were studied for mRNA levels of TGF-β1 ligand, TGF-β receptor1 & 2 (TGFβRI&II), Smad2 and Smad4 genes. mRNA expression was quantified by delta Ct (ΔCt) values obtained from quantitative PCR tests and fold change in expression by ΔΔCt values from ΔCt of reference endometrial sample. The association of these mRNA expressions with tumour-related characteristics and recurrences was assessed using non-parametric tests as Mann-Whitney U test & Kruskal Wallis test.

Results 49 patients were considered for analysis. Majority were of endometrioid histology, lower grade, and stage I. 84% of endometrial cancer samples demonstrated under-expression of Smad2. Loss of Smad2 was significantly associated with myo-invasive tumours and tumours >2 cm. Loss of TGFβRII expression was related to parametrial invasion and stage IV disease, while reduced TGFβRI expression to clear cell histology. During a median follow up of 15.4 months, there were three recurrences. Loss of TGFβRII expressions was significantly associated with recurrence. Mean ΔΔCt value of >1.950 for smad2 and TGFβRII expression was associated significantly with a reduced 1.5 year recurrence-free survival.

Conclusion TGFβ pathway components undergo changes in endometrial cancer. Impaired expression is observed at every level of signalling pathway, Loss of Smad mRNA expression and TGFβ receptor levels have certain associations with aggressive features and can predict recurrence risk.

2022-RA-627-ESGO PREOPERATIVE CIRCULATING TUMOR DNA LEVEL IS ASSOCIATED TO POOR OVERALL SURVIVAL IN PATIENTS WITH OVARIAN CANCER

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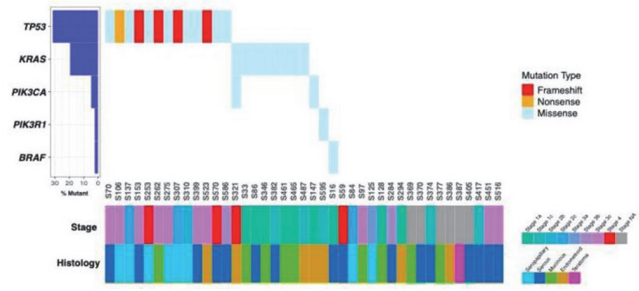
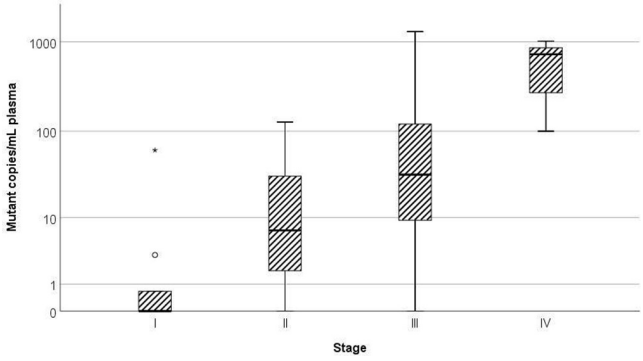
Introduction/Background Circulating tumor DNA (ctDNA), which is shed from tumor cells into the blood, is a promising minimal-invasive method for cancer diagnostics and monitoring. The aim of this study was to evaluate preoperative ctDNA levels in the plasma of patients with ovarian cancer and correlate the levels to clinico-pathological parameters and patient outcome.

Methodology Tumor DNA was extracted from ovarian tumor tissue from 41 patients. Targeted sequencing using a panel of 127 genes recurrently mutated in cancer was performed to identify candidate somatic mutations in the tumor DNA. SAGAsafe digital PCR (dPCR) assays targeting the candidate mutations were used to measure ctDNA levels in patient plasma samples, obtained prior to surgery, to evaluate ctDNA levels in terms of mutant copy number/mL and variant allele frequency.

Results Somatic mutations were found in 24 tumors, of which seven were from patients with borderline, and 17 with invasive cancer diagnosis. *TP53* was the most frequently mutated gene. Fifteen of 24 patients had detectable ctDNA levels in pre-operative plasma. Plasma ctDNA mutant concentration increased with higher stage (p_{trend} <0.001). Cancer patients with more than 10 ctDNA mutant copies/mL in plasma prior to surgery had significantly worse overall survival (p=0.008).



Abstract 2022-RA-627-ESGO Figure 1 Waterfall plot of validated somatic mutations in the patient tumors. Genes are indicated in rows and samples in columns. Mutated samples are show according to mutation type. Patient and tumor clinopathological variables are shown below the patient IDs



Abstract 2022-RA-627-ESGO Figure 2 Plasma circulating tum or (ctDNA) mutant concentration increased with higher stage (p_{trend}<0.001).Concentrations of circulating tumor DNA (ctDNA) in stage III and stage IV OvCa were significantly higher compared with stage I OvCa (p=0.025 and p=0.007 respectively) Bars include highest and lowest values, except outliers (o), which are 1.5 to 3 box lengths from the end of the box, and extremes (*) which are more than 3 box lengths from the end of the box

Conclusion Measuring ctDNA in pre-operative plasma may be useful as a predictive biomarker for tumor staging and prognosis in ovarian cancer patients.