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LETTER TO THE EDITOR

GENETIC DIVERSITY OF MEASLES VIRUS - RESURGENCE OF NEW GENOTYPE D8 IN SAO PAULO, BRAZIL

Sao Paulo, April 28, 2014

Dear Sir:

Measles virus (MV) has been under control in Brazil because of the high coverage rates of immunization. Emphasized by the measles control global program at the Pan American Health Organization, with the use of several strategies of vaccination programs to reduce the number of circulating chains of transmission of the virus, these programs have successfully decreased the incidence of measles on a global scale. However, measles outbreaks still occasionally occur in areas with high vaccine coverage as a result of imported transmission^{1,2}.

For the goal of MV elimination, genotypes characterization of circulating wild-type MV is useful to document the interruption of transmission of endemic measles infection. In a meeting organized by the World Health Organization (1998), a nomenclature of MV genotypes and the targets for molecular epidemiological studies were established. Currently, 24 genotypes of MV have been identified and they have been distributed by geographical patterns^{6,7}.

The Epidemiologic Surveillance Center and Adolfo Lutz Institute in São Paulo are consistent in the investigation and continuous analysis of the activity of the measles control program. Retrospective studies of the genetic diversity of MV in São Paulo indicated that genotypes D5 had been registered in 1995 and 1996 and that the circulation of genotypes D6 was responsible for the 1997 epidemic⁵. After this period, the MV was interrupted with the absence of endemic genotypes. However, cases of imported virus were registered - genotype D5 in 2000, 2001 and 2005, genotype D4 in 2011 and genotype D8 in 2012 and 2013^{2,3,4}.

A resurgence of indigenous MV cases has occurred in Sao Paulo in 2014. A total of 90 patients suspected of MV infection were analyzed for measles-specific immunoglobulin (IgM) by Elisa and Real-time quantitative PCR. Of these patients, MV infections were confirmed in seven cases. They did not receive the vaccine nor had any record of vaccination for MV; regarding age, patients were between eight month-old and 34 years-old.

The genetic analysis was carried out from the seven confirmed measles cases. The sequences of N gene were determined by means of comparison with those from the GenBank reference strains. The results in five cases showed the presence of genotypes D8, a new genotype circulating in Sao Paulo. This genotype had been previously reported with an imported case in 2012 and 2013. In one of these cases, the patient had traveled to Fortaleza (Brazil), where MV genotype D8 had been circulating, and returned to Sao Paulo.

In addition, we conducted the analysis of two imported cases, which the surveillance had reported as patients who had traveled to Europe and returned to Sao Paulo presenting symptoms. The phylogenetic analysis of one of these cases showed that MVs were genotype B3 and that the

other case was confirmed only by IgM and 4-fold increase in the IgG antibody titer in acute and convalescent serum specimens.

The government has been making great efforts to achieve the goal of measles elimination adopting surveillance programs to implement investigation strategies in susceptible populations and others to improve supplemental immunization.

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