INTRODUCTION The aim of our work was to validate the promising molecular biomarkers of high-grade cervical neoplasia and cancer in HPV-infected patients. For this purpose, we analyzed the profile of 21 different markers (expression of 6 microRNAs and 8 protein-coding genes, methylation level of 3 promoters) in 18 air-dried cervical PAP smears from patients of age risk group (average age 39) with the lesions of HSIL degree. The markers were selected by meta-analysis of related literature.

MATERIAL AND METHODS Cytological analysis was performed under an AXIOLAB microscope (Austria). Samples were classified according to the Bethesda system. Cervical epithelial scrapings were obtained and prepared by routine methods (MGG). Isolation of nucleic acids was performed by Boom method. In all samples, high-risk HPV DNA was detected by commercial kit (Vector-Best, Russia). MicroRNA and mRNA quantitation was performed by qPCR-based techniques. The relative level of methylation was estimated by methyl-specific PCR after bisulfite conversion. To identify levels on selected mRNAs and microRNAs and trained on larger samples of PAP smears corresponding to lesions of different severity.

RESULTS AND DISCUSSION Matching of molecular classifier conclusion and cytology was obtained for 14 (77.7%) samples. In 6 of these, increased level of promoter methylation was detected, and in 4 cases a borderline value for this criterion was obtained, possibly due to cell heterogeneity of the preparation. On the contrary, in 4 cases (22.2%) neither molecular classifier conclusions nor methylation level assessments pointed to high risk of malignancy, which may reflect relatively lower risk of malignant progression for these patients.

CONCLUSION The analysis of molecular biomarkers combined with cytology may provide the information useful not only for early diagnosis of cervical lesions, but also for estimating the risk of malignant transformation.