Royal Bengal tiger genome sequenced

It will help in precise understanding of tiger's evolutionary linkage

Y. MALLIKARJUN

For the first time, the genome of the Royal Bengal tiger, an endangered big cat, has been sequenced as part of plans to generate a high-quality draft genome sequence of the animal. Although endangered and threatened by various extinction risks, this tiger subspecies is the most populous one with the highest genetic diversity and the strongest chance of survival in the wild.

The high coverage genome sequencing and identification of genome variants in Bengal tiger (Panthera tigris tigris) were carried out by scientists from the Centre for Cellular and Molecular Biology (CSIR-CCMB) and a Hyderabad-based private company. The details of the study were published online in BioRxiv recently. This genome was compared with the genome of Amur or Siberian tiger. These two subspecies occur in diverse environments and the new data also reveals major variations between the two. While Amur tiger occurs exclusively in sub-tropical and snow-covered habitats, the Bengal tiger occupies diverse tropical habitats ranging from Himalayan foothills to Central India plateau and the Western Ghats.

Genome data provides an insight into the genetic differences at individual level – ranging from single nucleotide variations to large structural variants. It also provides a better understanding of how the gene variants play a role in adaptation to the environment and disease susceptibility. In other words, it will reveal the changes triggered in the genes due to the adaptability to different environments in the evolutionary time scale.

The study observed “For a very long time it was believed that single nucleotide variants (SNVs) contribute to a majority of the individual genomic variations. Now it is recognized, albeit poorly understood, that much larger changes in the genome like structural variants and copy number variants also contribute significantly to disease susceptibility, phenotypic variations and immunity”.

The researchers claim that this is the first report on the discovery of copy number variants and large structural variants in the genome of a wild, endangered species. The comprehensive data of Bengal tiger and Amur tiger genome sequences “will initiate our understanding on genomic changes and the species ability to adapt to discreet habitats”, the scientists write.

The identification of numerous Simple Sequence Repeats (SSRs) will help in gaining a better insight into population genetics and gene flow. Dr. P. Anuradha Reddy, the lead author of the paper said that the numerous SSRs and SNVs identified in the genome can be used to strengthen forensic evidence in tiger poaching cases.

Such studies will also help in improving conservation management as authorities attempting to relocate an endangered animal will have a better understanding of its adaptability to the new environment.

CCMB Director, Dr. Rakesh Mishra said that genome sequencing will help in precise understanding of the evolutionary linkage of the organism. Besides, epigenetic analysis becomes possible once the genome is available.