Chapter 4

Amplicon mapping and expression profiling identifies the Fas-Associated Death-Domain gene (FADD) as a new driver in the 11q13.3 amplicon in laryngeal/pharyngeal cancer

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ABSTRACT

Purpose: Amplification of the 11q13 region is a frequent event in human cancer. The highest incidence (36%) is found in head and neck squamous cell carcinomas. Recently, we reported that the amplicon size in 30 laryngeal and pharyngeal carcinomas with 11q13 amplification is determined by unique genomic structures, resulting in the amplification of a set of genes rather than a single gene.

Experimental Design: To investigate which gene(s) drive the 11q13 amplicon, we determined the smallest region of overlap with amplification and the expression levels of all genes within this amplicon.

Results: Using array CGH analysis we detected a region of -1.7 megabases containing 13 amplified genes in more than 25 of the 29 carcinomas. Quantitative RT–PCR revealed that overexpression of 8 potential driver genes including, cyclin D1, cortactin and FADD, correlated significantly with DNA amplification. FADD protein levels correlated well with DNA amplification, implicating that FADD is also a candidate driver gene in the 11q13 amplicon. Analysis of 167 laryngeal carcinomas showed that increased expression of FADD (p=0.007) and Ser194–phosphorylated FADD (p=0.011) was associated with a worse disease specific survival. FADD was recently reported to be involved in cell cycle regulation, and cancer cells expressing high levels of the Ser194–phosphorylated isoform of FADD proved to be more sensitive to taxol–induced cell cycle arrest.

Conclusion: Because the frequent amplification of the 11q13 region and concomitant overexpression of FADD in head and neck squamous cell carcinomas, we hypothesize that FADD is a marker to select patients that might benefit from taxol–based chemo–radiotherapy.
INTRODUCTION

Squamous cell carcinoma of the head and neck (HNSCC) is the fifth most common cancer with a worldwide incidence of approximately 780000 new cases per year. Traditionally, depending on tumor stage, patients are treated with surgery, radiotherapy alone or a combination of both. In early to intermediate stages of laryngeal carcinoma, radiotherapy is generally preferred because of better organ preservation and high rates of locoregional tumor control. However, in the more advanced carcinomas radiotherapy fails in local control in up to 50% of patients [309]. A recent clinical trial showed that concomitant chemo – and radiotherapy leads to improved locoregional control and laryngeal preservation in locally advanced laryngeal cancer as compared to conventional radiotherapy [310,311]. However, combining chemo – with radiotherapy also has unfavorable effects since it results in a significant increase in toxicity. Although various clinico–pathological parameters have been validated to classify patients according to their likelihood of responding to chemo–radiation, they are still generally of low predictive value [309]. Therefore there is a need for (molecular) markers to predict therapeutic outcome.

Chromosomal DNA amplification resulting in an increase in gene copy number, is a well–documented mechanism for cells to increase gene expression and has been used successfully as a prognostic marker for therapeutic outcome [19**,312]. DNA amplification has been reported in various human malignancies and numerous (candidate) oncogenes have been identified. Amplification of chromosome 11q13 is frequently found in human cancer and is most prominent (36%) in HNSCC [107**]. Within different cancer subtypes this amplification is associated with poor prognosis (reviewed in [107**,313]). These studies include HNSCC reporting on associations with the presence of lymph node metastasis, decreased disease free survival and overall survival [139,142,144**,222]. In the last 15 years many efforts were undertaken to identify the gene that is responsible for the biological behavior of the carcinomas with 11q13 amplification [107**,313]. We and others have identified several candidate genes in the amplified 11q13 region that showed increased expression upon amplification, including CCND1 (cyclin D1) [108**,314], CTTN (EMS1/cortactin) [108], MYEOV [315], ORAOV1 (TAOS1) [174**], EMSY [114] and SHANK2 [173]. CCND1 and CTTN were the genes identified first and studied most extensively, and expression of both genes has been correlated with prognosis (reviewed in [107**,313]). The function of cyclin D1, involved in cell cycle regulation, and cortactin, a regulator for actin–polymerization and cell migration and invasion [316–318], makes them both good candidates of being the drivers of 11q13 amplification. However, the function and role of the other amplified and overexpressed 11q13 genes is presently unknown. Furthermore, most studies fail in comprehensively studying both the copy number and expression of all genes present in the amplicon.

The completion of the human genome sequence has enabled the use of new techniques like array CGH (aCGH) to study genomic aberrations in more detail
The use of fluorescent probes in PCR analysis can be used to study gene expression (qRT–PCR) or microsatellites (QuMA) quantitatively. These techniques have previously been used successfully to identify possible target genes in an ampli-con [171**,319].

We generated a high–resolution aCGH (HR–aCGH) specific for the long arm of chromosome 11 [207]. In the present manuscript, we used these data to determine the Core Region of Amplification (CRA). Secondly, we used qRT–PCR for genes located in the CRA to search for candidate genes with a high relative expression. We found that not a single gene but 8 of the 13 genes in the CRA were overexpressed in at least 25/29 laryngeal/pharyngeal carcinomas with 11q13 amplification. In addition to cyclin D1, cortactin and ORAOV1, this is the first study reporting on FADD as a potential driver in the 11q13 amplicon. The possible role of FADD in the prognosis of laryngeal HNSCC was further studied immunohistochemically using antibodies against FADD protein and the phosphorylated isoform (pFADD) on a large subset of patients.

**MATERIAL AND METHODS**

**Patient material**

For HR–aCGH analysis, we used snap frozen tissues of squamous cell carcinomas from 42 patients. Selected carcinomas with a known 11q13 aberration originated from the larynx (n=19) or pharynx (n=11). The remaining 12 patients without an 11q13 aberration were diagnosed with laryngeal carcinomas. Nineteen patients (obtained from the Instituto Universitario de Oncología del Principado de Asturias, Oviedo, Spain) diagnosed with a laryngeal (L13–23) or pharyngeal (P01–08) carcinoma were previously screened for 11q13 abnormalities using conventional CGH [134*]. Five patients (L09–12 & A11; from the Leiden University Medical Center, Leiden, The Netherlands) were included because of previous 11q13 amplification detected by Southern blotting [143]. Eighteen patients with laryngeal (n=15) or pharyngeal cancer (n=3) were obtained from the University Medical Center Groningen, The Netherlands. These patients were pre–screened with whole genome aCGH [207] for the presence (L03–L07 and P09–P11) or absence (A01–A10) of 11q13 aberrations. For qRT–PCR, only laryngeal carcinomas were included (L01–08 & A01–10). The percentage of tumor cells in the frozen sections used for DNA and RNA isolation was estimated by Hematoxylin–Eosin staining judged by an experienced pathologist (JEvdW). All patient samples were primary tumors that had received no therapy prior to surgery. DNA from these patients was isolated using a standard high salt extraction method.

A total of 167 laryngeal squamous cell carcinomas were used for immunohistochemical analysis, including material from the laryngeal carcinomas that were also used for HR–aCGH analysis (L01–L23). Patient material and available clinico–
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pathological data were obtained from the University Medical Center Groningen (n=56), The Netherlands Cancer Institute – Antoni Van Leeuwenhoek Hospital, Amsterdam, the Netherlands (n=61), the Instituto Universitario de Oncología del Principado de Asturias (n=22) and the Leiden University Medical Center (n=28). Patients were diagnosed at a median age of 61 years (minimum: 34; maximum: 89) with a gender distribution of 135 males (88%) and 19 females (12%). T-status at diagnoses was subdivided in T1 (n=16; 10%), T2 (n=27; 17%), T3 (n=38; 24%) and T4 (n=75; 48%) according to the American Joint Committee on Cancer TNM system. At the time of diagnosis 63 patients (41%) were lymph node positive (N1=23, N2=35, N3=5) and 92 (59%) were lymph node negative (N0). Patients were treated with either primary surgery (n=54), primary radiotherapy (n=24) or a combination of both modalities (n=64). All patient samples were taken prior to treatment.

**HIGH resolution array CGH**

A detailed description of the generation of the high-resolution chromosome 11q13–specific CGH array, and the determination of the size of the amplified region as well as the copy number of the 11q13 region in the same 30 carcinomas used in this study was recently described elsewhere [207].

**Quantitative RT–PCR**

RNA was extracted from snap frozen tumor tissue or cell lines using Trizol® (Invitrogen, Breda, Netherlands) and cDNA was prepared. Quantitative measurements of mRNA content were performed using an ABI PRISM® 7900 HT and the SDS software 2.1 (Applied Biosystems, Nieuwerkerk a/d IJssel, The Netherlands). Taqman primers and probes are listed in Supplementary Table 1. No appropriate primer/probe sets could be designed for the hypothetical genes LOC390218, LOC399921 and LOC653621 (supplementary methods). No RNA–specific primer/probe sets could be designed for MRGPRD and MRGPRF. The relative copy number of each unknown sample (ΔCt) was obtained by normalization to TBP (TATA–box binding protein). Patients were divided into two groups on a gene by gene basis. The first group consisted of patients with 11q13.3 amplification containing the gene of interest and the second group included patients without the particular 11q13.3 amplification as determined by HR–aCGH. For a detailed description of the quantitative RT–PCR, see the supplementary methods online.

**Immunohistochemistry**

Paraffin–embedded, formalin–fixed sections of laryngeal carcinoma were deparaffinized and antigen retrieval was performed by overnight incubation at 80°C in Tris•HCL pH=9.0 (for FADD) or heating in a microwave oven for 15 min in EDTA pH=8.0 (for Ser–194 phosphorylated FADD and cleaved caspase 3). After blocking endogenous peroxidases with 0.3% H2O2, the sections were stained for 1 hour with a mouse IgG antibody against FADD (clone A66–2; 1:100, BD Pharmingen), caspase 3
The commonly amplified 11q13.3 region is 1.7 Mb and contains 13 genes

Using HR–aCGH, we recently showed gain (n=1) and amplifications (n=29) in all carcinomas with previously identified 11q13 amplifications, whereas normal copies were shown in all cases without previously identified 11q13 amplifications [207]. The amplified region in all 29 cases was located within the same 5 Mb region at 11q13.3 (position 67–72 Mbp; NCBI build 35) (summarized in Figure 1A). EMSY (position

Figure 1 (on next page): Detailed location of the core region of amplification at 11q13.3 as identified with 30 patients. Mapping of the amplified 11q13 regions in laryngeal carcinomas using a high–resolution chromosome 11q13 CGH–array as reported previously [207]. (A) For each patient the 2log ratios exceeding 0.5 that were detected by aCGH smooth [106•] are depicted as thick bars; detected gains (ratio below 0.5) are depicted as thin bars; normal ratios and deletions (no gain or amplification) are not included. (B) Detailed view with the core region of amplification shown by a gray background. The gray region illustrates part of the 11q13.3 region amplified in at least 25/29 cases. The highest overlap was found at the dark gray region (amplified in 28/29 cases). (C) The genes localized in the CRA are visualized as bars according to their location in megabases (Mb) on chromosome 11 (NCBI build 35.1).
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75.8 Mbp) recently identified as a BRCA2–inactivating protein which is amplified independent of CCND1 in breast cancer [114], was amplified only in two cases (L19 and L21). The 11q22 gene cluster containing matrix metallopeptidases (MMPs) and the inhibitors of apoptosis cIAP2 and cIAP3 was amplified in 3 of our 29 carcinomas (P10, L19 and L21). This finding is in agreement with a previous reports in esophagus cell lines (4/42 cases) [320].

**Table 1: Genes located in the 11q13.3 amplicon.**

<table>
<thead>
<tr>
<th>Position</th>
<th>Gene</th>
<th>Description</th>
<th>Amplified</th>
<th>Expression</th>
</tr>
</thead>
<tbody>
<tr>
<td>68281657</td>
<td>CPT1A</td>
<td>carnitine palmitoyltransferase 1A (liver)</td>
<td>8/29</td>
<td>0.002</td>
</tr>
<tr>
<td>68415323</td>
<td>MRPL21</td>
<td>mitochondrial ribosomal protein L21</td>
<td>8/29</td>
<td>0.005</td>
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<tr>
<td>68427948</td>
<td>IGHMBP2</td>
<td>immunoglobulin mu binding protein 2</td>
<td>8/29</td>
<td>0.014</td>
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<tr>
<td>68504066</td>
<td>MRGPRD</td>
<td>MAS–related GPR, member D</td>
<td>8/29</td>
<td>nd</td>
</tr>
<tr>
<td>68528443</td>
<td>MRGPRF</td>
<td>MAS–related GPR, member F</td>
<td>18/29</td>
<td>nd</td>
</tr>
<tr>
<td>68572941</td>
<td>TPCN2</td>
<td>two pore segment channel 2</td>
<td>25/29</td>
<td>0.0001</td>
</tr>
<tr>
<td>68818198</td>
<td>MYEOV</td>
<td>myeloma overexpressed gene</td>
<td>26/29</td>
<td>ns</td>
</tr>
<tr>
<td>68827449</td>
<td>LOC390218</td>
<td>similar to interferon–induced transmembrane protein 3 (1–8U); interferon–inducible</td>
<td>27/29</td>
<td>nd</td>
</tr>
<tr>
<td>68949639</td>
<td>LOC399919</td>
<td>hypothetical LOC399919</td>
<td>27/29</td>
<td>nd</td>
</tr>
<tr>
<td>69165054</td>
<td>CCND1</td>
<td>cyclin D1 (PRAD1: parathyroid adenomatosis 1)</td>
<td>27/29</td>
<td>0.0043</td>
</tr>
<tr>
<td>69177025</td>
<td>FLJ42258</td>
<td>hypothetical protein supported by AK124252 , FLJ42258</td>
<td>27/29</td>
<td>0.0019</td>
</tr>
<tr>
<td>69189515</td>
<td>ORAOV1</td>
<td>oral cancer overexpressed 1, TAOS1</td>
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<td>&lt;0.0001</td>
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<td>69222187</td>
<td>FGF19</td>
<td>fibroblast growth factor 19</td>
<td>27/29</td>
<td>0.019</td>
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<tr>
<td>69296978</td>
<td>FGF4</td>
<td>fibroblast growth factor 4</td>
<td>27/29</td>
<td>ns</td>
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<tr>
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<td>fibroblast growth factor 3</td>
<td>27/29</td>
<td>ns</td>
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<td>69579986</td>
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<td>hypothetical LOC399920</td>
<td>27/29</td>
<td>nd</td>
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<tr>
<td>69602294</td>
<td>TMEM16A</td>
<td>transmembrane protein 16A , TAOS2</td>
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<td>ns</td>
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<tr>
<td>69726917</td>
<td>FADD</td>
<td>Fas (TNFRSF6)–associated via death domain</td>
<td>28/29</td>
<td>&lt;0.0001</td>
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<tr>
<td>69794471</td>
<td>PPFIA1</td>
<td>protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interact‑ing protein (liprin), alpha 1</td>
<td>27/29</td>
<td>&lt;0.0001</td>
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<td>CTNN</td>
<td>cortactin , EMS1</td>
<td>27/29</td>
<td>0.013</td>
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<tr>
<td>69991609</td>
<td>SHANK2</td>
<td>SH3 and multiple ankyrin repeat domains 2</td>
<td>25/29</td>
<td>ns</td>
</tr>
<tr>
<td>70221832</td>
<td>LOC399921</td>
<td>similar to SH3 and multiple ankyrin repeat domains protein 2 (Shank2)</td>
<td>16/29</td>
<td>nd</td>
</tr>
</tbody>
</table>

Genes are ordered by their position on the chromosome (start–stop; Build 35). The number of patients with amplification of each gene as determined by array CGH is shown in the column “amplification” (29 cases tested). The column “expression” shows the p–value given by a Mann Whitney U–test comparing the expression level by quantitative RT–PCR of patients with amplification of this gene determined by array CGH compared to those cases without (see Figure 2). The CRA (core of region of amplification) includes all genes.

Within the 5Mb commonly amplified region, we defined a core region of amplification containing amplifications in at least 25 of the 29 cases (gray region in Figure 1B). This region is flanked by genes that are co–amplified at lower frequency (<18/29)
The core region of amplification extends from \textit{TPCN2} to \textit{SHANK2} and is approximately 1.7 Mbp in size (68.5–70.2 Mbp; build 35) containing 13 genes including previously identified 11q13.3 genes: \textit{MYEOV}, \textit{CCND1}, \textit{ORAOV1}, \textit{FGF3}, \textit{FGF4} and \textit{CTTN} [108',314,315,174''] and 3 hypothetical genes (not further analyzed in this study) (Figure 1C). Of these 13 genes, 9 are co–amplified in 27/29 cases (Table 1). The smallest overlapping region of amplification, found in 28 of 29 carcinomas, was restricted to a very small region of -50 kb at position 69.7Mb (NCBI build 35) and only contains a single gene, \textit{FADD} (dark gray region in Figure 1B–C and Table 1).

**DNA amplification results in increased expression of 11q13.3 genes.**

DNA amplification is generally accepted as a mechanism resulting in increased gene expression in drug–resistance or carcinogenesis [19'',254]. Based on these findings, we hypothesized that the key gene in the commonly–amplified 11q13.3 region should not only be amplified most frequently, but also be overexpressed when amplified. To identify the gene that fulfills this criterion the best, we designed a quantitative RT–PCR for all 13 genes (hypothetical genes were excluded) within the 1.7Mb CRA. As a control we also included 3 genes immediately centromeric of the CRA that were co–amplified in only 9/29 cases (\textit{CTP1a}, \textit{MRPL21} and \textit{IGHMBP2}) as well as 5 genes on the telomeric side of the CRA which were not frequently (co–)amplified in our series of carcinomas but have been described to be overexpressed in other studies (\textit{WNT–11}, \textit{UVRAG}, \textit{EMSY}, \textit{GARP} and \textit{PAK1}). From 8 patients (Figure 1: L03–L07 and P09–P11) and 10 without 11q13.3 amplification (A01–A10) total RNA was isolated from snap frozen primary laryngeal carcinomas. In order to calculate the effect of DNA amplification on gene expression of each separate gene, the normalized ΔCt ratios from the 10 patients without amplification were used as a calibrator (set at 1). FGF3 and FGF4 were excluded from further analysis because these genes were expressed in only 2 and none of the 18 carcinomas respectively (not shown). Relative expression analysis per patient revealed that every patient with 11q13.3 amplification showed an increased expression for multiple amplified genes. To identify the gene with the best relation between amplification and expression, we compared the relative expression levels for each gene in the amplified and non–amplified group using a one–tailed Mann Whitney U–test (Figure 2). This analysis revealed significant differences in gene expression for 8 of the 11 genes located in the CRA (Figure 2A and Table 1). From these 8 genes, the most significant relation (p<0.0001) between increased expression and amplification was observed for \textit{TPCN2}, \textit{ORAOV1}, \textit{PPFIA1} and \textit{FADD}. Correlating gene copy number to relative gene expression using linear regression analysis further confirmed this relation for these 4 genes (data not shown). Interestingly, high expression of \textit{CPT1a}, \textit{MRPL21} and \textit{IGHMBP2} was significantly correlated with amplification despite co–amplification in only 8 of the 29 cases (Figure 2B and Table 1). On the other hand, expression of \textit{WNT–11}, \textit{UVRAG}, \textit{EMSY}, \textit{GARP} and \textit{PAK1} (all located far outside the CRA) was not increased in carcinomas with amplification of the CRA (data not shown).
Figure 2: Gene expression of 18 patients with or without amplification. (A) Expression of genes in the CRA. (B) Expression of genes near the CRA. Patients are divided into two groups based on the copy number status of a gene. Gene expression levels for each patient (amplification in diamonds and normal in downward triangles) are shown as the $2^{-\Delta C_t}$ on the y-axis. The median expression is indicated per group by a horizontal line. Statistical analysis was performed with a Mann Whitney U test comparing gene expression for patients with amplification to those without.
**FADD is a new potential driver gene within the 11q13 amplicon in HNSCC**

When combining the findings obtained by HR–aCGH–mapping and expression analysis (summary in Table 1), *FADD* was one of the most likely potential driver genes. Of the 8 genes with a significant correlation between gene amplification and increased expression, FADD is amplified with the highest frequency (in 28 of 29 cases). To determine whether an increase in FADD mRNA due to DNA amplification also results in increased FADD protein expression, we performed immunohistochemistry on formaldehyde–fixed/paraffin–embedded tissues from the same laryngeal carcinomas used for both RT–PCR and HR–aCGH analysis. We used an anti–FADD antibody that was previously used to detect total FADD expression on archive material [32]. Normal epithelium present in most samples showed cytoplasmic staining of the supra–basal layer. In carcinoma cells FADD protein expression was found mainly in the cytoplasm also and very homogeneously distributed in most tumors. In cases with the strongest expression, the FADD protein was not only detected in the cytoplasm but also nuclear staining became apparent. However, the staining intensity was variable between different carcinomas. Using the normal epithelium as a reference for normal expression levels, we categorized all samples into low FADD (FADD− and FADD+) and high FADD (FADD++ and FADD+++) expressing (Figure 3). All 8 cases with high levels of FADD RNA, also showed high FADD protein expression levels, whereas only 2/10 cases with low FADD RNA levels

![Figure 3: Immunohistochemical comparison of FADD and pFADD expression.](image)

Protein expression for FADD and Ser–194 phosphorylated FADD is shown on sequential sections for 4 patients. Patients are ordered from left to right by their relative FADD expression (FADD−, FADD+, FADD++ and FADD+++). FADD− and FADD+ are considered FADD–Low and FADD++ and FADD+++ are considered FADD–High in this study.
had elevated protein expression. Western blot analysis using the same anti–FADD antibody of lysates from frozen tissues of 2 cases with high and 5 with low FADD protein levels showed similar results (data not shown). Since RNA levels correlated significantly with DNA amplification and protein levels were significantly increased at high RNA expression, logistic regression analysis revealed a significant relation between amplification and protein expression (Mann Whitney test: p=0.008). Because FADD is involved in regulation of apoptosis, we stained a subset of carcinomas for cleaved caspase 3 and found no correlation with FADD (not shown).

To investigate whether FADD expression is associated with clinico–pathological features, we determined expression levels in a series of 167 primary advanced stage laryngeal carcinomas of patients who did not receive other therapy prior to surgery. High FADD levels were observed in 62 of 140 tested laryngeal cases (44%). Univariate Cox regression analysis revealed that high FADD levels were related to an increased Hazard Ratio (HR) for worse overall survival (OS) (HR, 1.74; 95% CI, 1.07–2.83; p=0.025) and disease specific survival (DSS) (HR, 3.29; 95% CI, 1.39–7.80; p=0.007) (Figure 4A). Lymph node positivity (HR, 4.45; 95% CI, 1.94–10.20; p<0.001) and radiotherapy treatment (HR, 3.42; 95% CI, 1.24–9.43; p=0.018) also predicted a worse prognosis. A multivariate Cox regression model including FADD, lymph node metastasis, and treatment revealed that high FADD expression was significantly related to a worse prognosis (HR, 4.59; 95% CI, 1.56–13.47; p=0.004). Furthermore, survival curves stratified for FADD expression and lymph node positivity showed that high FADD expression independent of the lymph node status identifies patients with poor prognosis (Figure 4B).

**Figure 4:** Survival analysis related to FADD and pFADD expression. Kaplan–Meier analysis was performed for disease free survival (DSS). (A) Patients are shown as high or low FADD expressing. (B) The survival of lymph node positive (N+) and negative (N–) tumors stratified for FADD expression. (C) Disease specific survival for FADD stratified for Ser–194 phosphorylated FADD expression. The number of patients remaining after 5 years is shown underneath the plots. Significance was calculated using univariate Cox analysis and p–values are displayed on the bottom left of the plot.
Recently, nuclear localization of FADD has been ascribed to FADD phosphorylation at Ser–194 and important for its function in cell cycle control [322]. Because the antibody against FADD used in this study does not discriminate between Ser–194 phosphorylated (pFADD) and non–phosphorylated FADD, we also studied expression of pFADD using a specific anti–pFADD antibody. The immunohistochemical staining of pFADD was more heterogeneously distributed within tumor tissues compared to FADD and predominantly found within the nucleus. High pFADD levels were observed in 61 of 133 cases (46%). Even though, FADD and pFADD stainings were morphologically different, logistic regression revealed a relation between both stainings (RR, 2.26; 95% CI, 1.11–4.59; p=0.025). High expression of pFADD marked a worse OS (HR, 1.62; 95% CI, 0.98–2.68; p=0.061) and DSS (HR, 3.05; 95% CI, 1.29–7.22; p=0.011). When comparing patients with a low FADD, to patients with a high expression of both protein isoforms, survival rates declined even further (Figure 4C).

In summary, we show for the first time that amplification of the 11q13.3 region in head and neck cancer results in increased levels of the phosphorylated and non–phosphorylated FADD protein and that these increased levels are associated with a worse prognosis independent of the presence of lymph node metastasis.

**DISCUSSION**

Chromosomal DNA amplification is a well–documented mechanism for cells to increase gene expression of a driver gene involved in oncogenesis, development or multidrug resistance [19••,254]. In many amplicons the driver gene has yet to be identified. In search for such gene, any driver gene for amplification should fulfill at least two criteria: it should be most frequently amplified and have the most significant correlation between DNA amplification and expression levels. In the last 15 years many efforts were undertaken to identify the driver gene in the 11q13 ampli­con [107••,313] and numerous candidate genes were reported that showed increased expression upon DNA amplification, including CCND1 [108••,314], CTTN [108•], MYEOV [315], ORAOV1 [174••], EMSY [114] and SHANK2 [173•]. In this study we performed a comprehensive analysis of DNA amplification using HR–aCGH of the 11q13 region in combination with quantitative expression levels using qRT–PCR of all genes in the 11q13 region on a large series of laryngeal/pharyngeal carcinomas with 11q13 amplification (n=29). The core region of amplification contains 13 genes. Quantitative RT–PCR analysis revealed that not a single gene, but 8 genes showed overexpression upon DNA amplification (Table 1).

In agreement with our findings, very recently Järvinen and coworkers [208••] proposed that FADD and PPFIA1 are likely candidates implicating that these two genes are located near the core of the amplicon. However, our comprehensive analysis of all genes in the 11q13 region revealed that in addition to FADD and PPFIA1, 6 other likely candidate genes (TPCN2, CCND1, FLJ42258, ORAOV1, FGF19 and
CTTN) within the 11q13.3 CRA that are co-amplified in at least 25/29 cases and show a strong correlation between expression and amplification (Table 1). Of the genes in the 11q13.3 amplicon CCND1 [108,314] and CTTN [316–318,144”] were studied most extensively in the last fifteen years. They have been reported to be the best candidates for driving 11q13.3 amplification, because they are both frequently co-amplified and amplification correlates well with overexpression. Furthermore, the characterization of the cell biological properties of both these genes provided clear evidence for a function in processes related to tumorigenesis such as cell cycle control and cell migration [316,317,323,324]. ORAOV1 was described as a candidate in one study using quantitative copy number analysis (QuMA) with 11q13.3 markers in oral carcinoma cell lines [174”]. Here, we show that also in primary carcinomas of the head and neck ORAOV1 seems a good candidate (Table 1; Figure 2A) although the function of this gene is still unknown. PPFIA1 is involved in regulating the disassembly of focal adhesions [325] but its function has not yet been studied in relation to 11q13.3 amplification. The function of TPCN2, FGF19 and FLJ42258 has not yet been studied in relation to 11q13.3 amplification.

A general increase in the expression of numerous genes within an amplicon, known as a gene dosage effect, has previously been shown by several groups for other amplified chromosomal loci [67”*,319,326,327”]. Recently, we reported on the structural analysis of the amplified 11q13 region in the same 29 laryngeal carcinomas using a high resolution 11q13 specific CGH array [207]. We found that the boundaries of the commonly amplified region were restricted to four segments, coinciding with segmental duplications and syntenic breakpoints. These findings imply that the selection of genes in the 11q13.3 amplicon is determined by the ability to form DNA breaks within specific fragile regions and consequently would result in large amplicons containing multiple genes. Because of coincidental co-amplification, the increased gene dosage will result in increased expression of genes that either act as driver or are not harmful. To identify those overexpressed gene(s) that are relevant to tumor progression, functional analysis of all the 8 genes would be necessary. At present, the cell biological properties of CCND1 [323], CTTN [328] and FADD ([329”] and see below) have been reported. On the other hand, the existence of multiple driver genes cooperating at different time points in carcinogenesis or selected for at different stages of carcinogenesis is an attractive alternative when considering genes functions within in this amplicon. For instance, CCND1 might cause growth advantage and genetic instability at early stages [285”"], CTTN could enhance cell migration [316–318,324] and FADD may be involved in survival and therapy resistance (see below). In this way the same 11q13.3 amplicon is selected for at multiple stages of carcinogenesis.

**FADD, a new driver within the amplified 11q13.3 region in HNSCC**

In this study FADD was identified as one of the 8 potential driver genes in the 11q13 amplicon in head and neck cancer. In fact, FADD was amplified the highest
FADD as a new driver in the 11q13.3 amplicon in LSCC/ PSCC

(28/29) and its expression strongly correlated with DNA amplification. FADD (for Fas–Associated Death Domain–containing protein) was originally identified as a protein that binds to the cytosolic tail of the FAS–receptor (reviewed in [330]). The pro–apoptotic adapter molecule recruits caspases 8 and 10 to initiate the formation of the death–inducing signal complex (DISC) that mediates receptor–induced apoptosis. The recruitment of these caspases to the DISC leads to intracellular processing and activation of caspases eventually resulting in cleavage of downstream targets and apoptosis. Thus, increased expression should correlate with increased apoptosis. However, more recent studies demonstrated that FADD also plays an important role in growth and regulation of the cell cycle (reviewed in [331]). In both FADD–knockout and transgenic mice expressing human dominant–negative FADD, T–cells are defective in proper cell cycle entry in response to mitogens [332]. In vitro experiments showed that FADD was regulated during cell cycle progression. Cells treated with agents blocking the G2/M transition have higher levels of Ser–194 phospho–FADD [333]. Furthermore, expressing a ser194–phospho–mimicking FADD mutant caused G2/M cell cycle arrest [334] suggesting a key role in cell cycle regulation [334–336, 329].

Chen and coworkers [321] showed that increased expression of FADD and Ser–194 phosphorylated FADD were both associated with decreased survival of patients with lung adenocarcinoma. In contrast to head and neck carcinomas, in these lung adenocarcinomas DNA amplification of FADD was not detected [321]. Furthermore, patients with laryngeal/pharyngeal carcinomas with high levels of FADD and pFADD have a significantly decreased survival (Figure 4C). In patients with carcinomas containing high FADD expression and lymph node metastases, the prognosis is even worse (Figure 4B). This indicates that high FADD expression defines a worse prognosis for patients independent of other classical predictors such as lymph node status. Interestingly, in lung adenocarcinoma, the staining of pFADD was correlated with Ki–67, cyclin B1 and CCND1 staining, indicating that high pFADD levels are associated with increased cell proliferation at the G2/M phase of the cell cycle [321]. This is in concordance with in vitro studies [321, 322, 333, 335, 337]. Since this amplification is prominent in head and neck carcinoma [107] and results in increased expression of FADD (this study), FADD might be one of the genes to regulate cell cycle progression in laryngeal carcinomas with 11q13 amplification.

Perspectives on the role of FADD and chemotherapeutic drugs in hNSCC

The role of FADD in cell cycle regulation suggests that FADD is also implicated in the response to cytotoxic drugs. As described previously, taxol treatment arrests tumor cells at G2/M with concomitant phosphorylation of FADD [335]. Interestingly, both the G2/M arrest as well as cell growth suppression upon taxol treatment were abolished in transfected cells expressing a non–phospho–mimicking mutant of FADD [322, 329, 336]. Taken together, these data show that cells expressing high levels of phosho–FADD are [321] more sensitive to taxol–induced cell cycle arrest [322, 329].
than cells expressing non–phosphorylated FADD. Our data revealed that in HNSCC carcinomas with 11q13.3 amplification both FADD and pFADD are overexpressed (this manuscript). Several recent clinical studies in HNSCC have underlined a positive effect of chemo–radiation over radiotherapy alone [33,311]. We hypothesize that patients with HNSCC carcinomas with 11q13.3 amplification and concomitant pFADD overexpression might benefit from taxol–based chemo–radiotherapy over radiotherapy alone.

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