

## HEPATITIS A OUTBREAKS IN AUSTRALIA

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**Background:** Hepatitis A is a widespread infectious disease caused by hepatitis A virus (HAV) and its site of replication is the liver. In adults, symptoms include fever, malaise, anorexia, nausea, abdominal discomfort, and jaundice. Usual risk factors for hepatitis A infection in Australia include travel to endemic countries, male-to-male sexual contact, and close contact with a confirmed case. In industrialized countries, common source outbreaks are usually related to food contaminated by infected food handlers or food contaminated at the primary production stage. We investigated two recent outbreaks, one in 2009 associated with semi-dried tomatoes and the other in 2015 associated with frozen berries.

**Methods:** Serum samples were sent to VIDRL for HAV RNA testing. Samples shown to HAV RNA positive by the RealStar HAV assay (Altona Diagnostics) were subjected to an in-house RT-PCR and sequenced to determine genotype. The region amplified was the viral protein 1/ protein 2A (VP1/P2A) junction and provided sequence of approx. 300 base pairs in length. Sequences were aligned with CLUSTALX and phylogenetic analysis performed.

**Results:** Hepatitis A virus genotype IB was isolated and identified in 144 of 153 (94%) patients from the 2009 outbreak, and partial sequence analysis showed complete identity with an HAV isolate found in a sample of semidried tomatoes. Hepatitis A virus genotype IA was isolated and identified from 20 patients who had consumed frozen berries and the HAV sequences showed 100% identity.

**Conclusion:** The results from both the virus investigation and food testing implicated the semidried tomatoes and frozen berries, respectively, as the causes of the two hepatitis A outbreaks. VIDRL is currently re-sequencing HAV isolates according to the protocols set out by HAVNET, a global network of reference laboratories specifically focused on HAV. One of the aims of HAVNET is to map the worldwide distribution of HAV strains by creating a shared sequence database which includes epidemiological information. This should allow multi-country outbreaks to be traced to their original source.