Conclusion Robot assisted laparoscopic staging surgery is feasible and safe with early ovarian cancer. Additionally, prospective randomized clinical trials will be able to evaluate the clinical benefits of robot-assisted surgery.

2022-RA-837-ESGO
CHARACTERIZATION OF LONG-TERM SURVIVOR AND MAINTENANCE THERAPY IN RELAPSED OVARIAN CANCER (CAROLIN)- INTERGROUP STUDY NOGGO/ A-AGO

Introduction/Background Ovarian Clear Cell Carcinomas (OCCC) are characterized by a low response to chemotherapy and a poor prognosis in advanced stages. Several studies have demonstrated that OCCc is not a uniform entity. Previously, we have identified four potential molecular subtypes based on the mutational status of ARID1A and PIK3CA. This study aimed to examine and describe the association between different molecular profiles, Tumor Mutational Burden (TMB), and molecular signatures with the clinical outcome in OCCc.

Methodology We identified 55 OCCc cases with corresponding data and biological tissue samples in the Danish Gynecological Cancer Database (DGCD) in the period January 2005 to December 2016. The mutational profiling and Tumor Mutational burden (TMB) were performed using the Oncomine Tumor Mutational Load Assay. Chi square and Cox regression analyses were performed. P-values of <0.05 were considered statistically significant.

Results Mutations in the PIK3CA gene (p=0.04), as well as low TMB (p=0.05), were associated with the progression of the disease (yes vs no). In analyses adjusted for stage, patients with mutations in either ARID1A or PIK3CA were both associated with an impaired Progression Free Survival (PFS), and Overall Survival (OS) compared to cases who were wildtype for ARID1A and PIK3CA (undetermined subgroup) ((HR 5.42 and HR 2.77, respectively). High TMB status was associated with an improved PFS (HR 0.36) and OS (HR 0.46), although the latter only reached borderline significance. A trend toward an improved PFS in patients with APOBEC enrichment was observed (HR 0.45).

Conclusion We found that TMB-High is associated with decreased risk of progression and with an improved PFS and OS. Furthermore, a subgroup of OCCc with mutations in either the ARID1A and/or PIK3CA genes had a significantly impaired prognosis compared to the undetermined subgroup in analyses adjusted for stage.

2022-RA-840-ESGO
PROGNOSTIC IMPACT OF MOLECULAR PROFILES AND MOLECULAR SIGNATURES IN CLEAR CELL OVARIAN CANCER

Introduction/Background Ovarian Clear Cell Carcinomas (OCCC) are characterized by a low response to chemotherapy and a poor prognosis in advanced stages. Several studies have demonstrated that OCCC is not a uniform entity. Previously, we have identified four potential molecular subtypes based on the mutational status of ARID1A and PIK3CA. This study aimed to examine and describe the association between different molecular profiles, Tumor Mutational Burden (TMB), and molecular signatures with the clinical outcome in OCCC.

Methodology We identified 55 OCCC cases with corresponding data and biological tissue samples in the Danish Gynecological Cancer Database (DGCD) in the period January 2005 to December 2016. The mutational profiling and Tumor Mutational burden (TMB) were performed using the Oncomine Tumor Mutational Load Assay. Chi square and Cox regression analyses were performed. P-values of <0.05 were considered statistically significant.

Results Mutations in the PIK3CA gene (p=0.04), as well as low TMB (p=0.05), were associated with the progression of the disease (yes vs no). In analyses adjusted for stage, patients with mutations in either ARID1A or PIK3CA were both associated with an impaired Progression Free Survival (PFS), and Overall Survival (OS) compared to cases who were wildtype for ARID1A and PIK3CA (undetermined subgroup) ((HR 5.42 and HR 2.77, respectively). High TMB status was associated with an improved PFS (HR 0.36) and OS (HR 0.46), although the latter only reached borderline significance. A trend toward an improved PFS in patients with APOBEC enrichment was observed (HR 0.45).

Conclusion We found that TMB-High is associated with decreased risk of progression and with an improved PFS and OS. Furthermore, a subgroup of OCCC with mutations in either the ARID1A and/or PIK3CA genes had a significantly impaired prognosis compared to the undetermined subgroup in analyses adjusted for stage.