

High genetic diversity of species A rotaviruses detected in swine farms in Chile

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Resumen

Rotavirus A is one of the main causative agents of diarrhoea in lactating and weaned pigs worldwide. Its impact in the swine industry is well documented. However, in Chile, the current epidemiological status of rotavirus on porcine farms is unknown. This study evaluated the current epidemiologic status of rotavirus A infection in Chile using on-farm detection techniques, electrophoretic confirmation, genotyping and phylogenetic clustering by analysis of partial sequences of VP4 and VP7 genes. Rotavirus A was detected in four out of five farms with an overall prevalence of 17.7% in diarrhoeic pigs. The average age of diarrhoea onset was at 32 +/- 6.2 days, corresponding to weaning pigs, and rotavirus was not detected in lactating piglets. Molecular characterization indicated that genotypes G5, G3, P[7] and P[13] are currently the most widely represented on these pigs farms. The phylogenetic analysis showed that farms shared similar G types (VP7), which might denote a common origin. Meanwhile, [P] types (VP4) showed considerable genetic diversity, and this might represent a high rate of reassortment of this genetic segment in rotavirus circulating in the researched area. These findings demonstrate the importance of considering both the geographical and production factors to accurately determine rotavirus prevalence status at the national level, and have relevant implications in determining effective strategies for rotavirus infection control on porcine farms.

Palabras clave

Palabras clave de autor: [rotavirus](#); [molecular genotyping](#); [epidemiology](#); [pig](#); [Chile](#)

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