

WHAT DOES IT TAKE TO RESOLVE THE GUENON PHYLOGENY? NEXT-GENERATION SEQUENCING FROM 100-YEAR OLD MUSEUM SPECIMENS

K. Guschanski¹, J. Krause², S. Rankin², V. Savolainen¹

¹*Imperial College London, Silwood Park, Ascot, UK*, ²*Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany*

Presenter's Email: k.guschanski@imperial.ac.uk

Guenons (Cercopithecini) exhibited a rate of radiation unparalleled by any other African primate group. They show a wide geographical distribution, differ strongly in their ecological, behavioural, karyotypic characteristics and particularly morphological traits. Over 60 different species and subspecies have been described, mostly based on morphological and geographical information. However, guenon taxonomy remains controversial. Resolving evolutionary relationships among guenon taxa is hampered by the difficulty of obtaining samples from the wild. Museum collections offer a unique solution around these difficulties. However, working with museum samples represents a challenge, as the DNA retrieved from specimens is often of very low quality and quantity. New technological advances, such as next-generation DNA sequencing techniques, now allow to effectively use degraded DNA. We have sequenced complete mitochondrial genomes from representatives of ten species belonging to two genera (*Cercopithecus* and *Chlorocebus*) of the family Cercopithecidae. We extracted DNA from 100-year old museum specimens, enriched the extracts for mitochondrial fragments using a novel bead capture method, and sequenced the mtDNAs using a parallel-tagged high-throughput sequencing approach on the Illumina platform. This method overcomes some of the traditional drawbacks of mtDNA studies, such as erroneous phylogenetic interpretations based on the presence of nuclear insertions. The more than 16 kb sequences of the complete mitochondrial genome provide more informative and robust data than previous studies of short mitochondrial segments (COII, 12S rRNA). They depict the evolutionary relationships within the guenons and reveal divergence pattern for mitochondrial lineages of the various taxa.

Keywords: Cercopithecini, museum specimens, whole mitochondrial genome, new-generation sequencing