EV0098
ePoster Viewing
Viral molecular epidemiology (other than hepatitis & HIV)

Prevalence and genetic distribution of human papilloma virus in women with cervical intraepithelial neoplasia

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Background: Epidemiological and molecular studies have implicated the human papilloma virus (HPV) as the main risk factor for the development of cervical intraepithelial neoplasia (CIN) and cervical cancer. Each region has its own distribution and prevalence of HPV infections, together with its specific genetic distribution. The aim of this study was to evaluate the prevalence and genetic distribution of HPV infection in women with CIN in Skopje area.

Material/methods: We evaluated a selected group of 100 cervical specimens from women with previously detected CIN. The DNA extraction was performed with QIAamp DNA Mini Kit, Qiagene. Testing for HPV DNA presence was with Seeplex HPV4A ACE Detection kit, Seegene. The HPV typisation was with Opegen High Papilloma Strip kit, by Operon, a kit based on the principle of reverse hybridization for detection and identification of 19 high risk genital HPVs (16, 18,26, 31, 33, 35, 39, 45, 51, 52, 53, 56, 58, 59, 66, 68, 69, 73 and 82).

Results: Our data revealed that 29% of patients were positive for HPV DNA, present in single or co-infections, the most frequently in the age group between 26-35 years. Half of the patients had single high risk HPV genotype, and other half were with co-infection with multiple HPV genotypes. The genotypic distribution of the 29 HPV positive patients showed HPV 16 to be the most prevalent - in 9 cases alone and 9 cases combined with 35, 31 or 18 HPV type. That is followed by HPV 35 in 6 cases alone and 5 cases combined with HPV 31, 33 or 51. HPV 33, 31 and 52, were detected in 8, 7 and 5 cases, respectively.

Conclusions: The prevalence of the HPV infection correlates with the data published for this part of Europe. However, besides the introduction of the quadrivalent HPV vaccine since 2010, it is necessary to conduct regular HPV typisation due to the high incidence of HPV types 35, 31 and 33 in our population.

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PREVALENCE AND GENETIC DISTRIBUTION OF HUMAN PAPYLOMA VIRUS IN WOMEN WITH CERVICAL INTRAEPITHELIAL NEOPLASIA

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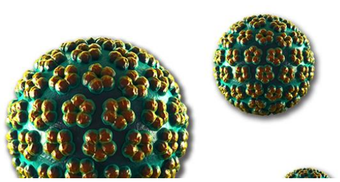
Background:

Epidemiological and molecular studies have implicated the persistent infections caused by human papilloma virus (HPV) as the main risk factor for the development of cervical intraepithelial neoplasia (CIN) and cervical cancer. To date, 184 HPV types have been identified. Among these, epidemiological data showed that HPV16 and HPV18 are responsible for 70% of cases of invasive cervical cancer worldwide. Moreover, other genotypes, such as HPV31, HPV33, HPV35, HPV45, HPV52, and HPV58, are involved in 18% of cases of squamous cell carcinoma cancer worldwide. Each region has its own distribution and prevalence of HPV infections, together with its specific genetic distribution.



Aim:

The aim of this study was to evaluate the prevalence and genetic distribution of HPV infection in women with CIN in Skopje area.

Material/methods:

We evaluated a selected group of 100 cervical specimens from women with previously detected CIN. The DNA extraction was performed with QIAamp DNA Mini Kit, Qiagene. Testing for HPV DNA presence was with Seeplex HPV4A ACE Detection kit, Seegene. The HPV typisation was with Opegen High Papilloma Strip kit, by Operon, a kit based on the principle of reverse hybridization for detection and identification of 19 high risk genital HPVs (16, 18,26, 31, 33, 35, 39, 45, 51, 52, 53, 56, 58, 59, 66, 68, 69, 73 and 82).

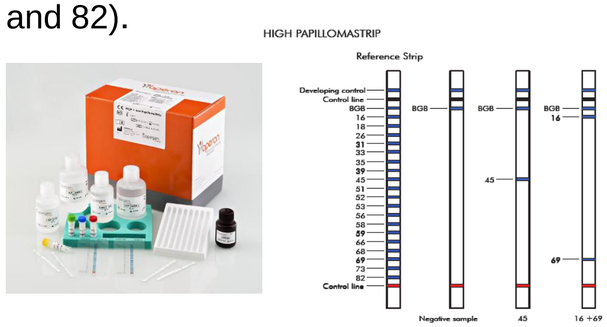


Image 1. High Papilloma Strip kit, Operon

Results:

Our data revealed that 29% of patients were positive for HPV DNA, present in single or co-infections, the most frequently in the age group between 26-35 years.

Age (years)	No. of specimens	No. of positive specimens
under 25	7	0
26-35	41	16
36-45	31	10
46-55	18	2
above 56	3	1
TOTAL	100	29

Table 1. Distribution of human papillomavirus-positive specimens by age

Half of the patients had single high risk HPV genotype, and other half were with co-infection with multiple HPV genotypes.

	Number of patients
HPV single infection	15
HPV multiple infection	14

Table2. HPV types prevalence

The genotypic distribution of the 29 HPV positive patients showed HPV 16 to be the most prevalent - in 9 cases alone and 9 cases combined with 35, 31 or 18 HPV type. That is followed by HPV 35 in 6 cases alone and 5 cases combined with HPV 31, 33 or 51. HPV 33, 31 and 52, were detected in 8, 7 and 5 cases, respectively.

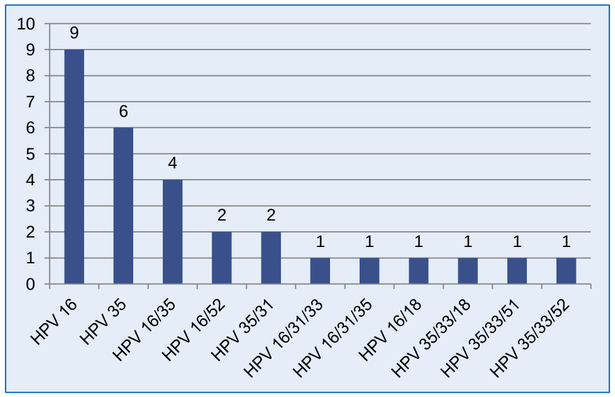


Chart 1. Distribution of HPV types as single and multiple infection

Conclusions:

The knowledge of regional human papillomavirus type distribution is essential for the optimization of prevention strategies and this study was carried out to explore the prevalence and type distribution of high-risk HPV in a screening population across the country. The prevalence of the HPV infection correlates with the data published for this part of Europe. However, besides the introduction of the quadrivalent HPV vaccine since 2010, it is necessary to conduct regular HPV typisation due to the high incidence of HPV types 35, 31 and 33 in our population.

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