ORIGINAL ARTICLE

HEPATITIS-C GENOTYPES DISTRIBUTION IN PROVINCE OF PUNJAB, PAKISTAN

Farheen Ansari[1], Rabia Nosheen[2]

Authors' Affiliation
[1,2]Institute of Molecular Biology and Biotechnology Department, The University of Lahore, Lahore

Corresponding Author
Rabia Nosheen.
Postgraduate Student, Institute of Molecular Biology and Biotechnology Department, The University of Lahore, Lahore
Email:rabianosheen1987@gmail.com

ABSTRACT

Objective: To determine the Hepatitis-C genotypes distribution in province of Punjab, Pakistan.

Material & Methods: This comparative investigation was conducted at Jinnah hospital in Lahore over a period of 14 months (Aug 2016 to Sep 2017). All the patients' referred to the Molecular Microbiology department of Jinnah hospital were enrolled for hepatitis C detection and genotyping.

Results: Total no of 300 positive patients were enrolled in the study. 106 (35.33%) were males and 194 (64.66%) were female patients with different age group. Frequency rate of HCV Genotype 1 was 8.4% (25), Genotype 2 was 1.0% (3), and Genotype 3 was 81.0% (243), Genotype 4 was 2.33% (7), untype capable genotype was 5.33% (16), Cross contamination with genotype 1 and 2 was 0.67% (02), Cross contamination with genotype 1 and 3 was 1.33% (04). This examination exhibits that HCV effluence in contaminated people is recognized dominating to viral genotype 3 in Pakistan with the rate of 81.0% in the Lahore.

Conclusion: Female population was viewed as logically affected with HCV when appeared differently in relation to male population. Since people developed among 36-45 years old are vibrant in public, they are in risk and acquire themselves.

Key Words: Genotype, Hepatitis, Liver, Virus

This article may be cited as: Ansari F., Nosheen R. Hepatitis-C genotypes distribution in province of Punjab, Pakistan. Ann Allied Health Sci. 2022; 8(1):18-22.

INTRODUCTION

HCV hepatotropic RNA infection have a place with the group of Flaviviridae with pretty much 9.6 kb single-abandoned, positive detect RNA genome.[1] Its genomes teach a poly protein predecessor of 3000 amino acids alongside non coding district (3' prime non coding region and 5'prime non coding region) which possess an inner ribosomal passage site (IRES) a significant for viral RNA cap self-sustaining transformation.[2] According to WHO gauges, 3% of the complete people is polluted with this infection (WHO, 2011). Around one-fourth of a 1million spending yearly occur taking into account a consistent liver sickness related with hepatitis C contamination.[3] These days hepatitis C is perceived as an illness of widespread significance. It is of worry for both creating and created countries occurrence of sick state interrelated with constant chronic hepatitis infection. As per the WHO information comprehensive 170 million of individuals are infected with persistent contamination, four million populaces are contaminated every day with this infection.[4]

Infectivity with HCV is not pretentious over all clinical concern. Ailment with this contamination is winding up elevated monetary, societal and prosperity inconvenience.[5, 6]

The incidence rate of the contaminated populace as per the WHO was unsurprising to be in Africa 31.8 million, areas of east Mediterranean 21.4 million, 62.2 million in west pacific locale, 13 million, in America, 32.2 millions in Southeast Asia, and 8.9 million cases was report in Europe nations (WHO, 2019). According to the most recent data by the WHO appraises that in regards

to three to four millions case are report' each year.[3,7] In Pakistan 10 million cases were accounted for 7 People who have liver sickness with infected with HCV Consistent reports of the rate of scattering of genotypes in Pakistan were arrange assessment reports smooth research article papers appropriated among 2010 to 2015 April, in documented and non-recorded journals, was unite contemporary examinations have not quite recently viewed as the prevalence HCV in the past in uncovered locales.[8, 9] Then again, strains that show less hereditary heterogeneity have a more limited acquired history and regularly draw a parallel with the modern preface and development correspondence rates.[10]

MATERIAL AND METHODS

This was the comparative investigation led at Jinnah hospital Lahore from (Aug 2016 to Sep 2017). Every one of the patients alluded to the molecular microbiology division of Jinnah emergency clinic were selected for hepatitis C discovery and genotyping. There incorporate patients of all ages, identity, preliminary point of home country instruction status and employment. The complete no of tests was 300. Four millimeters of fringe blood was gathered in an EDTA tube marked with patients' id no. Blood was isolated, and plasma moved into eppendrof tube for RNA extraction.

The smaller than usual INSTANT infection RNA kit (scientific Jena) for RNA extraction, and Geno Sen's standard arranged to use amplification component and genotypic innovation by utilizing kit and genotypic detection by using Third Wave Technology.

The HCV intensification was done by Real Time PCR utilizing the third wave technology. HCV genotyping was ended by Geno-Sen's genotyping unit on Rotor-Gene 2000/3000/6000 instruments.

Master Mix adds 10ul into each named tube with PCR. At the direct 15ul add toward the earlier isolated RNA to each example cylinder and blend well by pipetting all over in the equivalent way, 15ul of positive control and 15ul of water (water, PCR grade) utilized as a negative control. Cautiously close the cylinder covers and spot into the Rotor Gene TM instrument. These interactions all out require some investment is 2 hours and 20 minutes. Furthermore, show the diagram on screen, information assessment is performed with the rotor quality programming according to the assembling guidance physically exertion.

RESULTS

All out no of patients were noticed 300 surrounded by 300 patients, 106 (35.33%) were males and 194 (64.66%) were females patients were chosen from different region of Punjab area the recurrence affliction is found in the age social incident of 15-25years was 30(10.0%). Occurrence of HCV genotype 1 was 0.67%(2), genotype 2 was not identified, genotype 3 was 8.67% (26), genotype 4 was not recognized, untype capable genotypes 0.67%(2), Co- disease of genotypes 1 and 2 was not distinguished, Co-contamination of genotype 1 and 3 was not identified, Incidence of hepatitis C infection in 26-35 years of age was 85 (28.33%) genotype 1 was 2.0% (6), genotype 2 was 0.3% (01), genotype 3 was 23.0%(69), genotype 4 was 1.33% (04), untype capable genotype was 1.33% (04),Co-disease of g from various district of Punjab province the frequency sickness is found in the age social occasion of 15-25 years was 30 (10.0%). Incidence of HCV genotype 1 was 0.67% (2), genotype 2 was not detected, genotype 3 was 8.67% (26), genotype 4 was not detected, untype able genotypes 0.67% (2), Co-infection of genotypes 1 & 2 was not detected, Co-infection of genotypes 1 & 3 was not detected, Incidence of hepatitis C virus in 26-35 years old was 85 (28.33%), genotype 1 was 2.0% (6), genotype 2 was 0.3% (01), genotype 3 was 23.0% (69), genotype 4 was 1.33% (04), untype able genotype was 1.33% (04), Co-disease of genotype 1 and 2 was not recognized, Co- disease of genotype 1 and 3 was 1.33%(04), occurrence of HCV infection in 36-45 years of age was 34.0% (102), genotype 1 was 3.3% (10), genotype 2 was 0.3% (01), genotype 3 was 27.3% (82), genotype 4 was 1.33%(04), untype capable genotype was 1.33% (04), Co-disease of genotype 1 and 2 was 0.34% (01),Co-contamination of genotype 1 and 3 was not distinguished. Rate of hepatitis C infection in 46-55 years of age was 14.0% (42), genotype 1 was 0.67% (2), and genotype 2 was 0.34% (01), genotype 3 was 11.0% (33), and genotype 4 was

0.67% (02), untype capable genotype was 1.0% (3), Co-disease of genotype 1 and 2 was 0.34% (01), Co-contamination of genotype 1 and 3 was not distinguished. Occurrence of hepatitis c infection in 56-65 years of age was 32 (10.67%), genotype 1 was 1.67% (05), and genotype 2 was not recognized, genotype 3 was 8.34% (25), genotype 4 was not identified, untype capable genotype was 0.67% (2), Co-contamination of genotype 1 and 2 was not distinguished, Co-disease of genotype 1 and 3 was not identified. Frequency of hepatitis C in > 65 years of age was 9 (3.0%). Genotype 3 was 2.67% (8), untype capable genotype was 0.3% (01), different genotypes was not identified. The information was HCV-positive patients from Lahore, Sargodha, Mianwali, Kasur, Multan, Rawalpindi, Chicha watni, Pak pattan, Shekhupura, Faisalabad, and Okara, Narowal, Nankana Sahib, Khanewal, Sahiwal, Hafiz Abad, D.G Khan, regions, separately.

Among with 300 positive patients with hepatitis C frequency of genotype 1 was 8.4% (25), Genotype 2 was 1.0% (3), and Genotype 3 was 81.0% (243), Genotype 4 was 2.33% (7), untype capable genotype was 5.33% (16), Cross contamination with genotype 1 and 2 was 0.67% (02), Cross contamination with genotype 1 and 3 was 1.33% (04). This examination exhibits that HCV effluence in contaminated people is credited dominating to viral genotype 3 in Pakistan with the rate of 81.0% in the Lahore. **(Table1)**

Table No 1. : Frequency of genotype in male and female population

HCV Genotype	Male	Female	Total
Type 1	8	17	25
Type 2	_	3	3
Type 3	86	157	243
Type 4	2	5	7
1 & 2 Co infection	2	_	2
1 & 3 Co infection	2	2	4
Un-type able	7	9	16

DISCUSSION

With the pervasiveness pace of contamination viral illness of HCV getting elevated worldwide, accordingly its complexities and influencing factors are believed to be originate in all age groups. HCV is an infective microbe, Blood product and blood item because high hazards ailments in human. Who have frequently undergone blood transfusion.[11,12] chronic infection causes the significant sickness, in organization by method of the hepatic cell carcinoma and cirrhosis.[13] HCV infections keep on being the world's most essential sickness issues. As per the data 3% populaces of the overall are contaminated with this infection (WHO, 2011). Current investigation uncovered that hepatitis C infection is constantly in females (64.66%) of Lahore populace followed by in male (35.34%).The assessment was show infected patients mostly perceived genotype will be genotype 3 in Pakistan of the rate of (81.0%) in the city of Lahore. The results were examined by observance the unobstructed period and sex

inconsistent separated in to 6 distinguishing age groups. As per the current examination, Patients having a spot with to the age gathering (36-45years old) are progressively infected by genotype 3 other age gather. It was seen that 3a is the most unpreventable (41%) genotype. No massive difference Commonness as for any sexual direction or a particular age group.[14] Right now HCV genotype is in like manner recorded with regarding sexual orientation. It is uncovered that most raised transcendence of genotype 3 is found in females. Type 3 is prevails beside the patients living in city of Lahore, type 1 and type 4 tails it. This data favors the outcome of Ahmad. Ahmed announced for the most part recurrently recognized genotype in their assessment was genotype 3, among otherworldly subtype 3a and b15. Because product give you an idea about elevated result type 3 in Lahore population expected with others descriptions ponders, furthermore is comprehensive expectedness genotype 1a and un-type capable genotype build up in our assessment is throughout the raised subsequently behind the fundamentals HCV influence genotype Idrees showed that the reliability of HCV tainting in light of genotype 4 and genotype 1 is rising about to happen short on a growth in the genotype 3 in a variety of zone of Pakistan predominantly NWFP genotype1a, (6.56%), genotype4, (2.30%) and genotype1a, Baluchistan (25.80%) and genotype 4 is (4.03%). They guaranteed the incidence of type 4 in Pakistan in light of the fact that with (1.15%) ordinariness in the Punjab region which solidifies Lahore city consolidates Lahore city.[15,16] The assessment exhibited that tainting of HCV in certain. Patients are seen generally of viral genotype 3 in Lahore city by the speed of (81.0%) In addition, there was a for the most part distant above the position most prevalence of type1 (8.4%). Raised prevalence of genotype 3 in the nation of Pakistan showed to be unavailable for control disease of HCV.[15, 17] Genotype 3 requires more limited season of treatment as differentiate 1 by methods for its corresponded limited cost and side effects18. Dominance genotype 3 into our general population is according to prominence of genotype 3.[18,19] Advance requires to do out a bare essential examination on instant of HCV genotype close by the number of occupants in Lahore for the healthier control on reproduce of impenetrability.

CONCLUSION

The observations that most judiciously secure the theory are: the pace of HCV genotype 3 is high in size of test sample decided for study. Frequency rate of HCV together with the patients of Lahore was found logically impacted as difference with others spaces of Punjab domain. Female population was viewed as logically affected with HCV when appeared differently in relation to male population. Since people developed among 36-45years old are vibrant in public, they are in risk and acquire themselves. Progressively affected other age gathering the respondent had a spot with lower class they did not move toward enhanced environment of nature of living from this time forward are inclined to HCV infection. Innovative antiviral administrators being created consolidate inhibitors of viral compounds, for instance, protease enzyme, helicase enzyme and polymerase just as a few hereditary methodologies. And to access the nearness of HCV genotype on an enomerous arrangement of population demonstrating rise commonness collecting test samples from DHQ, THQ.

REFERENCES

1. Moradpour D, Penin F, Rice. Replication of hepatitis C virus Nature Reviews Microbiology 2007; 5:453–463.
2. Dubuisson J. Hepatitis C virus proteins World J Gastroenterology 2007; 17:2406 2415.
3. Lo Re V, Kostman JR. Management of chronic hepatitis C Post-graduate Medicine 2004; 81: 376-382.
4 WHO Factsheets [Internet]: World Health Organization, Hepatitis C Available from: 2009 ; http://www.who.int/mediacentre/factsheets/fs164/en/index.html3
5 Lavanchy D Evolving epidemiology of hepatitis C virus Clinical Microbial Infection 2011; 17:107-115.
6 Hajarizadeh B, Grebely J, Dore GJ Epidemiology and natural history of HCV

infection. Nat Rev of Gastroenterology Hepatology 2013; 10: 553–562.
7 Lo Re V, Kostman JR , Management of chronic hepatitis C. Post-graduate Medicine 2004; 81: 376-32
8 Higuchi M, Tanaka E, Kiyosawa K. Epidemiology and clinical aspects on hepatitis C. Journal Infectious Disease 2002; 55: 69-77.
9 Stoszek SK, Abdel-Hamid M, Narooz S, El Daly M, Saleh DA, Mikhail N, Kassem E, Hawash Y, El Kafrawy S, Said A El Batanony M, Shebl FM, Sayed M, Sharaf S, Fix AD, Strickland GT. Prevalence of and risk factors for hepatitis C in rural pregnant Egyptian women 2006; 100(2):102-107.
10 Zahran KM, Badary MS, Agban MN, Abdel Aziz NH. Pattern of hepatitis virus infection among pregnant women and their newborns at the Women's Health Center of International Journal of Gynecology & Obstetrics 2010; 111(2):171–174.
11 Jackowiak P, Kuls K, Budzko L, Mania A, Figlerowicz M, Figlerowicz M. Phylogeny and molecular evolution of the hepatitis C virus Infection Genetics and Evolution 2014; 21:67-82.
12 Muzafar F, Hussain I, Haroon TS. Hepatitis C: the dermatologic profile Journal of Pakistan Dental Association 2009; 15: 692-700.
13
14 Willems M, Metselaar HJ, Tilanus HW, Schalm SW, de Man RA. Liver transplantation and hepatitis C Transplant 2002; 15: 61-72.
15 Hammad Riaz Muhammad Zahid Latif Atif Qureshi Abdul Rouf. HCV Prevalence and its Predominant Genotypes in Sargodha Region of Pakistan Article. Pakistan Journal of Medical and Health Sciences 2016; 10(1): 6-10.
16 Ahmad S, Salati SAA, and Mattar EH, Al-Sabban AMH. Hamad IS Epidemiology of Hepatitis C Virus (HCV) Infection. Physicians Academy 2010; 4(8): 82–87.
17 Idrees M, Riazuddin Frequency distribution of hepatitis C virus genotypes in different geographical regions of Pakistan and their possible routes of transmission. BMC Infectious Disease 2008; 2334:8-69.
18 Qazi MA, Fayyaz M, Chaudhary GMD, Jamil A, Malik AH, Gardezi AI, Bukhari M.H Hepatitis C virus genotypes in Bahawalpur Biomedical 2006 ; 22: 13.
19 Abbas S, Ali M, Muhammad A, Shaw S, Abbas. Frequency of HCV infection and its genotypes among patients attending a liver clinic and voluntary blood donors in a rural area of Pakistan 2009; 25(4):579–582.

.