

Phylogenetic analysis of porcine gastrointestinal viruses identified in pig farms in Colombia

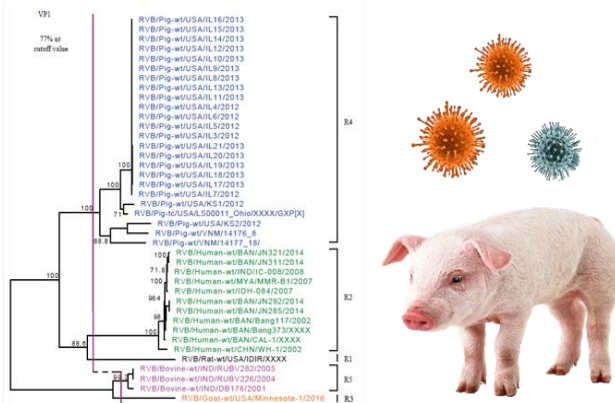
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Graphical Abstract



Abstract.

Neonatal diarrhea is a prevalent disease within the pig farms. The etiological agents involved include: Porcine Epidemic Diarrhea Virus (PEDv), rotavirus (RV), *Mamastrovirus*, among others. The aim of the present research is to analyze phylogenetically the PEDv and RV from diarrheic fecal samples collected from pigs farms in Colombia to study the evolution and genetic diversity of the strains present in the country. Materials and methods. The methodology will include the identification of PEDv and RV in fecal specimens of piglets up to 8 weeks of age, through viral RNA extraction and real-time reverse transcription-PCR amplification (RT-PCR). Confirming the presence of the viruses of interest, the genome will be sequenced using the Next Generation Sequencing (NGS) platform from Illumina®. Expectations: Providing information on the evolution and genetic diversity of PEDv and RV strains in Colombia, through the NGS sequencing of viral genomes identified with real time RT-PCR in young piglets with diarrhea.

Keywords: rotavirus, Porcine epidemic diarrhea virus, phylogeny.

Neonatal diarrhea is one of the most important diseases in pig farms, due to the considerable economic losses associated. These losses can be reflected in costly treatments, reduction in productivity and growth slowing (Chandler-Bostock et al., 2014). Increased mortality rates due to neonatal diarrhea can be seen in pigs within the first and second week of age (Lee, 2015).

Rotavirus (RV) is an important etiological agent that causes acute viral gastroenteritis in humans and young animals, including young calves, weaned and post-weaning pigs. The RVs are members of the *Reoviridae* family, with a genome consisting of eleven segments of double-stranded RNA, encoding six structural proteins (VP1-VP4, VP6 and VP7) and five or six non-structural proteins (NSP1-NSP5 / NSP6) (Shepherd et al., 2018; Vlasova, Amimo, & Saif, 2017). The etiology of Porcine Epidemic

Diarrhea (PED) is a highly infectious enteric coronavirus known as porcine epidemic diarrhea virus (PEDv) that affects pigs of all ages, being more severe in newborn piglets, where morbidity and mortality can reach the 100%. The PED is an emerging and re-emerging disease that appeared in the American continent in 2013, generating the death of 7 million piglets and losses of young animals in the United States (Cima, 2014). According to figures reported by The National Agricultural Statistics Service in that same year, the United States Department of Agriculture (USDA) reported an inventory of 65.07 million pigs, which dropped to 61.49 million in 2014 due to the negative effects of the disease. The virus spread to Canada, Mexico, Peru, Ecuador and in 2014 the virus entered in Colombia, confirming the presence of this exotic disease in the country (Jarvis, Lam, Rovira, & Marthaler, 2016).

Thus, the aim of the present study is to determine phylogenetically RV and PEDv in different cities of the country from diarrheic fecal samples from suckling and weaned pigs. One of the main objectives of the project is to provide information on the evolution and genetic diversity of the PEDv and RV strains in Colombia.

The methodology includes the identification of PEDv and RV through real-time reverse transcription PCR (rtRT-PCR) and genome sequencing using the Next Generation Sequencing (NGS) platform from Illumina® (Shepherd et al., 2018). For each phylogenetic analysis, the RV and PEDv nucleotide sequences for strains identified in Colombia will be employed, as well as sequences from other parts of the world. They will be obtained from the nucleotide database of the National Center for Biotechnology Information (NCBI) <https://www.ncbi.nlm.nih.gov/nuccore/>. The alignment of the nucleotide sequences will be used to generate the phylogenetic trees by means of specialized software. This kind of methodologies allows to understand the epidemiology and genetic diversity of RV and PEDv strains in Colombia, which will provide information for the prevention and effective control of the disease.

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