

# GENOMIC STUDIES ON RUSTY-SPOTTED CAT



**Shomita Mukherjee**

**Nandini Rajamani**

**Nayan Khanolkar**



भारतीय वन्यजीव संस्थान  
Wildlife Institute of India

Salim Ali Centre for Ornithology  
and Natural History,  
South India Centre of Wildlife  
Institute of India



Indian Institute of  
Science Education and  
Research, Tirupati

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***Correspondence:*** Shomita Mukherjee, [shomitam@gmail.com](mailto:shomitam@gmail.com)

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## Summary

In this report, we present the first sequence assembly and analysis of a Rusty-spotted Cat genome. The project was initiated as part of a larger project on small cats and a workshop on upgrading the Rusty-spotted Cat captive breeding facility in Sanjay Gandhi National Park (SGNP), Mumbai. At the time of writing the proposal, there were nine Rusty-spotted Cats in captivity at the breeding centre and there was a strong need felt to generate genomic data on them that would facilitate the captive breeding programme and aid their conservation in natural habitats.

Blood and buccal swabs of two captive female (siblings) Rusty-spotted Cats in SGNP were collected on 08 October 2022 by the Park veterinarian. Samples were collected in tubes coated with EDTA and were immediately couriered over cold gel packs to the laboratory at IISER Tirupati for further processing. DNA extracts were couriered to Neuberg Supratech laboratories, Ahmedabad for sequencing over Illumina Novaseq 6000 sequencer (150 bp paired-end) for 50x and 30x coverage. Standardised web-based pipelines and bioinformatic tools for genomic analyses were used to assemble the genome. Demographic change for the Rusty-spotted Cat over a period of 500,000 years (Late Quaternary) was performed through Pairwise Sequentially Markovian Coalescent (PSMC) analysis.

The 30x genome yielded 78.84 gigabases recorded in ~ 493 million Illumina short-read sequences. The Whole Genome Sequencing (WGS) of the second individual yielded more than 1.9 billion reads of 160 bp in length and generated 308.85 Gigabases. The size of the Rusty-spotted Cat genome was estimated at 2.350 Gbp which is similar to its congeners, the Asian Leopard Cat and Fishing Cat. The genome with 30x coverage was assembled first and the results of that are presented in this report. The preliminary PSMC analysis of the demographic history of the species suggests that there were dips in the effective population size during the glaciation times which correspond with results of an earlier study on their past climatic niches. However, given that the genome assembly is preliminary and further analysis is required for robust results, the patterns presented here should be treated with caution. Analysis of whole genomes is very time-consuming since web-based tools and pipelines are in heavy demand and not always available. The caveats of the project are discussed along with recommendations.