Scientific team reveals the correct evolutionary relationships among possums
18 August 2022, by Kathrin Kottke

Comparison of SINE presence/absence and classical DNA sequence analyses. Left: The common brushtail possum and the Leadbeater's possum share a diagnostic SINE (black ball) at an orthologous genomic position (pictured as gray area). The SINE was inherited from a shared common ancestor of Phalangeroidea plus Petauroidea and is absent (dashes) in Macropodiformes and all outgroup representatives. Right: The classical DNA sequence analysis compares orthologous conserved sequences that can be variably exposed to homoplasy depending on selection and drift. Both marker systems are equally exposed to homoplasy as a result of ILS. Credit: Systematic Biology (2022). DOI: 10.1093/sysbio/syac025

Phalangeroida and Petauroidea, but DNA sequence analyses challenged and undermined these results.

In contrast to previous genetic-based studies that examined gene sequences, we analyzed the more reliable insertions of jumping genes. Especially, short interspersed elements (SINEs), which a reliable source for resolving evolutionary relationships among species. "If we find a jumping gene in two species at the exact genomic location, we can be sure they are closely related, as such insertions do not happen by chance," Schmitz explained.

The team analyzed complete genomes from 12 different marsupials, enabling them to investigate thousands of genomic positions. Among these, they found 61 genomic insertions of jumping genes at the exact locations in the genomes of all possum families. "These genetic markers demonstrate that all the various possums evolved from a shared ancestor," says Doronina.

The team traveled back 50 million years to clarify this important part of marsupial evolutionary history. Sometimes it is necessary to shake up old scientific ideas to save the biodiversity of species. About 8% of all Australian species became endangered in the last five years. Such animals can be better recognized and protected to retain biodiversity after a reliable estimation of their relatedness.

The research is published in Systematic Biology.


Provided by University of Münster