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Assessment of Human Papillomavirus (HPV) type 16 and 18 status by nested multiplex PCR in cervical cancer patients and in healthy women from a tertiary care hospitalP. Arumugam^{1,*}, S.C. Parija², S. Habeebullah³¹ JIPMER, Puducherry, Puducherry, India² Jawaharlal Institute of Postgraduate Medical Education and Research, Puducherry, Puducherry, India³ JIPMER, Puducherry, India

Background: Cervical cancer is the most common malignancy in Indian women and approximately 130,000 women fall prey to cervical cancer every year. HPV DNA testing can be used as an adjunct to cytological screening of cervical samples of above 30 year old women and can be used as an optional test for follow-up in women who have slightly abnormal Pap test results. The aim of the study was to assess the HPV 16 and 18 status in cervical cancer patients and in healthy women visiting JIPMER, Pondicherry.

Methods & Materials: This study was approved by JIPMER Institute Ethics Committee. 171 biopsies from cervical cancer patients and 152 cytobrush samples from healthy women were collected. DNA was extracted using QIAamp DNA mini kit. The quality and quantity of the extracted DNA was determined by a spectrophotometer. The integrity of genomic DNA was checked by amplifying a 248-bp product of the human beta-globin housekeeping gene. A nested multiplex PCR was standardized and carried out to detect 2 high risk types, HPV 16 and HPV 18, further representative positive PCR amplicons were sequenced for confirmation.

Results: Out of 171 cervical cancer cases, 149 (87%) patient samples tested positive. Overall HPV-16 and 18 occurrence was found to be 87% in which HPV-16 was 64%, HPV 18 was 3% and mixed infection was 23%. Out of 152 healthy women cases, 78 samples were positive. Overall HPV-16 and 18 occurrence was found to be 51% in which HPV-16 was 22%, HPV 18 was 5% and mixed infection was 25%. Sequencing results were analyzed in NCBI BLAST to reconfirm the HPV genotype.

Conclusion: In our study, HPV -16 found to be the most common genotype in our region. Our study suggests that the HPV 16 and 18 mixed infection could be due to the consequence of poor genital hygiene and unsafe sexual behavior. In healthy women cases, it may be too early to come to a definitive conclusion about the HPV positivity because women under 30 who are sexually active are likely to have an HPV infection that will disappear on its own in future. But those women may need regular follow up.

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Is HLA-DRB1*13 allele a risk factor for prognosis of hepatitis C virus infection?N. Aydin^{1,*}, R. Bulbul², A. Coskun², S. Kirdar², S. Oncu², Y. Kilinc³¹ Adnan Menderes University Medical Faculty, Aydin, Turkey² Adnan Menderes University, AYDIN, Turkey³ Akdeniz University, Antalya, Turkey

Background: Hepatitis C virus infection, with its high rate of chronicity, is a serious public health problem. There are studies being conducted on the factors affecting the prognosis of the disease. Changes of alleles in the human histocompatibility antigens (HLA) have been reported to affect the prognosis of HCV infection. In this study, we aimed to investigate the effects of HLA-DRB1 alleles on the treatment response and prognosis of the HCV infection.

Methods & Materials: This study was conducted with a total of 65 chronic HCV patients at Adnan Menderes University Medical Faculty Hospital. These patients were divided into three groups according to the prognosis of the disease: 1) patients who have responded to the treatment, 2) patients who has not responded to the treatment or had recurrence of the disease, 3) patients who have recovered spontaneously. Determination of HLA-DRB1 alleles were performed using sequence specific oligonucleotide (SSO)-Luminex method.

Results: The patients were in 22–79 years age range, and the average age was 56.5 ± 12.9 . 43.1% of the patients (28) were male, and 56.9% (37) were female. Of the 65 patients with HCV infection in the study, 36 (% 55.4) responded to the treatment, 16 (24.6%) has not responded to the treatment or had recurrence of the disease, 13 (20%) have recovered spontaneously. The most common HLA-DRB1 alleles types found in patients were: HLA-DRB1*11 in 34 patients (26.15%), HLA-DRB1*4 in 20 patients (15.38%), HLA-DRB1*15 in 14 patients (10.17%), HLA-DRB1*13 in 13 patients (10%), HLA-DRB1*1 in 11 patients (8.46%). The patients who responded to treatment and patients who recovered spontaneously were found to carry the most HLA-DRB1*11 allele. The patients who have not responded to treatment or had recurrence of the disease were found to carry HLA-DRB1*13 allele the most, A statistically significant relationship ($p < 0.002$) was found between frequency of HLA-DRB1*13 allele and the response to treatment and prognosis of the disease.

Conclusion: We concluded that carrying the HLA-DRB1*13 allele may be a risk factor for prognosis and response to treatment of HCV infection. Therefore, determination of HLA-DRB1 alleles may be necessary for effective treatment planning for patients with HCV infection.

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