

Tracing Hepatitis A Through the Food Chain: Genomic Surveillance Challenges and Opportunities Across Fresh Produce, and Frozen Fruit, in Australia

Karolina Mercoulia^{1,2}, Sally Dougall¹, Mathilda Wilmot¹, Tuyet Hoang¹, Jake Lacey¹, Benjamin Howden^{1,2}

1. WHO Collaborating Centre for Foodborne Disease Surveillance and Genomics at the Microbiological Diagnostic Unit Public Health Laboratory, University of Melbourne, Melbourne, Victoria, Australia
2. Department of Microbiology & Immunology at the Peter Doherty Institute for Infection & Immunity, University of Melbourne, Melbourne, Victoria, Australia

Background: Hepatitis A virus (HAV) remains a public health concern in low-endemicity settings such as Australia, where food-borne transmission has repeatedly driven multi-state outbreaks. Imported foods such as berries have been implicated in national outbreaks in recent years. These events, together with sustained non-food-borne transmission in vulnerable populations, underscore the need for robust, harmonised food and clinical surveillance. Currently, Australian jurisdictions generate ad hoc national genomic surveillance reports from clinical specimens based on partial genome sequencing spanning the VP1/2A junction region. Regular comparison of new Australian sequences against the National HAV Database held at the Microbiological Diagnostic Unit Public Health Laboratory (MDU PHL) supports epidemiological investigation by linking domestic cases to international food and clinical strains.

Challenges in testing: Detecting and characterising HAV directly from food matrices remains a challenge. Fresh produce such as berries, and leafy vegetables typically carry low, unevenly distributed viral loads, often below the limit of detection of standard methods, and surface contamination can be difficult to recover efficiently. Across all food and environmental matrices, viral genomic material is frequently degraded or present in low numbers for sequencing approaches, meaning routine subtyping from non-human sources is rarely achieved outside of outbreak investigations. This gap limits the ability to confirm a source genomically, relying solely on epidemiological and traceback evidence. Whole genome sequencing (WGS) — from both clinical and food specimens — has historically been constrained by low sensitivity of direct metagenomic sequencing in complex matrices, and difficulty designing primer schemes that perform consistently across all six HAV genotypes. Recent proof-of-concept work, including a hybrid-capture enrichment approach validated on Australian clinical serum and berry specimens, demonstrates that near-complete and complete HAV genomes can now be recovered from low-titre samples without prior genotyping, offering a feasible route toward routine WGS-based surveillance that spans both clinical and food sources.

Discussion: Australia is actively transitioning toward WGS for HAV surveillance, building on this local proof-of-concept work, with the eventual goal of a standardised workflow linking clinical, food, and environmental detections. Realising this at a national scale requires harmonising sequencing methods across jurisdictions and establishing new data-sharing agreements to support timely, standardised genome comparison. Complementary food-testing capacity, strengthened by accredited ISO 15216 workflows for HAV detection, positions Australian laboratories to support this integrated approach and to contribute meaningfully to international harmonisation efforts in food safety control.