

# Unraveling the natural history of the lion using host and virus population genomics

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The lion (*Panthera leo*) is one of the world's most charismatic carnivores. In an article published November 7 in the open-access journal *PLoS Genetics*, an international team of researchers provides insights into the genetic structure and history of lion populations. Their work refutes the hypothesis that African lions consist of a single, randomly breeding (panmictic) population. It also indicates the importance of preserving populations in decline as opposed to prioritizing larger-scale conservation efforts.

Understanding the broader aspects of the evolutionary history of the lion has been hindered by a lack of comprehensive sampling and appropriately informative genetic markers. Nevertheless, the unique social ecology of lions and the well-documented infectious diseases they have experienced, including lion-specific feline immunodeficiency virus (FIVPle), provides the opportunity to study lion evolutionary history using both host and virus genetic information.

In total, a comprehensive sample of 357 individuals from most of the major lion populations in Africa and Asia were studied. The authors compared the large multigenic dataset from lions with patterns of genetic variation of FIVPle to characterize the genomic legacy of lion populations. The research reveals evidence of unsuspected genetic diversity even in the well-studied lion population of the Serengeti ecosystem, which consists of recently admixed animals derived from three distinct genetic groups.

Citation: Antunes A, Troyer JL, Roelke ME, Pecon-Slattery J, Packer C, et al. (2008) The Evolutionary Dynamics of the Lion *Panthera leo* Revealed by Host and Viral Population Genomics. PLoS Genet 4(11): e1000251. doi:10.1371/journal.pgen.1000251  
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