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Genetic diversity and amino acids variations at vaccine target sites in rabies viruses collected from different host species in Makueni and Siaya counties, Kenya

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Background: Rabies, a viral disease that causes lethal encephalitis is endemic in Kenya and is transmitted to humans mainly by domestic dogs. Rabies kills an estimated 2000 people annually, despite there being effective vaccines for dogs and humans. This study characterized the genetic diversity of RABV obtained from brains of suspected rabid animals from Makueni county, Eastern region and Siaya county, Western Kenya and determined variances within the antigenic sites of RABV vaccines currently in use in Kenya.

Methods: Brain biopsies (165) confirmed positive for rabies with rapid kits were collected between July 2021 and August 2022 from dogs, cats, cows, sheep and goats and re-screened for RABV by qPCR. Whole Genome Sequences (WGS) and individual Nucleoprotein (N) and Glycoprotein (G) genes were used for phylogeny. The amino acid variances in the N and G genes antigenic sites were compared to three RABV vaccine sequences: Pitman-Moore L503 (PM), Challenge Virus Standard (CVS) and the Pasteur Vaccine (PV) strains.

Results: Of the 165 brain samples, 156 were positive by qPCR and 141 (74 from Makueni and 67 from Siaya) produced useable sequences. Phylogenetic lineages drawn from WGS or from individual N and G genes showed two geographical distinct lineages: The Eastern Kenya sequences overwhelmingly (n=69) clustered with the Africa 1b lineage, with only 3 in Africa 1a. In contrast, the Western Kenya sequences (n=64) clustered with Africa 1a with only 3 in Africa 1b. The nearest common ancestor of the Africa 1a traced to Sudan, while the Africa 1b traced to Tanzania. The percent amino acid homologies of the N gene to the RABV vaccines were at least 97.6% for PV, 97.8% for CVS and 98.5% for PM. The homology with the G gene was at least 93.0% for PV, 93.3% for CVS and 92.2% for PM.

Conclusions: Our data confirm geographical isolation of RABV in Eastern and Western Kenya. The data suggests limited migration, probably through wild carnivore movement or translocation of domestic dogs by humans. The observed amino acid variances RABV vaccines antigenic sites would predict good vaccine efficacy, indicating that the RABV endemicity in Kenya is due limited programmatic vaccine coverage.