

post-activity assessment during the study period were included in the analysis. Overall, 35% and 59% of oncologists and gynecologists, respectively, improved their competence across the activity. Specific improvements included: 20% of oncologists and 27% of gynecologists improving their competence related to selection of PARP inhibitor maintenance regimens. Statistically significant improvements ($P < .001$) for both oncologists and gynecologists in their competence related to selection of frontline treatment regimens. As a result of the education, 30% of the oncologists and 43% of gynecologists had a measurable increase in confidence in their ability to select therapy for patients with newly diagnosed ovarian cancer ($P < 0.001$ for both specialties), which led to an average positive confidence shift of 47% for oncologists and 63% for gynecologists.

Conclusion This study demonstrated the effectiveness of an online, interactive, case-based educational activity on improving competence and confidence of oncologists and gynecologists in practically incorporating PARP inhibitor maintenance regimens into the treatment paradigm for patients with newly diagnosed advanced ovarian cancer.

2022-RA-1112-ESGO MFAP5 IS RELATED TO OVARIAN CANCER PROGRESSION BUT NOT SUITABLE AS PROGNOSTIC BIOMARKER

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Introduction/Background Previously, we identified a set of genes related to differential survival of patients with high-grade serous ovarian cancer (OC).¹ One of these was *Microfibrillar associated protein 5* (MFAP5). MFAP5 is poorly characterized, although some data suggest that it can promote cancer cell motility and invasiveness, as well as angiogenesis in OC. Our aim was to validate MFAP5 as prognostic biomarker. **Methodology** For survival analysis we used online tools: Kaplan-Meier Plotter and Microarray Gene Expression Database of OC Subtype (CSIOVDB). MFAP5 co-expressed genes were identified using cBioPortal; protein interaction networks were assessed by STRING. Immunohistochemical analysis was performed on 108 formalin-fixed paraffin-embedded OC samples and on tissue arrays (US Biomax), using anti-MFAP5 antibody (15727-1-AP, Proteintech); results were analyzed using Statistica-v.13.1 (StatSoft).

Results Kaplan-Meier Plotter and CSIOVDB analysis confirmed that MFAP5 mRNA level is significantly related to survival of OC patients. Also, patients with FIGO I&II had significantly lower MFAP5 expression than patients with advanced stage (FIGO III&IV) cancer; patients with well-differentiated (G1) tumors had lower MFAP5 expression than patients with G2&G3 tumors. Subsequently, we evaluated expression of MFAP5 protein by immunohistochemistry. Patients with highest MFAP5 level had shorter survival, however not statistically

significant. MFAP5 expression was also related to desmoplastic reaction. There was no correlation neither with stage, grade, nor histological type. MFAP5 is co-expressed with multiple genes coding for extracellular-matrix proteins (cBioPortal); STRING algorithm showed strong experimental evidence for MFAP5 interactions with ECM proteins, primarily with LOX family members and FBN1. MFAP5 was shown to be connected to the Notch signaling pathway.

Conclusion MFAP5 seem to be involved in the important cellular processes and signaling pathways engaged in cancer progression and its mRNA level is related to worse prognosis. However, MFAP5 is not suitable as prognostic marker for simple evaluation with IHC.

REFERENCE

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2022-RA-1114-ESGO BRCA I, BRCA II MUTATION IN HIGH GRADE OVARIAN CANCERS, FALLOPIAN TUBE CANCER, PRIMARY PERITONEAL CARCINOMA

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Introduction/Background BRCA1 and BRCA2 carriers have an increased risk of developing ovarian cancer (OC), fallopian tube carcinoma (FTC), and primary peritoneal cancer (PPC). Germline mutations in BRCA1/BRCA2 are responsible for the development of ovarian cancer in at least 10% of cases. The aim of study was to investigate the BRCA status of high-grade serous OC, FTC, PPC.

Methodology Patients with OC, FTC and PPC with high grade serous were recruited. Data and blood of patients, who treated at oncogynecologic department N.N. Alexandrov National Cancer Centre of Belarus between January 2022 and May 2022 were collected. Germline mutations in BRCA1/BRCA2 were tested and analyzed by polymerase chain reaction (PCR).

Results A total of 75 patients were analyzed: 65 patients with OC, 9 with FTC, 1 with PPC. BRCA negative status was observed in 43 patients, BRCA positive in 32 (43%). 31 patients had BRCA1 mutation and 1 patient had BRCA2 mutation. The most frequently BRCA 1 mutations were: 5382incC (20 exon) – n=15, slightly less (n=9) 4153delA (11 exon), 185delAG (2 exon) – n=2, 300T>G (5 exon) – n=5. One patient had BRCA 2 mutation (6174 delT). 75% of patients had a burdened family history and first-, second- and third-degree relatives with oncological diseases, mainly breast cancer, ovarian cancer, pancreatic cancer, prostate cancer.

Conclusion The high percentage BRCA 1, 2 mutations (43%) in patients with ovarian cancer, fallopian tube carcinoma, primary peritoneal carcinoma with high-grade serous carcinoma requires further research. Genetic counseling is also especially necessary not only for patients, but also for their relatives in order to identify hereditary mutations and carry out preventive measures.