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## MIGLIOR POSTER ANIV - SISVET 2021

**P285 - Genotyping of *Hepatitis E virus (Orthohepevirus A)* spread in wild boars in the Marche region, Italy**

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*Hepatitis E virus* (HEV), now named *Orthohepevirus A*, belongs to the *Orthohepevirus* genus in the family *Hepeviridae* and is associated in humans with outbreaks and sporadic cases of acute hepatitis. The virus is considered endemic in many tropical and subtropical countries, but its distribution is probably global. In Europe, the number of autochthonous cases in humans is increasing. In Marche region (Italy) several cases have been recently found to be caused by genotype 3 [1], which is most frequently detected in Italy in raw and dry pork liver sausages [2]. The aim of this study was to study the presence of and to genotype HEV in wild boars in Marche region, Italy.

Forty-five liver samples were collected from wild boars shot during the hunting seasons of 2018–2019 in six different municipalities in Marche region. A nested PCR protocol was used to amplify a specific part of the ORF2 [3]. Seventeen samples gave a PCR product of the expected size (348 bp) and were sequenced. The sequences were edited and aligned with representative sequences of all genotypes described so far [4]. The phylogenetic tree was inferred using the Maximum Likelihood method and the best-fitting nucleotide substitution model was Tamura-Nei with bootstrap values based on 1000 repetitions. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The rate variation model allowed for some sites to be evolutionarily invariable.

In all municipalities at least one animal was infected by HEV genotype 3. Three different HEV subtypes were found. HEV-3f was found in most samples, subtype 3e was found in 5 samples, and only one wild boar was infected by 3c subtype. In one municipality all three subtypes were found in wild boars shot in the same area.

The results show that HEV genotype 3 is widely spread in wild boars. The subtypes detected in the present study have been already found in Italy both in pigs and in wild boars [4,5]. Although subtype 3f has been frequently associated to disease in humans in some European countries e.g., France and England, subtypes 3e and 3c are the most frequently reported in humans in Italy, while subtype 3c is rarely reported in Italian suids [5]. HEV-3c, HEV-3e, and HEV-3f have been reported not only in humans and suids (pigs and wild boar) but also in contaminated food items of pork and wild boar (references are reported in [5]). Considering that traditional food products are widely made with uncooked wild boar liver in the geographic area included in this study, studies on the impact of the maturing process on HEV infectivity are required. In addition, the role of wild boars in maintenance and recombination of HEV should be monitored, as well as their role in transmitting the virus to free-range pigs.

[1] Tarantino et al. Locally acquired hepatitis E virus in Marche Italy: Clinical/laboratory features and outcome, *Dig Liver Dis*, 52(4):434-439, 2020. [2] Di Bartolo et al. Detection of hepatitis E virus in pork liver sausages. *Int J Food Microbiol*, 193:29-33, 2015. [3] van der Poel et al. Hepatitis E virus sequences in swine related to sequences in humans, *The Netherlands, Emerg Infect Dis*, 7(6):970-6, 2001. [4] Pierini et al. Hepatitis E virus (HEV) genotype 3 diversity: Identification of a novel HEV subtype in wild boar in Central Italy, *Transbound Emerg Dis*, in press.