

News

On the prowl for insights into lions' genetic evolution

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An international team of researchers has successfully traced the evolutionary history of the world's lions in unprecedented detail. The researchers' findings published online in the journal Public Library of Science (PLoS), indicate that there are 11 genetic subsets in today's lions that not only distinguish African from Asian populations but also separate genetic strands within the African population.

The subsets, most of which are determined by geographical clusters, include individual ones in Namibia, Kruger National Park (South Africa), Ngorongoro Crater (Tanzania), Kenya, Uganda and the Gir Forest in India as the only Asia subset. In addition, there are two distinct clusters in Botswana and three in Serengeti National Park (Tanzania).

The findings contradict the theory that African lions consist of a single, randomly breeding or so-called 'panmictic' population. The authors of the study, including researchers from Portugal, the UK, Africa and the US, conclude that greater efforts should go into preserving individual populations as opposed to large-scale conservation schemes.

'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,' the authors explain. In an effort to address that shortcoming, they examined the genetic makeup of 357 lions from Africa and Asia.

The scientists also analysed patterns and variations of viruses found in the big cats. 'The unique social ecology of lions and the fact that lions have experienced well-documented infectious disease outbreaks [...] provide a good opportunity to study lion evolutionary history using both host and virus genetic information,' the study reports. 'Indeed, population genetics of transmitted pathogens can accurately reflect the demographic history of their hosts.'

In this regard, the feline immunodeficiency virus (FIV), a retrovirus analogous to the human immunodeficiency virus (HIV), was particularly useful because, the authors explain, 'the virus is quite genetically diverse in lions, offering a unique marker for assessing ongoing lion demographic processes.'

According to the analysis, today's population of 50,000 free-ranging lions in sub-Saharan Africa and Asia derive from several habitats in Eastern and Southern Africa in the Pleistocene epoch (about 324,000 to 169,000 years ago). These genetically distinct populations spread into Central and Northern Africa and into Asia during the Late Pleistocene (about 100,000 years ago). Between 14,000 and 7,000 years ago, during the Pleistocene/Holocene transition, the big cats from habitats in the south spread again towards the north and east, so that there was interbreeding between populations.

Yet, the study concludes, 'in spite of the ability of lions to disperse long distances, patterns of genetic diversity suggest substantial population subdivision [...], and reduced gene flow, which, along with large differences in [...] six distinct FIV-Ple subtypes among lion populations, refute the hypothesis that African lions consist of a single panmictic population.'

For further information, please visit:

<http://www.plosgenetics.org/> [<http://www.plosgenetics.org/>]

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