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Genetic susceptibility of *HCV RNA* and gene polymorphism of IL-10 and IL-28B in various isonym groups of Pakistan

Rubi Ghazala and **Muhammad Aslamkhan**
University of Health Sciences Lahore, Pakistan

Introduction & Rationale: Hepatitis C, a widespread infectious disease targeting circa 130 million people worldwide, is caused by the Hepatitis C Virus (HCV). HCV genome, consisting of 9,600 nucleotides, is fully sequenced. Population specific high variation in HCV genome exists. HCV is classified into 7 different genotypes with several subtypes. Genotypes 1, 2 and 3 are found worldwide.

Objective: To find out the ecology and genetics of susceptibility of HCV RNA in various isonym groups of the Punjab population.

Subjects & Methods: A sample of 449 chronic HCV hospital patients were studied who were already taking the treatment of standard therapy of Interferon+Ribavirin thrice a week. The sample was divided into three groups based on the nature: Responder- patients who received the standard therapy and recovered/cured; Relapser- patients who after a course of therapy became negative for HCV RNA but after sometimes (6-18 months) became HCV positive again; Non-responder- patients who did not show positive response to therapy.

Results: It was found that HCV genotype 3a is very common (84.0%) among responders group while genotype 1a is more common in relapser (66.2%) and non-responders (54.0%). Five of the six main genotypes, namely, 1a (61.40%), 2a (0.50%), 2b (20.00%), 3a (13.70%) and an untypable (4.40%) were found among the 12 different castes/tribes/isonym ethnic groups. Genotype 4 was not found. The HCV frequency in 12 isonym groups is as follows: Arain (15.26%), Gujjar (10.02%), Jutt (18.91%), Kashmiri (10.02%), Malik (10.44%), Mughal (3.21%), Pathan (17.19%), Rajput (11.46%), Sheikh (3.43%), and Sayyed (4.87%). Jutt caste was found to have the maximum infection of HCV, while the minimum was found in Mughals. Genotype 3a among responder was most common in Rajput caste. Among the relapser 1a is most prevalent in Jutts. Pathans top the list of non-responders having 1a and 2b. Genotype 2a was found only in one sample of Rajput, who was non-responder. Gene-polymorphism in IL-10 and IL-28B genes to ascertain the genetic susceptibility among various isonym groups revealed six SNPs. In IL-10, SNP at 1082 position, AA (14.5%), GA (80.30%) and GG (5.20%); SNP at 819, AA (3.2%), AC (84.7%) and CC (12.0%); and SNP at 592 position, AA (6.0%), CA (69.9%) and CC (24.1%). CA was in high frequency than CC and AA homologous gene polymorphism. In IL-28B SNP at location a, GG (4.8%), TG (40.6%), TT (54.6%); SNP at location b, CC (34.9%), CT (58.2%), TT (6.8%) and CC (40.2%), CT (43.8%), TT (16.1%) was found. Frequency of TT homologous high at one position, CT hetrozygous polymorphism was frequent at second and third position.

Conclusion: Human genetic susceptibility to HCV genotypes appears to be of importance in getting the infection. The study suggests that IL-10 and IL-28B interleukin genes are common in two major castes of the Punjab. A cohort study needs to be done for better understanding of human susceptibility to HCV infection and its management.

Biography

Rubi Ghazala, MSc, MPhil, PhD, has 21 years of experience in Molecular Diagnostics. Her role involves molecular diagnostic planning, designing and new tests development with marketing along with pre commissioning and post commissioning. She is working on a project "Genetic Susceptibility of HCV in Ethnic groups of Pakistan". As a Molecular Pathologist, she established outreach clinical lab of AKUH in central Punjab region to cater the services for Punjab, North Punjab, KPK as well as Gilgit and remote areas. In this way, the business from North Punjab and KPK has been shifted to Lahore rather Karachi by this volume growth of molecular services has been reached to 27%. She developed and directly monitored the overall operations of the Clinical Molecular Laboratory. She supervises technical and non-technical staff. She was directly responsible for the startup of new molecular testing, technology evaluation, QA/QC, budget planning, equipment purchasing, and marketing along with lab administration, staff training, IQC training to staff, ISO audit, JCIA audit and PHC registration. The main focus of this molecular laboratory is to provide timely and accurate reporting of results and patient care. The laboratory is staffed for full consultation in all areas of molecular pathology and genetic testing. She actively participates in national and international CME and presented in more than 15 international conferences.

rubighazala@yahoo.com