

P0003

Paper Poster Session

Viral molecular epidemiology (other than Hepatitis/HIV)

Molecular epidemiology of measles viruses in Italy, 2014-2015

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Background: The Italian National Reference Laboratory for Measles and Rubella (NRL) is part of the WHO European Regional Network of Measles and Rubella Reference Laboratories with the goal of the measles elimination in Europe by 2015. This study describes the molecular characterization of measles virus (MV) strains identified in Italy during the years 2014-2015, as part of the laboratory measles surveillance activity. Clinical samples were collected from patients with suspected measles infection. Molecular tests were performed for MV detection and positive samples were sequenced and phylogenetically analysed.

Material/methods: Molecular detection was performed by real time PCR. A traditional RT-PCR was performed on positives for sequencing reactions. Sequences were compared aligning the fragment coding for the carboxyl terminus of the nucleoprotein (450 nucleotides) with those of reference strains. Sequence data were analyzed by using version 7.0 of BioEdit and phylogenetic analyses were performed using MEGA version 6. MV strains were named as designated by the World Health Organization.

Results: Between 2014 and 2015, a total of 119 samples positive for MV were sequenced and phylogenetically analysed. Phylogenetic analysis showed a steady circulation of genotype D8. Genotype B3 became endemic during 2014 and it has continued to co-circulate with D8. Sporadic cases belonged to genotypes D9 and H1 during all the reviewed period.

Conclusions: Positive measles samples were genotyped to identify MV strains circulating in Italy. Genetic characterization is an essential component of laboratory-based surveillance. It provides a means to study transmission pathways of the virus and find origins and routes of MV wild-type circulation. Knowledge of currently circulating MV genotypes in Italy will help in monitoring the success of the measles elimination programme and will contribute to evaluate the effectiveness of future vaccination campaigns.