ABSTRACT

Background: Simian immunodeficiency virus (SIV) naturally infects African non-human primates (NHPs) and poses a threat of transmission to humans through hunting and consumption of monkeys as bushmeat. This study investigated the as of yet unknown molecular diversity of SIV in free-ranging Chlorocebus species (African green monkeys—AGMs) and Papio anubis (olive baboons) within Mombasa, Kisumu and Naivasha urban centres in Kenya. Methods: We collected blood samples from 124 AGMs and 65 olive baboons in situ, and detected SIV by high-resolution melting analysis and sequencing of PCR products. Results: Simian immunodeficiency virus prevalence was 32% in AGMs and 3% in baboons. High-resolution melting (HRM) analysis demonstrated distinct melt profiles illustrating virus diversity confirmed by phylogenetic analysis. Conclusions: There is persistent evolutionary diversification of SIVagm strains in its natural host, AGMs and cross-species infection to olive baboons is occurring. Further study is required to establish pathogenesis of the diverse SIVagm variants and baboon immunological responses.

Keywords

African green monkeys, evolution, high-resolution melting analysis, olive baboon, SIVagm, strain diversity