TARGETED NEXT-GENERATION SEQUENCING OF ORAL CAVITY CARCINOMAS IN AN AUSTRALIAN COHORT

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Introduction

Oral squamous carcinomas (OSCC) are a heterogeneous group of malignancies with a diverse range of presentations. Clinical subgroups have been delineated and are of significant interest, particularly the non-smoking non-drinking (NSND) group and human papilloma virus (HPV) related tumours. Genomic characterisation of these clinical subgroups utilising next-generation sequencing techniques will help in understanding the genetic progression of oral carcinogenesis and guide us towards novel rational approaches for the treatment of this disease.

Methods

Two separate groups of patients were recruited from the Royal Melbourne Hospital: suitable patients were identified retrospectively from the BioGrid database, and prospectively from new cancer patients presenting at the RMH.

A 500kbp targeted custom capture library was designed based on an integrative analysis of the Cancer Genome Atlas (TCGA) database. Sequencing was performed on archival fresh frozen paraffin embedded (FFPE) tissue for the retrospective group, and on fresh frozen tumour and blood for the prospective group. Bioinformatic analyses were carried out to reduce paraffin related artefact and identify somatic mutations.

Results

60 patients were recruited to the retrospective group, and 70 patients to the prospective group. Mutation rates were very similar across both groups with a high number of mutations in the tumour suppressors TP53 and CDKN2A. A high rate of mutations were also seen in NOTCH pathway members.

Conclusions

We have sequenced a large number of tumours from patients presenting to our centre. Reduction of paraffin-induced sequence artefact was achieved and similar mutation rates were seen across both patient cohorts. Findings in specific clinical subgroups will be discussed further at the meeting.