#1063 IL-10 POLYMORPHYSMS AS OVARIAN CANCER RISK FACTOR IN GEORGIAN WOMEN

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10.1136/ijgc-2023-ESGO.897

Introduction/Background Ovarian cancer (OC) is considered to demonstrate multifactorial causes including multiple genetic contributors. Variants of many genes are suspected to participate in increasing the risk for OC. Some of those are genes involved in tumor microenvironment formation, an example of which is Interleukin-10 (IL-10) gene. We tried to analyze the single nucleotide polymorphism (SNP) (rs1800896) in the IL-10 gene in relationship to OC risk and correlated it with the levels of IL-10 in the peripheral blood of OC patients.

Methodology A case-control study was performed on a total of 20 women, with histologically confirmed epithelial ovarian cancers and 20 age-matched controls. SNP genotyping was performed with TaqMan Assay with Real Time-PCR. Statistical analyses were performed by GraphPad Prism 9.3.1 for macOS. Statistical significance for differences in genotype frequencies was determined by Chi-square and Fisher's exact test.

Results The genotype distributions of IL-10 gene polymorphisms among cancer and control groups were all according to the expected Hardy–Weinberg equilibrium. There was no statistically significant difference in frequency of genotypes and alleles between the two study groups.

In another analysis, the samples were grouped according to the polymorphic variant IL 10 (– 1082) A/G. Subjects having the homozygous variant (AA) had lower IL-10 mRNA levels than those with the homozygous wild (GG) genotype in both, ovarian cancer patients and controls, $p < 0.05$.

mRNA levels on IL-10, IL-8 were different among cases and controls ($p < 0.05$). Patients with OC had higher level of mRNA for IL-10 and IL-8 than controls.

Conclusion This relatively small-scaled study demonstrated, that mRNA levels of IL-10 and IL-8 are high in patients with OC and this goes along with the serum levels of proteins. However this difference is not determined by allelic differences, which means that other factors - epigenetic and regulatory - up-regulate expression of IL-10 and IL-8 genes in patients with OC.

Disclosures The study was supported by Shota Rustaveli National Science Foundation (Grant N YS-21-1216).

#1044 WHY WE REALLY NEED THE HUMAN EPIDIDYMIS PROTEIN 4 IN THE PREOPERATIVE ASSESSMENT OF PREMENOPAUSAL PATIENTS WITH PELVIC MASS

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10.1136/ijgc-2023-ESGO.898

Introduction/Background Human epididymis protein 4 (HE4) has been reported as a promising complement to CA125 in the assessment of the risk of malignancy in patients, diagnosed with pelvic mass. However, reference limits of HE4 do not provide clinically relevant discrimination between malignant and benign ovarian diseases. The clinical significance of well-known Risk of Ovarian Malignancy Algorithm (ROMA), which combines both HE4 and CA125, is still questionable. Recently, ESGO/ISUOG/IOTA/ESGE Consensus Statement on pre-operative diagnosis of ovarian tumors implied that neither HE4 nor ROMA improve the discrimination between benign and malignant masses compared with CA125 alone.

Methodology An external validation of the new algorithm, named Risk of Ovarian Cancer Kazan Index (ROCK-I), will be presented. A comprehensive analysis of the performance of ROCK-I will be presented with the focus on clinical utility of adding HE4 to CA125 and ultrasound evaluation.

Results A comprehensive analysis of the performance of ROCK-I will be presented with the focus on clinical utility of adding HE4 to CA125 and ultrasound evaluation.

Conclusion HE4 is a useful compliment to expert ultrasound and CA125

Disclosures Authors has nothing to disclosure

#1120 DURVALUMAB WITH PACLITAXEL/CARBOPLATIN + BEVACIZUMAB THEN MAINTENANCE DURVALUMAB, BEVACIZUMAB + OLAPARIB IN PATIENTS WITH NEWLY DIAGNOSED ADVANCED OVARIAN CANCER WITHOUT A TUMOUR BRCA1/2 MUTATION: RESULTS FROM THE DUO-O/ENGOT-OV46/AGO-OVAR 23/GOG-3025 TRIAL

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10.1136/ijgc-2023-ESGO.899

Introduction/Background Olaparib maintenance improved outcomes in patients with newly diagnosed advanced ovarian cancer (AOC) and a BRCAm (DiSilvestro JCO 2023), or with bevacizumab in patients with homologous recombination deficiency (HRD+) tumours (Ray-Coquard ESMO 2022) in response to first-line treatment; however, an unmet need remains.