

Population genetics of African Fruit Bats involved in ecology of Filoviridae (Ebola virus, Marburg virus) in West, Central and Southern Africa

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For several decades, the Filoviridae family including Ebola virus (EBOV) and Marburg virus (MARV) has been responsible for many haemorrhagic fever outbreaks in humans and great apes, mainly in Central Africa (*Rougeron et al. 2015*). Since 2005, several studies have shown that certain African fruit bat species might be potentially susceptible to transmit pathogens, including filovirus, between geographically distant African regions (*Olival et al., 2014; Richter et al. 2008*). The objective is to understand the spatial dynamics related to the migratory behaviour of these species through a study of the relationships existing between the populations of six frugivorous bat species (*Hypsignathus monstrosus, Epomops franqueti, Epomops buettikoferi, Eidolon helvum, Lissonycteris angolensis and Rousettus aegyptiacus*), throughout Western, Central and Southern Africa and which were found to be positive for the Zaïre strain Ebolavirus. Population genetics studies are achieved by single-nucleotide polymorphism (SNP) obtained through genotyping using sequencing methods (3Rad, *Bayona-Vásquez et al. 2019*). Our research based on 328 samples of all these species from 11 countries, gives a better knowledge on their mobility as well as on their genetic structures and population relationships. This information is essential to identify networks of contacts between bat populations and communities as well as interactions between humans and bats, in order to estimate risks of transfer of filoviruses among African regions. For *Eidolon helvum*, a species under focus of scientists due to its migrating behaviour as well as human cohabitation (urban roosts or feeding areas on fruit crops), 58 pooled libraries were sequenced resulting of an average of 7.2 million reads analyses per samples with 91.2 % sequences retained after filtering. Analyses of these data result of a panmictic distribution for *E. helvum* throughout its area distribution, implying possible transfer of virus across this area.

KEYWORDS. Ebola; Filoviridae; Outbreak; Disease; Chiroptera.

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