

## WIF1 AND DKK4 METHYLATION ANALYSIS IN CERVICAL INTRAEPITHELIAL NEOPLASIA

I. Gladchk, Kashtalian N.,  
Odessa National Medical University, Ukraine

Epigenetic gene silencing by excessive methylation was found in many tumors. Methylation of tumor suppressor genes is often found in cervical cancer, which is an important pathogenetic factor of oncologic process.

The aim was identify gene methylation of *WIF1* and *DKK4* events and their usefulness in distinguishing cancer and precancerous lesions from normal cervical cells that could have prospective efficacy in diagnostic testing for cervical precancer.

We examined methylation index of *WIF1* and *DKK4* genes in the tissue specimen of 42 women: CIN I in 9 cases, CIN II in 11 cases and CIN III in 10 cases, 7 samples included invasive cancer and control group of 5 normal cases.

In analysis of methylation level of *WIF1* and *DKK4* genes aberrant methylation of *WIF1* gene was found in women with CIN+ and aberrant methylation of *DKK4* gene was found in all women. There was a trend of methylation level increase according to the severity of the precancerous lesions with the maximum methylation levels in cases of invasive cervical cancer.

Methylation indexes determination in *WIF-1* and *DKK-4* genes is a perspective method of cervical precancer diagnostics.