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Letter to the Editor

Distribution of Human Papillomavirus Genotypes in Liquid-based Samples; Abundance of HPV-53 in Tehran, Iran

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Dear Editor-in-Chief

Cervical cancer adequately depends on Human papillomavirus (HPV) infection (1). To achieve high throughput implementation and monitoring of HPV vaccination programs, awareness about the frequent HPV genotypes would be helpful (2). Since there is little data in literature regarding the prevalence of HPV genotypes in Iran, we looked for the distribution of HPV genotypes in Iranian female patients. In this retrospective study, we assessed distribution of HPV genotypes among the HPV infected patients who were referred to Armin Pathobiology Laboratory (Tehran, Iran) for detection and genotyping of HPV in liquid-based samples.

The HPV genotyping was performed using INNO-LiPA HPV genotyping *Extra* kit (INNOGENETICS, Ghent, Belgium). Among the patients referred for HPV genotyping, we found 80 patients to be HPV positive. Out of 80 HPV positive samples, 40 (50%) patients were infected by one genotype of HPV, 25 (31.3%) were infected by two, 7 (8.7%) were infected by three, 5 (6.3%) were infected by four, 2 (2.5%) were infected by 5 and one (1.2%) patient was infected by 6 genotypes of HPV. The Fig. 1 demonstrates the distribution of the HPV genotypes in our study population. Among mono-infected patients, the most frequent genotype was HPV-6 (30%) which was followed by HPV-53 (15%), HPV-16 (12.5%), HPV-66 (7.5%), HPV-18 (7.5%), HPV-11 (7.5%), HPV-58 (5%), HPV-39 (2.5%), HPV-45 (2.5%), HPV-51 (2.5%), HPV-52 (2.5%), HPV-68 (2.5%), and HPV-82 (2.5%). In multiple-infected patients, the most frequent genotype was HPV-6 (40%) followed by HPV-53 (32.5%), HPV-66 (30%), HPV-16 (27.5%), HPV-52 (22.5%), HPV-39 (20%), HPV-18 (20%), HPV-51 (15%), HPV-11 (10%), HPV-56 (7.5%), HPV-33 (7.5%), HPV-31 (7.5%), HPV-54 (5%), HPV-58 (5%), HPV-82 (5%), HPV-35 (2.5%), HPV-44 (2.5%), HPV-45 (2.5%), HPV-68 (2.5%) and HPV-69/71 (2.5%).

Epidemiological studies demonstrated that the distribution and pathogenicity of HPV genotypes would be altered in different geographical regions (3). In this study, among high risk (HR) and probable high risk (pHR) genotypes, the most

prevalent HPV genotype was HPV-53 followed by HPV-16, HPV-66, HPV-18, HPV-52 and HPV-39. Abundance of HPV-53 in some studies was similar to our results (4, 5), while in other studies the frequency of HPV-53 was lower than our study (6, 7). These data clarified that in addition to the HR genotypes, pHR genotypes are frequent in Iran. In this study, whether we considered pHR genotypes as oncogenic types, the high prevalence of pHR genotypes in Iranian HPV infected patients would be challenging. To accomplish whether pHR genotypes are oncogenic or not, further studies would be conducted.

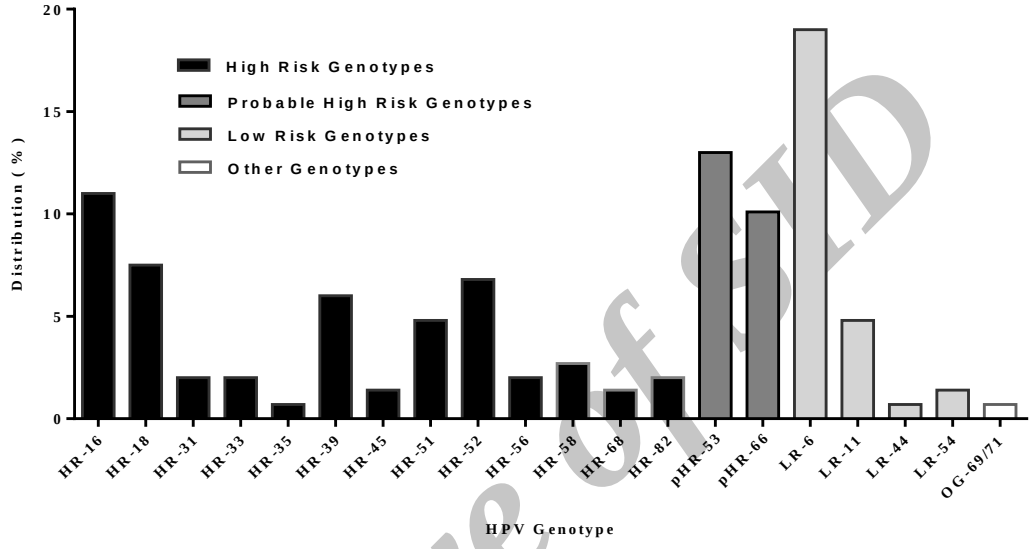

Fig. 1: Distribution of HPV genotypes in liquid-based samples among Iranian patients

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