



Category: Animal genomics

Genome –wide variation and demographic history of small cats with a focus on Felis species

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Abstract

Majority of the 38 known cat species are classified as small and they inhabit five of the seven continents. They survive in a vast range of habitats but still 12 out of the 18 threatened felids are small cats. However, there has not been enough progress in the field of small cat research as they generally get overshadowed by the charismatic big cats. Here we attempt to create a resource for small cat research especially of the genus Felis which has six species out of which two are classified as vulnerable by IUCN and at least one more is at risk. We collected tissue samples of four Felis chaus (Jungle cat) from central India and used available whole genome sequences of nine individuals from four other Felis species, two individuals of Prionailurus bengalensis and an Otocolobus manul. These whole genome sequences were filtered and aligned with the already published domestic cat (Felis catus) genome assembly. Felids are closely related species and reads from all species in our study aligned with the domestic cat genome with a rate of at least 93%. We estimated the existing genomic variation by calculating heterozygous SNP encounter rate. So far, it seems that all wild cats have more genetic variation than Felis catus species. This can be attributed to the inbreeding in these cats. Among the wild cats, Felis silvestris seems to have the highest level of genetic variation. To understand the reasons behind the distribution of genetic variation in small cats, we estimated the demographic histories of each of the species using PSMC. This method can only detect demographic changes more than 1000 generations ago. We observe that roughly all species share a parallel history in terms of population increase. The most interesting and important feature might be that all wild small cat population sizes increased exponentially around twenty thousand years ago as opposed to domestic cat and big cats which declined around this time. Another interesting feature of the demographic history is all the small cats seem to have recovered from the effects of Toba Volcano eruption which had triggered a glacial maximum leading a decline in big cat population. Thus it seems the partitioning of genetic variation has happened less than ten thousand years ago owing to anthropogenic activities?

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