Poster #15 | Mutational Landscape of Low-Grade Serous Carcinoma of the Ovary

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Topic: Ovarian

Objectives
Tumor genomic profiling is a critical component of precision oncology allowing the detection of genomic alterations (GA) that are potential therapeutic targets. We present an analysis of comprehensive genomic profiling (CGP) of a large series of low grade serous ovarian carcinoma patients assayed in a nationwide cancer network.

Methods
40 Pts with advanced low grade serous ovarian carcinoma (LGSOC) underwent hybrid-capture based CGP for up to 324 cancer-related genes on archival tumor tissue or 62 genes on circulating tumor DNA ordered during clinical care for treatment decision-making between 01-2013 thru 06-2021. Clinically relevant genomic alterations (CRGA) were defined as associated with targeted therapies or mechanism-driven clinical trials. The treatment histories for these patients were obtained with IRB-approved retrospective review.

Results
Median age was 44 years (range, 25-65), 68% were White and 23% were Black. Genomic alterations (GA) were identified in 80% (32/40) of LGSOC, of which 22 (55%) had a clinically relevant genomic alteration (CRGA). There were no apparent racial differences between mutation frequencies. The table below details the frequency of the most common of these clinically relevant mutations. Additionally, single cases of the following mutations were also noted: TSC1, PTCH1, PTEN, FGFR1, and AKT2.

Conclusions
In a large series of Low Grade Serous Ovarian Cancer patients assayed with CGP, 55% of pts had mutations potentially targeted by precision medicine therapy. The most common target is KRAS, seen in 33% of patients, these are potentially treatable with FAK and MEK inhibitors. Another 10% of patients had either a BRCA or ATM mutations making PARP inhibitor therapy another targeted treatment option. Single patients demonstrated EGFR or MTOR mutations which are also therapeutic targets. While mutations in the RAS pathway are most common in LGSOC they are not the only actionable target. The results of this study demonstrate the significant heterogeneity of genomic alterations in this rare cancer and highlight the importance of genomic profiling in this cancer which has a marked propensity for recurrence.

Abstract Table or Graph
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