

Original Article

Molecular, serological, and epidemiological characterisation of a hepatitis A virus outbreak in Maharashtra, India, 2025

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Background and objectives: Hepatitis A virus (HAV) remains a major cause of jaundice outbreaks globally, with 158.9 million infections reported in 2019 despite a 63% decline in mortality since 1990. Improved sanitation in many regions has shifted the age of primary infection from early childhood to older children and adults, increasing the risk of symptomatic and severe disease. In April–May 2025, we investigated an outbreak of HAV caused hepatitis that occurred in Rajur village, Ahilyanagar district, Maharashtra. A total of 327 suspected cases of acute hepatitis were reported, mainly affecting older children and young adults.

Methods: Suspected acute hepatitis cases were identified by clinical presentation and their epidemiological and clinical data were collected by questionnaire. Serum, stool, and potable water samples were collected and tested by anti-HAV IgM ELISA and/or real-time RT-PCR to confirm outbreak aetiology. Full HAV genome sequences were obtained from selected RT-PCR positive specimens.

Results: The age-specific attack rate for the 327 acute hepatitis cases was the highest in children aged 10–19 years (11.97%) and lowest in those ≥ 50 years. Anti-HAV IgM antibodies were detected in 32 of 45 (71.1%) available serum samples, and HAV RNA was detected in 7 of 22 (31.8%) serum and 19 of 31 (61.3%) stool samples tested. All 7 potable water samples tested negative for HAV RNA. Genomic analysis revealed strain details relevant to disease severity, providing insights into circulating HAV lineages in India.

Interpretation and conclusions: The findings highlight the need for continuous surveillance, genomic monitoring, and targeted prevention strategies to protect vulnerable, previously unexposed populations.

Keywords Acute hepatitis; Genotype III; Hepatitis A; Mutations; Nanopore; Outbreak