

Unlocking the past: museomics of African galagids

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Our understanding of primate phylogenetics is often limited by our ability to obtain high-quality data from wild populations. Developments in sequencing techniques have recently unlocked genetic access to millions of specimens housed in museum collections, providing an exciting alternative to overcome issues with sampling wild populations. Galagids are among the least studied primates and the lack of both comprehensive taxonomic and geographic sampling and genetic data has hindered our understanding of their evolutionary history. Here, we discuss the promise and challenges of using museum collections to study galagid evolution. We extracted over 150 specimens dated between 1912 and 1974 and we found that sample age was not a significant factor for determining DNA concentration ($R^2=0.035$, $F=2.335$, $p=0.1314$). We used target sequence capture to generate data at the genomic level. The final dataset contained 334 loci and a total of 1,108,850 bp. A total of 48 loriform specimens were included in the dataset, representing 13 galagid and 7 lorid species. The level of support for the monophyly of the family Lorisidae improves by increasing the number of loci included in a species tree analysis. Phylogenetic analyses confirm known phylogenetic relationships among galagid genera with high support, however, a few species were not recovered as monophyletic suggesting that either some museum specimens were mislabeled, or the current taxonomy does not reflect species diversity adequately. Future work will be focused on obtaining additional data for specific taxonomic groups to further advance our understanding of cryptic diversity within the Galagidae.

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