Characterizing FOLR1 expression in Low Grade Serous Ovarian Carcinoma

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Background

- Targeted therapy in folic receptor alpha (FOLR1)-positive high grade serous ovarian carcinoma (HG) is now a mainstay for platinum-resistant disease.
- The rate of FOLR1-positivity in low grade serous ovarian carcinoma (LG) is unknown.
- We compared the genomic and transcriptomic landscapes in FOLR1-positive/negative LG in comparison to its HG counterpart.

Methods

- LG (N = 281) and HG (N = 5086) tumors were tested at Caris Life Sciences (Phoenix, AZ) with NextGen Sequencing on DNA (592 genes or whole exome) and RNA (whole transcriptome).
- PD-L1+ (22C3, TPS > 1%) and FOLR1 (Positive [F+], >2%, >75%) expression was assessed by IHC.
- Mutations were defined as pathogenic SNVs/indels (-Mt).
- A transcriptomic signature associated with MAPK pathway activation (MPAS) was applied.
- Fisher’s exact/𝜒2 and Mann-Whitney U tests were applied as appropriate (p < 0.05, adjusted for multiple comparisons).
- Real-world overall survival (OS) was obtained from insurance claims and Kaplan-Meier estimates were calculated for molecularly defined patients.
- This study was reviewed by the Johns Hopkins Medicine IRB and determined to qualify as exempt human subjects research.

Results

- LG tumors have a lower rate of FOLR1+ as compared to HG.
- LG tumors are enriched for mutations in the MAPK pathway.

Conclusions

Though less prevalent than in HG disease, a notable portion of LG tumors were FOLR1+, which suggests that FOLR1 expression in LG could be a viable target for this rare histology, particularly in the recurrent setting.

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