Evolution and phylogeographic dissemination of endemic porcine picornaviruses in Vietnam

* Lu 2016
* Porcine picornaviruses
* uncorrelated lognormal relaxed molecular clocks and a constant-population coalescent process prior
* strong priors of substitution rate were chosen according to published evolution rates of the VP1 gene from related genera in the picornavirus family, including 17 seventeen enteroviruses (species/types) and 10 ten non-enteroviruses (species/types)
* MCMC chains were run for 100 million steps, sampled every 10,000 states with 10% burn-in.

Varying genera specific substitution rates/ Genus-Specific Substitution Rate Variability among Picornaviruses

* Hicks 2011
* Table is in paper
* The relaxed molecular clock was the best-fitting prior for CVB2, CVB4, EV71, PV1, and HPeV (logBF > 10 [BF is Bayes factor]), but the strict molecular clock was preferred for EMCV, PTV, FMDV-A, and HAV (logBF > 1.8; [Table 1](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3147923/table/T1/)). The constant demographic model was preferred for FMDV-A, HAV, and HPeV (logBF > 2), the exponential model was the best fitting for PV1 and EV71 (logBF > 2)
* These mean rates of enterovirus VP1 evolution range from 3.40 × 10−3 to 1.19 × 10−2 nucleotide substitutions per site per year (ns/s/y), and mean VP1 rates for nonenteroviruses range from 9.76 × 10−4 to 2.79 × 10−3 ns/s/y. The average of the 18 enterovirus mean rates was 6.50 × 10−3 ns/s/y (standard deviation [SD] = 2.61 × 10−3), while the average of the eight nonenterovirus mean rates was four times lower at 1.60 × 10−3 ns/s/y

Detection and genetic characterization of canine kobuvirus from stray dogs in Shanghai, China

* Deng 2023
* Bayesian skyline coalescent was set as the tree prior. Markov chain Monte Carlo (MCMC) sampling was run twice independently for 50,000,000 generations with 10% burn-in
* relaxed lognormal clock was used as the clock model

Molecular characterization of Porcine sapelovirus in Hunan, China

* Yang 2017
* a relaxed molecular clock with an uncorrelated log-normal distribution of rates and a chain length of 1108 generations was used, with sampling every 1000 generations, using an extended Bayesian skyline plot as a tree prior, and the burn-in was set at 10 % of the sampled states

Substitution rates for mada genera

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Substitution rate | Reference | Target |
| Lesavirus | Lesavirus 1 and 2 | 9.22 × 10−3 and 8.26 × 10−3 | Lim 2015 | VP1 |
| Mischivirus | Can’t find any papers |  |  |  |
| Kunsagivirus | Can’t find any papers |  |  |  |
| Kobuvirus | Canine kobuvirus | 1.36 × 10−4 | Deng 2023 | VP1 |
| Teschovirus and Sapelovirus |  | 1.62x10-3 | Hicks 2011 | VP1 |
| hepatovirus | Hepatitis C | 3.5 × 10–5 to 1.2 × 10–4 | Nakamura 2022 |  |
| Sapovirus |  | 1.32 × 10−3 to 3.38 × 10−3 | Tohma 2020 | VP1 |