**Title:** Full genome sequences of novel Nobecoviruses identified in endemic Madagascar fruit bats

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**Abstract:**

Bats are natural reservoirs for both Alpha- and Betacoronaviruses and the hypothesized original hosts of five of seven known zoonotic CoVs. To date, the vast majority of bat coronavirus research has been concentrated in Asia, though CoVs are globally distributed; indeed, SARS-CoV and SARS-CoV-2-related Sarbecoviruses have been identified circulating in Rhinolophid bats in both Africa and Europe, despite the relative dearth of surveillance in these regions. In part with a long-term study examining the dynamics of potentially zoonotic viruses in three species of endemic Madagascar fruit bat (*Pteropus rufus, Eidolon dupreanum, Rousettus madagascariensis*), we carried out metagenomic Next Generation Sequencing on a subset of fecal samples obtained from wild-caught individuals. We here report detection of Betacoronavirus RNA in samples derived from all three species and describe full genome sequences of novel Nobecoviruses in *P. rufus* and *R. madagascariensis,* the latter of which has not been previously identified as a CoV host*.* We discuss the implications of these findings in light of CoV capacity for recombination, the global circulation of SARS-CoV-2, and the frequency of bat-human contacts in Madagascar*.*