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Mapping the epigenetic landscape for sinonasal carcinoma

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Summary

Background: Malignancies of the sinonasal tract account for 3-5% of all head and neck cancers. The clinical presentation of sinonasal carcinomas are nonspecific and late detection is common. A high proportion of lesions are advanced stage at first diagnosis. Sinonasal carcinomas show histological heterogeneity, hence diagnostic classification can be challenging. Recently, genetic testing has identified specific sub-types of sinonasal carcinomas that have distinctive treatment pathways including their responsiveness to chemo-radiotherapy and prognosis.

There is limited literature investigating the genome of sinonasal carcinomas with substantially more limited or non-existent data on the epigenome and transcriptome. Additionally, the Human Papilloma Virus has been identified as an oncogenic driver of oropharyngeal carcinoma and postulated to play a role in sinonasal malignancies.

Aims: This study aims to establish the largest cohort of sinonasal carcinoma patients to date to investigate the genome and epigenome. Identification of genetic signatures and their associations with key patient events can help improve diagnosis, provide relevant clinical information regarding responsiveness to chemo-radiotherapy and inform patient prognosis. Substantial genetic findings can improve our understanding of the cancer biology, help revise the current classification and provide clinical-pathological data to inform future studies and clinical trials.

Methods: DNA and RNA will be extracted from paraffin embedded tissue and exploratory target sequencing conducted to identify key mutations in commonly mutated candidate genes. In addition, methylation and copy number analysis will be performed to provide an epigenetic insight for each patient and this linked to their clinical outcomes.

Keywords

'Genetics', 'Sinonasal carcinoma', 'Prognosis', 'Research'