

# METHYLATION PROFILING OF HOMEOTIC AND CHROMATIN REMODELING GENES IN CANCEROUS OVARIAN TISSUE

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Ovarian cancer is the third most common gynecologic cancer in the world and has the highest mortality rate of all gynecologic cancers [1]. Due to asymptomatic progression, ovarian cancer is diagnosed in 4 out of 5 cases in advanced stages (III or IV), when cancer has spread and control of the disease is difficult [2]. Ovarian cancer is heterogenic disease, which complicates the diagnosis of the disease and the selection of the optimal treatment strategy, however, approximately 75% of ovarian cancer cases are high-grade serous carcinomas. Current diagnostic methods for ovarian cancer lack specificity and sensitivity, thus it is important to search for new modern diagnostic tools. In recent years, promoter hypermethylation of tumor suppressor genes has gained a lot of attention for its potential to be applied as a cancer biomarker. Methylation studies of homeotic and chromatin remodeling genes attracted clinicians because they are important for the development of various organs, including ovaries and are critical for maintaining normal functions and homeostasis. Therefore, dysfunctions of homeotic and chromatin remodeling genes are associated with various diseases, including the development and progression of ovarian cancer.

This study aimed to evaluate promoter methylation profiles of homeotic (*ALX4*, *CDX2* and *HOPX*) and chromatin remodeling (*ARID1A*) genes that act as tumor suppressor genes in cancerous ovarian tissues as potential ovarian cancer biomarkers for more accurate and specific diagnostics. In total methylation profile was evaluated in 51 tissue biopsy samples using methylation-specific PCR (MSP).

The results demonstrated that methylation profile of *HOPX* gene significantly differ between benign gynecological tumors and high-grade ovarian carcinoma patients, while methylation profiles of *ALX4* and *CDX2* genes showed tendency between benign gynecological tumors and high-grade ovarian carcinoma patients, and other less common types of gynecologic cancer patients. Methylation profile of *ARID1A* gene showed no significant differences.

Thus, we found out that homeotic genes have the potential to be used for the early detection of disease and prediction of response to therapeutic interventions and prognosis of outcome, improving the quality of patients lives. However, more extensive analysis must be performed to validate the studied biomarkers.

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