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Porcine noroviruses: towards a better understanding of strains circulating in North-East Italy

Project coordinator: Maria Serena Beato

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 five genogroups (G), from GI to GV, which are further subdivided into 29 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 adult pigs in Japan and Europe, and GII NoV antibodies in US swine have raised public health concerns about the zoonotic potential of porcine NoVs.

Although such potential has been called for, little is known about the genotype distribution and related epidemiological characteristics of NoVs in pig farming, including their genetic relationship with human strains. In Italy, little information is available on the distribution of porcine NoVs, nor on their relationship with human NoVs.

This project aims at investigating the prevalence of porcine NoVs circulating in North-East Italy, including their genetic characterization and elucidation of possible routes for zoonotic transmission.