

An update on circulating Hepatitis delta virus genotypes in Australia

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Background: Hepatitis delta virus (HDV) is a small satellite RNA virus which requires the presence of the HBsAg in order to propagate, and therefore infects only individuals infected with HBV. HDV infection may occur simultaneously with HBV, or later as a superinfection. HDV is estimated to infect between 12 – 60 million people worldwide, with prevalence and genotype distribution varying globally.

A previous study has shown three out of eight recognised HDV genotypes circulated in Australia from 2010 to 2016; genotype 1 (80.5%), genotype 5 (16%), and genotype 2 (3.5%). This current study expands on this knowledge, and assesses the distribution of HDV genotypes over the period of 2017 to 2024.

Methods: Patient samples which tested positive for HDV RNA between 2017 and 2024 were reflexed to genotyping by sanger sequencing. Two primer sets were utilized, to maximise coverage of the HDV genome.

Results: Sequences were obtained for a total of 170 patients over the study timeframe. The genotype distribution was similar to that observed in the previous study, with genotype 1 being most prevalent (84.7%), followed by genotype 5 (11.8%), and genotype 2 (3.5%). Combining the results of the current study with the previous study shows the globally distributed HDV genotype 1 to be most prevalent in Australia (82.6%), followed by genotype 2 (13.9%) which is found predominantly in Asia and genotype 5 (3.5%) originating from Africa.

Conclusion: The prevalence of each of the HDV genotypes present in Australia has remained steady since the previous study in 2016, with a slight increase in genotype 1, and a corresponding decrease in genotype 5. This distribution is likely a reflection of immigration patterns in Australia, alongside local transmission in PWID. Data is limited by the testing algorithm in Australia, potentially due to HDVPCR testing not being a Medicare rebatable test.

Disclosure of Interest Statement: None to declare.