Identification and validation of gene expression models that predict clinical outcome in patients with early-stage laryngeal cancer.

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Source

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Abstract

BACKGROUND:

Despite improvement in therapeutic techniques, patients with early-stage laryngeal cancer still recur after treatment. Gene expression prognostic models could suggest which of these patients would be more appropriate for testing adjuvant strategies.

MATERIALS AND METHODS:

Expression profiling using whole-genome DASL arrays was carried out on 56 formalin-fixed paraffin-embedded tumor samples of patients with early-stage laryngeal cancer. We split the samples into a training and a validation set. Using the supervised principal components survival analysis in the first cohort, we identified gene expression profiles that predict the risk of recurrence. These profiles were then validated in an independent cohort.

RESULTS:

Gene models comprising different number of genes identified a subgroup of patients who were at high risk of recurrence. Of these, the best prognostic model distinguished between a high- and a low-risk group (log-rank P<0.005). The prognostic value of this model was reproduced in the validation cohort (median disease-free survival: 38 versus 161 months, log-rank P=0.018), hazard ratio=5.19 (95% confidence interval 1.14-23.57, P<0.05).

CONCLUSIONS:

We have identified gene expression prognostic models that can refine the estimation of a patient's risk of recurrence. These findings, if further validated, should aid in patient stratification for testing adjuvant treatment strategies.