

Mane event: Recombination in lion feline immunodeficiency virus

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Parts of feline immunodeficiency virus (FIV) isolated from wild lions have undergone substantial genetic recombination, says research published in the online open access journal *BMC Genomics*. The sequencing of the two full FIV genomes of different lion subtypes shows the importance of whole-genome analysis in understanding complex genetic events. These findings will be relevant to big cat conservation and developing more effective animal models for HIV.

FIV is a member of the lentivirus family of retroviruses, as is HIV. The feline virus causes similar disease progression to HIV in domestic cats, and is used by researchers as an animal model for human disease.

FIV also infects a number of other cat species, many of which are endangered. The virulence and pathogenicity of the virus varies between species, but the genetic contribution to this variation is unclear. Full-length viral genome sequences are vital for scientists to understand the extent of genetic involvement yet, until recently, only six species-specific strains of FIV had been sequenced in full: Pallas cat, domestic cat (subtypes A, B and C) and puma (subtypes A and B).

Now, Jill Pecon-Slattery and Stephen J. O'Brien from the National Cancer Institute's Center for Cancer Research in Frederick, MD, USA and colleagues from the USA and Botswana have sequenced the genomes of two lion FIV subtypes in full: FIVPle subtype B, isolated from lions in the Serengeti National Park in Tanzania, and FIVPle subtype E, isolated from lions in the Okavango Delta in Botswana. Using

comparative genomics methods the team found that the two viral subtypes shared a common evolutionary history – confirming earlier research that suggested FIV has evolved in a species-specific manner.

However, the lion viruses showed substantial variation in the env gene region, which encodes the envelope glycoprotein essential for viral binding and entry. Lion virus subtype E was more closely related to domestic cat virus than to lion subtype B or Pallas cat virus. The researchers suggest this is due to recombination between strains in the wild, either involving an unidentified lion FIV strain or a strain from another African cat species.

The authors write: “The changes observed in the env gene as a consequence of recombination in FIV_{Ple} will provide important clues to the natural history of these viruses and their hosts, and may lead to insights into genetic determinants of pathogenicity and virulence differences between domestic cat and lion FIV; findings with important implications for HIV pathogenesis in humans and virus attenuation in wild populations of endangered species.”

Source: BioMed Central

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