**Original Article**

**Epidermal growth factor receptor gene amplification in atypical adenomatous hyperplasia of the lung**

Maria G. McIntire¹, Sandro Santagata¹, Keith Ligon¹ and Lucian R. Chirieac¹

¹Department of Pathology, Brigham and Women's Hospital, and Harvard Medical School, Boston, MA, USA.

Received April 21, 2010; accepted May 10, 2010, available online May 16, 2010

**Abstract:** Atypical adenomatous hyperplasia (AAH) is postulated to be the earliest morphologic precursor lesion in lung carcinogenesis. The epidermal growth factor receptor (EGFR), one of the members of the Erb-2 family of receptors, is commonly expressed in non-small cell lung carcinoma (NSCLC). A subset of the patients with NSCLC has molecular abnormalities in the EGFR gene, including missense mutations and deletions and/or abnormal gene copy numbers, and the relative importance of each of these for patient outcome is an area of great interest. Recent reports show that EGFR mutations are rare or absent in AAH and are rare in bronchioloalveolar carcinoma (BAC). However, the EGFR gene copy number status in AAH is unknown. In this study, we examined the EGFR gene copy number status in lung adenocarcinomas, synchronous AAH, and BAC in surgical pathology resection specimens. EGFR gene copy number was analyzed by chromogenic in situ hybridization (CISH) using formalin fixed paraffin embedded tissue sections and EGFR probes as recommended by the manufacturer. A known positive case of high-grade glioma was used as a positive control. The results indicate that four of eight adenocarcinomas (50%) had more than five EGFR signals per nucleus, suggesting a gain in copy number. Interestingly, in four of nine cases of AAH (44.4%) more than three EGFR signals per nucleus were noted, with scattered cells showing up to 6 signals per nucleus. In addition, in five of 12 cases of BAC (42%), more than three EGFR signals per nucleus were noted. In the remaining cases two to three intranuclear dot-like peroxidase positive signals were present consistent with non-amplification of the gene. Our study reveals an abnormal EGFR gene copy gain in several cases of AAH. In our cohort, the rate of EGFR gene copy abnormalities in AAH appears similar to BAC and lower than in lung adenocarcinomas. These findings suggest that although EGFR gene copy abnormalities may be an early event in lung carcinogenesis, they are associated with tumor progression to invasive cancer and highlight the complexity of tumor morphogenesis.

**Keywords:** EGFR, lung cancer, chromogenic in situ hybridization, copy number

**Introduction**

Dysregulation of epidermal growth factor receptor (EGFR) signaling has been implicated in the pathogenesis of numerous carcinomas, most notably non-small-cell lung carcinoma (NSCLC) [1]. Recognized mechanisms of EGFR gain of function in NSCLC include somatic activating mutations in the exons encoding the tyrosine kinase domain [2] and EGFR gene amplification [3]. A hypothesis of multi-step tumorigenesis of lung adenocarcinoma starting with atypical adenomatous hyperplasia (AAH), progressing to bronchioalveolar carcinoma (BAC), and ultimately to invasive adenocarcinoma has been proposed and widely considered [4-6]. Although there have been intensive efforts to characterize the molecular abnormalities of BAC and invasive adenocarcinoma, the molecular alterations of precursor AAH are an area of more recent investigation [7-11]. Furthermore, the genetic alterations in the EGFR signaling pathway, which have been shown to characterize the late-stage of certain lung adenocarcinomas, are not clearly defined in AAH [12]. Studies have identified somatic mutations of the EGFR gene in lung adenocarcinoma [13, 14]. However, EGFR mutations are relatively uncommon in AAH and likewise rare in BAC [8]. Similarly, copy number changes of EGFR have also been identified in
adenocarcinomas [15, 16] but to our knowledge, EGFR copy number changes in AAH have not been demonstrated in detail [17].

In this study, we therefore examined the extent of copy number variations in patients with AAH, BAC, and invasive lung adenocarcinoma by chromogenic in situ hybridization (CISH). CISH utilizes a peroxidase reaction to detect the locus of interest and can be performed in the clinical immunohistochemistry laboratory on formalin fixed paraffin embedded archival tissue and interpreted by standard light microscopy [15]. Recent studies from our group and others’ have shown that CISH is a useful assay for detecting EGFR gene amplification in patients with NSCLC and has an important role for identification of patients with a high number of EGFR copies [15, 18, 19]. Furthermore, the reliability of CISH as a technique for detecting gene amplification has been established for HER-2 in breast cancer specimens [20-22]. We therefore used CISH to investigate whether early morphologically detectable lesions such as AAH manifest copy number changes in the EGFR locus. The specimens used in this study were from patients with lung adenocarcinomas and synchronous AAH, in addition to patients who exclusively had pure BAC.

Materials and methods

We studied ten consecutive patients who had NSCLC with synchronous AAH (seven of the ten) in their surgical pathology lung specimens, and 12 patients with BAC, who were treated at Brigham and Women’s Hospital between 1999 and 2004. This study was approved by the local Institutional Review Board. Routine hematoxylin and eosin-stained slides from formalin-fixed, paraffin-embedded tissue sections were reviewed and classified according to the WHO criteria [5, 23] and staged according to the American Joint Committee on Cancer [24]. Representative areas containing carcinoma and AAH were selected for CISH analyses on 5 mm tissue sections.

Chromogenic in situ hybridization

Paraffin-embedded tissue sections were deparaffinized in two changes of xylene for 5 minutes each; xylene was removed in three washes of ethanol for three minutes each (100%, 100% and 95%) and the slides were washed in distilled running water for 5 minutes. The slides were placed in heated (>90°C) CISH Pretreatment Buffer (Invitrogen, Carlsbad, CA) and microwaved on high power for 30 minutes, then rinsed in distilled water for 5 minutes at room temperature. The tissue was digested for 10 minutes with pepsin digestion solution (Invitrogen, Carlsbad, CA) at room temperature, washed twice in distilled water for five minutes each, dehydrated in 90, 95, and 100% alcohol for 2 minutes each, then dried in a 37°C oven.

Five to seven µl of EGFR Amplification Probe (Invitrogen/Zymed, South San Francisco, CA) were applied to the designated area and a coverslip was applied and sealed with rubber cement. Slides were dried at 37°C, followed by probe denaturation at 95°C for five minutes and hybridization at 37°C overnight in a Thermobrite oven (MarketLab, Caledonia, MI). The slides were washed in 0.5% SSC for five minutes at room temperature, followed by 0.5% SSC for five minutes at 75°C, and water for five minutes at room temperature.

For immunodetection, slides were placed in 3% hydrogen peroxide in absolute methanol for ten minutes, and then washed in phosphate buffered saline with 0.025% Tween 20 (PBST) three times for 2 minutes each. Slides were incubated with nonspecific blocking solution (Zymed/Invitrogen, South San Francisco, CA) for 10 minutes at room temperature, then incubated with mouse anti-digoxigenin antibody for 30 minutes at room temperature, washed in PBST twice for two minutes each, and incubated with horseradish peroxidase-conjugated goat anti-mouse antibody for fifteen minutes, and finally washed again with PBST twice for two minutes each. Slides were then incubated with DAB Chromagen (Zymed/Invitrogen, South San Francisco, CA) for 30 minutes at room temperature, and washed in distilled water twice for two minutes each, and were counterstained with hematoxylin.

The CISH-prepared slides were examined at 400X magnification by bright field microscopy. Two pathologists (SS and LRC) examined the cases concomitantly and agreed on CISH scores; cases for which there was disagreement were further reviewed and a consensus was established. Both examiners were blinded to the FISH results. As in prior studies [15, 25], 200 tumor nuclei were examined in each case. In
cases where the number of signals per tumor nucleus varied between tumor cells, the range of signals counted was recorded for each case. Further validation of this work comparing CISH to FISH was recently published [15].

**Statistical analysis**

A geometric average was calculated from the range of CISH scores to represent the point estimate for each case. CISH scores were correlated between groups using nonparametric analysis (Spearman correlation).

**Results**

From the records of our institution, we identified seven patients with lung adenocarcinomas and synchronous AAH in the surgical pathology specimens, one patient with adenocarcinoma alone, two patients with AAH alone, and 12 patients with BAC. The clinical and pathologic features of the patient groups are summarized in Table 1. All surgical pathology specimens were reviewed morphologically and classified according to the WHO criteria [23], and each was subjected to analysis of *EGFR* gene copy number using CISH. We sought to examine whether gene amplification of *EGFR* was present in precursor lesions of lung adenocarcinomas. Using surgically resected specimens of lung adenocarcinomas that demonstrated concurrent AAH, we used CISH to evaluate *EGFR* gene amplification. All specimens were from formalin fixed paraffin embedded tissue sections and EGFR probes were used as recommended by the manufacturer. Cases of BAC had features of involvement of alveolar walls by a proliferation of cuboidal

<table>
<thead>
<tr>
<th>Case Nr</th>
<th>Age/Sex</th>
<th>Smoking</th>
<th>Type of Lesion</th>
<th>EGFR Copy Number</th>
<th>Surgical Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>50/F</td>
<td>40</td>
<td>AAH/ACA</td>
<td>3/3</td>
<td>RLL/RUL wedges</td>
</tr>
<tr>
<td>2</td>
<td>58/F</td>
<td>Unknown</td>
<td>AAH/ACA</td>
<td>2/2</td>
<td>RLL/RUL wedges</td>
</tr>
<tr>
<td>3</td>
<td>56/F</td>
<td>Never</td>
<td>AAH/ACA</td>
<td>5/7</td>
<td>RUL wedge</td>
</tr>
<tr>
<td>4</td>
<td>58/F</td>
<td>Unknown</td>
<td>AAH</td>
<td>2</td>
<td>Left lung, EPP</td>
</tr>
<tr>
<td>5</td>
<td>72/F</td>
<td>55</td>
<td>ACA</td>
<td>7</td>
<td>RUL wedge</td>
</tr>
<tr>
<td>6</td>
<td>62/F</td>
<td>45</td>
<td>AAH/ACA</td>
<td>4/10</td>
<td>LUL lobectomy</td>
</tr>
<tr>
<td>7</td>
<td>75/F</td>
<td>Never</td>
<td>AAH/ACA</td>
<td>2/2</td>
<td>RML lobectomy</td>
</tr>
<tr>
<td>8</td>
<td>69/F</td>
<td>12</td>
<td>AAH/ACA</td>
<td>6/2</td>
<td>LLL wedge</td>
</tr>
<tr>
<td>9</td>
<td>76/M</td>
<td>Unknown</td>
<td>AAH</td>
<td>2</td>
<td>RUL lobectomy</td>
</tr>
<tr>
<td>10</td>
<td>58/F</td>
<td>Unknown</td>
<td>AAH/ACA</td>
<td>6/9</td>
<td>LUL lobectomy</td>
</tr>
<tr>
<td>11</td>
<td>58/F</td>
<td>27</td>
<td>BAC</td>
<td>3</td>
<td>RUL wedge</td>
</tr>
<tr>
<td>12</td>
<td>59/F</td>
<td>Never</td>
<td>BAC</td>
<td>3</td>
<td>RUL wedge</td>
</tr>
<tr>
<td>13</td>
<td>49/F</td>
<td>Unknown</td>
<td>BAC</td>
<td>3</td>
<td>RUL lobectomy</td>
</tr>
<tr>
<td>14</td>
<td>66/F</td>
<td>25</td>
<td>BAC</td>
<td>5</td>
<td>RLL, wedge</td>
</tr>
<tr>
<td>15</td>
<td>69/F</td>
<td>Unknown</td>
<td>BAC</td>
<td>6</td>
<td>RUL wedge</td>
</tr>
<tr>
<td>16</td>
<td>80/M</td>
<td>10</td>
<td>BAC</td>
<td>3</td>
<td>RLL lobectomy</td>
</tr>
<tr>
<td>17</td>
<td>71/M</td>
<td>Occasion</td>
<td>BAC</td>
<td>6</td>
<td>RML wedge</td>
</tr>
<tr>
<td>18</td>
<td>66/F</td>
<td>Unknown</td>
<td>BAC</td>
<td>5</td>
<td>RUL lobectomy</td>
</tr>
<tr>
<td>19</td>
<td>56/M</td>
<td>20</td>
<td>BAC</td>
<td>5</td>
<td>RML wedge</td>
</tr>
<tr>
<td>20</td>
<td>75/F</td>
<td>Unknown</td>
<td>BAC</td>
<td>3</td>
<td>RLL wedge</td>
</tr>
<tr>
<td>21</td>
<td>79/M</td>
<td>40</td>
<td>BAC</td>
<td>3</td>
<td>LUL wedge</td>
</tr>
<tr>
<td>22</td>
<td>66/F</td>
<td>Unknown</td>
<td>BAC</td>
<td>2</td>
<td>LUL wedge</td>
</tr>
</tbody>
</table>

*ACA, adenocarcinoma; RLL, right lower lobe; RUL, right upper lobe; RML, right middle lobe; LLL, left lower lobe; LUL, left upper lobe.*
cells with severe atypia, but without evidence of invasion. In contrast, the cases of AAH were localized proliferations of pneumocytes less than 0.5cm with marked hobnailing and mild to moderate atypia lining the alveolar walls and/or respiratory bronchioles. We were able to identify increased CISH signals representing amplification of the *EGFR* gene in cases of AAH (Figure 1A, B), suggesting the presence of increased *EGFR* gene copy number in this proposed earliest morphologic precursor of lung adenocarcinoma. We found up to six *EGFR* signals per nucleus (Figure 1B) in a case of AAH. In addition, we were able to detect increased copy numbers of *EGFR* by CISH in BAC. As previously reported, increased *EGFR* copy number was also identified in lung adenocarcinomas, with one example demonstrating up to ten *EGFR* signals per nucleus (Figure 1D).

To determine whether there might be a correlation between early lesions of lung adenocarcinoma with *EGFR* gene amplification, we examined whether there was a progressive increase in *EGFR* gene expression as a function of proposed tumor development. We found an abnormal *EGFR* gene copy gain in several cases of AAH (mean 3.5 signals, 95% CI 2.2 to 4.9) and a progressive increase in the rate of *EGFR* gene copy abnormalities to invasive ACA (mean 5.3 signals, 95% CI 2.4 to 8.1). In four of 9 cases of AAH (44.4%) more than three *EGFR* signals per nucleus were noted (Figure 2).

**Discussion**

In the current study, we used CISH to determine whether copy number changes to the *EGFR* locus might be an early event in lung tumorigene-
EGFR copy number in AAH

EGFR copy number changes in atypical adenomatous hyperplastic lesions, which are thought to represent the earliest morphologic entity that can be discriminated from either normal or reactive pulmonary epithelium. Although a previous report evaluated the prevalence of EGFR copy number abnormalities by CISH in AAH and lung adenocarcinoma [17], our findings are the first to demonstrate evidence for EGFR gene amplification in atypical adenomatous hyperplasia. The number of EGFR copies detected by CISH was higher in invasive adenocarcinoma than BAC and atypical adenomatous hyperplasia. Overall, we found that EGFR gene copy number in AAH is lower than in adenocarcinoma and very similar to that of BAC. Two other studies by Sakuma et al. found EGFR mutations by PCR-based methodology to be present in 32% of AAH cases, 88% of pure non-mucinous bronchioloalveolar carcinomas and 75% of invasive adenocarcinomas with a non-mucinous bronchioloalveolar component [26, 27]. Nevertheless further studies are needed to define this relationship. One limitation of our study was that most of the AAH were found concurrently in cases with invasive cancer. Ideally, examination of EGFR by CISH would occur in specimens devoid of an invasive lesion in order to definitively determine whether EGFR gene amplification is indeed an early event, or simply a correlate seen in cases of invasive adenocarcinoma with concurrent AAH. However, this would be difficult given that AAH lesions are small and are not usually or likely to be discovered by clinical or pathologic examination.

Activation of the EGFR signaling cascade has been shown to be due to a subset of mutations in the EGFR receptor kinase domain, which have been reported to occur with a frequency of 10% [1]. Such mutations appear to be more common in the adenocarcinoma histologic types and tend to be found in young, Asian women who have never smoked [28-30]. Notably, these patients appear to benefit substantially from inhibitors targeting EGFR. Other mechanisms of activation of the EGFR signaling cascade include gene amplification. Recent studies have highlighted the prognostic value of EGFR gene amplification in response to EGFR-inhibitor therapies [31-34]. Cappuzzo et al. showed that there was an increased responsiveness to kinase therapy in patients with lung adenocarcinomas that harbored increased EGFR gene copy number determined by FISH [31]. Similarly, Hirsch et al. demonstrated that increased EGFR gene copy number was associated with increased sensitivity to kinase inhibitors in patients with BACs [34]. Adenocarcinomas with increased EGFR copy number were also found to correlate with EGFR overexpression in NSCLC and showed a trend towards poorer prognosis [16]. Importantly then, both mutations in EGFR and gene amplification are correlated with subsequent responsiveness to kinase inhibitor therapy. However, whether defects in kinase signaling are by themselves sufficient to induce malignancy is still unknown. Further research into the early mechanisms of lung tumorigenesis may reveal new strategies for the development of specific molecular therapeutics as well as provide for novel prognostic and diagnostic markers.

Our findings show that EGFR gene abnormalities are associated with tumor progression to invasive cancer and highlight the complexity of tumor morphogenesis.

Acknowledgments

This study was supported by Specialized Programs of Research Excellence (SPORE) grant in Lung Cancer CA090578 from the National Cancer Institute. Dr. Chirieac is supported by W81XWH06-1-0303 from the Department of

Figure 2. Scatter diagram illustrating the correlation between EGFR copy number and tumor progression, in AAH, BAC and lung adenocarcinoma. In four of 9 cases of AAH (44.4%) more than three EGFR signals per nucleus were noted. Horizontal bars represent the median value of EGFR copy number for each of the groups evaluated.
EGFR copy number in AAH

Defense. We are indebted to Ms. Lillian Cruz for laboratory assistance and Ms. Brittany MacFarland for her editorial assistance in preparing the manuscript.

Please address correspondence to: Lucian R. Chirieac, MD, Department of Pathology, Brigham and Women’s Hospital, 75 Francis Street, Boston MA 02115, USA. Tel: 617 732-8126, Fax: 617 264-5118, E-mail: lchirieac@partners.org

References


