

Abstract

Novel Insights for Biosurveillance of Bat-Borne Viruses [†]

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Abstract: Bats are rich reservoirs of viruses, including several high consequence zoonoses. In this study, high throughput sequencing was used to characterize the virome through a longitudinal study of a captive colony of lesser dawn bats, species *Eonycteris spelaea*, in Singapore. This study utilized viral RNA extracted from swabs of four body sites per bat per timepoint. Swabs of the exterior of the bat (head and body) were used to evaluate virus populations and demonstrate utility as a sample site for future surveillance to extrapolate population-level infection. Through unbiased shotgun and target-enrichment sequencing, we identified both the known and previously unknown viruses of zoonotic relevance and defined the population persistence and temporal patterns of viruses from families that have the capacity to jump the species barrier. We observed the population persistence of three zoonotic-related viral families that are known to be associated with spillover from bats to humans: *Paramyxoviridae*, *Reoviridae*, and *Coronaviridae*. To our knowledge, this is the first study that combines probe-based viral enrichment with high-throughput sequencing or that creates a viral profile from multiple swab sites on individual bats and their cohorts. This work demonstrates temporal patterns of the lesser dawn bat virome, including several novel viruses. Noninvasive surveillance methods that target the body of bats not only detect viruses shed within the colony but can also represent viral populations dispersed throughout the entire colony. New knowledge of persistent viral families should inform future directions for the biosurveillance of viruses that have the potential to cross the species barrier from bats to humans or other amplifying hosts.

Keywords: *Eonycteris spelaea*; virome; bat; metagenomic; sequencing; viral genomics



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