

# Interleukin-28B SNPs rs12979860 and rs8099917 allele frequencies from North India using a novel in-house multiplex T-ARMS-PCR

Rohit Randhawa<sup>1</sup> and Harish Changotra<sup>2</sup>

<sup>1,2</sup>*Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat, Solan 173 234, Himachal Pradesh*

---

**Background:** SNPs, rs12979860 and rs8099917, upstream to IL28B gene are strong predictor of sustained virological response of anti-Hepatitis C Virus (HCV) treatment. The purpose of this study was to develop a novel multiplex tetra primer amplification refractory mutation system polymerase chain reaction (T-ARMS PCR) assay for genotyping these two polymorphisms simultaneously and apply this assay to find the allele frequencies in North Indian population.

**Materials and Methods:** DNA isolated from healthy individuals from North India were genotyped using PCR-RFLP assay. DNA from the known genotypes were used to develop multiplex T-ARMS-PCR which was later used to genotype 94 samples, further sample collection is in progress.

**Results:** The results of the T-ARMS-PCR assay were concordant with the PCR-RFLP method. Frequencies of CC, CT, and TT genotypes of rs12979860 were 27.66% (n=26), 63.83% (n=60) and 8.51% (n=8), respectively, while GG, GT and TT genotypes of rs8099917 were 2.12% (n=2), 29.79% (n=28) and 68.08% (n=64), respectively.

**Conclusion:** We have development a novel multiplex T-ARMS-PCR assay for simultaneously genotyping rs12979860 and rs8099917. This would be helpful in the management of HCV treatment. Furthermore, we report allele frequencies for rs12979860 (C=0.60 and T=0.40) and rs8099917 (G=0.17 and T=0.83) from North Indian population.