Genomic Alterations in the RB Pathway Indicate Prognostic Outcomes of Early-Stage Lung Adenocarcinoma

Seongmin Choi¹,², Hyeong Ryul Kim³, Chang Ohk Sung⁴, Jongkyu Kim¹,², Sukjun Kim¹,², Sung-Min Ahn⁵,⁶,⁷, Chang-min Choi⁸, Sung-Min Chun⁹, Eun Kyung Choi⁹, Sang-We Kim⁶, Yong-Hee Kim³, Ji-Young Lee¹⁰, Joon Seon Song⁴, Deokhoon Kim⁷, Farhan Haq⁷,¹¹, Sun Young Lee⁷, Jong-eun Lee¹², Wang-rim Jung¹², Hye Yoon Jang¹², Eunho Yang¹², Charles Lee¹³,¹⁴, Eunsil Yu⁴, Gu Kong¹⁵, Daehyun Baek¹²,¹⁶, and Se Jin Jang¹⁴

Abstract

Purpose: To better understand the complete genomic architecture of lung adenocarcinoma.

Experimental Design: We used array experiments to determine copy number variations and sequenced the complete exomes of the 247 lung adenocarcinoma tumor samples along with matched normal cells obtained from the same patients. Fully annotated clinical data were also available, providing an unprecedented opportunity to assess the impact of genomic alterations on clinical outcomes.

Results: We discovered that genomic alterations in the RB pathway are associated with significantly shorter disease-free survival in early-stage lung adenocarcinoma patients. This association was also observed in our independent validation cohort. The current treatment guidelines for early-stage lung adenocarcinoma patients recommend follow-up without adjuvant therapy after complete resection, except for high-risk patients. However, our findings raise the interesting possibility that additional clinical interventions might provide medical benefits to early-stage lung adenocarcinoma patients with genomic alterations in the RB pathway. When examining the association between genomic mutation and histologic subtype, we uncovered the characteristic genomic signatures of various histologic subtypes. Notably, the solid and the micropapillary subtypes demonstrated great diversity in the mutated genes, while the mucinous subtype exhibited the most unique landscape. This suggests that a more tailored therapeutic approach should be used to treat patients with lung adenocarcinoma.

Conclusions: Our analysis of the genomic and clinical data for 247 lung adenocarcinomas should help provide a more comprehensive genomic portrait of lung adenocarcinoma, define molecular signatures of lung adenocarcinoma subtypes, and lead to the discovery of useful prognostic markers that could be used in personalized treatments for early-stage lung adenocarcinoma patients. Clin Cancer Res; 21(11); 2613–23. © 2014 AACR.

See related commentary by Collisson, p. 2418

Introduction

Worldwide, lung cancer is the leading cause of cancer-related mortality (1). The incidence of lung adenocarcinoma continues to rise and is now the most frequent histologic subtype according to nationwide surveys in East Asian countries (2, 3) and the United States (4). Recent large-scale genomic studies have identified novel therapeutic targets and accelerated the development of personalized treatment for lung adenocarcinoma.
Translational Relevance

Lung cancer is the leading cause of cancer-related mortality worldwide and its most predominant subtype is lung adenocarcinoma. For early-stage lung adenocarcinomas, surgical resection has been shown to increase curative outcomes and thus remains the recommended treatment approach. However, the survival rate after curative resection in early-stage lung adenocarcinoma cases is still lower than 50%. In our present study, we performed microarray analyses of 247 lung adenocarcinomas to detect copy number variations and also sequenced the complete exomes of these tumor specimens. As a result, we discovered that genomic alterations to the RB pathway are strongly linked to a significantly shorter disease-free survival outcome for early-stage lung adenocarcinoma patients. The current treatment guideline for early-stage lung adenocarcinoma patients comprises mainly follow-up without adjuvant therapy after resection. However, our current findings raise an interesting possibility that additional clinical interventions might provide medical benefit for early-stage lung adenocarcinoma patients who have genomic alterations to the RB pathway.

Materials and Methods

Patients and tumor specimens

This study included a whole-exome and CNV analysis of 247 Korean patients with lung adenocarcinoma. Lung adenocarcinoma tumor and matched normal tissue samples were obtained from two independent patient cohorts that include a discovery cohort (n = 170) and a validation cohort (n = 77). Patients in both cohorts had completely annotated clinical data, including overall survival, recurrence, histologic subtype, clinical stage, tumor stage, and smoking status. All specimens used in this study were obtained with the approval of the Institutional Review Board of Asan Medical Center (Seoul, South Korea), and documented informed consent was obtained from all patients. The specimens and data used in this study were provided by the Asan BioResource Center of the Korea Biobank Network (Seoul, South Korea).

Sample preparation and evaluation

Sections of 291 flash-frozen samples were stained with hematoxylin and eosin (H&E) and subjected to histologic examination by pathologists to determine tumor area in the slides (coverage area) and cellularity. DNA was only extracted from the 256 tumors with coverage areas ≥80% and tumor cellularity ≥60%. Genomic DNA was extracted using the QiAamp DNA FFPE Tissue Kit (Qiagen) according to the manufacturer’s instructions. After elution in DNase- and RNase-free water, genomic DNA was quantified using the NanoDrop spectrophotometer and PicoGreen system (Invitrogen). Six samples failed DNA quality control and the final 247 samples were sequenced. Then, from the 247 patients, 170 patients were randomly chosen to be the discovery cohort, leaving 77 patients in the validation cohort. Using a multiheaded microscope, H&E-stained tumor sections were reviewed by two pathologists (J.S. Song and S.I. Jang) blind to the study protocol, and were evaluated simultaneously until a consensus was reached. Tumor subtypes were classified according to the IASLC/ATS/ERS classifications (13). Minimaly invasive and invasive adenocarcinomas were divided into five subtypes: papillary-predominant, acinar-predominant,
micropapillary-predominant, solid-predominant, and invasive mucinous adenocarcinoma.

**Exome capture and massive parallel sequencing**

SureSelect sequencing libraries were prepared using the SureSelect All Exon 50 Mbp Kit (Agilent) according to the manufacturer’s instructions. The quality of the amplified fragment libraries was verified by capillary electrophoresis using the Agilent Bioanalyzer. Cluster generation in the flow cells was achieved using the cBot automated cluster generation system (Illumina). Then, the flow cells were loaded onto an Illumina HiSeq2000 sequencing system, and sequencing was performed using a read length of 2 × 100 bp.

**Validation of detected mutations, bioinformatics, and statistical analyses**

Detailed methods for validation of detected mutations, IHC, bioinformatics, and statistical analyses can be found in the Supplementary Methods.

**Results**

**Clinicopathological features of studied population**

We obtained tumor and matched normal tissue samples from two independent patient cohorts (n = 247): a discovery cohort (n = 170) and a validation cohort (n = 77). Demographics of patients’ information including smoking status, histologic subtype, and recurrence are provided in Table 1. According to the staging criteria of the American Joint Committee on Cancer, 157, 44, 40, and 6 patients were classified as clinical stage I–IV, respectively. About half were never-smokers (n = 122), and the rest were either former or current smokers (n = 125). Such fraction shows a clear difference from previous studies, which include only 10% to 15% of never-smokers (6, 8). Almost all smokers were male (94%), and the positive association between smoking status and sex was statistically significant (P < 2.2 × 10⁻¹⁰; Fisher exact test). Most tumor samples included a heterogeneous mixture of multiple histologic subtypes. By assessing the most predominant subtype, we classified each tumor sample as one of the following five major subtypes according to new international classifications (13): acinar, papillary, solid, micropapillary, or mucinous. Accordingly, we identified 81 acinar, 66 papillary, 64 solid, 20 micropapillary, and 16 mucinous subtypes.

**Detection of potential cancer drivers and CNVs**

To discover genes that are specifically mutated in cancer cells, we attempted to detect genes that accumulated significantly more mutations than the estimated number of mutations calculated from their background mutation rates (BMR). To compute the BMR, we estimated the nonsynonymous BMR from the synonymous BMR of each gene to reflect the fluctuating local mutation rate (Supplementary Methods). We also analyzed each base type separately to reflect the different mutation rate of each base type. This approach seems to improve the overall detection accuracy compared with previous approaches (Supplementary Table S4 and Supplementary Methods; refs. 6, 19). Using this improved method, we detected 48 significantly mutated genes (Supplementary Table S5). To further filter out potential false positives, we used the expression data obtained from 87 patients with lung adenocarcinoma (9) and filtered out genes not likely to be expressed in lung adenocarcinoma (Supplementary Methods), to determine our final list of 22 significantly mutated genes (Fig. 1A and Table 2). Among these, six genes have already been

<table>
<thead>
<tr>
<th>Attribute</th>
<th>Trait</th>
<th>Discovery (n = 170)</th>
<th>Validation (n = 77)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex</td>
<td>Male</td>
<td>95 (56%)</td>
<td>46 (60%)</td>
</tr>
<tr>
<td></td>
<td>Female</td>
<td>75 (44%)</td>
<td>31 (40%)</td>
</tr>
<tr>
<td>Age, years</td>
<td>≥70</td>
<td>31 (38%)</td>
<td>12 (16%)</td>
</tr>
<tr>
<td></td>
<td>&gt;70</td>
<td>77 (45%)</td>
<td>36 (47%)</td>
</tr>
<tr>
<td></td>
<td>&lt;70</td>
<td>62 (56%)</td>
<td>29 (38%)</td>
</tr>
<tr>
<td>Smoking status</td>
<td>Never-smoker</td>
<td>82 (48%)</td>
<td>40 (52%)</td>
</tr>
<tr>
<td></td>
<td>Smoker</td>
<td>88 (52%)</td>
<td>37 (48%)</td>
</tr>
<tr>
<td>Overall stage</td>
<td>I</td>
<td>110 (65%)</td>
<td>47 (61%)</td>
</tr>
<tr>
<td></td>
<td>II</td>
<td>28 (16%)</td>
<td>12 (16%)</td>
</tr>
<tr>
<td></td>
<td>III</td>
<td>28 (16%)</td>
<td>12 (16%)</td>
</tr>
<tr>
<td></td>
<td>IV</td>
<td>4 (2%)</td>
<td>2 (3%)</td>
</tr>
<tr>
<td>Predominant subtype</td>
<td>Acinar</td>
<td>53 (33%)</td>
<td>28 (36%)</td>
</tr>
<tr>
<td></td>
<td>Papillary</td>
<td>48 (28%)</td>
<td>18 (23%)</td>
</tr>
<tr>
<td></td>
<td>Solid</td>
<td>45 (26%)</td>
<td>19 (25%)</td>
</tr>
<tr>
<td></td>
<td>Micropapillary</td>
<td>13 (8%)</td>
<td>7 (9%)</td>
</tr>
<tr>
<td></td>
<td>Mucinous</td>
<td>11 (6%)</td>
<td>5 (6%)</td>
</tr>
<tr>
<td>Adjuvant chemotherapy treatment</td>
<td>Treated</td>
<td>30 (18%)</td>
<td>21 (27%)</td>
</tr>
<tr>
<td></td>
<td>Untreated</td>
<td>140 (82%)</td>
<td>56 (73%)</td>
</tr>
<tr>
<td>Recurrence status</td>
<td>Recurrent</td>
<td>80 (47%)</td>
<td>26 (34%)</td>
</tr>
<tr>
<td></td>
<td>Not recurrent</td>
<td>77 (45%)</td>
<td>47 (61%)</td>
</tr>
</tbody>
</table>

* Determined according to AJCC criteria (7th edition). See Supplementary Table S14 for additional stage classification data (TNM).
* Recurrence data on 17 patients are missing; these patients were excluded from subsequent analyses.

**Results of whole-exome sequencing and validation**

The whole exomes of the tumor and normal samples obtained from patients in both cohorts were analyzed using high-throughput sequencing. After applying multiple stringent filters, we obtained a median of 28 Mbp of exome sequences that have sufficient coverage (≥10×). Overall, the mean depth was 49.8 × (range: 13.9–117.3 ×; Supplementary Table S1). To reduce potential false positives, which were caused by a lenient parameter cutoff recommended by the published bioinformatics tool that we utilized (18), we used a more stringent cutoff (Supplementary Table S2). We obtained a mean rate of 3.9 mutations (substitutions and small indels) per Mbp, which is lower than that of a previous study (8), perhaps because of the larger number of never-smokers included in our cohort. The overall pattern of detected mutations is fairly similar to those of previous reports (8, 9). Smokers demonstrated a higher overall mutation rate than never-smokers (5.5 vs. 1.9 per Mbp, P = 1.3 × 10⁻⁹, rank-sum test), as previously reported (6, 8, 9). Especially, C to G and C to A substitutions demonstrated pronounced differences dependent on smoking status consistently with a previous study (Supplementary Fig. S1 and Supplementary Table S3; ref. 8).

To evaluate the accuracy of the whole-exome sequencing, we performed Sanger sequencing on 161 randomly chosen mutations (31 small indels and 130 substitutions). The validation rate was 100% for small indels (31 of 31), 95% for substitutions (123 of 130), and 96% for both types of mutations combined (154 of 161). Furthermore, we used mass spectrometry to independently validate additional 90 randomly chosen substitutions and obtained an overall validation rate of 71% (64 of 90; see Supplementary Methods). The high validation rates of these two independent technologies show that rigorous filtering is able to detect somatic mutations with a high level of accuracy.
reported (EGFR, TP53, KRAS, PIK3CA, RB1, and SETD2) and the other 16 genes seem to be novel driver candidates. Consistently with previous reports (6, 8, 20), there was a significant association between EGFR and KRAS mutations ($P = 8.2 \times 10^{-3}$, Fisher exact test). Possibly due to our stringent cutoff criteria, some previously reported genes were absent from our final list; however, we were able to detect 21 mutation(s) in each of previously reported 29 genes (Supplementary Table S6; refs. 6, 8, 9). The known functions of these 16 novel driver candidates suggest that some of them might be related to lung adenocarcinoma occurrence or progression. For instance, COL11A1 has been proposed as a poor prognostic marker for non–small cell lung cancer (21). CENPF, a centromere protein-coding gene, and COL6A3 have been identified as poor prognostic markers for breast cancer (22, 23). SLIT2, which is involved in the SLIT/ROBO-signaling pathway, is also associated with poor prognosis in lung cancer (24, 25).

To detect the CNVs associated with lung adenocarcinoma, we used CNV arrays for 247 pairs of tumor and their matched normal samples (Supplementary Methods) and processed them using a publicly available tool (26). After removing CNV regions that did not harbor any genes expressed in lung adenocarcinoma, 13 significantly altered CNV regions (including 60 genes) were detected. Among these, six CNV regions have been previously reported (8), including regions that encompass TERT, CDKN2A, MDM2, MYC, ERBB2, and RB1 (Fig. 1B and Supplementary Table S7). In addition, dozens of novel driver candidates within the 13 significantly altered CNV regions were identified (Supplementary Table S7). For instance, FOXA1 has been reported as a driver candidate in prostate cancer and identified as a therapeutic target for breast cancer (27, 28), YEATS4 has been identified as a novel oncogene that regulates the p53 pathway (29), and the amplification of a potential oncogene ZNF217 has been shown to regulate expression of ErbB3 receptor tyrosine kinase in breast cancer (30).
We searched for drugs that could potentially target the significantly altered genes in the discovery cohort. When looking at the 22 significantly mutated genes and the 60 genes located on the 13 significantly altered CNV regions, eight of them can be targeted by known drugs (Supplementary Table S8). Among these eight genes, four can be targeted by drugs with known tumor-inhibiting activities. The oncogenes EGFR, ERBB2, PIK3CA, and TERT can be targeted by tailored drugs such as erlotinib (15), trastuzumab (31), NVP-BEZ235 (32), and GRN163L (33), respectively. These target drugs and their respective target genes are presently model in different pathways (Supplementary Fig. S2). The expanded list of novel driver candidates discovered in this study suggests that additional investigations into these candidates might lead to the discovery of novel drug targets for the treatment of lung adenocarcinoma.

Association between RB pathway alterations and poor prognosis in early-stage lung adenocarcinoma patients

We performed pathway enrichment tests on the 22 significantly mutated genes and 60 genes within significantly altered CNVs. We detected 19 significantly enriched pathways (Supplementary Table S9), almost all of which are related to cancer, including non–small cell lung cancer (KEGG pathway, \(P = 1.6 \times 10^{-9}\), modified Fisher exact test). This is another indication that these significantly mutated genes and CNVs are involved in lung adenocarcinoma occurrence or progression.

Next, we examined whether genomic alterations accumulated on the genes of known pathways could result in differential clinical outcomes (Fig. 2A–D). We found that genomic alterations in the RB pathway (Supplementary Fig. S3) are strongly associated with significantly shorter disease-free survival in stage I and II lung adenocarcinoma patients (\(P = 1.4 \times 10^{-3}\) and \(q = 0.031\), log-rank test; Fig. 2A). When we excluded early-stage lung adenocarcinoma patients who were treated with adjuvant chemotherapy from the analysis, we observed an even stronger association (\(P = 6.7 \times 10^{-3}\) and \(q = 0.026\), log-rank test; Supplementary Fig. S4A). On the other hand, this association was not observed in stage III or IV lung adenocarcinoma patients, regardless of including patients treated with adjuvant chemotherapy (\(P = 0.11\) and \(q = 0.21\), log-rank test; Fig. 2C) or not (\(P = 0.28\) and \(q = 0.33\), log-rank test; Supplementary Fig. S4C).

To rule out the possibility that this discrepancy originated from the small number of late-stage patients included in our discovery cohort, we repeated our analysis using the same number of randomly sampled early-stage patients and found that the observed association between RB pathway mutations and poor disease-free survival is specific to early-stage lung adenocarcinoma patients, regardless of including patients treated with adjuvant chemotherapy (\(P = 0.025\), log-rank test; Supplementary Fig. S5) or not (\(P = 0.020\), log-rank test; Supplementary Fig. S4E). Furthermore, our independent validation cohort of 77 patients with lung adenocarcinoma confirmed this association (\(P = 0.017\) and \(4.0 \times 10^{-3}\) respectively, log-rank test; Fig. 2B and Supplementary Fig. S4B). When the discovery and validation cohorts were combined, the association was statistically significant (\(P = 5.2 \times 10^{-5}\), log-rank test).

To verify that the association between RB pathway alterations and poor prognosis was not due to confounding effects (e.g., sex, age at diagnosis, node metastasis), we performed univariable and multivariable Cox regression analyses. Accordingly, we found that RB pathway alterations were significantly associated with poor prognosis in the discovery cohort, regardless of correcting for the confounding factors in the survival prediction model (\(P = 4.6 \times 10^{-4}\), multivariable Cox regression analysis; Supplementary Table S10) or not (\(P = 9.4 \times 10^{-3}\), univariable Cox regression analysis; Supplementary Table S11). These results were also reproduced in the validation cohort (\(P = 9.4 \times 10^{-3}\) and 0.024 according to multivariable and univariable Cox regression analyses, respectively). In contrast with the current treatment guidelines for early-stage lung adenocarcinoma patients, which recommends follow-up without adjuvant therapy after complete resection except for high-risk patients (10), these results raise the interesting possibility that early-stage lung adenocarcinoma patients with genomic alterations in the RB pathway might benefit from additional medical interventions.

**RB1 inactivation alters expression of cell-cycle–related proteins in lung adenocarcinoma tumors**

We evaluated whether RB1 inactivation, resulting from mutations or CNV deletion, is associated with protein level changes of other genes related to cell-cycle regulation. Protein expression levels of pRB1, E2F1, cyclin D1, and cyclin E1 within 247 tumor samples were evaluated by IHC and compared for statistical differences (Fig. 3A). Tumors with inactivated RB1 exhibited significantly lower pRB1 expression but higher E2F1 expression (\(P = 3.2 \times 10^{-4}\) and \(1.0 \times 10^{-4}\), respectively, rank-sum test; Fig. 3B), consistent with previous reports (34, 35). Higher E2F1 expression correlated with higher expression of cyclin E1 (\(P = 5.5 \times 10^{-4}\), Fig. 3C). In addition, tumors with inactivated RB1 exhibited...
significantly lower expression of cyclin D1 \((P = 1.6 \times 10^{-5}; \text{Fig. 3B})\), consistent with a previous report that demonstrated that \(RB1\) mutations promote cyclin degradation, leading to lower expression of cyclin D1 \((36)\). Taken together, these results indicate that tumors with inactivated \(RB1\) have altered expression of other proteins essential to cell-cycle regulation, providing a possible link between RB pathway alterations and poor prognosis in early-stage lung adenocarcinoma patients.

**Molecular definitions of lung adenocarcinoma subtypes**

To gain more comprehensive insight into the molecular definitions of lung adenocarcinoma subtypes, we investigated the associations between significantly mutated genes and tumor subtypes, which were classified on the basis of the most up-to-date tumor classification criteria \((13)\).

The overall molecular definition demonstrated the similarities between the acinar and the papillary subtypes, and between the micropapillary and the solid subtypes \((\text{Fig. 4A})\). Consistent with this observation, when subjected to hierarchical clustering according to the mutation profile, the acinar and the papillary subtypes were included in the same cluster, whereas the micropapillary and the solid subtypes formed another cluster \((\text{Fig. 4B})\). These clustering patterns agree with the known histologic and morphologic characteristics of these tumor subtypes \((13)\).

The molecular definitions of the acinar and the papillary subtypes seem to be dramatically different from those of the micropapillary and the solid subtypes. One of main reasons for this discrepancy stems from \(EGFR\) mutations, which are strongly associated with the papillary subtype \((P = 4.7 \times 10^{-6}; \text{Fisher exact test})\) and inversely associated with the solid \((P = 1.5 \times 10^{-3}; \text{Fisher exact test})\), the mucinous \((P = 2.7 \times 10^{-3}; \text{Fisher exact test})\), and the micropapillary subtypes \((P = 8.0 \times 10^{-3}; \text{Fisher exact test})\). Some of these associations have been previously reported \((16)\), but our large-scale dataset enabled us to look into these associations more completely. Interestingly, the mucinous subtype demonstrated a unique mutation profile, in that the most prevalent mutations accumulated in \(KRAS\) \((\text{Fig. 4A})\). It is also noteworthy that the solid subtype demonstrated a very heterogeneous mutation profile \((\text{Fig. 4A})\), which is consistent with the observation that this subtype often demonstrates unusual histologic and morphologic characteristics that are fairly different from other subtypes \((13)\). Taken together, our detailed analyses call for a more careful investigation of the molecular definitions of the lung adenocarcinoma subtypes and indicate that a better tailored therapeutic approach should be used when treating patients with lung adenocarcinoma to improve overall therapeutic outcomes.

**Discussion**

For this study, we generated the whole exome and CNV dataset together with fully annotated clinical data on 247 lung adenocarcinomas, which provide an unprecedented opportunity for investigating the genomic architecture of lung adenocarcinoma and genomic alternations associated with clinical phenotypes and outcomes.

By processing the exome data according to our stringent statistical approaches, we detected 22 significantly mutated genes...
with either base substitutions or small indels, which account for 78% of our discovery cohort. Sixty-nine percent of the discovery cohort had such mutations in six previously reported genes (EGFR, TP53, KRAS, PIK3CA, RB1, and SETD2). The remaining 9% of cases had base substitutions or small indels that accumulated in the 16 novel driver candidates, including COL11A1, CENPF, COL6A3, LRBA, and SLIT2. Another 6% of the discovery cohort demonstrated significant CNV(s), leaving 15% of lung adenocarcinomas unexplained by our exome or CNV data (Supplementary Fig. S6). Potential reasons for the 15% of unexplained lung adenocarcinomas include tumor impurity, relatively low overall depth of exome sequencing, translocation or fusion genes such as EML4-ALK (37, 38), genomic alterations accumulating in noncoding regions, epigenetic changes (39, 40), and technical underrepresentation by exome capture. This large-scale effort extensively utilized whole-exome sequencing, Sequenom technology, and CNV arrays to detect dozens of novel driver candidates and CNVs, and yet only a small fraction (9% + 6% = 15%) of lung adenocarcinomas can be additionally explained by these genomic alternations compared with 69% of lung adenocarcinomas that can be explained by the genomic alternations that accumulated on six previously reported genes (Supplementary Fig. S6). To comprehensively verify the molecular causes responsible for the 15% of unexplained lung adenocarcinomas, we speculate that future efforts should be directed toward utilizing multiplatform technologies that concurrently monitor the transcriptome, methylome, and noncoding genome, in addition to coding genomes and CNVs.

Although we detected a large number of significantly mutated genes in most of the 170 patients in our discovery cohort, the overall prevalence of mutations in a few genes was lower than previously reported. For instance, KRAS has been reported as mutated in about 12% of Asian patients with lung adenocarcinoma (9), whereas in the present study, KRAS was only affected in 6% of patients in both the discovery and validation cohorts. To validate the prevalence of KRAS and a few other genes in our dataset, we used the more sensitive Sequenom approach, which utilizes mass spectroscopy-based genotyping. Accordingly, 81%

**Figure 3.** Rb1 gene inactivation associated with expression changes of cell-cycle-related proteins in lung adenocarcinoma tumors. A, protein expression of cell-cycle-related proteins in 170 tumor samples as measured by IHC (see Materials and Methods). B, altered protein expression of cyclinD1, E2F1, and pRB1 in tumors with inactivated Rb1 compared with tumors with unaltered Rb1. C, elevated protein expression of cyclinE1 in tumors with high expression of E2F1.
of EGFR substitutions (29 of 36) and 100% of BRAF substitutions (3 of 3) detected by the Sequenom technology were also detected by exome sequencing (Supplementary Table S12). However, only 21% of KRAS substitutions (3 of 18) detected using this technology were detected in our exome dataset.

To understand the underlying reasons for this discrepancy, we looked at the depths of the sequence reads and found that the median read depth of the first KRAS exon (where the recurrent mutations were located) was significantly lower than that in other KRAS regions ($P < 2.2 \times 10^{-16}$, rank-sum test). However, this phenomenon seems to be specific to our exome data because another exome sequencing study on AML-M5 did not show a lower read depth for the first KRAS exon (Supplementary Fig. S7; ref. 41). Therefore, we speculate that the low detection sensitivity of our exome data may be due to low capturing efficiency in specific regions of the exome, including the first KRAS exon. In support of this hypothesis, the read depth of the first KRAS exon in patients in whom we were unable to detect KRAS mutations was significantly lower than in patients who have detectable KRAS mutations ($P < 2.2 \times 10^{-16}$, rank-sum test; Supplementary Fig. S7C). These findings illustrate that, depending on the exome-capturing platform, genomic studies based on exome sequencing might include significantly underrepresented regions. Thus, alternative technologies should be used to compensate for low detection sensitivity in such regions. In this study, we complemented EGFR, KRAS, and $PIK3CA$ mutations using Sequenom-detected mutations. This increased the overall prevalence of EGFR, KRAS, and $PIK3CA$ mutations from 28%, 6%, and 5% to 44%, 14%, and 6%, respectively.

There are several genes that have been previously reported to be driver candidates in lung adenocarcinoma but that were not detected in our analysis, such as KEAP1 and STK11 (6, 8, 20). Of the 247 patients, only 4 patients had KEAP1 mutations, and only 2 patients had STK11 mutations. The lower prevalence of these mutations, compared with a previous study done in the United States where 22 and 27 out of 183 patients bore mutations in KEAP1 and STK11, respectively (8), may be the major reason these genes were not detected as driver candidates in our analysis. The low prevalence of mutated KEAP1 and STK11 may be due to the low capture efficiency discussed above or to the different ethnic backgrounds of the study populations. The median sequence depths of KEAP1 and STK11 (22 and 7, respectively;
Supplementary Fig. S8) are much lower than the median depth of 40 for the overall tumor samples and are lower than the depths of known driver genes such as EGFR, KRAS, and BRAF (45, 48, and 43, respectively), indicating that the lower capture efficiency may be at least partially responsible for the low prevalence. It is also possible that the prevalence of these genes in the Asian population may differ from that of Western populations. Supporting this possibility, another independent exome study on patients with lung adenocarcinoma in South Korea reported low prevalence of mutated STK11 (2 out of 87) and KEAP1 (3 out of 87; ref. 9).

The Cancer Genome Atlas (TCGA) recently reported a comprehensive molecular profile of 230 patients with lung adenocarcinoma with diverse ethnic backgrounds (20). Although the TCGA study agrees well with ours on many key findings such as a higher overall mutation rate in smokers than in never-smokers and the negative association between EGFR and KRAS mutations, there are noticeable differences between the two studies. For example, among the 18 and 22 significantly mutated genes detected in the studies, TCGA and ours, respectively, only six genes (EGFR, TP53, KRAS, PIK3CA, RB1, and SETD2) were found to be present in both lists. Also, the prevalence of EGFR mutations was much higher in our study (42.4%) than in the TCGA study (14.3%). These differences may have originated from the differences in ethnic backgrounds and the relative fraction of smokers included in the analysis. Indeed, the TCGA study had a smaller fraction of never-smokers (14.3%, n = 33) than in ours (49%, n = 122) and the different mutation profiles related to ethnic backgrounds have been previously reported (9, 42). These two studies should be complementary to each other, providing a more comprehensive molecular profile of lung adenocarcinoma and a useful resource for future comparative studies that aim to analyze the complexity and the heterogeneity of lung adenocarcinoma.

To reduce potential false positives in this study, we used a more stringent MuTect parameter, and by doing so, we might have sacrificed the overall detection sensitivity. To estimate the number of mutations we might be missing due to our stringent parameters, we compared the overall detection sensitivity between our current stringent parameter (MuTect \( \theta_T = 8.0 \)) and the more lenient default detection parameter (MuTect \( \theta_T = 6.3 \)). The more lenient cutoff increased the total number of detected mutations by 50%, from 25,065 to 37,548. However, the prevalence of known driver genes was not significantly affected. For instance, the prevalence of EGFR was 42.9% using the lenient cutoff compared with 42.4% using our current stringent cutoff. Similarly, the prevalence of TP53 and PIK3CA only increased marginally, from 25.3% to 28.8% for TP53 and from 14.1% to 14.7% for PIK3CA. The prevalence of other driver genes was similarly unchanged (Supplementary Table S13). For 45 known driver genes, using the more stringent cutoff reduced the average prevalence only by 0.5% in comparison with the default parameter, indicating that the additional mutations detected using the lenient cutoff might include a high fraction of false positives.

It has been reported that lung adenocarcinoma has a high overall mutation rate (MR), and that the MR is higher in smokers than in never-smokers (8, 43). In comparison with previous reports, our overall MR was a bit lower, probably due to our high detection stringency. Using the current stringent cutoff, we obtained MRs of 5.5/Mbp and 1.9/Mbp for smokers and never-smokers, respectively (Supplementary Fig. S9A). When the lenient cutoff was applied, the MR of smokers increased to 7.7/Mbp. However, the MR of never-smokers also increased, to 4.4/Mbp, resulting in too little difference in MR between smokers and never-smokers (Supplementary Fig. S9B). Repeated analysis with an even more lenient parameter (\( \theta_T = 5.5 \)) resulted in nearly equal MRs (11.1/Mbp for smokers and 8.5/Mbp for never-smokers, Supplementary Fig. S9C). These analyses also suggest that the additional substitutions detected using the lenient cutoff might include many false positives. We concluded that the stringent cutoff results in a more robust set of substitutions at the expense of lowered detection sensitivity. Therefore, we decided to continue to use the more stringent parameter instead of the lenient parameter.

It is noteworthy that the current treatment guidelines for early-stage lung adenocarcinoma provided by the National Comprehensive Cancer Network recommend follow-up without adjuvant therapy after complete resection, except for patients who have residual tumors or those considered at high risk (10). However, because the long-term treatment failure rate is close to 50% (10), it is important to identify subgroups of patients who may benefit from adjuvant treatments such as chemotherapy, even in early-stage lung adenocarcinoma. Our discovery that RB pathway mutations are associated with poor prognosis calls for additional clinical interventions that could improve the clinical outcomes of early-stage lung adenocarcinoma patients. In particular, a set of validated diagnostic markers that could detect genomic alterations in the RB pathway would be useful for patient stratification.

RB protein acts as a tumor suppressor that inhibits cell-cycle progression by binding and inhibiting transcription factors of the E2F family. When RB is phosphorylated to pRB by cyclin-dependent kinases, it is unable to form a complex with E2F, which allows E2F to promote cell-cycle progression (44). In this study, lower levels of pRB and cyclin D1 and higher levels of E2F1, a member of the E2F family, were detected in tumors with RB1 alterations compared with tumors without RB1 alterations. These findings agree with a previous report showing a lack of cyclin D1 overexpression and high E2F1 levels in tumors with RB loss (36). Lack of cyclin D1 overexpression in RB loss can be explained by the increased disassembly of cyclin D-cdk4 complexes and increased cyclin D turnover (36, 45). We also observed that tumors with RB1 alterations are characterized by low pRB levels and high E2F1 levels, which may explain the poor prognosis of these patients. In addition, our study reveals that high E2F1 protein expression is associated with high cyclin E1 levels, which is consistent with the fact that E2F binds the promoter of the cyclin E gene and increases its expression. High levels of E2F1 and cyclin E1 in tumors with RB1 alterations suggest that the prognostic effect of RB1 alterations may be related to the actions of these downstream molecules of Rb1. Our analysis suggests that either pan-CDK inhibitors or selective CDK inhibitors, being used more frequently in clinical trials (46), might be effective to target these downstream molecules of Rb1.

Our analysis of the whole exome, CNV dataset, and fully annotated clinical data provide comprehensive insights into the genomic portrait of lung adenocarcinoma and help define the molecular signatures of lung adenocarcinoma subtypes. These findings could lead to the discovery of useful prognostic markers and help devise personalized treatment strategies for patients with early-stage lung adenocarcinoma.

**Disclosure of Potential Conflicts of Interest**

No potential conflicts of interest were disclosed.
Choi et al.

Authors' Contributions

References


Grant Support
This work was supported by the National Project for Personalized Genomic Medicine, Ministry of Health and Welfare of Korea (A111218-SC01), by the Leading Foreign Research Institute Recruitment Program (2011-0030105) and the Basic Science Research Program (2011-0014523), the Ministry of Education, Science, and Technology of Korea, and by the Institute for Basic Science (EM1302). The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked advertisement in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

Published OnlineFirst October 7, 2014; DOI: 10.1158/1078-0432.CCR-14-0519

Clinical Cancer Research

2622 Clin Cancer Res; 21(11) June 1, 2015

Downloaded from clinicaners.acrjjournals.org on June 4, 2017, © 2015 American Association for Cancer Research.


Genomic Alterations in the RB Pathway Indicate Prognostic Outcomes of Early-Stage Lung Adenocarcinoma

Seongmin Choi, Hyeong Ryul Kim, Chang Ohk Sung, et al.


Updated version
Access the most recent version of this article at:
doi:10.1158/1078-0432.CCR-14-0519

Supplementary Material
Access the most recent supplemental material at:
http://clincancerres.aacrjournals.org/content/suppl/2014/10/08/1078-0432.CCR-14-0519.DC1

Cited articles
This article cites 45 articles, 9 of which you can access for free at:
http://clincancerres.aacrjournals.org/content/21/11/2613.full.html#ref-list-1

Citing articles
This article has been cited by 1 HighWire-hosted articles. Access the articles at:
/content/21/11/2613.full.html#related-urls

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.