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Bats are natural reservoirs for both *Alpha*- and *Betacoronaviruses* and the hypothesized original hosts of five of seven known zoonotic coronaviruses. To date, the vast majority of bat coronavirus research has been concentrated in Asia, though coronaviruses are globally distributed. As part of a long-term sampling study in three species of endemic Malagasy fruit bats, we carried out metagenomic Next Generation Sequencing on urine, throat, and fecal samples obtained from wild-caught individuals. We describe three full genome sequences of novel *Betacoronaviruses* in the subgenus *Nobecovirus*, identified in two endemic Malagasy bat species. Recombination analysis indicates that significant selection has taken place in the spike, nucleocapsid, and NS7 accessory protein regions of the genome for viruses derived from both bat hosts. One of these sequences appears highly divergent from previously described *Nobecoviruses,* which our analyses indicate group into five distinct clades with disparate Asian and African origins.Madagascar offers a unique phylogeographic nexus of bats and viruses with both Asian and African phylogeographic origins, providing opportunities for unprecedented mixing of viral groups. As fruit bats are handled and consumed widely across Madagascar for subsistence, understanding the landscape of potentially zoonotic coronavirus circulation is essential for mitigation of future zoonotic threats. This research fills a gap in coronavirus surveillance outside of Asia and elucidates the evolutionary history of the *Nobecovirus* subgenus.