

## PREVALENCE OF ANTIVIRAL RESISTANCE IN AN AUSTRALIAN HEPATITIS C POPULATION

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**Background:** Hepatitis C virus (HCV) is the main cause of liver transplantation and liver cancer in Australia. New directly acting antivirals (DAAs) have significantly improved cure rates and are now licensed for use in Australia, but the emergence of antiviral resistance remains a concern.

The Q80K mutation in NS3 and several NS5A mutations confer reduced susceptibility to DAAs in clinical trials. Treatment guidelines in the USA recommend resistance testing in patients who have failed treatment with an NS5A inhibitor and for cirrhotic patients with HCV genotype 1a infection being treated with simeprevir and sofosbuvir.

This study examines the prevalence of NS3 and NS5A resistance mutations among Australian patients with HCV genotype 1a infection.

**Methods:** A single centre study was performed at Westmead Hospital, using 380 samples submitted for hepatitis C genotyping between 2011 and 2012.

Total RNA was extracted and reverse transcribed into cDNA. HCV NS3 and NS5 regions were analysed by PCR and Sanger sequencing. In-house next generation sequencing and bioinformatics analysis was also performed for comparison, using the Illumina platform.

**Results:** The Q80K simeprevir resistance mutation was detected in 21 samples by Sanger sequencing, giving a prevalence of 5.6%. Rates of other resistance mutations obtained by next generation sequencing, including minority species prevalence, will also be presented.

**Conclusion:** This study demonstrates the baseline prevalence of resistance mutations among people in Australia living with hepatitis C. We are currently optimising the assay for diagnostic use, to monitor for emergence of antiviral resistance and guide antiviral therapy.

**Disclosure of interest statement:** None