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Characterization of human papillomavirus (HPV) genotypes among patients referred to gynecology clinics, Laleh Hospital

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Background: Human papillomavirus (HPV) infection is the main cause of cervical cancer (CC) worldwide. HPV is a necessary, but not a sufficient factor for acquiring CC. The aim of this study was to explore the prevalence of HPV and its genotypes among outpatients referred to Laleh Hospital from December 2014 to December 2017.

Methods: 307 patients who referred to Gynecologic clinic were included in a cross sectional study. Fresh cervical secretions (collected in ThinPrep tubes), wart biopsies and male genital secretions were collected and were transferred to the genetics lab for molecular analysis. Viral nucleic acids were extracted manually by High Pure Viral Nucleic Acid kit and subsequently, a multiplex real time PCR differentiating 14 high risk HPV genotypes plus HPV-6 and HVP-11 was carried out. Patient history, details of therapy, laboratory and radiographic details were analyzed using SPSS software.

Results: 176 (58%) of specimens were positive for at least one HPV genotype. (77%) and (23%) were female and male, respectively. 135 (57%) and 41 (59%) of females and males were positive for HPV, respectively. 242 (77%) and 54 (63%) were positive for HPV high risk genotypes, respectively. On the other hand, 71 (23%) and 32 (37%) were positive for HPV low risk genotypes, respectively. Totally, the rates of multiple genotypes (at least two genotypes) were 88 (50%) which was distributed as 64 (47%) and 24 (59%) to females and males respectively (P value 0.551). Among males, (80%) and (20%) of positive samples were belonged to warts and genital secretions, respectively. The mean ages among females and males were 34.1 and 32.9, respectively. In both genders, the highest prevalence was found between age group of 30 and 40 years old. The highest HPV prevalence in order was: 6%, 16%, 39% and 66%.

Conclusion: HPV-39 and HPV-66 genotypes have not been included in current HPV vaccines. Unusual finding of these genotypes among patients heralds their prevalence among Iranian populations which necessitate public health interventions.

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