

## **P325. Prevalence of HPV genotypes in the senese female population undergoing cervical screening**

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**Context:** Human papillomaviruses (HPVs) are naked viruses belonging to Papillomaviridae family. There are over 200 types of HPVs, some of which are almost exclusively associated with benign lesions while others are mainly associated with high grade lesions and invasive carcinoma. The identification of HPV as the cause for uterine cervical cancer development and the detection of variable oncogenic potential HPV types enabled the implementation of new screening strategies based on molecular tests (liquid-based HPV DNA test). These tests have more sensitivity in detecting women at risk of developing a high grade lesion or invasive carcinoma.

**Objective:** To analyze viral genotypes in order to provide an evaluation of the prevalence and distribution of HPV infections in the Senese area.

**Methods-Patients:** This retrospective cohort study involved 491 women from the Senese University Hospital Cervical-Vaginal Pathology Center between 1st January 2016 and 31st July 2017.

**Interventions:** Patients underwent Pap-smear/HPV DNA-TEST and/or colposcopy with portio biopsy for subsequent typing analysis.

**Main Outcome Measures-Results:** In our study infection is particularly prevalent in the range from 36 to 40 years and then declines progressively. The most frequently found genotypes are 16 (which is ranked first in frequency and represents nearly 30% of positivities), 31, 33 and 67 among high oncogenic risk types; 6 and 81 among low oncogenic risk types. Furthermore some infections are transient with a negativization rate about 20%. Finally, we found that all HSIL diagnoses in our sample are associated with high-risk HPV in 100% of cases, whereas LSIL and ASCUS diagnoses are associated with high-risk HPV about in 60% of cases and with low-risk HPV about in 40% of cases.

**Conclusions:** The prevalence of cervical HPV infection in the sample was 18.9% and it varies in relation to the different age groups, with a linear decrease with age. The most interesting result is the total absence of HPV 18 isolation during the observational period in our patients. In the future it would be advisable to evolve and optimize the vaccine offer according to the different geographical distribution of HPV genotypes.

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