THE 67TH INTERNATIONAL

OPEN READINGS

CONFERENCE FOR STUDENTS OF PHYSICS AND NATURAL SCIENCES

BOOK OF ABSTRACTS | 2024

Vilnius University

VILNIUS UNIVERSITY PRESS

Editors:

Martynas Keršys
Rimantas Naina
Vincentas Adomaitis
Emilijus Maskvytis

Cover and Interior Design:

Goda Grybauskaitė

Vilnius University Press
9 Saulėtekio Av., III Building, LT-10222 Vilnius
info@leidykla.vu.lt, www.leidykla.vu.lt/en/
www.knygynas.vu.lt, www.journals.vu.lt

Bibliographic information is available
on the Lithuanian Integral Library Information System (LIBIS) portal www.ibiblioteka.lt
ISBN 978-609-07-1051-7 (PDF)

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

Rugilė Gineikaitė[1,2], Ieva Vaicekauskaitė[1,2], Rūta Čiurlienė[1], Rasa Sabaliauskaitė[1,2]

[1]Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania
[2]National Cancer Institute, Vilnius, Lithuania
rugile.gineikaite@gmc.stud.vu.lt

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 remodelation 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 remodelation 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.

Acknowledgements: This study was funded by the National Cancer Institute.

[1] Momenimovahed, Z., Tiznobaik, A., Taheri, S. and Salehiniya, H. (2019). Ovarian cancer in the world: Epidemiology and risk factors. International Journal of Woman Health, 11, 287-299.
[2] Menon, U., Karpinskyj, C. and Gentry-Maharaj, A. (2018). Ovarian Cancer Prevention and Screening. Obstetrics and Gynecology, 131(5), 909-927.