

EXPRESSION ANALYSIS OF THE COMPONENTS OF HIPPO SIGNALING PATHWAY IN OVARIAN CANCER

Kornelia Gurska², Rūta Čiurlienė³, Rasa Sabaliauskaitė^{1,2}, Ieva Vaicekauskaitė^{1,2}

¹Lithuania, Vilnius, National Cancer Institute

²Lithuania, Vilnius, Life Science Center, Institute of Biosciences

³Lithuania, Vilnius University Hospital Santaros Clinics, National Cancer Center
kornelia.gurska@gmc.stud.vu.lt

Ovarian cancer is one of the most common women's reproductive system malignancies [1]. The most common subtype of ovarian cancer is high-grade serous ovarian carcinoma (HGSOC), which is characterized as an aggressively spreading malignancy. Furthermore, due to its non-specific symptoms, ovarian cancer is hard to diagnose in an early stage, which explains the high mortality rate of this disease.

Cancer development is often described by dysregulation of signaling pathways. Studies show that Hippo signaling pathway plays a crucial role in the ovary organ size control, development and regeneration [2]. Main components of this pathway are YAP, MST1/2, TAZ and LATS1/2 protein kinases, which control cell proliferation by regulating gene expression. Dysregulation of this pathway leads to uncontrolled cell proliferation and tumor progression.

This research aimed to analyze the expression of *YAP1*, *MST1*, *TAZ* and *LATS1* genes and identify their diagnostic potential. To achieve our aim, we performed a reverse transcriptase quantitative polymerase chain reaction (RT-qPCR) with 42 HGSOC, 14 other gynecological and 9 benign tumor tissue samples. The results were normalized to a reference gene *GAPDH*.

The ROC curve analysis when comparing HGSOC and benign cases showed an AUC of 0.94 for *TAZ*, 0.89 for *LATS1* and 0.87 for *YAP1* with a high sensitivity and specificity. Also, there was a high AUC, specificity and sensitivity rate when comparing HGSOC and other gynecological malignancies for *MST1* (AUC 0.74, specificity 0.79, sensitivity 0.71). Hippo pathway genes were downregulated in HGSOC and other tumor samples compared to benign cases ($p < 0.05$).

Our research suggests that the components of Hippo signaling pathway could be considered as a potential biomarker for ovarian cancer diagnosis. Further research is needed to validate this suggestion.

[1] B. Smolarz et al., "Ovarian Cancer—Epidemiology, classification, pathogenesis, treatment, and estrogen receptors' molecular backgrounds," *International Journal of Molecular Sciences*, vol. 26, no. 10, p. 4611, May 2025, doi: 10.3390/ijms26104611.

[2] K. L. Clark et al., "Hippo signaling in the ovary: Emerging roles in development, fertility, and disease," *Endocrine Reviews*, vol. 43, no. 6, pp. 1074–1096, May 2022, doi: 10.1210/endrev/bnac013.