

Determining population structure among Argentinian jaguars (*Panthera onca*)

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The jaguar (*Panthera onca*) is the largest felid in America and the most emblematic South American predator. This carnivore species holds a high environmental importance in all ecosystems it inhabits for its apex predator role. Jaguar populations have suffered an important decline over the last century and today this species is considered as critically endangered in Argentina. Ensuring the sustainability of the remaining jaguar populations demands a high degree of knowledge about the current state of their genetic variability levels and a description of population structure is essential, especially to allow rational translocation and reintroduction actions. The first jaguar reference genome was released in 2017 (Figueiro *et al.* 2017) by the Jaguar Genome Project, a consortium we integrate.

With the aim of generating useful resources and information for the jaguar genetics and conservation from the genomic perspective, we carried out the whole genome sequencing of 9 jaguar samples using Illumina 2500 NSG technology. Here we present the first results obtained from these 9 genomes compared to the reference. We performed a population structure analysis in order to estimate the optimal number of populations present in our data and a Multiple Correspondence Analysis (MCA) clustering of our samples based on over 280.000 homozygous variable positions in their genomes. The estimation of the optimal number of populations present among our samples resulted in 6, according to the Structure analysis. However, the MCA clustering analysis only revealed 5 groups of individuals. The main genetic cluster of animal obtained is integrated by captive animals from zoos and natural reserves and surprisingly a Paraguayan male. Apart from this central group, a wild Argentinian sample from Misiones (a province in the north-east of the country) was located. Also, an animal of Uruguayan origin and the reference, built from a Brazilian animal, located in individual clusters.

More work including heterozygous variable position analysis will be performed to better describe the genetic variability among the sequenced jaguar genomes and accurately describe the current genetic situation and population structure of this species in Argentinian territory.