

Complete genome and pathogenesis of a novel recombinant Senecavirus A isolate in China

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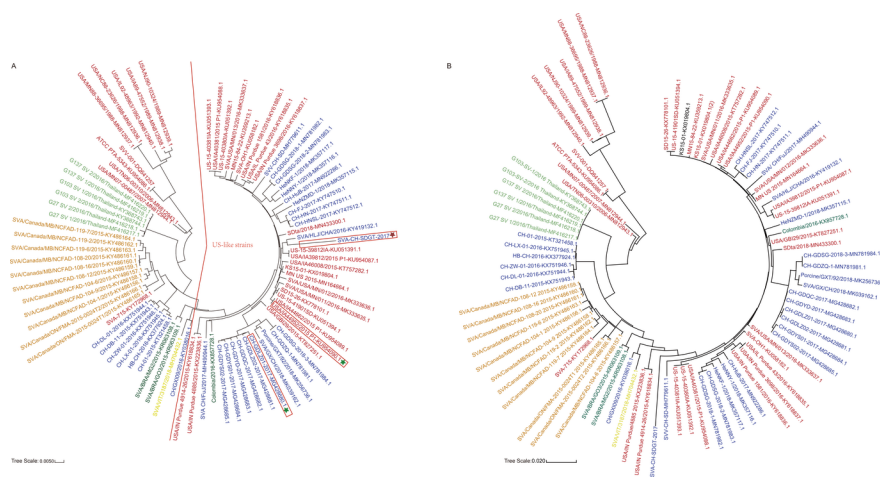
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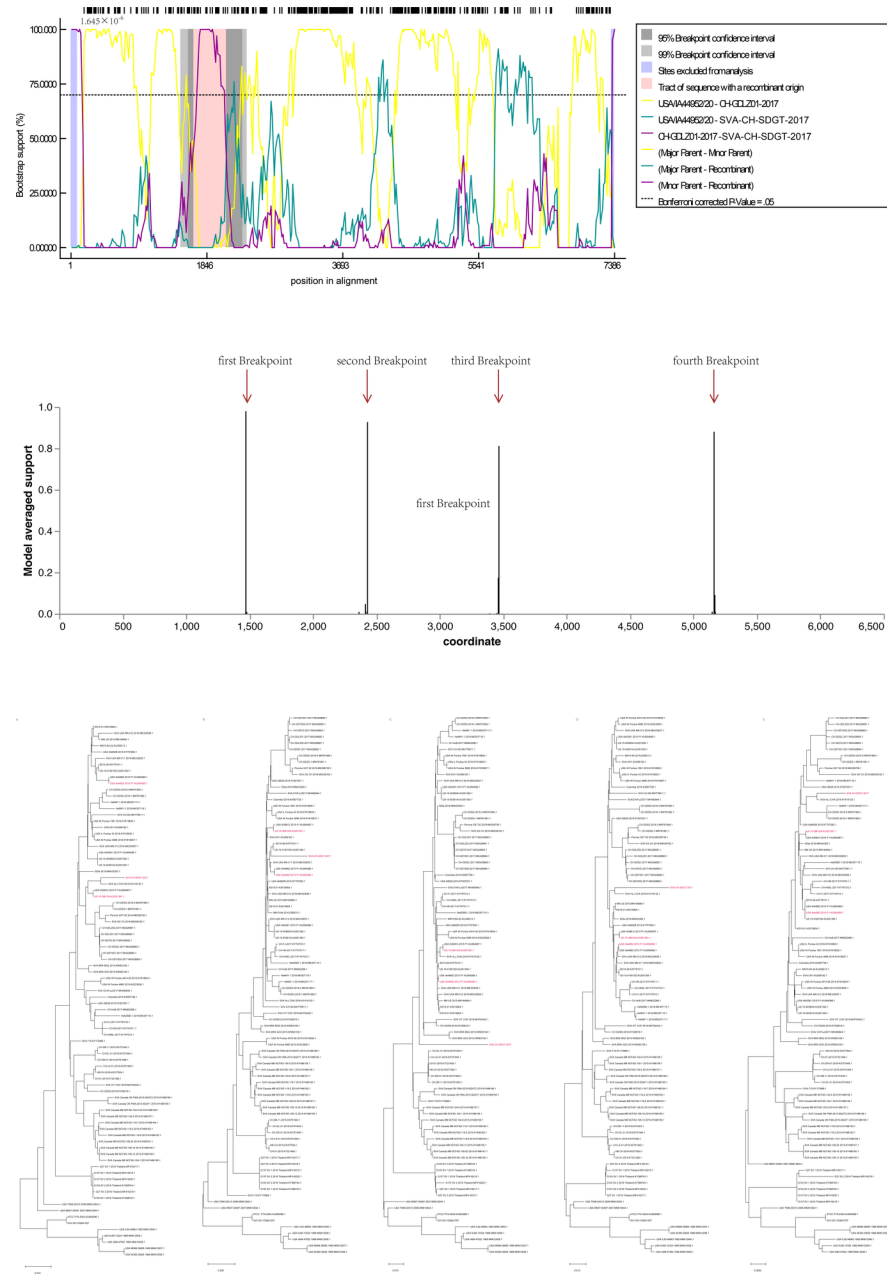
Abstract

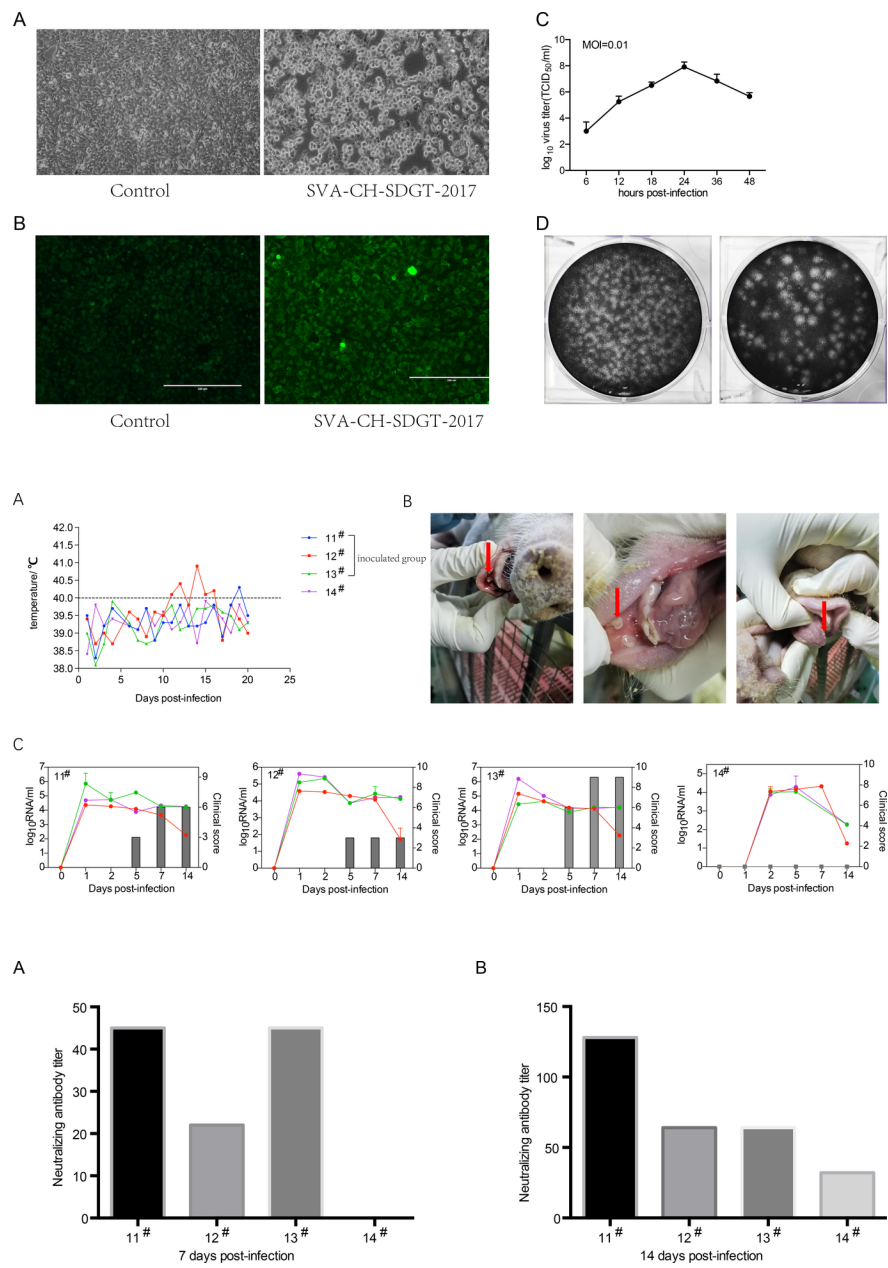
The Senecavirus A (SVA), formerly called Seneca Valley virus (SVV) which was first isolated in the United States (US) in 2002. In this study, a SVA strain was isolated from a pig herd in Shandong Province in China and designated as SVA-CH-SDGT-2017. The full-length genome, excluding the poly (A) tail of the SVA isolates, was 7280 nucleotides long, with the genomic organization resembling and shares high nucleotide identities of 90.7% to 96.9% with other previously reported SVA isolates. To investigate the pathogenicity of the SVA isolate, experimental infections of pigs were performed. The SVA strains successfully infected the pigs, evidenced by presence of virus shedding and robust serum neutralizing antibody responses. Moreover, the contact-exposed pigs showed 100-fold reduction compared to that of inoculated group. Our findings provide useful data for studying the pathogenesis and transmission of SVA in pigs.

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