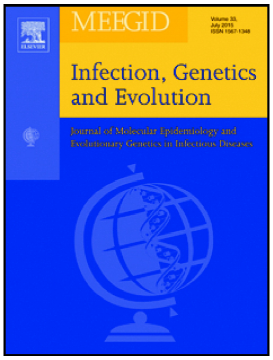

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High-resolution phylogeny providing insights towards the epidemiology, zoonotic aspects and taxonomy of sapoviruses

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Abstract

The evolution, epidemiology and zoonotic aspects of Sapoviruses (SaV) are still not well explored. In this study, we applied high-resolution phylogeny to investigate the epidemiological and zoonotic origins as well as taxonomic aspects of animal and human SaV. Bayesian framework analyses showed an increase in porcine SaV (PoSaV) population dynamics between