

# Field study shows tigers in India follow corridors between groups to maintain gene flow

July 31 2013, by Bob Yirka

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Image: Wikipedia.

(Phys.org) —A team of researchers working in India has found that tigers living in separate geographic areas mate with tigers from other groups by traversing natural corridors. In their paper published in *Proceedings of the Royal Society B*, the team explains how they analyzed tiger DNA samples from different groups to learn more about their mating patterns.

Tigers are native to India—part of a tract of land that once stretched from the far eastern parts of Russia to Turkey. As the population of the country has increased, sadly, the population of tigers has dwindled. Now, instead of roaming vast forests, tigers inhabit small geographical zones,

where groups of the [big cats](#) survive only through the efforts of [conservationists](#). Recent reports suggest that tigers now inhabit just seven percent of the land area in the country. Because of their isolation from other groups researchers have worried that the tigers will all die out due to such a small [gene pool](#). In this new effort, the researchers sought to learn whether tigers from the separated groups are breeding with one another, helping to keep the gene pool diverse enough to be sustainable.

To find out, the researchers went into the jungle and collected tiger hair and feces samples from four [geographic areas](#) where tigers are allowed to roam free. They brought the samples back to the lab and analyzed the DNA found in them. In so doing, they were able to see that the DNA was from 273 individual tigers and that the four areas were actually just two—two pairs were separated by long thin, natural channels which tigers are still able to traverse. Because of that, the researchers feel confident that the gene pool can be maintained, provided the channels the tigers use are left open. Unfortunately, that might not happen, as the channels are privately owned and one of them has already been leased to a [mining company](#).

In studying the tiger DNA the researchers were also able to see periods of sharp decline in genetic diversity over time. The first occurred approximately 700 years ago when human invaders arrived and started clearing forests for agriculture. The second was approximately 200 years ago as India became a part of the British Empire and wood from its forests was felled for timber shipped back to Europe

**More information:** Forest corridors maintain historical gene flow in a tiger metapopulation in the highlands of central India, Published 31 July 2013 [doi: 10.1098/rspb.2013.1506](https://doi.org/10.1098/rspb.2013.1506)

## **Abstract**

Understanding the patterns of gene flow of an endangered species

metapopulation occupying a fragmented habitat is crucial for landscape-level conservation planning and devising effective conservation strategies. Tigers (*Panthera tigris*) are globally endangered and their populations are highly fragmented and exist in a few isolated metapopulations across their range. We used multi-locus genotypic data from 273 individual tigers (*Panthera tigris tigris*) from four tiger populations of the Satpura–Maikal landscape of central India to determine whether the corridors in this landscape are functional. This 45 000 km<sup>2</sup> landscape contains 17% of India's tiger population and 12% of its tiger habitat. We applied Bayesian and coalescent-based analyses to estimate contemporary and historical gene flow among these populations and to infer their evolutionary history. We found that the tiger metapopulation in central India has high rates of historical and contemporary gene flow. The tests for population history reveal that tigers populated central India about 10 000 years ago. Their population subdivision began about 1000 years ago and accelerated about 200 years ago owing to habitat fragmentation, leading to four spatially separated populations. These four populations have been in migration–drift equilibrium maintained by high gene flow. We found the highest rates of contemporary gene flow in populations that are connected by forest corridors. This information is highly relevant to conservation practitioners and policy makers, because deforestation, road widening and mining are imminent threats to these corridors.

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