



VIRAL DISEASES

VVD-069

NOROVIRUS IN FAECES OF HEALTHY PIGS IN NORTH-EAST ITALY

L. Cavicchio¹, G. Rizzo¹, L. Amato¹, T.J. Vieria¹, M. Forzan², M. Ustulin³, I. Monne¹, D. Vio³, L. Bonfanti¹, M.S. Beato¹.

¹IZSVE, Legnaro, Italy; ²University of Pisa, Pisa, Italy; ³IZSVE, Pordenone, Italy.

Introduction

Norovirus (NoV) has emerged as one of the major causative agents of non-bacterial, food- and water-borne gastroenteritis in humans all over the world. NoVs are classified into six groups (G), from GI to GVI, which are further subdivided into 30 genotypes. NoVs identified in human gastroenteritis cases are only GI, GII, and GIV. NoVs have also been isolated from several animal species, including pigs, dogs, cattle, rodents and lions. The detection of GII NoV from pigs in Japan and Europe, and GII NoV antibodies in US swine have raised public health concerns about the zoonotic potential of porcine NoVs.

Material & Methods

Faeces were collected at slaughterhouse in 2017 in two regions of North-East Italy. Forty-six samples originated from Veneto and thirty-three from Friuli Venezia Giulia regions, covering seven and three provinces, respectively, were analysed for presence of Calicivirus. A two-step RT-PCR targeting the RdRP gene using the p290-p110 primer pairs was used. Sanger sequence was conducted on samples presenting enough amount of the target amplified DNA. Phylogenetic analysis was carried out using the neighbour-joining method and Kimura two-parameter substitution model using MEGA7 software.

Results

Fourteen samples collected in Veneto region, were PCR positive. Nucleotide sequence of about 300bp were obtained from only two samples. BLAST analysis showed a homology between 89 and 92% with swine NoV detected in Europe. Phylogenetic analysis showed that Italian strains belong to the GII.11 and cluster with other swine NoV from USA and Asia.

Discussion and Conclusion

This study identified GII.11 NoVs in the swine population of North-East Italy, similarly to a previous report in 2011. Further molecular analysis on the VP1 gene are ongoing on positive samples. The real distribution and the role of NoVs in swine needs to be further investigated by proper sampling approach and full genome analysis.