Next-generation sequencing reveals high intra-individual molecular concordance between primary head and neck tumors and matched local or distant recurrences

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Background: Recurrent or metastatic head and neck squamous cell carcinoma (HNSCC) is an incurable disease and is responsible for 4,000 deaths every year in France. Targeted therapies improve outcomes in several types of cancer and lead to development of the prescription of drugs according to the molecular features of the tumor, called “precision medicine”. The need to perform recent biopsy to perform those molecular analyses is a critical restriction and limits inclusion of patients into precision medicine programs.

Methods: To compare molecular profiles of primitive tumor and recurrence, we analyzed molecular alterations in primary HNSCC and paired local or distant recurrences from 31 patients using targeted next-generation sequencing (MiniSeq, Illumina), of 42 “cancer-associated” genes (Solid Tumor Solution, Sophia Genetics).

Results: Primary tumors and recurrences harbored alterations common in HNSCC. The most frequent were TP53 mutations (76%), CDKN2A mutations (21%), PIK3CA mutations (16%), MET mutations (16%) and EGFR amplifications (8%). Twenty-six patients (83.9%) showed concordant molecular profiles between primary tumors and matched local or distant recurrences. Fifteen patients harbored alterations with potential therapeutic implications (mostly tyrosine kinase receptor genes or oncoproteins activation) according to local Molecular Tumor Board criteria. Twenty-seven out of the 31 patients (87.1%) had concordant molecular profile between primary and recurrence when considering only these “druggable” alterations.

Conclusions: HNSCC primary tumors and metastases exhibit an intra-individual high genomic concordance. As these patients had limited therapeutic options, inclusion in precision medicine programs represents an important opportunity and should be allowed regardless of the origin of the sample, the primary tumor or its recurrence.

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