Detection of Orthopoxviruses in multiple small mammals in the Democratic Republic of the Congo

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Background: This study aimed to detect and characterize the mpox virus in wild animal species to identify which species are involved in zoonotic transmission events in the Democratic Republic of the Congo (DRC). Methods: Between 2010 and 2024, various species of bats, shrews, rodents including squirrels, small mammals and primates were sampled in the provinces of Equateur, Tshopo, Tshuapa, Bas-Uele, South Ubangi, Kinshasa and South Kivu. Animals were identified to species level using cytochrome b sequencing. Molecular detection of mpox was performed using Real‑time PCR targeting the OPXV P4A gene of all orthopoxviruses and/or orthopoxvirus PCR targeting a 269 bp fragment of the haemagglutinin (HA). For PCR positive samples whole genome sequencing was attempted to confirm mpox infection followed by phylogenetic analysis with mpox strains from humans in DRC Results: A total of 2,115 animals were captured and tested, among which 33.7% (714/2,115) bats, 15.5% (327/2,115) shrews, 1.9% (42/2,115) small mammals, 0.2% (5/2,115) primates and 76.2% (1612/2,115) rodents, including 587 squirrels. Orthopoxviruses were molecularly confirmed in 4 rodents. One Jackson's soft-furred mouse (Praomys jacksoni) and one squirrel (Paraxerus sp) from Tshopo province and another squirrel (Funisciurus anerythrus) from Bas Uele Province were confirmed as mpox by whole genome sequencing and clustered closely to human Clade Ia mpox strains from the same geographic area. In one Crocidura cf. denti from Tshopo province sequencing revealed the presence of Taterapoxvirus. Conclusion: This study shows that different rodent species can harbor mpox viruses and that other orthopoxviruses circulate in shrews.

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