Occurrence of measles genotype D8 during a 2014 outbreak in Banjarmasin, South Kalimantan, Indonesia Tahun Terbit 2017

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Short Communication

Occurrence of measles genotype D8 during a 2014 outbreak in Banjarmasin, South Kalimantan, Indonesia

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SUMMARY

Objectives: An outbreak of measles symptoms occurring in children in Banjarmasin, South Kalimantan, Indonesia in 2014 was investigated.
Methods: Nasal swabs were collected from 23 children (median age 41 months) with fever and other symptoms of measles hospitalized in Ulin General Hospital and Islamic Hospital, Banjarmasin, South Kalimantan. Viral RNA was extracted for cDNA synthesis, followed by PCR and sequencing using paramyxovirus family consensus and N-gene primers.
Results: Sixteen measles-positive patients (70%) were identified. Fifteen virus strains belonged to genotype D8 and the remaining one strain was confirmed as belonging to genotype D9.
Conclusion: Measles virus genotype D8 was detected in an outbreak of measles in South Kalimantan, Indonesia, in 2014.
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1. Introduction

Measles is an acute, highly contagious illness caused by an enveloped virus in the family *Paramyxoviridae*, genus *Morbillivirus*. Measles is a vaccine-preventable disease, and the currently available vaccine is expected to provide protection against all circulating strains.

Three genotypes of measles have previously been reported to circulate in Indonesia: genotypes G2, G3, and D9.[1] The Ministry of Health, Republic of Indonesia reported that measles vaccination coverage of children was 94.7% in 2014, but 69.5% in South Kalimantan Province.[2] Despite vaccination efforts in Indonesia, a total of 12 943 measles cases were reported in 2014, which was an increase from the 11 521 cases reported in 2013; the incidence rate (IR) was 5.13/100 000 in 2014 and 4.64/100 000 in 2013.[2] An investigation of the virus responsible for an outbreak involving children with measles symptoms in Banjarmasin, South Kalimantan is reported herein.

2. Methods

Nasal swabs were collected in viral transport medium (VTM) from children presenting with fever and other symptoms of measles. Samples were taken <5 days after illness onset from patients who were hospitalized in the pediatric wards of Ulin General Hospital and Islamic Hospital, Banjarmasin, South Kalimantan, from October to November 2014. A history of travel or any contact with travelers was not reported for any of the patients. The testing of outbreak specimens was approved by the Eijkman Institute Research Ethics Commission (number 66, November 18, 2013).

Detection of the virus causing the outbreak was conducted as part of ongoing research into a fever study algorithm, designed for the surveillance of viruses of pandemic potential (USAID PREDICT Project). Viral RNA was extracted from all nasal swab specimens for cDNA synthesis, followed by PCR amplification using paramyxovirus family consensus primers.[3] Positive amplicons were sequenced using the Sanger method and a BLAST search was performed in the GenBank database. All positive samples, as identified by sequencing, went through further amplification and sequencing of 450 nucleotides in the N-gene region recommended for measles virus genotyping, following the procedure described by Chibo

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et al.[4] All positive samples were sent to PT Bio Farma, the World Health Organization (WHO) reference laboratory located in West Java, Indonesia, for sequence confirmation.

3. Results

During the outbreak, 23 swabs were collected from as many patients. These patients ranged in age from 6 months to 11 years (median age 41 months); 11 were male and 12 were female. Clinical presentations included fever ($n = 23$, 100%), severe rash typical of measles ($n = 21$, 91%), cough ($n = 23$, 100%), nausea and vomiting ($n = 15$, 65%), sore throat ($n = 16$, 70%), stomach ache ($n = 4$, 17%), and seizures ($n = 2$, 9%). All patients recovered without further complications and were discharged an average of 2.8 days after hospitalization. The vaccination status of the patients was determined through a review of the records and parental report,

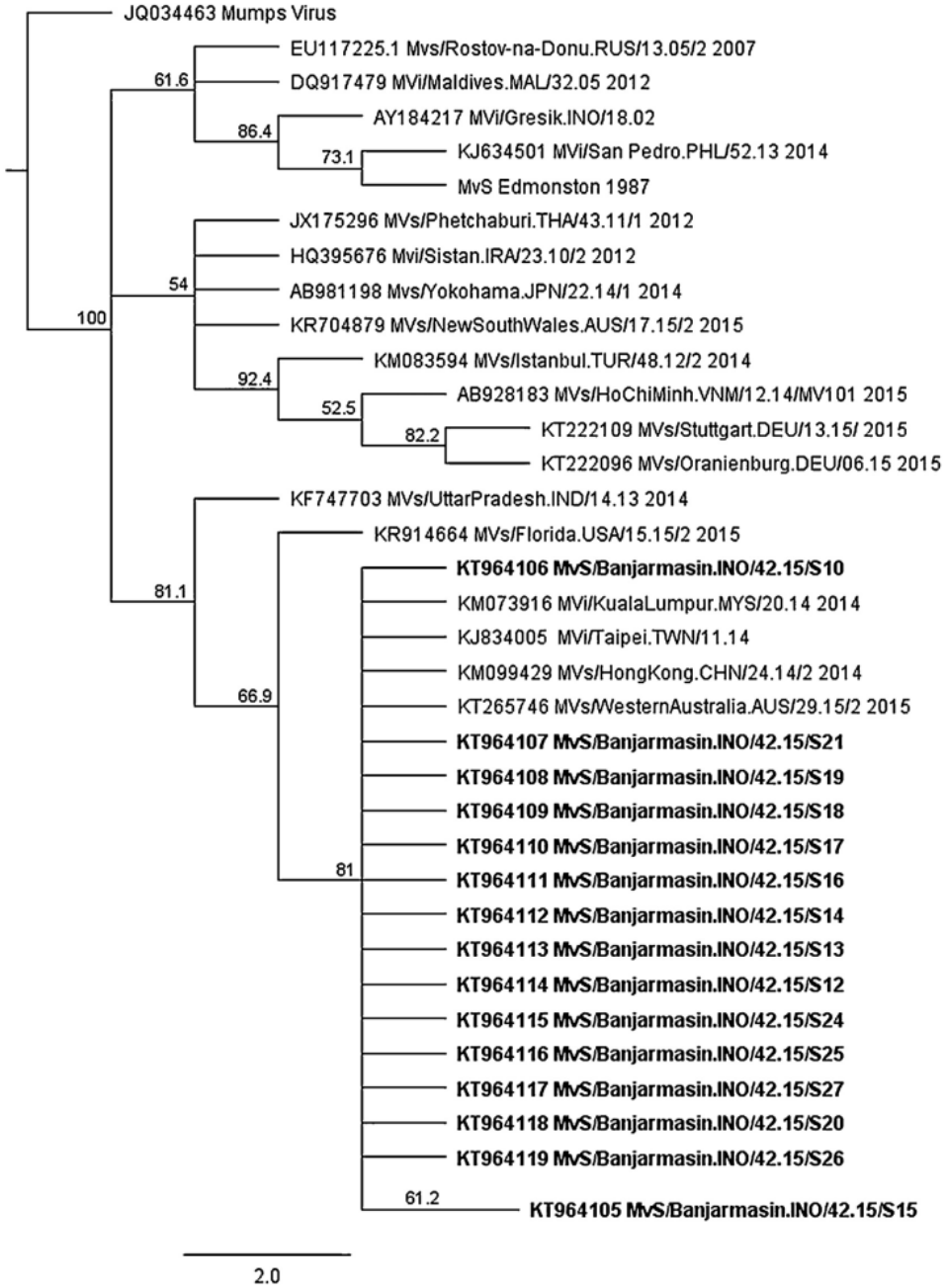

Figure 1. Phylogenetic tree of measles virus sequences from the outbreak in Banjarmasin and other genotype D8 strains circulating in the region (a total of 19 reference strains obtained from the GenBank database and a WHO reference strain). Accession numbers are given on the phylogenetic tree. The sequences cover 450 nucleotides encoding the C-terminal hypervariable region of the N-gene recommended for measles genotyping. The phylogenetic tree was constructed using Geneious software version 8.1.5, applying the neighbor-joining model and the Kimura 2-parameter method with 1000 bootstrap replicates.

revealing 14 to be vaccinated and seven to be unvaccinated; the vaccination status was uncertain for two patients.

Sixteen of the patients were found to be positive for measles. PT Bio Farma confirmed 15 virus strains to be genotype D8 and one strain to be genotype D9. The sequences of the D8 strains were 99% similar to other D8 strains circulating in the region (Figure 1). All sequence data for the genotype D8 strains reported in this study have been deposited in GenBank (gene accession numbers **KT964105**–**KT964119**).

4. Discussion

Up until 2009, measles outbreaks in Indonesia were associated with genotypes G2, G3, and D9.[1] Measles genotype D8 (MV-D8) has already been reported to be circulating and is associated with sporadic cases in many countries in the Southeast Asia region, including Thailand, Vietnam, Nepal, India, and Bangladesh.[1] Recently, MV-D8 was reported in two Taiwanese travelers visiting Indonesia.[5] According to a WHO report[6] and personal communication with an Indonesian Ministry of Health representative and PT Bio Farma, MV-D8 was detected co-circulating with genotypes D9 and B3 in 2013 and 2014 in Sumatera and Jakarta, Indonesia. It is possible that MV-D8 has been circulating within Indonesia in areas of low vaccination coverage, but the origin of the strain is difficult to specify.

Measles vaccination coverage for children in South Kalimantan has been reported to be 69.5%, with two doses given as part of the national immunization program (one at 9 months and one at 24 months of age). This is lower than the minimum vaccination coverage required to protect the population from a large outbreak, which is >93–95% of the population immunized.[7] This coverage can be improved through more active, routine vaccination and/or campaigns aimed at providing the two doses of vaccine.[8] Failure to maintain coverage with the vaccination will lead to a resurgence of measles.[8] Moreover, the interval between the first and second dose of the vaccine will leave several birth cohorts protected with only one dose, which has only about 85% protection efficacy.[9]

According to RISKESDAS, a health survey performed by the Indonesian Ministry of Health in 2007, 2010, 2013, and 2014, measles vaccination coverage for babies 12–23 months of age in South Kalimantan decreased from 81.7% to 75.2%, 74.1%, and then 69.5%, respectively.[2,10–12] This decrease in vaccination coverage might have an impact on the occurrence of measles outbreaks.

This study has some limitations. Serum samples were not available from any of the patients to assess their immunity status. The breakthrough infection in 11 cases could have been due to the children only having received one dose of the vaccine and to the variability in immune response to the measles vaccine.[13]

The recovery of MV-D8 from an outbreak in Banjarmasin, South Kalimantan is reported. This information might be beneficial for directing public health action in Indonesia and for informing strategies to increase vaccine coverage. The results should alert the responsible health authorities to increase measles surveillance, as well as to determine the immunity status among vaccinated children in order to assess the effectiveness of the measles vaccine and the measles elimination program.

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Conflict of interest: No conflict of interest to declare.

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