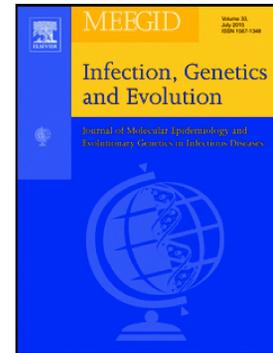


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## Newly Emerged Porcine Enteric Alphacoronavirus in Southern China: Identification, Origin and Evolutionary History Analysis

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**Abstract:** Coronaviruses have a wide host range and can cause a variety of diseases with varying severity in different animals. Several enteric coronaviruses have been identified that are associated with diarrhea in swine and that have caused substantial economic losses. In this study, a newly emerged porcine enteric alphacoronavirus (PEAV), PEAV-GD-CH/2017, was identified from suckling piglets with diarrhea in southern China, and a full-length genome sequence of PEAV was obtained for systematic analysis. The novel PEAV sequence was most identical to that of bat-HKU2, and the differences between them were comprehensively compared, especially the uniform features of the S protein, which was shown to have a close relationship with betacoronaviruses and to perhaps represent unrecognized betacoronaviruses. In addition, Bayesian analysis was conducted to address the origin of PEAV, and the divergence time between PEAV and bat-HKU2 was estimated at 1926, which indicates that PEAV is not newly emerged and may have circulated in swine herds for several decades since the interspecies transmission of this coronavirus from bat to swine. The evolutionary rate of coronaviruses was estimated to be  $1.93 \times 10^{-4}$  substitutions per site per year for the RdRp gene in our analysis. For the origin of PEAV, we suspect that it is the result of the interspecies transmission of bat-HKU2 from bat to swine. Our results provide valuable information about the uniform features, origin and evolution of the novel PEAV, which will facilitate further

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