P1401
Poster Session V
Molecular and non-molecular diagnostics of viruses

INFLUENCE OF HETEROGENEITY OF AMINO ACID SEQUENCE VARYING CONSIDERABLY ON IMMUNOREACTIVITY ANTIGEN REGION OF HCV NS5 PROTEIN FROM POSITION 2212 TO 2313

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There are a very little data regarding the influence of genetic heterogeneity of NS5 protein on the efficiency of antibody detection.

Aim: The purpose of this study was evaluating diagnostic relevance of sequence heterogeneity of HCV NS5 proteins.

Objectives and methods: 9 different synthetic genes encoding epitopes of HCV NS5A proteins containing HCV regions at position 2212 -2313 aa of genotypes 1a, 2a, 2b, 3a, 3b, 4a, 5a, 6a were assembled by PCR from oligonucleotides and expressed as fusion proteins with Glutathione S-transferase in E. coli. Immunoreactivity of these artificial proteins was evaluated by testing well defined anti-HCV positive (n=80) sera samples with different genotypes obtained from patients infected with HCV from Russia and anti-HCV negative (n=82) samples in ELISA.

Results: All proteins have very different immunoreactivity. NS5-1 (1a) had the most level of immunoreactivity and detected anti-HCV in 60.0 % of positive samples. NS5-3 (2b) had the lowest immunoreactivity and detected anti-HCV in 2.5 % of samples. NS5-2 (2a) detected anti-HCV in 51% of samples, NS5-4 (3b) – in 40.6%, NS5-5 (2a) – in 45%, NS5-6 (4a) – in 42.5%, NS5-7 (6a) – in 6.25%, NS5-8 (3a) – in 18.75%, NS5-9 (5a) – in 43.75%. Complex of three proteins NS5-1 (1?), NS5-5 (2a), NS5-8 (3a) made possible to detect anti-HCV in 75 % of positive samples, complex of four proteins NS5-1 (1a), NS5-2 (2a), NS5-5 (2a) and NS5-8 (3a) – in 80%.

Conclusion: These data demonstrate that variation in the primary structure has a significant effect on the antigenic properties of the HCV NS5 protein and should be taken into a consideration when selecting diagnostic target for the development of highly specific and sensitive diagnostic assays for the detection of anti-HCV activity in sera specimens.