Conclusion Severe persistent LLL occurred rarely after surgical pelvic LN staging in cervical cancer patients. Contrary to our expectations, de-escalation from systematic PLND to SLN biopsy was not associated with a significantly decreased risk of mild-to-moderate LLL.

11. Translational research/biomarkers

#64 HOMOLOGOUS RECOMBINATION DEFICIENCY (HRD) TESTING ON CELL-FREE TUMOR DNA FROM PERITONEAL FLUID OF PATIENT WITH EPITHELIAL OVARIAN CANCER

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Introduction/Background Knowledge regarding homologous recombination deficiency (HRD) status at diagnosis is essential to manage patients with advanced epithelial ovarian cancer (EOC). These genomic tests are performed on tumor samples and unfortunately the analysis of tumor DNA are missing 15–19% of cases.

Methodology We collected ascites or peritoneal washings (20ml) from 53 patients undergoing primary or secondary laparoscopy for suspicion of EOC, or therapeutic paracentesis. A Cancer Gene Panel (CGP) was analyzed by Next generation sequencing (NGS) for TP53 genes and HR genes and shallow Whole Genome Sequencing (sWGS) was used to measure genomic instability on cftDNA from peritoneal fluid

Results A total of 53 patients were included. Cell-free DNA (cfDNA) was detectable in 49/53 patients (92,5%) even when there was little peritoneal fluid (<100cc) at laparoscopy (n=7). Median cfDNA extracted from 20ml peritoneal fluid or washings was high at 3700 ng/ml (range 109 – 65 000 ng/ml) and median turn-around testing time was 21 days. 42 patients (86%) had a TP53 pathogenic variant, all cases were HGSOC. Seven (14%) and 5 (10%) had a BRCA1 or BRCA2 pathogenic variant, respectively. The sensitivity, specificity and concordance of acfDNA compared with tumor testing for TP53 pathogenic variant detection were 97% (95% IC : 86%-100%), 83% (95% IC : 43%-100%) and 95% (K = 0,81: P <0,001) respectively. NGS CGP on cftDNA was contributive in 5 patients with failed NGS CGP on tumor DNA from tissue, including one patient with a BRCA2 pathogenic variant identified in cftDNA. Genomic instability was assessed by sWGS on cftDNA and provided a contributive result for all samples tested, including 7 for which matching tissue-based GIS testing failed.

Conclusion Genomic profiling on cftDNA from peritoneal fluid is feasible and yields high quantity of tumor DNA.HRD testing on cfDNA from peritoneal fluid should be proposed to every patient undergoing primary laparoscopy.

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#71 INTEGRATED MULTI-OMIC AND CLINICOPATHOLOGICAL ANALYSIS OF HIGH-GRADE SEROUS OVARIAN CANCER IN BRCA1/2 MUTATED PATIENTS WITH POOR SURVIVAL: IDENTIFICATION OF PREDICTIVE BIOMARKERS FOR PERSONALIZED TREATMENT

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Introduction/Background Pathogenic germline BRCA1/2 alterations (gBRCA) are common in patients with high-grade serous ovarian carcinoma (HGSOC) and are generally associated with better chemotherapy response and longer 5-year-survival. However, fewer gBRCA1-carriers are alive at 10 years compared to non-carriers and gBRCA2-carriers. Clinicopathological and multi-omic features of HGSOC were compared in BRCA1/2-mutated patients with short and long-term survival to identify factors influencing clinical outcomes.

Methodology Whole-genome-sequencing, RNA-sequencing and clinicopathological analysis on primary HGSOC tumors from 35 advanced-stage BRCA1/2-mutant with short survival (≤3-years) was compared with data from 84 patients with >3-year survival (44 BRCA-mutant, 40 BRCA-wildtype), and 35 BRCA-wildtype patients with short survival. We also assessed clinicopathological features and tumor immune markers by multiplexed immunofluorescence in 293 and 146 gBRCA-carriers, respectively.

Results Prognostic features including residual disease, age, grade, FIGO stage, primary site, and BRCA type (BRCA1 vs BRCA2) could not explain short survival in BRCA-mutants relative to those with longer survival. Somatic mutation and neoantigen burden were equivalent between the two survival groups of BRCA-mutants, however the homologous recombination DNA repair deficiency (HRD) score was significantly higher in BRCA-mutants with long survival compared to those with short survival (73.6 vs 65.5, p=0.007). T-cell (PD1+,CD4+) density was associated with good outcomes in BRCA-mutants (p=0.003). Mutational signature clustering identified a group of BRCA-mutants characterised by short survival, low HRD-scores, and DNA copy number signature CN9 which is associated with increased leucocyte fraction and poor disease-specific survival. PIK3CA alterations were enriched in BRCA2-mutants with short survival (5/10, 50%, p=0.061).

Conclusion Survival in BRCA-mutants with HGSOC was associated with distinct mutational signatures, differential immune responses, somatic gene alterations, and differences in the extent of HRD. Integration of multi-omic data with clinical variables can enhance the accuracy of predictive models and