P245

VIROLOGIA

PHYLOGENETIC CHARACTERIZATION OF WEST NILE VIRUS (WNV) STRAINS CIRCULATING IN EMILIA-ROMAGNA REGION, 2013-2018

S. Lafratta [1], M.C. Re [1], G. Rossini [1]

[1]*Centro di Riferimento Regionale Emergenze Microbiologiche (CRREM), Unità Operativa di Microbiologia, Policlinico di Sant'Orsola, Bologna*

INTRODUZIONE

West Nile virus (WNV) is a mosquito-borne RNA virus belonging to the genus Flavivirus. Despite the majority of WNV infections in humans are asymptomatic (80%), some infected patients develop West Nile fever (WNF, 20%) and a small subset (<1%) develop severe neuroinvasive disease (WNND), which may include meningitis, meningoencephalitis and acute flaccid paralysis. In Italy, the first human cases were reported in 2008, and since then the virus has circulated in many regions and more than 400 autochthonous cases of human WNND were notified. Since 2008, various WNV strains, belonging both to lineage 1 and lineage 2, have circulated in Italy. Aim of this study was to characterize the molecular epidemiology of WNV strains circulating in Emilia-Romagna region during 2013-18.

METODI

Urine samples were collected from 19 WNV infected patients residing in the provinces of Bologna (n.4), Modena (n.6), Ferrara (n.4), Reggio nell'Emilia (n. 2), Parma (n.2) and Piacenza (n.1), during years 2013-18. Urine samples were processed for viral RNA extraction and PCR amplification of a region of 1306 nt in WNV NS5 gene. Amplicons were bidirectionally sequenced and multiple alignments of the new sequences, along with the corresponding sequences from other WNV strains available in GenBank were generated by MAFFT software. Phylogenetic analysis was inferred by using MEGA 7 software.

RISULTATI

Phylogenetic analysis of WNV genomes detected in Emilia-Romagna region in 2013-2018 showed that they all belonged to the Central/Southern European lineage 2 (Hungarian clade). Strains isolated in Emilia-Romagna grouped with WNV strain isolated in others Italian regions forming a single monophyletic group within the large European clade. Interestingly, within the Italian clade two significant sub-cluster could be identified: one included strains circulating in 2013 and the other one included strains circulating in 2014-2018. WNV strains circulating in 2013 were characterized by unique sets of amino acid substitutions in NS5 protein.

CONCLUSIONI

The results of this study provide further information on WNV lineage 2 transmission dynamics in Italy, and emphasize the need for WNV surveillance activities to monitor viral evolution and diversity.