



VVD-068

## **CHARACTERIZATION OF ASTROVIRUS CAUSING GASTROENTERIC DISEASE IN PIGLETS IN ITALY BY A METAGENBOMIC APPROACH**

L. Tassoni<sup>1</sup>, G. Zamperin<sup>2</sup>, E. Schiavon<sup>2</sup>, V. Vendramin<sup>3</sup>, F. Tonon<sup>4</sup>, I. Monne<sup>2</sup>, M.S. Beato<sup>5</sup>.

<sup>1</sup>IZSVE, Legnaro, Italy; <sup>2</sup>Istituto Zooprofilattico Sperimentale delle Venezie, LEGNARO, Italy; <sup>3</sup>IGA Technologies, Udine, Italy; <sup>4</sup>SUIVET, Treviso, Italy; <sup>5</sup>Istituto Zooprofilattico Sperimentale Delle Venezie, Padova, Italy.

### **Introduction**

Astroviruses are emerging viruses, Family Astroviridae, that infect mammalian and avian species. They are non-enveloped viruses with a single-stranded positive sense RNA genome. They are detected in the intestines and several other organs in diseased and healthy animals. Porcine astroviruses (PoAstVs) belong to the Mamastrovirus genus and are distributed worldwide and divided into five lineages possibly reflecting different species of origin, interspecies transmission and recombination events. Here we report a diagnostic case of acute gastroenteritis in piglets in Italy with the involvement of PoAstVs.

### **Materials and methods**

In November 2015, an acute episode of gastroenteritis was observed in an open cycle farm of about 460 sows in North-East Italy, Treviso province. Piglets during post weaning presented diarrhea, reduction of food intake, high morbidity and low mortality. Faecal samples were collected from diseased piglets and analysed by electron microscopy (EM) and a pan mamastrovirus RT-PCR. Whole genome sequence was obtained with a metagenomic approach, from EM positive faeces.

Assembled sequence of length comparable to Astrovirus length (6-8 Kb) was selected as consensus sequence and confirmed by BWA. Phylogenetic analysis was performed on the deduced amino acid sequence of ORF2, using maximum likelihood method in PhyML3.1 and including representative strains from PoAstV1-5.

### **Results**

The phylogenetic analysis showed the Italian virus belongs to the PoAstV2 lineage 1, clustering with viruses from Asia. Based on the ORF2 aa sequence the Italian strain shares the highest similarity (73.2%) with PoAstV2/Bel-12R021/2012 from Belgium.

### **Discussion and conclusions**

The present case report indicates that: PoAstVs2 may be involved in enteric disorders in piglets and the low number of PoAstV sequences available rises the complexity of PoAstVs classification. Still fragmentary data are available on the role of PoAstV in the multifactorial enteric disorders of pigs. Better surveillance and diagnosis may clarify the epidemiology and taxonomical classification of PoAstVs.

 P  
O  
S  
T  
E  
R