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Full genome analysis of swine genotype 3 hepatitis E virus isolated from eastern China

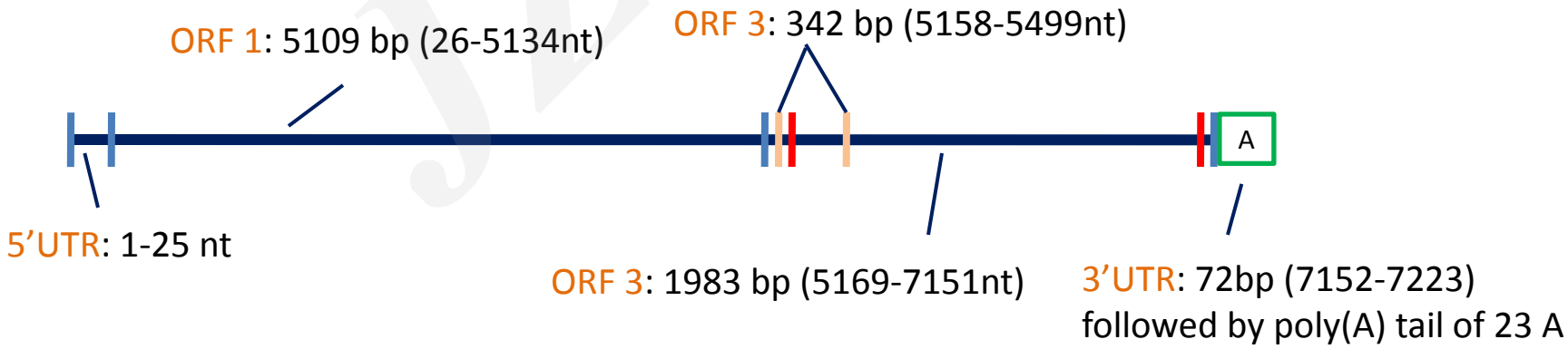
Key words: Swine hepatitis E virus; Full genome sequence; Phylogenetic analysis; Genotype 3

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Research Summary

The first full genome sequence of the swine genotype 3 HEV strain from Zhejiang province (ZhJ-PJ050-3) was determined using RT-PCR and rapid amplification of cDNA ends (RACE) and analyzed.

- The genome consists of 7223 nucleotides, excluding the 23 nt of poly (A) tail at 3'-terminus
- Containing three major ORFs
- One amino acid deletion of Leu residue at position 1048 in the ORF1 protein



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ZhJ-PJ050-3

- exhibits the highest genomic nucleotide similarity of 87.9% to the only reported HEV 3 strain SAAS-JDY5 (FJ527832) isolated from Shanghai, China

- clustered in subtype 3b together with most Japanese isolates

- was most closely related to SAAS-JDY5

