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Title: POPULATION GENOMICS OF IBERIAN LYNX (Lynx pardinus)
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Abstract
Iberian Lynx (Lynx pardinus) is considered to be the most endangered felid worldwide. The only two known breeding populations are located in Spain, one in Sierra Morena mountains and the other in Doñana National Park. The later being the smallest and most threatened one. Within the Lynx Genome Project, 11 lynx males have been sequenced with high coverage (~26X). This data have offered the opportunity of calling and genotyping 1.4 million SNPs and also to study the demographic history of the species. Analyses of genome-wide SNP data, have provided insight into the inbreeding coefficients, the extent of linkage disequilibrium and also pinpointed areas of strong differentiation between the extant populations. Finally, a coalescent model was used to reconstruct the historical variation of effective population size of Iberian and Euroasian lynx (Lynx lynx). The observed fluctuations of population size are coincident with severe climatic changes during the Pleistocene that may have affected similarly to other European and Eurasian animals.