Transcriptional activity of human epidermal growth factor receptor family and angiogenesis effectors in locoregionally recurrent head and neck squamous cell carcinoma and correlation with patient outcome.

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Source

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Abstract

Locoregional recurrence is the most common failure pattern in patients with head and neck squamous cell carcinoma (HNSCC). We retrospectively identified 41 HNSCC patients with locoregional relapse and used kinetic reverse transcription-polymerase chain reaction (kRT-PCR) in order to study fresh-frozen tumour messenger RNA (mRNA) levels of the Human Epidermal growth factor family members HER1-4, the Vascular Endothelial Growth Factors (VEGFs) A, B, C, D, and their receptors VEGFR1, 2, 3. High VEGF-C and VEGFR3 tumour mRNA expression correlated with relapse beyond the primary locus (neck nodes or soft tissues, $P < .05$). Tumours with regional nodal involvement at diagnosis more often exhibited high transcriptional activity of VEGFR1 and VEGFR3 at the time of relapse ($P < .05$). At a median follow-up of 52 months from the time of locoregional recurrence, patients with high VEGF-C tumours at relapse had significantly poorer postrelapse progression-free survival (R-PFS, 5 versus 47 months, log-rank $P = .052$) and a trend for inferior postrelapse overall survival (R-OS, 22 versus 44 months, log-rank $P = .076$) in comparison to low VEGF-C tumours. Similar association with dismal outcome was seen for its receptor, VEGFR3 tumoural mRNA levels (log-rank $P = .060$). In contrast, suppressed tumour transcription of VEGF-D was associated with poorer post-relapse survival, though statistical significance was not reached. Active transcription of the VEGF-C/VEGFR3 axis in recurrent HNSCC is associated with failure at neck soft tissues/lymph nodes and inferior survival post-relapse.