Impact of Smoking Cessation on Global Gene Expression in the Bronchial Epithelium of Chronic Smokers

Li Zhang,¹ J. Jack Lee,¹ Hongli Tang,² You-Hong Fan,² Lianchun Xiao,¹ Hening Ren,² Jonathan Kurie,² Rodolfo C. Morice,² Waun Ki Hong² and Li Mao²

Abstract

Cigarette smoke is the major cause of lung cancer and can interact in complex ways with drugs for lung cancer prevention or therapy. Molecular genetic research promises to elucidate the biological mechanisms underlying divergent drug effects in smokers versus non-smokers and to help in developing new approaches for controlling lung cancer. The present study compared global gene expression profiles (determined via Affymetrix microarray measurements in bronchial epithelial cells) between chronic smokers, former smokers, and never smokers. Smoking effects on global gene expression were determined from a combined analysis of three independent data sets. Differential expression between current and never smokers occurred in 591 of 13,902 measured genes ($P < 0.01$ and $>2$-fold change; pooled data)—a profound effect. In contrast, differential expression between current and former smokers occurred in only 145 of the measured genes ($P < 0.01$ and $>2$-fold change; pooled data). Nine of these 145 genes showed consistent and significant changes in each of the three data sets ($P < 0.01$ and $>2$-fold change), with eight being down-regulated in former smokers. Seven of the eight down-regulated genes, including CYP1B1 and three AKR genes, influence the metabolism of carcinogens and/or therapeutic/chemopreventive agents. Our data comparing former and current smokers allowed us to pinpoint the genes involved in smoking-drug interactions in lung cancer prevention and therapy. These findings have important implications for developing new targeted and dosing approaches for prevention and therapy in the lung and other sites, highlighting the importance of monitoring smoking status in patients receiving oncologic drug interventions.

Chronic cigarette smoking is the major cause of lung cancer and remains so for years even after smoking cessation (1, 2). Therefore, the development of agents for controlling lung cancer generally targets, virtually by default, current and former heavy smokers. Smoking status, however, seems to influence response to various chemopreventive and chemotherapeutic agents and clinical outcomes of their use (3, 4). Three large randomized clinical trials to prevent lung cancer—the Alpha-Tocopherol, Beta-Carotene Prevention Study (5), Carotene and Retinol Efficacy Trial (6), and Lung Intergroup Trial (7)—showed that current heavy smokers had harmful interactions (higher lung cancer mortality, incidence, and recurrence) with preventive agents (versus control arms); agent effects in former smokers were generally neutral and were not readily interpretable in never smokers because of the exclusion or very limited number of these patients in these trials. Certain lung cancer therapy regimens have been shown to be less effective in current smokers than in former and never smokers (8, 9). Smoking can stimulate the metabolic clearance of targeted anticancer therapies, undoubtedly diminishing therapeutic benefit (9, 10). These data highlight the importance of understanding the biological effect of chronic smoking on lung tissue.

To understand why smokers and former smokers have differential responses to agents for preventing or treating lung cancer, we analyzed and compared global gene expression profiles in three independent cancer-free cohorts comprising current, former, and never smokers.

Materials and Methods

Study population

This study included current smokers, former smokers, and never smokers with no evidence of cancer and collected from separate, independent studies conducted at The University of Texas M. D. Anderson Cancer Center (MDACC; two studies) and the Boston Medical Center (BMC; one study). The three data sets associated with the three studies are called MDACC-1, MDACC-2, and BMC throughout this article. Former smoking was defined as having quit smoking for at least...
12 months before study entry. Participants included in the MDACC-1 and MDACC-2 data sets came from the placebo arm of an ongoing chemoprevention trial done at M. D. Anderson Cancer Center. All MDACC subjects were clinically free of cancer at enrollment and underwent a bronchoscopy at baseline. Bronchial brushes were done at six predetermined sites including the entry area at each of the five main lobes and the carina, as previously described (11). The study was approved by the MDACC Institutional Review Board, and all MDACC participants gave signed informed consent. BMC data set participants had a bronchoscopy at the BMC and were analyzed in a previously reported study (12) as well as in the current study. Potential subjects for the MDACC or BMC data sets in the current study were excluded if their specimen images (produced as discussed below in “cRNA preparation and microarray hybridization”) had defects, evidence of blood contamination, or other problems that did not meet image quality criteria applied consistently across all three data sets. All MDACC patients had smoking history, with average pack-years of 40.6 ±(13). Their average age is 58 (±8) years. Sixty-one percent of them are male and 78% of them are White. More details about the demographic data of MDACC data sets can be found in Supplementary Table S2.

**Bronchial brush processing and RNA extraction**

For samples in MDACC-1 and MDACC-2, brushes were placed on bronchoscopy in 3 mL of plain DMEM culture (Life Technologies, Inc.) in sterile tissue culture tubes and stored at 4°C for processing the same day. The tubes were vortexed lightly to detach cells from the brushes. After removal of the brush from the tube, the cell suspension was centrifuged at 2,500 rpm for 5 min. Cell pellets were then washed with 2 mL of PBS twice, and an aliquot of material was saved at −80°C until RNA extraction. For the microarray analysis, cells from the six brushing sites of the same individual were pooled together for RNA extraction. We also ignored data of MM probes. We used PM probes common to U133A and U133 Plus 2 arrays to perform quantile normalization on the probe level data (14). The procedure was done so that the distributions of the probe signal intensities of a sample are identical for all samples within a data set. Then, we used PDNN model (15) to quantify the gene expression values from the normalized probe signal intensity data. We then applied median-centering normalization on the probe set level data so that the median of expression values of a sample was made to be the same for all the samples in all of the data sets.

**Identification of differentially expressed genes**

Differential expression was identified to be similar to that described by Wang et al. (16). We used Z values (defined below) to assess differentially expressed genes between current and never or former smokers, in whom the magnitude of the Z values is assumed to represent the effect of smoking cessation. For a given data set containing nA and nB samples in groups A and B, respectively, we compute the following test statistic Z for each probe set:

\[
Z = D/\sigma
\]

(A)

where D is average difference between the log expression values between A and B groups, \(\sigma\) is the estimated standard deviation (SD) of D:

\[
\sigma = \sqrt{(n_A \sigma_1^2 + n_B \sigma_2^2) / (n_A + n_B)}
\]

(B)

where \(\sigma_1^2\) and \(\sigma_2^2\) are estimated variances of log expression values in groups A and B, respectively. These variances were estimated using Loess fit between the mean log expression values and the SD of the log expression values. The underlying assumption is that the mean and the SD are related by a smooth function, which allows the analysis method to treat the SD as if it were known.

**Combining Z values from different data sets**

The Z values obtained from the three data sets can be combined using the following formula:

\[
Z = (Z_1 / \sigma_1^2 + Z_2 / \sigma_2^2 + Z_3 / \sigma_3^2) / \omega^2
\]

(C)

\[
\omega^2 = 1 / \sigma_1^2 + 1 / \sigma_2^2 + 1 / \sigma_3^2
\]

(D)

where \(Z_1, Z_2,\) and \(Z_3\) were calculated using Eq. A from MDACC-1, MDACC-2, and BMC data sets, respectively; \(\sigma_1, \sigma_2,\) and \(\sigma_3\) were calculated using Eq. B from MDACC-1, MDACC-2, and BMC data sets, respectively.

The test statistic Z is supposed to form a T distribution if the log expression values are normally distributed. However, the observed data slightly deviate from the normal distribution because they contain more extreme values. Consequently, the significance of Z can be overestimated. To alleviate the bias due to the assumption of normal distribution, we used permuted data to compute Z*. The expression values are randomly permuted for each probe set within each data set. The permutation was done 10 times to construct an empirical cumulative distribution function of Z*. This distribution was assumed to be...

**Table 1. Sample sizes and array types of the microarray data sets**

<table>
<thead>
<tr>
<th>Data set</th>
<th>FS</th>
<th>CS</th>
<th>NS</th>
<th>Array type</th>
</tr>
</thead>
<tbody>
<tr>
<td>MDACC-1</td>
<td>7</td>
<td>11</td>
<td>0</td>
<td>U133A</td>
</tr>
<tr>
<td>MDACC-2</td>
<td>8</td>
<td>15</td>
<td>0</td>
<td>U133 Plus 2</td>
</tr>
<tr>
<td>BMC</td>
<td>9</td>
<td>30</td>
<td>19</td>
<td>U133A</td>
</tr>
</tbody>
</table>

Abbreviations: FS, former smoker; CS, current smoker; NS, never smoker.

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the distribution of \( Z \) values under null hypothesis (i.e., no differential expression), and it was used to estimate the \( P \) values and the false discovery rate associated with \( Z \) values. The permutation was done within each of the data sets, but never across the data sets. Note that other than the permutation step, our method is the same as that described by Wang et al. (16).

**Results**

Our overall study population numbered 99 individuals, composed of 56 current smokers, 24 former smokers, and 19 never smokers from three independent data sets (Table 1). The MDACC-1 and MDACC-2 data sets included 41 chronic smokers (26 current, 15 former) enrolled in an ongoing chemoprevention trial at M. D. Anderson Cancer Center. All 41 of these subjects had at least a 20-pack-year smoking history. Demographic characteristics of the MDACC cohorts are included in Supplementary Table S1. The BMC data set was composed of 75 current, former, and never smokers. Never smokers with significant environmental cigarette exposure and subjects with respiratory symptoms or who regularly use inhaled medications were excluded. We selected 58 members of the BMC cohort for the present analysis (Table 1) and excluded 17 subjects. Exclusions from either the BMC or MDACC data sets were based on image quality criteria applied consistently across all three data sets.

First, we determined \( Z \) values (defined in Materials and Methods) in the three data sets separately. Then, we compared the \( Z \) values from each data set and, as shown in Fig. 1, we found that the genes with the most significant differential expressions (shown in red) are similar among the three data sets. The largest \( Z \) values mostly are located in the first and third quadrants in the scatter plots of Fig. 1, indicating that these

![Fig. 1. Comparison of \( Z \) values obtained from the three data sets (BMC, MDACC-1, and MDACC-2). Each point in these scatter plots represents a probe set. The probe sets with absolute \( Z \) values >5 in all three data sets are shown in red. Detailed data on these probe sets are in Table 2.](image1)

![Fig. 2. Quantile-quantile plots of \( Z \) values. A, quantile of \( Z \) values versus quantile of \( Z \) values obtained from permuted data. B, quantile of \( Z \) values from permutation data versus quantile values of standard normal distribution.](image2)
changes in gene expression are consistent among the three data sets.

To further assess the statistical significance of the changes in gene expression between former and current smokers, we used quantile-quantile plots (Fig. 2) of Z values and BUM plots (Fig. 3) to evaluate the distribution of P values. Figure 2A compares the quantiles of Z values calculated from combining all three microarray data sets and the quantiles of Zp (Z values calculated from permuted data). With permuted data, Z values are bounded between −10 and 10. The Z values from observed data contain clear outliers >10. Without differential expression, the data points in Fig. 2A should be close to the diagonal line (shown in red). Ideally, if the gene expression data obey normal distributions and are independent from each other, we would expect values of Zp to form a standard normal distribution. However, Fig. 2B shows that Zp’s have wider ranges than that from standard normal distribution. Consequently, we used the distribution of Zp, as that from the null hypothesis (no differential expression between former and current smokers) to compute the P values of Z instead of using the standard normal distribution.

The BUM plot (17) presented a histogram of the P values. Under the null hypothesis, the P values should form a uniform distribution. The sharp spike at the left side of Fig. 3 represents the effects of differential expression contradicting the null hypothesis. The uniform part of the histogram is indicated by the red line in Fig. 3. The area above the red line contains ~1,200 probe sets, which is our estimated number of genes that are differentially expressed between the former smokers and current smokers. Only a subset of these genes is identifiable, however. According to the BUM method (17), we found 345 probe sets that were differentially expressed at a P value of <0.01, for which the false discovery rate was estimated to be 32%. Of the 345 probe sets, 176 have a >2-fold difference in expression (details of these 176 probe sets are shown in Supplementary Table S2). These 176 probe sets represent 145 nonredundant significantly differentially expressed genes (>2-fold change; P < 0.01). These 145 genes include 9 genes (Table 2) with consistent and significant changes in each of the three data sets (P < 0.01; >2-fold change). Eight of the nine genes are down-regulated after smoking cessation; one is up-regulated. To test the general accuracy of our microarray measurements, we compared them with reverse transcription-PCR measurements of a selected panel of genes, finding that the reverse transcription-PCR and microarray measurements were highly correlated, 96% [e.g., in the case of ALDH3A1 (Supplementary Fig. S1), which is the gene with the largest change between former and current smokers (Table 2)].

Furthermore, although not calculated, the false discovery rate for the subset of 176 probe sets

<table>
<thead>
<tr>
<th>Gene</th>
<th>Fold changes</th>
<th>P (comb.)</th>
<th>Full name</th>
<th>RefSeq</th>
<th>Probe set</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALDH3A1</td>
<td>6.9</td>
<td>9.4</td>
<td>4.0 6.2 0.0000 aldehyde dehydrogenase 3 family, member 1</td>
<td>NM_000691</td>
<td>205623_at</td>
</tr>
<tr>
<td>CYP1B1</td>
<td>4.2</td>
<td>5.7</td>
<td>6.7 4.9 0.0000 cytochrome P450, member 1B1</td>
<td>NM_000104</td>
<td>202436_s_at</td>
</tr>
<tr>
<td>MUC5AC</td>
<td>2.2</td>
<td>9.6</td>
<td>3.0 3.5 0.0000 mucin 5AC, oligomeric mucus/gel-forming</td>
<td>XM_001130382</td>
<td>214385_s_at</td>
</tr>
<tr>
<td>AKR1C2</td>
<td>3.3</td>
<td>4.2</td>
<td>3.5 3.5 0.0000 aldo-keto reductase family 1, member C2</td>
<td>NM_001354</td>
<td>209699_x_at</td>
</tr>
<tr>
<td>AKR1B10</td>
<td>3.2</td>
<td>4.2</td>
<td>3.8 3.5 0.0000 aldo-keto reductase family 1, member B10</td>
<td>NM_020299</td>
<td>206561_s_at</td>
</tr>
<tr>
<td>AKR1C1</td>
<td>2.8</td>
<td>4.0</td>
<td>3.3 3.2 0.0000 aldo-keto reductase family 1, member C1</td>
<td>NM_001353</td>
<td>204151_x_at</td>
</tr>
<tr>
<td>NQO1</td>
<td>2.8</td>
<td>2.3</td>
<td>2.4 2.6 0.0001 NAD(P)H dehydrogenase, quinone 1 member C3</td>
<td>NM_00903</td>
<td>210519_s_at</td>
</tr>
<tr>
<td>AKR1C3</td>
<td>2.5</td>
<td>2.1</td>
<td>3.1 2.5 0.0000 aldo-keto reductase family 1, member C3</td>
<td>NM_003739</td>
<td>209160_at</td>
</tr>
<tr>
<td>SCGB1A1</td>
<td>−2.0</td>
<td>−2.4</td>
<td>−2.6 −2.4 0.0001 secretoglobin, family 1A, member 1</td>
<td>NM_003357</td>
<td>205725_at</td>
</tr>
</tbody>
</table>
should be lower than that (32%) estimated for the 345 probe sets, and the false discovery rate for the nine changed genes that were validated across three data sets should be lower still because each subset adds new criteria that increase reliability.

For comparison, we also examined differential gene expression between current and never smokers (Fig. 4A). Similar to that in Fig. 3, the peak volume above the red line represents the number of differentially expressed genes, which is ~11,000 probe sets. This number is >9 times greater than the number detected in the comparison between former and current smokers (Fig. 3). We found 591 nonredundant genes with statistically significant changes (>2-fold change and \( P < 0.01 \)) in pooled data of the three data sets, a group that is >4 times larger than the group of such differentially expressed genes detected in the comparison between current and former smokers. Of the 145 significantly changed genes between current and former smokers, 77 are consistent with, and 68 are not consistent with, the 591 such genes between current and never smokers (Supplementary Table S2). The nine genes with consistent and significant changes between former and current smokers in each of the three data sets are in the subset of 77 common, significantly changed genes. Figure 4B compares former smokers with never smokers.

The scope of differential expressions in Fig. 4A is much larger than that in Fig. 3, which may be due to differences in sample size. A principal component analysis (Fig. 5), however, supported the conclusion that the larger differential expression in Fig. 4A compared with that in Fig. 3 is not simply due to sample size. The gene expression profile of each patient is represented by its two main principal components. Two distinct clusters emerge in Fig. 5, and the cluster to the left (Comp1 < −10) contains mostly never smokers. The right-side cluster is predominated by a mixture of current and former smokers, which supports the conclusion that former smokers are more similar to current smokers than to never smokers.

**Discussion**

In probing 13,902 genes, we found that 591 were differentially expressed in current versus never smokers and that only 145 of these 591 (25%) were also differentially expressed in current versus former smokers. Among these 145 genes, 9 were significantly differentially expressed (8 overexpressed, 1 underexpressed; Table 2) by >2-fold in current versus former smokers in each \( (P < 0.01) \) and in the pooled data \( (P < 0.0001) \) of the three data sets (two MDACC, one BMC) included in this study. Therefore, our present study pinpoints and validates nine differentially expressed genes in former versus current smokers.

Seven of the eight validated genes overexpressed in current smokers—CYP1B1, four AKRs, ALDH3A1, and NQO1 (Table 2)—are involved in drug and/or carcinogen metabolism (9, 10, 18–27). Polycyclic aromatic hydrocarbons in tobacco smoke are known to bind to and activate the aryl hydrocarbon receptor and thus induce CYP1B1 (10). CYP1B1 expression is of special interest because it may contribute both to increased drug metabolism and to carcinogenesis of the aerodigestive tract (1, 18–20). The metabolic clearance of docetaxel, tamoxifen, gefitinib, erlotinib, and other cancer prevention and therapy drugs is enhanced by YP1B1 (9, 21–23). Upregulation of CYP1B1 and the six other validated overexpressed metabolizing genes by smoking is likely involved in the adverse interactions between smoking and drugs for lung cancer prevention and therapy; smoking cessation down-regulates these gene expressions and thus may reduce or eliminate the adverse drug interactions.

Four of the eight most-up-regulated genes we detected in current smokers (Table 2) are members of the AKR
extended their earlier study, as do the complementary and publication, the Spira group published another report (34) that our MDACC data sets. As we prepared our present results for our gene expression analyses by adding the BMC data set to provided us with the opportunity to increase the robustness of oxidant genes in current versus former smokers; ref. 12) prod- broad array of differentially expressed metabolizing and anti- environmental influences. A report by Spira et al. (on a relatively duals, however, because of genetic variations and different en- lungs. Gene expression patterns vary greatly between indivi-
ded in this study.

Various biases can produce inconsistencies between similar data sets. These biases can stem from differences in age, race, sex, smoking history, and sample processing. Regarding sample processing, for example, MDACC-1 and MDACC-2 samples involved two rounds of RNA amplification versus a single round in the BMC set. Two rounds of amplification are known to cause loss of signals for probes that target far away from the 3′ end of mRNA sequences. The consistent changes in smoking cessation–related genes in all three independent data sets support the robustness of our present findings.

Gene expression profiling in bronchoscopy specimens offers a direct assessment of the effects of cigarette smoking in the lungs. Gene expression patterns vary greatly between individuals, however, because of genetic variations and different environmental influences. A report by Spira et al. (on a relatively broad array of differentially expressed metabolizing and anti-
reviews of our interrelated findings and thus their appeal for hyp-
thesis generation.

our present results for publication, the Spira group published another report (34) that extended their earlier study, as do the complementary and confirmatory findings we report here. We were able to identify the specific drug-metabolizing genes involved in smoking-
drug interactions, including the overexpressed genes in cur-
rent versus former smokers, because of the cross validation and increased statistical power provided by adding the BMC data set (12) to our MDACC-1 and MDACC-2 data sets. The combined effect of these reports is to increase the robust-

We combined the effects of smoking and drug interactions, including the overexpressed genes in current versus former smokers, because of the cross validation and increased statistical power provided by adding the BMC data set (12) to our MDACC-1 and MDACC-2 data sets. The combined effect of these reports is to increase the robustness of the pathways for drug-metabolizing genes that were validated in this study.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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