Carcinoma of unknown primary (CUP): The role of tumor genomic profiling

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- CUP is a heterogenous group of cancers characterized by early metastatic dissemination from an unknown site of origin.1
- Overall survival is a dismal 6-12 months and untreated CUP is associated with a 4 week life expectancy.2,3
- A 2014 review of the molecular profile of 1806 cases of CUP within the Caris Life Sciences database identified biomarkers with potential therapeutic benefits in over 96% of cases 4
- CUP continues to be a diagnostic and treatment challenge and comprehensive genomic profiling may provide therapeutic insight.

Study Methods

- Molecular profiles of tumors noted as 'unknown' for tumor primary site within the CARIS Life Sciences database were analyzed utilizing CODEai, a platform that integrates real-world clinical information obtained from insurance claims and medical records with genomic data.
- This real-world cohort consisted of 3,841 tumors:
  - 2,137: Adenocarcinoma (ADC)
  - 385: Squamous cell carcinoma (SQ)
  - 1,319: Carcinoma not otherwise specified (NOS)
- CUP-ALL: CUP-ADC + CUP-SQ + CUP-NOS
- Overall survival (OS) was calculated from time of tissue collection to last contact assessed by Kaplan-Meier estimates.

Result

- The findings from this large real-world cohort demonstrate that key molecular alterations have prognostic and predictive roles in CUP.
- To maximize clinical benefit, prospective studies with various therapeutic classes of cancer treatments exploiting these differences are warranted.

Background

- The role of tumor genomic profiling
- Carcinoma of unknown primary (CUP)

Figure 1. Within CUP-ALL, the targeted therapy cohort had a longer mOS of 638 days compared to 374 days in the chemotherapy cohort.

Figure 2. Within CUP-ALL, the immunotherapy cohort had a longer mOS of 601 days compared to 372 days in the chemotherapy cohort.

Figure 3. In CUP-ADC, tumors with KRAS wild type had a longer mOS of 202 days compared to 374 days in tumors with a KRAS mutant variant.

Figure 4. In CUP-SQ, tumors positive for PD-L1 had a longer mOS of 769 days compared to 508 days in tumors negative for PD-L1.

Conclusion

- The findings from this large real-world cohort demonstrate that key molecular alterations have prognostic and predictive roles in CUP.
- To maximize clinical benefit, prospective studies with various therapeutic classes of cancer treatments exploiting these differences are warranted.

References