

The Asian elephant joins the ever-growing list of animals with sequenced genomes. Recent analyses throws light on the genetic bases of evolution in these intelligent, social animals. Researchers at Prof. R. Sukumar's lab in the Indian Institute of Science (IISc) Bangalore and Prof. Sanjeev Galande's lab at the Indian Institute of Science Education and Research (IISER) Pune have analyzed the genome and transcriptome sequences of an Asian elephant in their report published in the December issue of the Journal of Biosciences.

India is home to the largest population of the Asian elephant, *Elephas maximus*, an endangered species with less than 50,000 individuals remaining in the wild. The Asian and the African elephants are the largest living land mammals; have a shared evolutionary history dating back about 7 million years ago, yet exhibit species-specific differences. Most of the research on elephants so far has been focused on themes such as ecology, behavior, demography, reproductive biology, welfare and conservation. However, there have been very few studies on understanding the genetic bases of evolutionarily important traits and processes. This study demonstrates the power of next generation sequencing and comparative genomics and transcriptomics in the study of functional genetics in a non-model species.

The authors have sequenced the genome of an Asian elephant from Karnataka in south India and identified more than 1500 genes that harbor changes specific to the Asian elephant when compared to the African elephant. One of the most significant subset of these genes were found to be involved in olfaction, and possibly indicate an evolutionary adaptation to differences in the chemical signals that the Asian elephant lineage encountered after it moved out of Africa. The authors have also reported the first transcriptome sequence in the Asian elephant. Analyses of the Asian elephant transcriptome from blood lymphocytes has uncovered the expression of numerous novel transcripts, as well as confirmed the expression of genes and non-coding RNAs that are known to be expressed in lymphocytes of other mammals. Further, the authors have identified proteins with domain architectures unique to elephants in comparison with three other related species of the superorder Afrotheria. Many of these genes and transcripts might have important roles in determining species-specific traits and warrant detailed investigations in the future.

Genome sequencing and comparative analyses of the Asian elephant reveal interesting insights

In summary, the authors have developed a useful resource and provide a proof of concept for comparative sequence analyses, which combined with the already available genome sequence of Asian elephant can be used for functional genetics research of elephantids in the future. Future research can also be directed towards the study of evolutionary relationships and trait-/species-specific evolutionary processes both within the elephantids, as well as between elephants and other mammals.