**Cyclin D1 Gene Amplification in Human Laryngeal Squamous Cell Carcinomas: Prognostic Significance and Clinical Implications**

Alfonso Bellacosa, Giovanni Almadori, Salvatore Cavallo, Gabriella Cadoni, Jacopo Galli, Gabriella Ferrandina, Giovanni Scambia, and Giovanni Neri

Institutes of Medical Genetics [A. B., S. C., G. N.], Otorhinolaryngology [G. A., G. C., J. G.], and Obstetrics and Gynecology [G. F., G. S.], Catholic University Medical School, Largo F. Vito 1, 00168 Rome, Italy

**ABSTRACT**

The cyclin D1 (CCND1) gene is amplified, rearranged, and overexpressed frequently in human cancer, including squamous cell carcinoma. The gene dosage of CCND1 was examined in 51 primary laryngeal squamous cell carcinomas, and amplification of the gene was found in 9 (17.6%) cases. CCND1 amplification did not correlate with age, tumor localization and extension, cervical lymph node involvement, histopathological grading, and epidermal growth factor receptor levels. In a univariate analysis, CCND1 amplification, tumor extension, lymph node involvement, poor histological differentiation, and high epidermal growth factor receptor levels were correlated significantly with shorter overall survival. In a median follow-up period of 29 months, the overall survival rate was 71.4% for patients affected with tumors displaying a normal CCND1 dosage and only 25.0% for patients affected with tumors carrying amplified CCND1 (P = 0.0288). In a multivariate analysis, only CCND1 and tumor extension retained statistically significant prognostic values (P = 0.037 and 0.041, respectively).

This is the first report in which CCND1 amplification is identified as a significant independent prognostic factor in laryngeal carcinoma. Evaluation of CCND1 amplification could be applicable to the clinical management of laryngeal cancer, allowing identification of patients with poor prognoses.

**INTRODUCTION**

Laryngeal SCC accounts for approximately 2% of all cancers in the United States and Southern Europe, is more prevalent in males than in females, and usually develops in the sixth and seventh decades of life (1).

The predicted mortality is 32%, with an overall survival rate of approximately 70% at 5 years (2). The TNM classification is a reliable prognostic determinant of survival. However, prognosis is far from being determined accurately in laryngeal cancer, and it is influenced by many host and tumor factors (3, 4). In recent years, considerable efforts have been made in the identification of biological factors that could have prognostic value, such as DNA index and ploidy, ras and p53 mutations, and EGFR expression or amplification (5–9).

Amplification of the chromosome 11q13 region is a frequent genetic alteration in SCCs of several tissues (10), including esophagus (11, 12) and lung (13). This region is also amplified in breast (14–16), bladder (17), and liver (18) carcinomas and rearranged in parathyroid adenomas at the PRAD1 locus (19, 20) and in centrocytic lymphomas at the BCL1 locus (21). The 11q13 region harbors several genes that could play a role in tumorigenesis, including the proto-oncogenes INT2 and HST1 (10) and EMS1, which encodes a putative src kinase substrate (22). However, the single most important molecular target and driving force of amplifications and rearrangements of this region seems to be the CCND1 gene, which is overexpressed frequently and consistently following those genetic alterations (15, 19, 23–25). CCND1 corresponds to the PRAD1 gene and is the most likely candidate for the BCL1 proto-oncogene (19–21). Cyclin D1 is known to regulate cell cycle progression at the G1-S checkpoint, and its overexpression, as a result of amplifications and rearrangements, is expected to drive the cells through the G1-S transition, thus contributing to oncogenesis (26).

CCND1 and 11q13 amplification also has been detected in laryngeal SCC (27–30), but a precise estimate of the frequency of this phenomenon is lacking. In fact, amplification has been evaluated usually in the context of the head and neck tumor group, which includes carcinomas of the mouth, tonsils, tongue, pharynx, larynx, salivary glands, and upper esophagus. Only a single study has investigated the amplification of the CCND1 gene in a collection of laryngeal tumors (25). In this study, amplification and overexpression correlated with advanced-stage laryngeal carcinomas, suggesting that CCND1 gene alterations might identify aggressive tumors.

---

1 The abbreviations used are: SCC, squamous cell carcinoma; CCND1, cyclin D1 gene; EGFR, epidermal growth factor receptor; CDK, cyclin-dependent kinase.

2 To whom requests for reprints should be addressed, at Institute of Medical Genetics, Catholic University Medical School, Largo F. Vito 1, 00168 Rome, Italy. Phone: +39-6-30154927/4606; Fax: +39-6-3050031.

3 The predicted mortality is 32%, with an overall survival rate of approximately 70% at 5 years (2). The TNM classification is a reliable prognostic determinant of survival. However, prognosis is far from being determined accurately in laryngeal cancer, and it is influenced by many host and tumor factors (3, 4). In recent years, considerable efforts have been made in the identification of biological factors that could have prognostic value, such as DNA index and ploidy, ras and p53 mutations, and EGFR expression or amplification (5–9).

**INTRODUCTION**

Laryngeal SCC accounts for approximately 2% of all cancers in the United States and Southern Europe, is more prevalent in males than in females, and usually develops in the sixth and seventh decades of life (1).

The predicted mortality is 32%, with an overall survival rate of approximately 70% at 5 years (2). The TNM classification is a reliable prognostic determinant of survival. However, prognosis is far from being determined accurately in laryngeal cancer, and it is influenced by many host and tumor factors (3, 4). In recent years, considerable efforts have been made in the identification of biological factors that could have prognostic value, such as DNA index and ploidy, ras and p53 mutations, and EGFR expression or amplification (5–9).

Amplification of the chromosome 11q13 region is a frequent genetic alteration in SCCs of several tissues (10), including esophagus (11, 12) and lung (13). This region is also amplified in breast (14–16), bladder (17), and liver (18) carcinomas and rearranged in parathyroid adenomas at the PRAD1 locus (19, 20) and in centrocytic lymphomas at the BCL1 locus (21). The 11q13 region harbors several genes that could play a role in tumorigenesis, including the proto-oncogenes INT2 and HST1 (10) and EMS1, which encodes a putative src kinase substrate (22). However, the single most important molecular target and driving force of amplifications and rearrangements of this region seems to be the CCND1 gene, which is overexpressed frequently and consistently following those genetic alterations (15, 19, 23–25). CCND1 corresponds to the PRAD1 gene and is the most likely candidate for the BCL1 proto-oncogene (19–21). Cyclin D1 is known to regulate cell cycle progression at the G1-S checkpoint, and its overexpression, as a result of amplifications and rearrangements, is expected to drive the cells through the G1-S transition, thus contributing to oncogenesis (26).

CCND1 and 11q13 amplification also has been detected in laryngeal SCC (27–30), but a precise estimate of the frequency of this phenomenon is lacking. In fact, amplification has been evaluated usually in the context of the head and neck tumor group, which includes carcinomas of the mouth, tonsils, tongue, pharynx, larynx, salivary glands, and upper esophagus. Only a single study has investigated the amplification of the CCND1 gene in a collection of laryngeal tumors (25). In this study, amplification and overexpression correlated with advanced-stage laryngeal carcinomas, suggesting that CCND1 gene alterations might identify aggressive tumors.
In the present study, we analyzed CCND1 gene amplification in a large, single-institution, homogeneous series of laryngeal SCC to evaluate its correlation with clinical outcome. CCND1 gene amplification was found to be a significant independent prognostic indicator in laryngeal SCC.

MATERIALS AND METHODS

Patients and Tumor Specimens. Laryngeal carcinoma specimens were obtained during 1988–1993 from patients undergoing surgery at the “A. Gemelli” Catholic University Hospital of Rome. In many cases, normal laryngeal mucosa adjacent to the tumor was also removed during surgery. Tissue samples were snap-frozen in liquid nitrogen and stored at −80°C until further processing. We evaluated a total of 51 primary neoplastic specimens from 51 patients (median age, 64; range, 37–85 years), 48 males and 3 females. According to location, tumors were defined as supraglottic, glottic, or transglottic (when extension of the tumor did not allow identification of the original site), and they were staged following the International Union Against Cancer TNM classification (31). All tumors were epidermoid SCC, and they were graded as well (G1), moderately (G2), or poorly (G3) differentiated. Clinicopathological characteristics of the patients are summarized in Table 2.

Surgical treatment was aimed at the complete removal of the tumoral mass and, therefore, differed in different patients according to the extension of the tumor. Radical laryngectomy was performed on 27 patients. Twenty-four patients underwent conservative surgery, i.e., cordectomy (n = 3), horizontal supraglottic laryngectomy (n = 18), and hemilaryngectomy (n = 3). In all cases, the margins of resection were judged to be free of disease both macroscopically and microscopically. At the time of surgery, 12 patients underwent neck dissection due to lymph node involvement. Eight of 12 lymphadenectomies revealed nonspecific reactive lymphadenitis, whereas the remaining 4 cases displayed infiltration of cancer cells. Two of these 4 cases had evidence of extracapsular spread, one of which was positive for CCND1 amplification. The number of involved lymph nodes ranged from two to five. Stage IV patients with positive lymph nodes (5 patients) received postoperative radiotherapy, following the standard protocol of treatment at our institution. Of the patients receiving radiotherapy, one had CCND1 amplification. None of the patients received chemotherapy.

Survival analysis was conducted on 50 patients. (One patient of the series, carrying an amplified CCND1, died of intercurrent disease and was not enrolled in the analysis.) The median follow-up period was 29 (range, 2–60) months; for those still alive, 37.5 months. The probe used for the Southern blot analysis of CCND1 amplification was the 1.4-kb EcoRI insert of the plasmid pPL-8, containing the partial cDNA of the PRAD-1/CCND1 gene (kindly provided by Dr. Andrew Arnold, Massachusetts General Hospital, Boston, MA); Ref. 20].

EGFR Assay. EGFR was determined by a radioreceptor method, as described previously (8). Briefly, tumor specimens were homogenized in TENG buffer (25 mM Tris-HCl, 1.5 mM EDTA, 5 mM Na2SO4, and 20% glycerol) supplemented with 0.1% monothioglycerol. Following an initial centrifugation at 7,000 × g for 20 min, the supernatant was spun at 105,000 × g for 75 min. The resulting membrane pellet was resuspended in TENG buffer containing 10 mM MgCl2, and 100-μl aliquots (300–500 μg protein) were incubated with 125I-labeled EGF (2.6 nm) in the presence or absence of unlabeled EGF (1 μM) at room temperature for 18 h in a 400-μl volume. Following a centrifugation at 2,000 × g for 20 min, the pellets were counted in a gamma counter. An EGFR level of 16 fmol/mg protein was shown to be the best discriminating value for prognostic assessment and was chosen as the cutoff value to define EGFR status.

Statistical Analysis. The χ² and two-tailed Fisher’s exact tests were used to evaluate the correlations between amplification of CCND1 and clinicopathological parameters. The distribution of EGFR levels according to CCND1 status was analyzed by the Wilcoxon rank-sum test. For disease-free and overall survival analysis, all medians and life tables were computed using the product-limit estimate by Kaplan and Meier, and the curves were examined by log-rank test (37, 38). Multivariate analysis was performed with BMDP statistical software.

A. Bellacosa and P. N. Tsichlis, unpublished data.
observed a trend toward positive correlations between amplification of *CCND1* and high histological grade (*G*3; *P* = 0.10) and high EGFR levels (*P* = 0.09). The latter potential correlation was explored further by evaluating the distribution of EGFR levels according to *CCND1* status. The results, although not statistically significant, confirmed that EGFR levels tend to be higher in tumors with *CCND1* amplification than in tumors with normal *CCND1* (median, 22.58; range, 4.00-49.90 fmol/mg protein; versus median, 6.06; range, 0-169.90 fmol/mg protein; *P* = 0.0962).

It should be noted that, although *CCND1* amplification and TNM classification both correlated with clinical outcome (see below), they did not correlate with each other in a statistically significant manner.

**CCND1 Amplification and Risk of Progression.** To determine whether the *CCND1* status is associated with unfavorable clinical outcome, the disease-free and overall survival of patients with or without *CCND1* amplification were examined. Disease-free survival was defined as the time interval from surgery to local recurrence or cervical lymph node involvement. Complete follow-up data were available for 50 patients. Higher survival rates were found in patients with the normal *CCND1* gene dosage (30 (71.4%) of 42 surviving) than in patients with amplification [2 (25.0%) of 8 alive]. Analysis of the overall survival curves revealed that *CCND1* amplification is associated significantly with a shorter overall survival (*P* = 0.0288). The association with disease-free survival, although showing the same trend, was not statistically significant (*P* = 0.12; Fig. 2). The disease-free survival rate was 59.5% for patients with the normal *CCND1* copy number and 25% for patients with amplification.

In the univariate analysis, shorter overall survival was associated significantly not only with *CCND1* amplification but also with T3-T4 tumors, lymph node involvement, poor histological differentiation, and high EGFR levels. However, when all the above parameters were submitted to multivariate analysis using a backward stepwise procedure, only *CCND1* gene amplification and tumor classification retained statistically significant prognostic values (*P* = 0.037 and 0.041, respectively; Table 3).

**DISCUSSION**

*CCND1* and 11q13 amplification has been detected previously in laryngeal SCC, yet the analysis has been confined to cell lines or small series of primary laryngeal neoplasms, evaluated in the general context of head and neck carcinomas (27-30). In the present study, evaluation of the *CCND1* copy number was performed on a large series of primary laryngeal carcinomas, and the frequency of amplification was estimated around 17.6%. In a recent survey, which also examined a large number of primary laryngeal carcinomas (*n* = 46), the reported frequency of *CCND1* amplification was 37% (25). It is conceivable that this discrepancy might reflect differences in the populations studied. We also used more stringent criteria to assess gene amplification. In fact, by using a control probe mapping on chromosome 11 (*ETS1*), polysomy of this chromosome was not scored as amplification. Chromosome 11 polysomy has been reported in head and neck carcinomas (40) and was detected,

**RESULTS**

**CCND1 Is Amplified in Laryngeal Carcinomas.** In Southern blots of EcoRI-digested tumor DNAs, three bands of 4.0, 2.2, and 2.0 kb were detected by the *CCND1* probe. The control *ETS1* probe hybridized to a 6.4-kb fragment, whereas *BCL3* detected bands of approximately 8 and 4.5 kb. Amplification of *CCND1* was found in 9 (17.6%) of 51 cases of laryngeal SCC (Fig. 1). Densitometric analysis, corrected for the level of the internal control *ETS1* band, showed that amplification of *CCND1* ranged from 3- to 18-fold relative to placenta or normal laryngeal mucosa DNA. When using the *BCL3* densitometric signal as a control, two additional specimens displayed an increased *CCND1* signal, which was interpreted as polysomy of the whole chromosome 11 and was not scored as actual amplification. No rearrangements were detected in any tumor specimen. The clinicopathological characteristics of the tumors with *CCND1* amplification are shown in Table 1.

**Correlations with Clinicopathological Parameters.** The correlations between amplification of *CCND1* and clinicopathological parameters are summarized in Table 2. The following parameters were evaluated: age at diagnosis; TNM T and N classification; stage and grade; tumor site; and EGFR levels. We
Table 1  Clinicopathological characteristics of laryngeal carcinomas with CCND1 amplification

<table>
<thead>
<tr>
<th>Patient</th>
<th>Age at diagnosis (yr)</th>
<th>Sex</th>
<th>Site</th>
<th>TNM</th>
<th>Stage</th>
<th>Grade</th>
<th>EGFR (fmol/mg protein)</th>
<th>CCND1 amplification (fold)</th>
</tr>
</thead>
<tbody>
<tr>
<td>7010</td>
<td>61</td>
<td>Male</td>
<td>Supraglottic</td>
<td>TaN_M0</td>
<td>IV</td>
<td>2</td>
<td>26.48</td>
<td>4</td>
</tr>
<tr>
<td>7016</td>
<td>65</td>
<td>Male</td>
<td>Supraglottic</td>
<td>TaN_M0</td>
<td>IV</td>
<td>3</td>
<td>18.68</td>
<td>3</td>
</tr>
<tr>
<td>7032</td>
<td>58</td>
<td>Male</td>
<td>Transglottic</td>
<td>TaN_M0</td>
<td>IV</td>
<td>3</td>
<td>31.39</td>
<td>7</td>
</tr>
<tr>
<td>7045</td>
<td>59</td>
<td>Male</td>
<td>Supraglottic</td>
<td>TaN_M0</td>
<td>I</td>
<td>3</td>
<td>NA*</td>
<td>5</td>
</tr>
<tr>
<td>7049</td>
<td>55</td>
<td>Male</td>
<td>Transglottic</td>
<td>TaN_M0</td>
<td>II</td>
<td>2</td>
<td>5.00</td>
<td>18</td>
</tr>
<tr>
<td>7057</td>
<td>49</td>
<td>Male</td>
<td>Supraglottic</td>
<td>TaN_M0</td>
<td>II</td>
<td>3</td>
<td>4.02</td>
<td>3.5</td>
</tr>
<tr>
<td>7068</td>
<td>56</td>
<td>Male</td>
<td>Transglottic</td>
<td>TaN_M0</td>
<td>II</td>
<td>2</td>
<td>9.52</td>
<td>17</td>
</tr>
<tr>
<td>7084</td>
<td>71</td>
<td>Female</td>
<td>Transglottic</td>
<td>TaN_M0</td>
<td>III</td>
<td>2</td>
<td>49.90</td>
<td>4.5</td>
</tr>
<tr>
<td>7091</td>
<td>72</td>
<td>Male</td>
<td>Transglottic</td>
<td>TaN_M0</td>
<td>IV</td>
<td>3</td>
<td>35.40</td>
<td>6</td>
</tr>
</tbody>
</table>

* NA, not available.

Indeed, in two specimens when using BCL3 as a control probe. Taken together, both studies are consistent with the hypothesis that CCND1 amplification plays a role in the pathogenesis of laryngeal SCC.

This conclusion is supported further by the novel finding presented here that CCND1 status is a prognostic indicator for laryngeal carcinomas, independent of the generally accepted survival predictor TNM. Previous studies had suggested a link between CCND1 and 11q13 amplification and advanced, poorly differentiated head and neck or laryngeal carcinomas (25, 27–30). However, the present report represents the first instance in which amplification of the CCND1 gene is associated significantly with a subgroup of laryngeal tumors characterized by

Fig. 2  A, overall survival rates according to CCND1 status. a, normal CCND1 copy number; patients entered, 42; died, 12; b, amplified CCND1: patients entered, 8; died, 6. B, disease-free survival rates according to CCND1 status. a, normal CCND1 copy number; patients entered, 42; relapsed, 17; b, amplified CCND1 patients entered, 8; relapsed, 6.
poor prognosis, much like breast (14–16) and esophageal (11, 12) carcinomas.

The mechanisms by which CCND1 amplification might contribute to SCC pathogenesis need further investigation. In recent years, substantial experimental evidence has accumulated, linking deregulation of cell cycle progression to malignant transformation. The progression through the different phases of the cell cycle is regulated at several checkpoints, and the late G1 checkpoint is altered frequently in tumor cells (26). This checkpoint is regulated by D-type cyclins (D1, D2, and D3), which bind to and activate CDK4 (and, to lesser degree, CDK5 and CDK6). The D-type cyclin-CDK complex is likely responsible for the phosphorylation of the retinoblastoma tumor suppressor protein, which in turn allows the cell to enter S-phase (26). It is possible that tumors carrying an amplified CCND1 gene have a high proliferation rate (26), which also could account for the clinical aggressiveness.

Recently, in an in vitro model, forced cyclin D1 expression has been shown to inhibit myoblast differentiation (41). It would be important to determine whether cyclin D1 overexpression also can inhibit differentiation of SCC cells. Such an effect could account for the tendency of association between CCND1 amplification and poor histological differentiation observed in this study.

Expression of the short-lived, D-type cyclins is increased by growth factors, and it has been suggested that their function is to sense growth stimuli, thus integrating external signals in the cell cycle machinery (42). Overexpression of cyclin D1, which follows CCND1 amplification in laryngeal cancer consistently (25), is expected to relieve or decrease the dependence of the cell from growth factor stimulation. Remarkably, the two tumors in our series with the highest CCND1 copy numbers had very low levels of EGFR. In those other cases with a lesser degree of amplification, increased levels of EGFR could be interpreted as a synergistic mechanism to stimulate cell proliferation. This would explain the trend in the association between CCND1 amplification and increased EGFR levels. Be that as it may, the interactions between EGF and EGFR and cyclin D1 are likely to be complex and to require further investigation.

The finding that the G1 checkpoint is altered critically in a large fraction of laryngeal SCCs might indicate that some tumors with a normal CCND1 gene could have a functionally equivalent defect in inhibitors of the cyclin D1-CDK complex, such as p16. Interestingly, mutations of the p16 gene and loss of heterozygosity at its locus on chromosome 9p21 have been detected frequently in head and neck SCC (43). Therefore, it will be of interest to assess the prognostic significance of p16 and 9p21 alterations alone or with respect to the CCND1 status.

In previous studies, we showed that high EGFR levels are an independent prognostic variable in predicting disease-free survival (8). The possible correlation between CCND1 and EGFR might explain why, in the present analysis, EGFR levels did not retain independent prognostic significance when challenged with the CCND1 copy number in the multivariate analysis.

Our study suggests that evaluation of CCND1 amplification and/or overexpression might integrate the established prognostic indicators for laryngeal SCC, helping in the identification of patients with poor prognoses, who could be enrolled in protocols including more aggressive surgery and adjuvant radiotherapy or chemotherapy. For this purpose, a rapid and reliable assay, based, for instance, on immunohistochemistry or quantitative PCR, would be ideally suited.

ACKNOWLEDGMENTS

We thank Dr. Andrew Arnold for providing the PRAD1/CCND1 probe. We are indebted to Drs. Maurizio Genuardi, Stefan Hohaus, and Maria Teresa Voso for helpful comments and critical reading of the manuscript.

REFERENCES

Cyclin D1 gene amplification in human laryngeal squamous cell carcinomas: prognostic significance and clinical implications.

A Bellacosa, G Almadori, S Cavallo, et al.