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**Epidemiological survey of PRRS and genetic variation analysis of the ORF5 gene in Shandong Province, 2020-2021**

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**Abstract:**

Since the rise of porcine reproductive and respiratory syndrome virus (PRRSV) in China, mutations have occurred regularly. In particular, the emergence of HP-PRRSV has significantly improved the pathogenicity of PRRSV. It has brought huge economic losses to the Chinese pig farming industry. To understand the current prevalence and evolution of PRRSV in Shandong Province, 1,344 samples suspected of having PRRSV were collected from local hog farms of different sizes. Genetic variation in the isolated PRRSV ORF5 gene was analyzed using the RT-PCR method. The results showed that the detection rate of PRRSV in the collected samples was 25.44%. The predominant strain of PRRSV in Shandong Province is still NADC30-like. However, it cannot be ignored that NADC34-like is also starting to become a prevalent strain. Mutations in ORF5 amino acids 13, 151 and neutralizing epitope (aa36-aa52) in some isolates can cause changes in virulence and ability to escape immunity. This study enriches the epidemiological data on PRRSV in Shandong Province, China. It provides an important reference for the development of new vaccines and for the prevention and control of PRRSV.

**Keywords:** PRRSV, GP5, epidemiology, genetic evolutionary analysis, prevention and control