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Sequence analysis of S gene of Tibetan pig Porcine epidemic diarrhea virus in Ganzi Prefecture of Sichuan Province

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Abstract: In order to understand the molecular characteristics of S gene of Tibetan Porcine epidemic diarrhea virus (PEDV) in Ganzi Prefecture, in this study, 144 fecal samples from 12 Tibetan Pig farms in four counties of Ganzi Prefecture were collected from January 2018 to December 2018 for PEDV detection and molecular characterization of S gene. The results showed that the positive rate of PEDV was 43.06% (62/144), the positive rate of PEDV in 12 Tibetan Pig farms was 91.67% (11/12), and complete S gene sequences of seven PEDV strains from Tibetan pigs were obtained by PCR amplification and cloning. The length of S genes ranged from 4 146 to 4 158 bp. The nucleotide similarity of seven PEDV strains from Tibetan pig were 95.7%-99.9% and the deduced amino acid sequence were 93.8%-99.9%, which shared 93.1%-98.3% identity with S gene nucleotide sequence and 91.0%-98.1% identity with S gene amino acid sequence. S gene of seven strains of PEDV from Tibetan pigs formed two separate independent branches between G1 and G2 branches, indicating that they might represent two novel S genotypes. The mutation of L535I amino acid mutation was firstly found in COE and epitope in the S protein. These results indicated that the infection rate of PEDV in Tibetan pigs in Ganzi Prefecture of Sichuan Province was high, and the S gene showed a unique genetic evolution trend.

Keywords: Ganzi Prefecture; Tibetan pigs; Porcine epidemic diarrhea virus; S gene; genetic variation

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