

GENETIC CHANGES IN SPORADIC KERATOCYSTIC ODONTOGENIC TUMOUR (ODONTOGENIC KERATOCYST)

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INTRODUCTION: Little is known about the genetic background of keratocystic odontogenic tumour (KCOT, odontogenic keratocyst). Our aim was to characterize genomic aberrations in sporadic KCOT using cDNA-expression arrays and array-comparative genomic hybridization.

METHODS: For cDNA-expression arrays, 10 KCOT specimens and 20 fetal tooth germs were studied. Quantitative real-time reverse transcription-polymerase chain reaction and immunohisto-chemical studies were also undertaken.

RESULTS: Several genes were over-expressed in 12q13 including cytokeratin 6B (KRT6B) (~10 fold), epidermal growth factor receptor ERBB3 (~4.7 fold) and glioma-associated oncogene homologue 1 (GLI1) (~5–12-fold). One amplicon (~0.7 Mbp), covering several genes involved in regulation of cell growth was found in 12q13.2. Deletions were found in 3q13.1, 5p14.3 and 7q31.3 including cell adhesion-related genes cadherin 18 (CDH18) and leukocyte cell adhesion molecule (ALCAM, MEMD).

DISCUSSION & CONCLUSIONS: Over-expressed and amplified genes in 12q13, also reported in several other tumours and cell lines, may contribute to the persistent growth characteristics of KCOT.

KEY WORDS: genomic aberrations; gene expression; keratocystic odontogenic tumour; odontogenic keratocyst.

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