

The aim of this thesis was to track the impact of selected herpesviruses, polyomaviruses, Chlamydia trachomatis and methylation of tumor suppressor genes at the development and progression of high grade-lesion in HPV - positive patients by means of molecular-genetic techniques. Confirmation of these markers presence in women with severe lesions of cervix would help to raise necessary specificity of molecular genetics HPV testing and recommend it as a primary screening test for cervical carcinoma prevention. HPV testing could thus replace currently prevailing cytology which has relatively low sensitivity and therefore the number of false negative results.

The analyzed samples consisted of cytological cervical smears of 51 HPV positive women, with histologically confirmed presence of severe lesions, collected in liquid medium. Samplings from 51 women without infection were used as a control.

The possible effect on disease progress was confirmed only in the case of gene promoters' methylation whose presence was detected in up to 26 patients. It is, however, very unlikely that cancer would develop in all these women. This marker could thus help to stratify patients at risk but only to some extent. Although the individual effect of remaining markers has not been established in the carcinogenesis of cervical cancer, there is conceivable synergy between them or a role in conjunction with positive methylating status. To confirm these hypotheses other studies are needed.