

Recent Updates on the Epidemiology and Immunizations of Measles Virus in Ethiopia

Aschalew Gelaw^{1*}

¹University of Gondar, College of Medicine and Health Sciences, School of Biomedical and Laboratory Sciences, Department of Medical Microbiology

Corresponding author: aschalew3@gmail.com

Citation: Gelaw A. Recent Updates on the Epidemiology and Immunizations of Measles Virus in Ethiopia. *Ethiop J Health Biomed Sci* [Internet]. [cited 2024 Apr. 11];13(2):1-3.

DOI: <https://doi.org/10.20372/ejhbs.v13i2.713>

Article History

Received: December 05, 2023

Revised: December 10, 2023

Published: December 30, 2023

Key words:

Publisher: University of Gondar

Editorial

Measles virus (MeV) remains a major cause of morbidity and mortality worldwide, with an increasing burden on children under five years of age (1). The disease is highly contagious and characterized by a prodromal illness of fever, coryza, cough, and conjunctivitis followed by the appearance of a generalized maculopapular rash. The primary routes of measles transmission are person-to-person via aerosolized droplets or by direct contact with nasal and throat secretions (2). The World Health Organization (WHO) reported an estimated 128,000 deaths globally attributable to measles in 2021(3). In Ethiopia, 182 deaths were recorded between 2021 and 2023, resulting in a case fatality ratio (CFR) of 1.1%. Since 2021, the annual number of confirmed measles cases has increased significantly, from 9291 in 2021 to 9291 in 2022 and 6933 in 2023. There was an approximately fivefold increase in confirmed measles cases between 2021 and 2022. Surprisingly, among the confirmed measles cases, more than 64% have not received the vaccine (4).

MeV is a negative-sense single-stranded RNA virus belonging to the family *Paramyxoviridae* (5, 6). The genome of MeV is approximately 15.9 kb long (1). The virion is composed of six types of proteins. Among these proteins, hemagglutinin (H), fusion (F) and matrix (M) proteins make up the envelope, whereas nucleoprotein (N), phosphoprotein (P) and large protein (L) make up the nucleocapsid. Although measles is a monotypic virus, genetic and antigenic variation has been detected in wild-type viruses (7). On the basis of genetic variability in the nucleoprotein (N), eight (A-H) clades and 24 distinct genotypes (A, B1-B3, C1-C2, D1-D11, E, F, G1-G3, and H1-H2) of MeV are recognized (6, 8–11). The genotypic distribution of MeV varies across the six WHO regions. According to the few available reports, genotype B3 is endemic in African countries, including Ethiopia (9, 12). Studies on the genetic diversity of MeVs help to trace transmission pathways, allow the detection of imported cases, and classify suspected cases as caused by vaccine or wild-type strains (13). Due to the limited

Copyright: © 2024 Gelaw et al. This is an open access article distributed under the terms of the Creative Commons Attribution-NonCommercial 4.0 (CC BY NC 4.0) License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

number of virology laboratories in resource-limited countries, there is a paucity of information on the genotypic distribution of MeV. Several immunoassay techniques are available for the detection of measles virus from oral secretions, blood and urine samples. Nucleic acid based detection methods such as Reverse transcriptase polymerase chain reaction (RT-PCR) are highly sensitive and specific, and provides genotypic information. However, RT-PCR assays are expensive and rarely available. Enzyme linked immunosorbent assays (ELISAs) based detection of measles specific IgM is the commonly used method in the routine surveillance and detection of measles in Ethiopia (14).

The disease is vaccine preventable. Cognizant of this, the WHO introduced the measles vaccine in 1963 for the first time (1). The vaccine is based on a live attenuated strain of measles prepared in lyophilized form. The WHO recommends two doses of the vaccine: the first dose of measles-containing vaccine (MCV1) at nine months of age and the second dose (MCV2) at least one month after the first dose (15). In Ethiopia, vaccination started in 1980 with the use of MCV1 (16). Later, in 2019, MCV2 vaccination was started. In 2021, the rates of vaccination coverage of MCV1 and MCV2 were estimated to be 54% and 46%, respectively (4, 17). Studies indicated that the coverage of MCV2 could be as low as 12.4% nationally, with some areas showing higher rates (42.5%) but still far from the ideal 95% coverage (18).

Despite the use of both the MCV1 and MCV2 vaccines, measles outbreaks persist in Ethiopia, particularly affecting children under five years of age. Evidently, outbreaks were reported in 44 woredas in eight regions of the country (4). To identify the actual causes for the frequent outbreaks, nationwide assessment is necessary. Different fragmented studies reported that low subnational vaccination coverage, poor nutrition, and the clustering of unvaccinated children were the contributing factors (16). In recent years, conflict, forced displacement and other humanitarian crises have disrupted childhood vaccinations and contributed to the resurgence of measles in Ethiopia. Furthermore, cultural beliefs, insufficient awareness, and behavioral characteristics of the population have affected treatment and other management strategies for this disease (4).

The prevention and control measures for the elimination of measles virus are clear. Prioritizing measles vaccination, strengthening surveillance, and conducting catch-up campaigns are essential for controlling outbreaks and maintaining elimina-

tion. Research into barriers to vaccination, molecular epidemiology, and vaccine storage and handling is crucial. Adequately equipping healthcare workers and establishing robust surveillance systems are paramount to swiftly identifying and containing outbreaks. Building resilient public health infrastructure and ensuring uninterrupted vaccination can prevent measles outbreaks, ensuring a healthier future for Ethiopian children.

References

1. Melissa M. Coughlin, Andrew S. Beck, Bettina Bankamp and Paul A. Rota: Perspective on Global Measles Epidemiology and Control and the Role of Novel Vaccination Strategies.
2. WHO Regional Office for Africa: African Regional Guidelines for Measles and Rubella Surveillance. Harare: 2015.
3. WHO, Measles. June: Key facts: WHO. <https://www.who.int/news-room/fact-sheets/detail/measles>. Accessed 2024.
4. WHO. Measles in Ethiopia: WHO. <https://www.who.int/emergencies/disease-outbreak-news/item/2023-DON460>. Accessed November 2023.
5. Knipe DM, Howley P: Fields Virology. Philadelphia, Wolters Kluwer, 2015.
6. Fields BN, Knipe DM, Howley PM: Fields virology, 5th ed. Philadelphia, Wolters Kluwer Health/Lippincott Williams & Wilkins, 2007.
7. Tamin A, Rota PA, Wang ZD, Heath JL, Anderson LJ, Bellini WJ.: Antigenic analysis of current wild type and vaccine strains of measles virus. *Journal Infectious diseases* 1994;170:795–801.
8. Alya D, Rebecca LL, Claudia S, Laure D, Mick NM, Katrina K, James PA, Paul A. Rota, James LG: Progress Toward Regional Measles Elimination Worldwide, 2000–2017;67(47):1323-1329
9. WHO: Genetic diversity of wildtype measles viruses and the global measles nucleotide surveillance database (MeaNS). *Weekly epidemiological record* 2015; 90 (30):337-380.
10. WHO: measles virus nomenclature update: 2012. *Weekly*

- epidemiological record 2012; 87(9): 73-80.
11. William J. Bellini, Paul A. Rota: Genetic Diversity of Wild-Type Measles Viruses: Implications for Global Measles Elimination Programs. *Emerging infectious diseases* 1998; 4:29–35.
 12. Rota PA, Brown K, Mankertz A, Santibanez S, Shulga S, Muller CP, Hübschen JM, et al: Global distribution of measles genotypes and measles molecular epidemiology. *J Infect Dis* 2011;204 Suppl 1:S514-23.
 13. Patel MK, Gacic-Dobo M, Strebel PM, Dabbagh A, Mulders MN, et al: Progress Toward Regional Measles Elimination - Worldwide, 2000-2015. *MMWR Morb Mortal Wkly Rep* 2016; 65:1228–1233.
 14. Lenessa W, Rimantas S, Kaw Bing C, Wondatir N, Kevin E B, Kestutis S, Dhanraj S, David B: A point-of-care test for measles diagnosis: Detection of measles-specific IgM antibodies and viral nucleic acid. *Bull World Health Organ* 2011;89:675–682.
 15. WHO: Measles vaccines: WHO position paper – April 2017. *Weekly epidemiological record* 2017;92
 16. Akalu HB: Review on Measles Situation in Ethiopia; Past and Present. *J Trop Dis* 2015;4.
 17. WHO/UNICEF estimates of national immunization coverage: <https://www.who.int/teams/immunization-vaccines-and-biologicals/immunization-analysis-and-insights/global-monitoring/immunization-coverage/who-unicef-estimates-of-national-immunization-coverage>
 18. MDPI Study: Low Measles Vaccination Coverage and Spatial Analysis of High Measles Vaccination Dropout in Ethiopia's Underprivileged Areas: [DDhttps://www.mdpi.com/2076-393X/12/3/328](https://www.mdpi.com/2076-393X/12/3/328).