PS105 MEASLES VACCINE IN AFRICA & ELSEWHERE

Abstract: 223

MOLECULAR EPIDEMIOLOGY OF MEASLES VIRUS IN IRAN

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Purpose/Objective

Measles virus (MV) genotyping is an important component of measles surveillance in the context of monitoring immunization program effectiveness towards measles elimination. The molecular epidemiology and genetic variability of circulating MV strains in Iran during the 2010–May 2013 were studied in consecutive MV isolates.

Materials and Methods

Specimens of blood, urine and throat swab from suspected cases of measles were collected from different regions of Iran. Detection of IgM specific antibodies to measles in sera was performed using a commercial ELISA kit. Virus isolation was performed on urine and throat swabs of confirmed serologically measles cases. For virus isolation, the specimens were inoculated onto Vero/hSLAM cell line. Partial nucleoprotein gene segments of MV including the 456 N-terminal nucleotides were amplified by RT-PCR. PCR products were sequenced in both directions. Sequenced data were analyzed by Bioinformatics software.

Results

From confirmed cases by ELISA, 57 (25.6%) were obtained from viral isolates using cell culture and the 166 (74.4%) were obtained directly from clinical samples.

Conclusions

Although vaccination programs have decreased successfully the incidence of the disease, sporadic cases and outbreaks continue to occur. During 2010-May 2013, genotypes B3 and D8 (for the first time), H1 (for the second time) and D4 were detected mainly in persons living within communities that had low vaccination status such as inland rural areas and hard-tor each community with traditional lifestyle. According to the new measles elimination strategic plan of the WHO/EMRO, Iran as one of the member of this region aimed to eliminate MV by 2020.