

Analysis of *IL28B* polymorphism among chronic HCV patients in Mongolia

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Both of the sustained virological response and spontaneous viral clearance for HDV patients are associated with several polymorphisms located around the *IL28B* gene. In this study, we have identified genotypes of rs12979860 locus of *IL28B* gene by PCR-RFLP method for 61 randomly selected patients with HCV chronic infection. Genotyping analysis showed that observed frequencies of CC, CT, TT genotypes were 0.63, 0.36, and 0, 0% respectively. From this frequencies, it is known that the frequency of C allele is 0, 79 and the frequency of T allele is 0.21. Our study indicates that the allele frequencies of C and T of *IL28B* rs129798601 in chronic HCV patient group are significantly higher than that of normal population of countries located around Mongolia. This result could lead us to assume that Mongolian patients with chronic HCV infection may have influence from *IL28B* polymorphism. The correlation of *IL28B* rs12979860 polymorphism distribution and fate of chronic HCV patients should be assessed by comparing to normal population groups in enough number of individuals.