Rubella Virus Genotype 1E in Travelers Returning to Japan from Indonesia, 2017

Daiki Kanbayashi, Takako Kurata, Yuka Nishino, Fumi Orii, Yuki Takii, Masaru Kinoshita, Toshitake Ohara, Kazushi Motomura, Takahiro Yumisashi

Author affiliations: Osaka Institute of Public Health, Osaka, Japan (D. Kanbayashi, T. Kurata, K. Motomura, T. Yumisashi); Osaka Prefectural Government Department of Health and Medical Care, Osaka (Y. Nishino, F. Orii, Y. Takii, M. Kinoshita); Osaka Prefectural Government Ikeda Healthcare Center, Osaka (T. Ohara)

DOI: https://doi.org/10.3201/eid2409.180621

Although rubella is epidemic in Indonesia, the phylogenetic profile of circulating rubella virus strains has not been clarified. In 2017, rubella virus was detected in 2 travelers who returned from Indonesia to Japan. These strains were classified into genotype 1E lineage 2, which may be an indigenous strain in Indonesia.
imported from African countries, such as the Democratic Republic of the Congo and Tunisia. 1E-L4 strains are detected in Sudan, Yemen, and Uganda. Both RVs/Osaka. JPN/41.17[1E] and Hendersonville.NC.USA/15.11 belonged to 1E-L2; these sequences were closely related to the recently identified 1E-L2 sequences. We also detected RVs/Yokohama.JPN/3.17[1E] in a traveler who returned to Japan from Indonesia in January 2017 (deposited in GenBank under accession no. LC215401) who had contact with a local rubella patient. Our findings indicate that 1E-L2 strains may circulate as indigenous strains in Indonesia.

To verify rubella elimination, interruptions in transmission of indigenous or imported rubella virus strains must be confirmed through effective surveillance systems (9). However, it is difficult to distinguish imported strains from endemic strains and to confirm the control status on the basis of genotype information because the genotypes of global epidemic strains converge to genotypes 1E and 2B (3,7,8,10).

**Figure.** Maximum-likelihood phylogram of the molecular window region (739 nt) within the E1 gene of rubella virus genotype 1E from a 29-year-old man in Japan who had traveled to Indonesia (black circles). We constructed a phylogenetic tree using 61 strains, including the genotype reference strains and the candidate lineage reference strains, using MEGA version 7.0 (http://www.megasoftware.net) and the Tamura-Nei model.

Numbers at nodes indicate the bootstrap support values, given as a percentage of 1,000 replicates (values <45 are omitted). The genotype 1D reference strain (RVi/Saitama.JPN/0.94/[1D]) is included as an outgroup. White circles indicate the genotype 1E strain detected in patients returning to the United States from Indonesia in 2011. Black squares indicate candidate genotype 1E lineage reference strains. White squares indicate the strains detected in Japan from 2012–2017. Each strain identification consists of a 3-letter country name abbreviation and detection year. Accession numbers are shown in parentheses. Scale bar indicates nucleotide substitutions per site.

COD, Democratic Republic of the Congo; FRA, France; JPN, Japan; KAZ, Kazakhstan; CHN, China; MYS, Malaysia; ROU, Romania; RUS, Russia; SDN, Sudan; TUN, Tunisia; UGA, Uganda; UKR, Ukraine; USA, United States of America.
Therefore, several studies were conducted to subdivide the genotypes on the basis of detailed phylogenetic analysis (7,8). We reported that a large epidemic in Japan in 2013 might have occurred due to the transport of multiple lineages of rubella virus from rubella-endemic countries (7). According to the National Epidemiological Surveillance of Infectious Diseases (NESID) of Japan, during 2015–2017, ≈100 cases of rubella, which is a notifiable disease in Japan, were reported annually (5), and genotype 1E strains, including a strain closely related to RVs/Osaka, were detected. Although these strains might have been transported from countries with endemic rubella, their origin remains unclear because of insufficient genomic information.

Japan has a high risk for subsequent rubella epidemics because the proportion of persons susceptible to rubella virus (≈9.0%) has not changed since 2013. In addition, an epidemic can occur when rubella virus is transported from rubella-endemic countries and the infection occurs in susceptible populations, as happened in Japan in 2013. Of the 11 imported cases of rubella to Japan reported in 2017, 4 were from Indonesia, according to the NESID of Japan. In the case we describe, we identified the rubella-exporting country and clarified the genetic information of the strain, which may contribute to countermeasures for worldwide importation of rubella virus. Rubella control by 2020 is the flagship goal of the World Health Organization South-East Asia region. Indonesia is conducting rubella immunization campaigns targeting ≈70 million children in 2017–2018. Therefore, constructing effective surveillance systems, accumulating genetic information, and promoting immunization in rubella-endemic countries are steps toward the global elimination of rubella.

Acknowledgments

We thank the staff of Osaka Prefectural Government, Yokohama City Institute of Public Health, Yokohama City Public Health Center, and Yokohama City Ward Health and Welfare Centers for supporting our work. We thank Yoshio Mori for review of this manuscript and Enago for the English language review.

This study was partially supported by JSPS KAKENHI grant number 16H00425, 18K17367 to D.K. and a grant-in-aid from the Japan Agency for Medical Research and Development, AMED (JP17fk0108213).

About the Author

Mr. Kanbayashi is a researcher at the Osaka Institute of Public Health. His research interests include rubella.

References

1. Reef S, Plotkin SA. Rubella vaccine. In: Plotkin SA, Orenstein W, Offit P, editors. Vaccines, 6th ed. Philadelphia: Saunders; 2013. p. 688–717.
2. Plotkin SA. The history of rubella and rubella vaccination leading to elimination. Clin Infect Dis. 2006;43(Suppl 3):S164–8. http://dx.doi.org/10.1086/505950
3. Lambert N, Strebel P, Orenstein W, Icenogle J, Poland GA. Rubella. Lancet. 2015;385:2297–307. http://dx.doi.org/10.1016/S0140-6736(14)60539-0
4. Cutts FT, Vynnycky E. Modelling the incidence of congenital rubella syndrome in developing countries. Int J Epidemiol. 1999;28:1176–84. http://dx.doi.org/10.1093/ije/28.6.1176
5. World Health Organization. WHO vaccine-preventable diseases: monitoring system [cited 2018 Jul 10]. http://apps.who.int/immunization_monitoring/globalsummary/
6. Okamoto K, Mori Y, Komagome R, Nagano H, Miyoshi M, Okano M, et al. Evaluation of sensitivity of TaqMan RT-PCR for rubella virus detection in clinical specimens. J Clin Virol. 2016;80:98–101. http://dx.doi.org/10.1016/j.jcv.2016.05.005
7. Mori Y, Miyoshi M, Kikuchi M, Sekine M, Umezawa M, Saikusa M, et al. Molecular epidemiology of rubella virus strains detected around the time of the 2012–2013 epidemic in Japan. Front Microbiol. 2017;8:1513. http://dx.doi.org/10.3389/fmicb.2017.01513
8. Rivailler P, Abernathy E, Icenogle J. Genetic diversity of currently circulating rubella viruses: a need to define more precise viral groups. J Gen Virol. 2017;98:396–404. http://dx.doi.org/10.1099/jgv.0.00680
9. Framework for verifying elimination of measles and rubella. Wkly Epidemiol Rec. 2013;88:89–99. PubMed
10. Abernathy ES, Hübschen JM, Muller CP, Jin L, Brown D, Komase K, et al. Status of global virologic surveillance for rubella viruses. J Infect Dis. 2011;204(Suppl 1):S524–32. http://dx.doi.org/10.1093/infdis/jir099

Address for correspondence: Daiki Kanbayashi, Osaka Institute of Public Health, 1-3-69 Nakamichi, Higashinari-ku, Osaka 537-0025, Japan; email: kanbayashi@iph.osaka.jp

Spondweni Virus in Field-Caught Culex quinquefasciatus Mosquitoes, Haiti, 2016

Sarah K. White,1 John A. Lednicky, Bernard A. Okech, J. Glenn Morris, Jr., James C. Dunford

Author affiliations: University of Florida, Gainesville, Florida, USA (S.K. White, J.A. Lednicky, B.A. Okech, J.G. Morris, Jr.); US Navy and Marine Corps Public Health Center, Portsmouth, Virginia, USA (J.C. Dunford)

DOI: https://doi.org/10.3201/eid2409.171957

1Current affiliation: Brammer Bio, Alachua, Florida, USA.