

Tilmelding af Foredrag

Foredragets titel

Genomic alterations in the stepwise progression from normal mucosa to metastasizing oral squamous cell carcinoma

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Uddannelsesniveau

Læge

Introduktion

The aim of this study was to investigate the genomic changes that occur in the development from dysplasia, to cancer, and further to regional metastases, in patients with oral cavity squamous cell carcinoma (OSCC).

Materiale/metode

We included OSCC patients with lymph node metastases at diagnosis, treated with primary surgery at Rigshospitalet, University of Copenhagen in the period from 2007 to 2014. The resected tumor specimens were evaluated by a pathologist, who marked areas of morphologically normal tissue and dysplasia surrounding the cancer, two areas from the cancer tissue, and one area within the lymph node metastases. From these areas a punch biopsy was taken, and DNA was extracted and sequenced using Illumina's TSO500 cancer panel.

Resultater

From 51 OSCC patients, 205 samples were included, comprising a wide variety of genomic alterations. Substantial intratumor heterogeneity was found as well. The most common mutated gene was TP53, mutated in 65% of all samples. Only two patients had no TP53 mutation in any samples. We found that morphologically normal appearing mucosa as well as surrounding dysplasia also contained malignant mutations, supporting the theory of field cancerization. There was a significant lower average tumor mutational burden (TMB) in the lymph node metastases compared to the primary tumors. This supports the theory of clonal selection.

Diskussion

We found substantial inter- and intratumor genomic heterogeneity. Mutation of TP53 was the most common and was present in all but two patients. Our data strongly supports the theory of clonal selection and the theory of field cancerization.

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