

Research program IZS VE 07/16

Influenza D: toward a better understanding of the infection dynamics of an emerging animal virus in north-eastern Italy

Project coordinator: Isabella Monne

A novel emerging pathogen within the Orthomyxoviridae family, tentatively named Influenza D virus (IDV), has been recently identified in the USA, China and Europe. This virus was shown to infect swine, cattle, sheep and goats and to efficiently replicate and transmit in guinea pigs and ferrets, highlighting the potential threat of the virus to public health. Cattle have been proposed as the reservoirs for IDV. In these animals, the virus has been demonstrated to be able to be transmitted efficiently, although it causes only a mild respiratory disease. However, metagenomic characterization of the virome associated with bovine respiratory disease (BRD) showed a significant association of IDV with this syndrome.

In Italy, IDV was identified in samples collected between 2014 and 2015 from cattle and swine herds in North Italy affected by respiratory disease. However, its spread throughout the country and the emergence threats associated with IDV circulation have not been assessed yet.

In this light, our project aims at

- 1) investigating the circulation of IDVs among pigs and cattle in north-eastern Italy
- 2) exploring the complexity of viral communities and the virus associations in respiratory diseases in pigs using a metagenomic approach
- 3) studying the global genetic diversity, evolution and geographical spread of IDV and
- 4) understanding its fitness and tropism in pigs, small ruminants and cattle using an ex vivo organ culture (EVOC) system.