



# Molecular characterization and phylogenetic analysis of porcine epidemic diarrhea virus samples obtained from farms in Gansu, China

M.Z. Huang<sup>1,2,3</sup>, H. Wang<sup>1,2,3</sup>, S.Y. Wang<sup>1,2,3</sup>, D.A. Cui<sup>1,2,3</sup>, X. Tuo<sup>1,2,3</sup> and Y.M. Liu<sup>1,2,3</sup>

<sup>1</sup>Engineering and Technology Research Center of Traditional Chinese Veterinary Medicine of Gansu Province, Lanzhou Institute of Husbandry and Pharmaceutical Sciences of Chinese Academy of Agricultural Sciences, Lanzhou, Gansu, China

<sup>2</sup>Key Lab of New Animal Drug Project of Gansu Province, Lanzhou Institute of Husbandry and Pharmaceutical Sciences of Chinese Academy of Agricultural Sciences, Lanzhou, Gansu, China

<sup>3</sup>Key Lab of Veterinary Pharmaceutical Development of Ministry of Agriculture, Lanzhou Institute of Husbandry and Pharmaceutical Sciences of Chinese Academy of Agricultural Sciences, Lanzhou, Gansu, China

Corresponding author: Y.M. Liu  
E-mail: myslym@sina.com

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**ABSTRACT.** Porcine epidemic diarrhea poses significant sanitation problems in the porcine industry, and has negatively affected the economy in recent years. In this study, 48 fecal specimens were collected from piglets from four intensive swine farms located in the Gansu Province of China. The molecular diversity and phylogenetic relationships between porcine epidemic diarrhea viruses (PEDV) prevalent in Gansu were probed, and the resultant proteins were characterized. Sequence analysis of the spike protein (S) genes showed that each specimen had unique characteristics, and that the PEDV1/S/4 strain could be differentiated from the others via a unique mutation of the S gene. The phylogeny of S glycoprotein showed

that all strains were clustered into two major groups. The four Gansu PEDV field strains were characterized into different groups; this finding was consistent with the results of the protein characterization prediction. This analysis additionally revealed the unique characteristics of each specimen. The results of this study could be used to elucidate the prevalence of PEDV and contribute to the prevention of PEDV in Gansu.

**Key words:** Porcine epidemic diarrhea; Virus; Gene; Phylogenetic analysis