Differences in the genomic and transcriptomic landscapes of Human Papillomavirus (HPV)-positive neuroendocrine neoplasms and HPV-positive carcinomas

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Methods

- 101,343 solid tumors were sequenced at Caris Life Sciences (Phoenix, AZ) with NextGen Sequencing (NGS) of DNA (whole or hybrid exome) and RNA (whole or hybrid transcriptome) and assayed for HPV16/18 positivity via DNA sequencing.
- Mutation prevalence for pathogenic SNVs/indels (-Mt) and copy number amplification (CNA) were calculated.
- Expression of Ki-67 mRNA (MKI67) was used to infer high-grade vs low-grade NEN.
- Differentially regulated pathways were assessed by gene set enrichment analysis (GSEA).
- Fisher’s exact²chi² tests were applied as appropriate with p-values adjusted for multiple comparisons (p < .05).

Results

- Pan-tumor prevalence of HPV16/18
- NEN prevalence of HPV16/18 by site and grade

Conclusions

- We uncovered a category of HPV+ NENs with distinct genomic and transcriptomic landscapes compared to non-NEN tumors.

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