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Genomes Map Elephant Populations, History

By: Arathi Menon

A recent genome study of elephants in India sheds new light on their population, divergence, and history. The study identifies five distinct genetic populations of elephants in the country, with a divergence history dating back as far as 70,000 years.

Asian elephants are one of the better studied species in the country. Yet, every new study provides a fresh glimpse into the secret world of jumbos. A recently published [study](#) on the genetic history of Asian elephants in India reveals some new findings — there are five genetically distinct populations of elephants in the country and their history is much older than previously thought.

Uma Ramakrishnan, a professor at the National Centre for Biological Sciences (NCBS) and one of the researchers associated with the study, says that animal genomics reveal intriguing aspects of the country’s wildlife history. “It’s fascinating to use DNA to reconstruct the past of various wildlife species. As we continue this work with different species, we’ll gain insights into India’s wildlife past,” she informs Mongabay India. She adds that it was important to explore this, especially since most impacts on wildlife have occurred in the last 200 years due to habitat fragmentation, increasing human populations, and other factors.

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India is home to approximately [30,000 Asian elephants](#) which constitute 60% of the global Asian elephant population spread across South and Southeast Asia. The current study done by researchers at the NCBS and the Indian Institute of Sciences (IISc) found five genetically distinct populations — one each in the north and central India and three in south India. Blood samples were collected from wild elephants in captivity for these regions and whole genome sequences were analysed to reach the conclusion.

Conservation ecologist Aritra Kshetry of WWF-India sees the genome study as an important milestone in elephant conservation that expands its scope. Earlier studies pointed to [three to four populations](#) with the north and northeastern populations being unique and distinct from each other. The [current study](#) adds one more population while arguing that the north and northeastern populations are a single cluster.

While the Palghat Gap in the south has historically played a key role as a barrier in species diversity and dispersal, the study finds another potential barrier for elephants in the south — the Shencottah (officially, Sengottai) Gap. The south of the Gap has a small genetically distinct population that’s low on genetic diversity and hence, believed to be more vulnerable to adversities. The three South Indian populations are found in the north of Palghat Gap, the south of Palghat Gap and the south of Shencottah Gap.

Go the extra mile

Another fascinating discovery is the species’ divergence and long history — estimated to be between 20,000 and 70,000 years — shares lead author Anubhab Khan from the IISc. “The northern population split into two, forming the northern (Terai) and northeastern populations. We believe the central Indian population diverged from the northeastern population around 50,000 years ago. The population north of the Palghat Gap diverged from the northeastern population 70,000 years ago. A subset of this population migrated to the south of the Palghat Gap, while a subset from the southern Palghat Gap population moved to the south of the Shencottah Gap approximately 20,000 to 30,000 years ago,” explains Khan, who adds that these are incredibly long histories not often come across in wildlife studies.

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The study reveals an intriguing narrative of elephant colonisation in the country. The antiquity of divergence also signals strong and big genetic differences between the populations, as Ramakrishnan notes. Khan explains, “This history of how they moved, or how they colonised the country, has also shaped their genetic diversity and genetic load. The genetic load is essentially the amount of disease

causing alleles the populations have.” The **genetic load** refers to the reduction in the mean fitness of a population relative to a population composed entirely of individuals having optimal genotypes. In simpler terms, genetic load indicates the presence of unfavourable genetic material in the genes of a population.

The study, published in *Current Biology*, observes that as the population diverged and migrated from north to south, the deleterious alleles — the gene variants that reduce the fitness of an individual — became diluted, with the southern population exhibiting fewer of them. The presence of these deleterious alleles, which leads to lower fitness, could manifest as reduced lifespan or fewer offspring per generation.

Does that mean the southern population is healthier than the northern ones? Not necessarily, says Khan. The southern population has a higher chance of expressing deleterious alleles due to increased **homozygosity**, which is the likelihood of inheriting two identical forms of a particular gene, one from each parent.

Inbreeding weakens

These findings point to a “serial founder effect”, often observed in populations that migrate long distances. In these cases, a limited number of individuals from each population move away to establish new ones, resulting in smaller populations that are more prone to inbreeding. Consequently, the new population may inherit harmful genetic variants from both parents due to breeding among related individuals.

Researchers predict multiple applications of the study in science and conservation. Ramakrishnan highlights that genome sequencing enables scientists to develop a **SNP (single nucleotide polymorphism) panel**, or a smaller set of markers that will help uniquely identify individuals. The study provides a database of genomes and variations that can serve as a reference for future research and for developing tools for application in conservation genetics.

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Kshetry sees greater potential for genomics in population estimation and accurately identifying individuals. This could be especially useful in the event of a seizure, helping to reduce poaching. He explains that, with the aid of genetic data, a seized item can be traced back to the individual or population, which can, in turn, have positive implications for elephant conservation. Ramakrishnan adds that the study serves as an indicator for conservation prioritisation. “Smaller, vulnerable populations, like the one south of the Shencottah Gap, can be better assessed and prioritised for conservation, as the study suggests low genetic variation and high inbreeding in that population. Similarly, better connectivity between the northern and northeastern populations is advisable because we don’t want multiple isolated populations there,” she says, adding, “The central Indian population is colonising many parts of Chhattisgarh, and it is imperative to understand their movement patterns and genetic variation as they expand.”

Many states across India are witnessing elephants moving closer to human habitations, resulting in increased conflicts with people. Researchers focused on conflict mitigation believe that genomics can significantly contribute to identifying viable solutions. Researcher-conservationist Tarsh Thekaekara from the Nilgiris-based The Shola Trust, which works on identifying elephants and mitigating conflicts in high-conflict areas such as Gudalur in the Nilgiri Biosphere Reserve, hopes that building upon this study can help shift conflict mitigation from being reactionary to science-based. “While the findings do not have an immediate application in the field of conflict mitigation, they hopefully encourage managers to consider long-term solutions to a serious wildlife concern,” says Thekaekara, one of the co-authors of the study.

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