

Rabies virus in Namibian Kudus - Exploring the Genetic Diversity of Lyssaviruses

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While rabies is one of the oldest known zoonotic diseases, knowledge of important key mechanism like adaption processes of rabies lyssavirus (RABV) to new host species is still incomplete. Rabies in the Greater Kudu (*Tragelaphus strepsiceros*) in Namibia is unique, found in such magnitude as has not been reported elsewhere in southern Africa. To elucidate the potential genetic diversity of the RABV genome in Kudus that may explain species adaption, a sample set of salivary gland and brain material from infected Kudus was selected and subject for next generation sequencing approaches. The results revealed the consistency of the viral consensus sequence in both organs of an infected individual. However, several substitutions distributed across the whole virus genome, except the N gene, with frequencies ranging from 1.6 % up to 39 % were identified, most of them located in coding regions of different genes. Among these substitutions, a high number of nonsynonymous mutations exist, leading to various amino acid exchanges within most of the viral proteins. The frequencies of the observed mutations changed between brain and salivary gland material, demonstrating the genetic variability and potential adaptability of RABV in the Greater Kudu underneath the consensus level.

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