29th ECCMID Amsterdam, Netherlands 13 – 16 April 2019

The congress of ESCMID

P0776 Naturally occurring NS5A and NS5B resistance-associated variants in HCV and HCV/HIV patients in Iranian population

Arezoo Aghakhani[1], Kazem Baesi[1], Mohammad Banifazl[2], Minoo Mohraz[3], Farzin Khorvash[4], Majid Yaran[4], Payam Tabarsi[5], Anahita Bavand[6], Amitis Ramezani*[1]

[1] Pasteur Institute of Iran, Tehran, Iran, [2] Iranian Society for Support of Patients with Infectious Disease, Tehran, Iran, [3] Tehran University of Medical Sciences, Tehran, Iran, [4] Isfahan University of Medical Sciences, Esfahan, Iran, [5] Shahid Beheshti University of Medical Sciences, Tehran, Iran, [6] Pasteur institute of Iran, Tehran, Iran

Background: The introduction of direct acting antivirals (DAAs) for hepatitis C virus (HCV) treatment promises shorter treatment duration, higher cure rates and fewer side effects. Naturally occurring Resistance Associated Variants (RAVs) are major challenge to the success of the HCV antiviral therapy. In this study we aimed to determine the naturally occurring NS5A and NS5B RAVs in Iranian HCV and HCV/human immunodeficiency virus (HIV) patients.

Materials/methods: A total of 209 DAA-naïve chronic HCV patients were enrolled in this study, including 104 HCV mono-infected and 105 HCV/HIV co-infected cases. Amplification and sequencing of NS5A and NS5B regions of HCV genome were carried out. The amino acid sequence diversity of the NS5A and NS5B regions were analyzed using geno2pheno HCV.

Results: Overall, baseline NS5A RAVs were detected in 21.5% of all amplified NS5A region sequences. Clinically relevant NS5A RAVs were seen in 11%, 40% and 5% of GT1a, GT1b and GT3a infected cases respectively. The most commonly detected clinically relevant NS5A RAVs in GT1a were Q30 H/R and M28 V/T each with the baseline prevalence of 6.5%, L28M in GT1b with prevalence of 30% and Y93 H/N in GT3a with prevalence of 3.3%.

Natural occuring NS5A RAVs were seen in 25.5% of HCV mono-infected and 16.9% of HCV/HIV co-infected cases with no significant difference between two groups. In HCV cases, clinically relevant RAVs were L28M followed by M28Vand Q30H and Y93 H/N. In HCV/HIV subjects, clinically relevant RAVs were Y93 H/N followed by L28M and P58T and M28 V/T and Q30R.

Natural occuring NS5B RAVs were observed in 11.8% of HCV and 5.9% of HCV/HIV subjects with no significant difference between two groups. The most common detected mutations were V321 A/I/H/L/S followed by C316 L/Y/G, S282 R/N and L159 F/P.The major S282T mutation was not detected.

Conclusions: The emergence of RAVs is a growing issue and although currently, screening of RAVs is not recommended before DAA treatment, it should be consider in patients with therapeutic failure. Therefore screening of naturally occurring RAVs may be useful as a strategy to overcome drug resistance in some cases and minimize the risk of treatment failure.