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**MOLECULAR EPIDEMIOLOGY AND GENETIC CHARACTERIZATION OF MEASLES VIRUS IN IRAN IN 2013-2014**

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**Background and aims:** Molecular epidemiology of measles viruses (MV) helps to identify transmission pathways of the virus and to document the interruption of endemic virus circulation. We carried out a phylogenetic analysis of measles virus circulating in Iran over the period 2013–2014.

**Methods:** Specimens of serum, throat swab and urine from suspected cases of measles were collected from different provinces of Iran. All sera were screened for measles IgM specific antibody using ELISA kits. Virus isolation was performed on throat swabs and urine of confirmed serologically measles cases. For virus isolation, the specimens were inoculated onto mycoplasma free Vero/hSLAM cell line. Partial nucleoprotein gene segments of MV were amplified by RT-PCR. PCR products were sequenced in both directions. Sequenced data were analyzed by Bioinformatics software.

**Results:** A total of 98 cases of measles were serologically confirmed. 17 sequences (17.4%) were obtained from viral isolates using cell culture and the 81 (82.6%) were obtained directly from specimens. The age of cases ranged from 2.5 month to 44 years. The vaccination history showed that among all confirmed cases, 8 (8.16%) had been vaccinated, 83 (84.7%) had not been vaccinated, and 7 (7.14%) had unknown vaccination status.

**Conclusions:** In spite of progress in measles surveillance, outbreaks were reported from some parts of Iran over the last 2 years. Genotypes B3 (92.86%), D4 (5.1%) and D8 (2.04%) were detected mainly in non-vaccinated persons. This information is valuable to inform vaccination strategies with a focus on those populations who remain susceptible to measles infection.