On the other hand, it confirms that hybridization processes between crocodylians are more common than we think, highlighting the approach that we must address in sympatry areas between species that can potentially hybridize in Central and South America and attending to the evolutionary effects of hybridization as a natural process in wildlife.

Keywords: Hybridization, Evolution, Crocodylians, Species boundaries.

Type of presentation: Oral

Thematic area: Research and Knowledge (P3: Systematic and Evolutionary Biology).