P090 - Environmental surveillance of Hepatitis A Virus: evaluation of urban sewages and shellfish farms contamination during the ongoing outbreak in Sicily

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Introduction: Hepatitis A virus (HAV) is an enteric picornavirus, typically transmitted by the fecal-oral route through exposure to contaminated food (shellfish, strawberries, etc) or water, that causes acute hepatitis in humans. HAV is classified in 6 genotypes (I to VI), divided into subtypes A and B. Recently, several outbreaks due to HAV-IA have been reported in men who have sex with men (MSM), demonstrating new transmission routes in industrialized countries. From 2017, Italy is involved in a large HAV outbreak (2017 incidence: 5,8 x 100.000 inhabitants). Also in Sicily the number of cases has considerably increased in 2017 (126 cases notified) and apparently the infection is spreading from MSMs to the general population, also involving women and children.

Materials and Methods: From May 2017, HAV genome has been searched on urban sewages, collected by the Acute Flaccid Paralysis Sicilian Regional Reference Centre from wastewater treatment plants of the main Sicilian towns. Sewage samples have been concentrated following the guidelines for environmental surveillance of polioviruses (WHO 2003) and HAV VP1/2A region has been amplified by nested-PCR using pan-genotypic primers. At the same time, shellfish samples were collected from harvesting areas, dispatch centres, restaurants, fish markets and supermarkets, during official monitoring programs, and tested according to ISO/TS 15216-2:2013 at the Experimental Zooprophylactic Institute of Sicily "A. Mirri".

Results: HAV-RNA was detected in 10/16 (62%) urban sewages collected from May to September 2017 in Trapani (1/1), Messina (3/3), Catania (2/5) and Syracuse (4/7). Sequence analyses demonstrated the co-circulation of two HAV-IA strains, named VRD-521-16 and RIVM-HAV16-090, currently involved in a large European outbreak in MSM population (>3000 confirmed cases in 22 EU/EEA countries). During Fall/Winter only sewages collected from Trapani and Catania were still contaminated. Starting from March 2018, HAV genome reappeared in wastewater from Syracuse, but nucleotide sequences were related to older HAV-IA clones or to the HAV-IA V16-25801 variant, recently spreading in Germany, UK and Spain among MSMs. Surveillance on shellfish showed the presence of HAV genome in only 1/23 samples analyzed. The HAV-positive

shellfish sample was collected in Syracuse on May 2017 and the strain belonged to HAV-IB subtype.

Discussion and conclusions: Environmental surveillance demonstrated that the widespread circulation of HAV-IA strains in Sicily, is probably not linked to marine and shellfish contamination but to person-to-person transmission, including MSMs sexual contact, as recently reported in other European countries.