

Whole-genome sequences shed light onto demographic history and contemporaneous genetic erosion of free-ranging jaguar (*Panthera onca*) populations

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Abstract

The vast amount of data contained in a single genome represents a detailed record of past events in that lineage and may forecast its evolutionary potential in the face of environmental changes. Here we employed whole-genome sequence (WGS) data to infer the demographic history and assess signals of recent inbreeding in jaguar (*Panthera onca*) populations. We analyzed whole genomes from 13 individuals (nine of which are reported here for the first time) sampled in seven different biomes across the species' range, including its northernmost extreme in the Mexico/USA border region. We modelled demographic history using the PSMC method, and analyzed long runs of homozygosity (ROH) to assess signals of population bottlenecks and inbreeding. PSMC plots were very consistent among individuals, indicating that the jaguar lineage had an effective population size of up to 100,000 individuals ca. 1 million years ago, then sharply declined and rebounded during the Late Pleistocene, followed by a more gradual decline in the last 40,000 years. This decline was more pronounced in the North/Central American genomes, likely reflecting population bottlenecks during the south-north colonization towards the edge of the species' current range. The ROH analysis revealed a relatively small burden for most jaguars, indicating a recent history of outbreeding and large-scale connectivity among regional populations. However, northern range-edge individuals and those from severely fragmented populations showed signals of recent bottlenecks and, in the latter case, inbreeding. Our results illustrate the power of WGS data to survey and monitor the genetic erosion triggered by anthropogenic habitat fragmentation.

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