EP221/#521 HIGH EXPRESSION OF VACUOLAR-ATPASE SUBUNIT ATP6V1B1 PROMOTES POOR PROGNOSIS AND TUMORIGENIC CHARACTERISTICS IN EPITHELIAL OVARIAN CANCER

[1]Hee Yun, [2]Gwan Hee Han*, [3]Hyosun Kim, [4]Joon-Yong Chung, [5]Sunghoon Kim, [5]Jae-Hoon Kim, [1]Hanbyoul Cho. *[1]Gangnam Severance Hospital, Yonsei University, Department of Obstetrics and Gynecology, Gangnam-gu,, Korea, Republic of; [2]Kyunghee University Hospital at Gangdong, Obstetrics and Gynecology, Gangdong-gu, Korea, Republic of; [3]Gangnam Severance Hospital, Yonsei University, Obestetrics and Gynecology, Gangnam-gu,, Korea, Republic of; [4]National Institutes of Health, Molecular Imaging Branch, Center For Cancer Research, National Cancer Institute, Bethesda, USA; [5]Institute of Women's Medical Life Science, Yonsei University College of Medicine, Department of Obstetrics and Gynecology, Seoul, Korea, Republic of*

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Objectives Vacuolar-ATPase subunit ATP6V1B1 belongs to the ATP6V1s which participates in the biological process of transporting hydrogen ions and are associated with various cancers, while its role its role in epithelial ovarian cancer (EOC) has not been clarified yet. Therefore, we aim to evaluate the function, molecular mechanism and clinicopathological significance of ATP6V1B1 in EOC.

Methods Expression level of ATP6V1B1 was screened by RNA sequencing of 10 EOCs and normal epithelial ovarian tissues. Expression levels of ATP6V1B1 were evaluated by immunohistochemistry staining of EOC, borderline, benign and normal epithelial tissues. Associations of clinicopathological features and prognosis with ATP6V1B1 in EOC patients were analyzed both our recruited cohort and GEO datasets. Also, the functional roles of ATP6V1B1 were evaluated in EOC cell lines.

Results ATP6V1B1 protein was elevated in EOCs according to a GEO and TCGA datasets. High mRNA and protein levels of ATP6V1B1 were observed in EOCs compared to borderline, benign and normal nonadjacent ovarian epithelial tissues. High expression level of ATP6V1B1 was associated poor overall survival and disease-free survival. In vitro results demonstrated the knockdown of ATP6V1B1 was associated with decreased cell proliferation and colony forming abilities, supporting the oncogenic role in EOC. Also, cell cycle analysis revealed a higher proportion of cells in G1 phase after knockdown of ATP6V1B1.

Conclusions Our study is the first work to identify an oncogenic role of ATP6V1B1 in EOC tissues and cell lines which may provide insights into the application of ATP6V1B1 as a novel predictor of clinical outcome and a potential therapeutic target in EOC patients.

EP222/#606 ACID CERAMIDASE (ASAH1) EXPRESSION IS ASSOCIATED WITH IMPROVED OVERALL SURVIVAL IN PATIENTS WITH HIGH-GRADE SEROUS OVARIAN CANCER FROM THE ICON-7 TRIAL

[1]Lars Hanker*, [2]Ahmed El-Balat, [2]Thomas Karn, [2]Uwe Holtrich, [1]Benedikt Decker, [3]Jacobus Pfisterer, [4]Heide Gevensleben, [5]Stefan Kommoss. *[1]University Hospital Schleswig-Holstein, Campus Luebeck, Gynecology and Obstetrics, Luebeck, Germany; [2]University Hospital Johann Wolfgang Goethe-University, Department of Gynecology and Gynecologic Oncology, Frankfurt, Germany; [3]Gynecologic Oncology Center, Gynecologic Oncology, Kiel, Germany; [4]Institute of Pathology, University Hospital, Bonn, Germany; [5]University of Tuebingen, Department Gynecology & Gynecologic Oncology, Tübingen, Germany*

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Objectives Despite recent progress in the treatment of epithelial ovarian cancer the cure of this disease remains a challenge. Therefore new treatment options along with new prognostic and predictive makers are urgently needed. The enzyme acid ceramidase (AC) plays a central role in the sphingolipid network which is involved in tumorigenesis and progression. Furthermore AC directed therapies are currently under development. We investigated the expression of AC and its prognostic impact on ovarian cancers.

Methods Patients of the AGO-cohort of the ICON-7 trial were analysed. In this randomized trial patients with advanced EOC received carboplatin+paclitaxel vs. carboplatin+paclitaxel +bevacizumab. Tissue micro arrays (TMAs) were constructed for performing immunohistochemical analysis of AC. The results were correlated with clinico-pathological characteristics and survival data.

Results Kaplan-Meier analysis (n=351) revealed that high levels of AC were associated with improved progression-free survival (PFS; 24.12 months [95% confidence interval (CI): 19.36 – 28.86] vs. 16.69 months [95% CI: 14.91 – 18.71], p < 0.0001) and overall-survival (OS; 66.83 months [95%CI: –] vs. 44.12 months [95%CI: 37.37 – 50.87], p < 0.0001). Subsequently, the prognostic value of AC expression together with clinical factors (i.e. FIGO stage, grading, histological subtype, bevacizumab medication and residual tumour burden after surgery) was further confirmed in multivariate Cox regression analysis in n= 426 patients (PFS: hazard ratio (HR) = 0.69 [95% CI: 0.550 – 0.877], p = 0.002; OS: HR = 0.67 [95% CI: 0.504 – 0.881], p = 0.004).

Conclusions Our data identify high levels of AC expression as a strong favorable prognostic marker in ovarian cancer patients.

EP223/#762 DISTINCT VAGINAL MICROBIOME IN NEWLY DIAGNOSED OVARIAN CANCER PATIENTS

Ronli Hershkovitch Neiterman*, Lina Salman, Shilhav Meisel Sharon, Shay Hantisteanu, Raphy Zarecki, Leah Reshef, Hallak Mordechai, Haim Werner, Ilan Bruchim. *Gynecology Laboratory, Department of Obstetrics and Gynecology, Hillel Yaffe Medical Center, Department of Obstetrics and Gynecology, HADERA, Israel*

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Objectives Microbiome plays an important role in the development of different cancer types. Vaginal microbiome constitutes a new study field. We aim to examine the vaginal microbiome profile in patients with newly diagnosed epithelial ovarian cancer (EOC) compared to healthy women.

Methods A prospective cohort study was conducted for evaluating the vaginal microbiome in patients with newly diagnosed EOC who are chemotherapy-naïve, compared to healthy controls. Samples were collected using a swab. DNA was extracted and amplified by PCR using universal primers of the prokaryotic 16S ribosomal RNA gene. Next-generation sequencing and taxonomical classification of bacterial species was performed.

Results Vaginal swab samples were collected from 18 EOC patients, and 22 controls. Higher rates of menopausal status were demonstrated in cancer patient (77.8% to 41% P=0.041). The microbiome profile analysis revealed statistically significant differences between groups; Peptoniphilus coxii and Veillonella dispar/parvula were found to be more abundant in the cancer patients (p=0.034 and p=0.022,