

Comparative prognostic value of epidermal growth factor quantitative protein expression compared with FISH for head and neck squamous cell carcinoma.

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Source

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Abstract

PURPOSE:

Epidermal growth factor receptor (EGFR) overexpression correlates with recurrence and with treatment resistance in head and neck squamous cell carcinoma (HNSCC). The aim of this study was to evaluate the relationship of EGFR gene copy number utilizing FISH and protein expression with automated quantitative analysis (AQUA) and to correlate those with patient outcome.

EXPERIMENTAL DESIGN:

A tissue microarray composed of 102 HNSCC treated with (chemo)radiation was constructed and analyzed for EGFR copy number by FISH (Vysis; Abbott Laboratories) and EGFR protein expression using AQUA analysis of EGFR staining scored on a scale of 0 to 255. We evaluated associations of EGFR FISH status and AQUA score with clinicopathologic parameters and survival prognosis.

RESULTS:

Eleven (17.2%) of 64 tumors with FISH results showed EGFR high polysomy and/or gene amplification (FISH positive). Protein levels assessed by AQUA in FISH-positive cases were significantly higher ($P = 0.04$) than in FISH-negative cases. Using the continuous AQUA scores for EGFR expression, AQUA and FISH showed significant agreement (Pearson's $\rho = 0.353$, $P = 0.04$). Patients with high tumor EGFR protein expression had inferior 5-year overall survival (27.7%) compared with those with low tumor EGFR expression (54%; $P = 0.029$). There was no significant association between EGFR FISH status and overall survival ($P = 0.201$). In the multivariate model, high tumor EGFR protein expression status remained an independent prognostic factor for overall survival ($P = 0.047$).

CONCLUSIONS:

EGFR protein content correlates with gene copy number if protein content is quantitated and automatically analyzed, as with AQUA. EGFR protein levels assessed by AQUA strongly predict for patient outcome in HNSCC, whereas EGFR FISH status does not provide prognostic information.