

Novel Association of Genetic Markers Affecting CYP2A6 Activity and Lung Cancer Risk

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Abstract

Metabolism of nicotine by cytochrome P450 2A6 (CYP2A6) is a suspected determinant of smoking dose and, consequently, lung cancer risk. We conducted a genome-wide association study (GWAS) of CYP2A6 activity, as measured by the urinary ratio of *trans*-3'-hydroxycotinine and its glucuronide conjugate over cotinine (total 3HCOT/COT), among 2,239 smokers in the Multiethnic Cohort (MEC) study. We identified 248 CYP2A6 variants associated with CYP2A6 activity ($P < 5 \times 10^{-8}$). CYP2A6 activity was correlated ($r = 0.32$; $P < 0.0001$) with total nicotine equivalents (a measure of nicotine uptake). When we examined the effect of these variants on lung cancer risk in the Transdisciplinary Research in Cancer of the Lung (TRICL) consortium GWAS dataset (13,479 cases and 43,218 controls), we found that the vast majority of these individual effects were directionally consistent and associated with an

increased lung cancer risk. Two hundred and twenty-six of the 248 variants associated with CYP2A6 activity in the MEC were available in TRICL. Of them, 81% had directionally consistent risk estimates, and six were globally significantly associated with lung cancer. When conditioning on nine known functional variants and two deletions, the top two SNPs (rs56113850 in MEC and rs35755165 in TRICL) remained significantly associated with CYP2A6 activity in MEC and lung cancer in TRICL. The present data support the hypothesis that a greater CYP2A6 activity causes smokers to smoke more extensively and be exposed to higher levels of carcinogens, resulting in an increased risk for lung cancer. Although the variants identified in these studies may be used as risk prediction markers, the exact causal variants remain to be identified. *Cancer Res*; 76(19): 5768–76. ©2016 AACR.

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Introduction

Globally, lung cancer is both the most common cancer and the leading cause of cancer-related deaths (1). Even though smoking is the primary cause of lung cancer, there is growing evidence for the involvement of genetics in the susceptibility to this disease. Genome-wide association studies (GWAS) have identified over ten genetic regions associated with lung cancer risk, which, combined, explain only a modest fraction of lung cancer heritability (8%; ref. 2). Expanding GWAS datasets should continue to yield new lung cancer susceptibility loci. However, it is also estimated that genetic determinants of smoking behavior account for a greater percentage (24%) of lung cancer's heritability (2). Indeed, there is growing evidence that tobacco carcinogen uptake by smokers and, consequently, lung cancer risk is strongly affected by two genetically determined traits: nicotine dependence and self-dosing of nicotine.

GWAS have demonstrated that variation at chromosome 15q25.1, which includes the nicotinic receptor subunit genes *CHRNA5-CHRNA3-CHRNA4*, is the strongest susceptibility locus for nicotine dependence and lung cancer (3–5). These studies have particularly highlighted the role of SNP rs16969968, which results in a functional *CHRNA5* variant (D398N). Smokers with this variant have been shown to not only smoke more cigarettes but also to uptake more nicotine and carcinogens per cigarette (6).

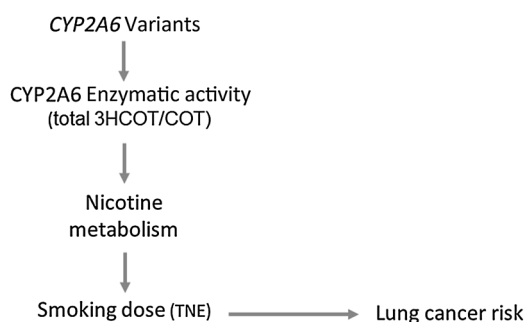


Figure 1.

Causal model in smokers. In order to achieve the desired psycho-pharmacologic effects of nicotine, smokers adjust their cigarette consumption to maintain stable levels of nicotine in the circulation. A high nicotine metabolism rate, as measured by the urinary ratio of *trans*-3'-hydroxycotinine and its glucuronide conjugate over cotinine (total 3HCOT/COT), causes the individual to smoke more extensively (i.e., smoke more cigarettes per day and/or extract a greater nicotine dose per cigarette) to reach the same plasma nicotine level as an individual who metabolizes nicotine less rapidly. Smoking more extensively results in a greater exposure to tobacco smoke carcinogens and, hence, likely to a higher risk of developing lung cancer.

Fewer large studies have focused on the metabolism of nicotine, as a determinant of smoking dose and lung cancer risk. Cytochrome P450 2A6 (CYP2A6)-catalyzed C-oxidation accounts for at least 75% of nicotine metabolism (7). Nicotine is metabolized into cotinine (COT), which is further metabolized to *trans*-3'-hydroxycotinine (3HCOT) primarily by the same enzyme. 3HCOT is further metabolized by glucuronidation, and quantifying the sum of 3HCOT and its glucuronide conjugate, referred to as "total 3HCOT," captures the total conversion of cotinine to 3HCOT. The ratio of total 3HCOT to COT has traditionally been used to assess CYP2A6 activity (8). Differences in the rate of nicotine metabolism have been shown to contribute to interindividual variation in smoking behavior (9, 10) and, consequently, lung cancer risk (11–13). In order to achieve the desired psycho-pharmacologic effects of nicotine, smokers have been shown to adjust their cigarette consumption to maintain stable levels of nicotine in the circulation (14). A slower nicotine metabolism rate causes the individual to smoke less extensively (i.e., smoke fewer cigarettes per day (CPD) and/or extract lower nicotine dose per cigarette) to reach the same plasma nicotine level as an individual who metabolizes nicotine more rapidly (Fig. 1; ref. 15). Smoking less extensively results in a lower exposure to tobacco smoke-derived carcinogens and, hence, likely to a lower risk of developing lung cancer. While genetic variation in CYP2A6 has been shown to influence smoking behavior (2), to date, GWAS have not identified CYP2A6 as a risk variant for lung cancer.

We report here on a large genome-wide investigation of the genetic variants affecting CYP2A6 activity among smokers in the Multiethnic Cohort (MEC) Study (16) and on their associations with lung cancer risk in the largest GWAS dataset available to date for this disease, the Transdisciplinary Research In Cancer of the Lung (TRICL) consortium (17). These two agnostic association studies, one of a biomarker trait that affects the primary exposure and the other of the disease itself, allowed us to empirically consider biological plausibility and internal validity, in addition to the usual GWAS criteria for independence of effects and

genome-wide statistical significance, in interpreting each variant's association with lung cancer.

Methods for the MEC smokers GWAS

Study population

The MEC is a prospective cohort study that investigates lifestyle and genetic risk factors for cancer and other chronic diseases (16). The MEC is comprised of 215,251 men and women ages 45 to 75 at baseline and includes five ethnic/racial groups: African Americans and Latinos mostly from Los Angeles, and Japanese Americans, Native Hawaiians, and Whites, mostly from Hawaii. Potential participants were identified from drivers' license files, voter registration lists, and Health Care Financing Administration files. Each participant entered the study between 1993 and 1996 by returning a self-administered questionnaire detailing demographics, diet, smoking, medical history, and other lifestyle factors.

Approximately 10 years after cohort entry, MEC participants were requested to provide a blood sample and an overnight urine collection in Hawaii or first morning urine sample in California. At that time, they also completed a questionnaire recording the number of cigarettes smoked per day during the past two weeks, and a record of current medications. The overnight urine collection in Hawaii started between 5 and 9 pm and included all urine passed during the night, as well as the first morning urine. Urine collections at both study sites were kept on ice until processing. Aliquots were subsequently stored in a -80°C freezer until analysis. The Institutional Review Boards at the University of Hawaii, the University of Southern California, and the University of Minnesota approved the present study. All MEC participants in the MEC Biospecimen Subcohort who were current smokers at the time of urine collection and cancer-free at selection ($N = 2,393$) were included in this study.

Phenotypes

Total and free nicotine, COT, and 3HCOT in urine were analyzed by LC/MS/MS in a 96-well plate format using methods previously described (18). For the analysis of total 3HCOT, the samples were treated with β -glucuronidase prior to analysis. The coefficients of variation among 10 blinded replicates of 22 samples were 16.7% for total nicotine, 10.1% for total cotinine, and 11.4% for total 3HCOT. The main phenotype of interest, CYP2A6 activity, was assessed from the ratio of total 3HCOT to COT. To account for dose, total nicotine equivalents (TNE), which is the sum of nicotine and its metabolites (total nicotine, total cotinine, and total 3'-hydroxycotinine, including their glucuronides), and nicotine *N*-oxide were used for adjustment in analyses as described earlier (18). Individuals with a TNE less than 1.4 nmol/mL ($n = 80$) were excluded from this analysis.

Genotyping and quality control

Blood leukocyte DNA samples were genotyped using the Illumina Human1M-Duo BeadChip (1,199,187 SNPs). Quality control procedures were applied to the genotyping data as previously described (19). Imputation of untyped variants included in the 1000 Genomes Project (<http://www.1000genomes.org/>) was performed using SHAPEIT (20) and IMPUTE2 (21) using a cosmopolitan reference panel (all groups included). Post imputation, we included SNPs with an IMPUTE2 info score of ≥ 0.30 and minor allele frequency (MAF) $>1\%$ in any MEC ethnic group in our

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association testing. A total of 2,239 study participants with complete genotype and phenotype data, and 11,892,802 SNPs/indels (1,131,426 genotyped and 10,761,376 imputed) were included in the GWAS analysis of CYP2A6 activity (ratio of total 3HCOT to COT).

Statistical analysis

Least-square means (or geometric means) were estimated and compared between populations for the smoking variables. Principal components (PC) were estimated using 19,059 randomly selected autosomal SNPs with frequency $\geq 2\%$ in the combined multiethnic sample. The 10 leading eigenvectors from this matrix were included in the analysis to adjust for population stratification (22). The per allele association of each SNP/indel with geometric mean CYP2A6 activity levels was evaluated using linear regression models, with adjustment for age at the time of urine collection, sex, self-reported ethnicity, TNE, body mass index (BMI, kg/m²), and the first 10 principal components described above. A *P* value cut-off of 5×10^{-8} was used to establish genome-wide significance (23). Ethnic-specific analyses were also performed to search for loci that may be important in individual populations. To determine the relative importance of multiple SNPs in a region or genome-wide, we used multiple regression methods. All SNPs showing globally significant associations were allowed to compete in forward selection regression models, and all variables that entered with a significance level of *P* < 0.001 were retained (19). This allowed us to estimate the number of independent signals that may be involved in each region associated with each phenotype of interest. *R*² value was used to assess the percentage of variation of CYP2A6 activity accounted for by the variants examined.

Methods for the TRICL Lung Cancer GWAS Consortium

Study population

The association study with lung cancer risk was conducted using the GWAS data assembled by the TRICL consortium. The overall study design and methods for TRICL have been described in detail elsewhere for most studies (17). The meta-analysis was based on summary data from 19 GWAS undertaken by eight analytic centers providing genotype data on 13,479 patients with lung cancer and 43,218 controls of European descent: the MD Anderson Cancer Center lung cancer study (24); the NCI lung cancer GWAS including the Environment and Genetics in Lung Cancer Etiology (EAGLE) study (25) and the Prostate, Lung, Colon, Ovary Screening Trial (PLCO; ref. 26); the International Agency for Research on Cancer (IARC) lung cancer GWAS (5) including Central Europe GWAS (27); the Carotene and Retinol Efficacy Trial (CARET) cohort lung cancer GWAS (28); the HUNT2/Tromsø 4 study (29); several lung cancer GWAS studies from Central Europe and France (30); the lung cancer study from Estonia (31); the German Lung Cancer Study (GLC; ref. 32); the Greater Toronto Area lung cancer study (ref. 5; 331 cases and 499 controls); and the Icelandic Lung Cancer Study (deCODE; 1,319 cases and 26,380 controls; ref. 3). Each TRICL study requested from each smoker (defined as individuals who smoked at least 100 cigarettes in their life) the number of cigarettes smoked per day and the number of years smoked. Pack years was then calculated as cigarettes per day/20 times number of years smoked. Lung cancer diagnosis was based on histopathology or cytology. A written informed consent was obtained from each participant, and this study was approved by

the Institutional Review Boards of the University of Hawaii and University of Southern California. The lung cancer GWAS were approved by each of the participating institutions.

Genotyping and quality control

Standard quality control on samples was performed on all scans, excluding individuals with low call rate (<90%) and extremely high or low heterozygosity ($P < 1.0 \times 10^{-4}$), as well as all individuals evaluated to be of non-European ancestry (using the HapMap phase II CEU, JPT/CHB, and YRI populations as a reference). In each study, genotyping was performed using the Illumina HumanHap 300 BeadChips, HumanHap550, or 610 Quad arrays. Untyped SNPs were imputed using the IMPUTE2 (21), MACH1 (33) or minimac (34) software, and HapMap Phase II, Phase III, and/or 1000 Genome Project data release 2010-08 or 2010-06 reference genotypes. Imputation uncertainty was accounted for by using posterior means or allele dosage in logistic regression (17). The meta-analysis of imputed genotypes included all studies. Poorly imputed SNPs defined by an RSQR < 0.30 with MACH1/minimac or an information measure *I*_s < 0.40 with IMPUTE2 were excluded from the analyses. A subset of 12,000 ancestry markers was used to calculate principal components to estimate genetic ancestry using EIGENSTRAT (35). These PCs of genetic ancestry were included in regression models to adjust for potential population stratification.

Statistical methods

To estimate the association between each SNP and risk of lung cancer, genotyped or imputed allele dosage for each SNP was tested for association in unconditional logistic regressions assuming an additive genetic model for the effect of risk allele. Each study center provided summary statistics from the initial model which were adjusted for age, sex, country/study center, and PCs of genetic ancestry. A secondary model using only ever smokers was fit and further adjusted for pack-years. A meta-analysis under fixed and random-effects models was conducted. The regression estimates were combined across studies using inverse-variance weighted, fixed-effect meta-analysis using METAL, a tool for meta-analysis of genome-wide association scans (36). The Cochran Q statistic was used to test for heterogeneity and to quantify the proportion of the total variation due to heterogeneity. Quantile-quantile (Q-Q) plots of association test statistics showed minimal over-dispersion consistent with limited cryptic population stratification between cases and controls. Conditional analysis for lung cancer risk in the TRICL data was performed using Genome-wide Complex Trait Analysis (GCTA) based on summary statistics (37).

Results

Selected characteristics of the 2,239 MEC smokers (437 Whites, 364 African Americans, 453 Latinos, 674 Japanese Americans, and 311 Native Hawaiians) included in the GWAS analysis of CYP2A6 activity are presented in Table 1. As reported previously, significant differences were observed among ethnic groups in cigarettes per day and TNE, with Whites reporting smoking the highest and Latinos the lowest number of CPD during the previous 2 weeks (18, 19). In contrast, mean TNE (a marker of total nicotine uptake) was highest in African Americans and lowest among Japanese Americans. Significant differences in mean-adjusted CYP2A6 activity levels were noted

Table 1. Descriptive characteristics of the MEC smokers ($N = 2,239$)

	African Americans		Native Hawaiians		Whites		Latinos		Japanese Americans	
	N	Mean (SE)	N	Mean (SE)	N	Mean (SE)	N	Mean (SE)	N	Mean (SE)
Age (y)										
All	364	64.86 (0.38)*	311	61.36 (0.41)***	437	63.69 (0.35)	453	65.53 (0.34)***	674	63.60 (0.29)
Male	111	63.49 (0.65)	114	63.08 (0.64)	190	63.36 (0.50)	237	66.43 (0.45)	388	63.62 (0.36)
Female	253	65.39 (0.47)	197	60.28 (0.54)	247	63.92 (0.48)	216	64.58 (0.51)	286	63.69 (0.47)
CPD ^a										
All	364	11.72 (0.48)***	311	15.52 (0.52)***	437	18.02 (0.43)	453	9.31 (0.43)***	674	13.76 (0.37)***
Male	111	11.98 (0.91)***	114	17.00 (0.91)**	190	21.00 (0.70)	237	10.87 (0.64)***	388	15.58 (0.51)***
Female	253	10.79 (0.53)***	197	14.27 (0.61)	247	15.47 (0.53)	216	8.14 (0.57)***	286	12.05 (0.53)***
TNE ^b										
All	364	44.35 (1.99)***	311	29.43 (1.42)	437	33.05 (1.33)	453	29.60 (1.18)	674	23.72 (0.79)***
Male	111	48.10 (3.94)	114	31.70 (2.58)*	190	40.44 (2.53)	237	31.76 (1.80)**	388	26.65 (1.18)***
Female	253	40.40 (2.12)***	197	27.54 (1.63)	247	28.01 (1.46)	216	28.24 (1.58)	286	21.36 (1.06)***
BMI ^c										
All	364	27.45 (0.26)***	311	26.83 (0.28)***	437	25.03 (0.22)	453	26.87 (0.23)***	674	24.19 (0.17)**
Male	111	26.17 (0.39)	114	26.98 (0.40)**	190	25.53 (0.29)	237	26.41 (0.27)*	388	24.87 (0.20)
Female	253	28.00 (0.35)***	197	26.65 (0.38)***	247	24.65 (0.31)	216	27.37 (0.37)***	286	23.37 (0.27)**
CYP2A6 activity ^d										
All	354	3.95 (0.16)	296	2.78 (0.12)***	418	3.94 (0.14)	431	4.66 (0.16)**	601	1.76 (0.05)***
Male	109	3.64 (0.26)	110	2.88 (0.20)*	182	3.56 (0.19)	225	4.38 (0.21)**	355	1.72 (0.07)***
Female	245	4.18 (0.20)	186	2.74 (0.15)***	236	4.27 (0.20)	206	4.93 (0.25)*	246	1.77 (0.08)***

NOTE: P values across ethnic groups (with Whites as the reference) were indicated where significant as *, $P < 0.05$; **, $P < 0.005$; and ***, $P < 0.0005$.

^aCPD, cigarettes/day. P values and least square means for CPD were adjusted for BMI, age (and gender where appropriate).

^bTNE is the sum of total nicotine, total cotinine, total 3-hydroxycotinine, and nicotine N-oxide expressed as nmol/mL. TNE was log transformed to maintain normality, and the means were back transformed to their original scale. P values and geometric least square means for TNE have been adjusted for BMI, age (and gender where appropriate).

^cBMI expressed as kg/m². BMI was log transformed to maintain normality, and the means were back transformed to their original scale. P values and geometric least square means of BMI were adjusted for age (and gender where appropriate).

^dCYP2A6 activity is the ratio of (total 3-hydroxy cotinine/free cotinine), expressed as percent nmol/mg. CYP2A6 was log transformed to maintain normality, and the means were back transformed to their original scale. P values and geometric least square means of CYP2A6 activity were adjusted for BMI, age, TNE (and gender where appropriate).

across populations, with Japanese Americans having significantly lower levels compared with any other ethnic group. Overall, the correlation between CYP2A6 activity and TNE adjusted for age, sex, race, and BMI was 0.31 ($P < 0.0001$), and this correlation was not affected when further adjusted for CPD ($r = 0.32$; $P < 0.0001$).

In the GWAS analysis of CYP2A6 activity among the MEC smokers, there was little evidence of genomic inflation in the test statistic in the overall sample ($\lambda = 1.0$). We found 251 variants with globally significant associations with CYP2A6 activity at $P < 5 \times 10^{-8}$. All but three were located in a 41.1–41.5 Mb region encompassing the CYP2A6 gene on chromosome 19q13.2, encoding for a family of cytochrome P450 enzymes (Supplementary Table S1). The three other variants associated with CYP2A6 activity were located near the gene *MTDH* on chromosome 8q22.1. However, these three variants together explain far less of the variability of CYP2A6 activity than the variants near CYP2A6, and we do not focus on these here.

Of the 248 globally significant SNP associations with CYP2A6 activity on chromosome 19, 226 (202 imputed, 22 genotyped) were available in the TRICL GWAS dataset and were the focus of our analyses onwards (Supplementary Table S2). Through forward regression analysis of the 226 variants in the MEC cohort, we identified 13 independent signals; together, these 13 SNPs explain 13.6% of variability in CYP2A6 activity (Table 2) in the MEC smokers. The strongest of these associations is with rs56113850, which on its own explains 6.2% of variability in CYP2A6 activity.

When the forward selection analysis was performed separately for each of the five ethnic groups, we found the number of

independent signals to range from one to eight; among Japanese Americans, eight independent signals were found to explain 27.9% of variability in CYP2A6 activity, whereas three signals explained 24% of variability among Latino Americans and two signals each explained 14.5% and 11.6% of variability in CYP2A6 activity among African Americans and Whites, respectively. A single SNP explained 9.1% of variability noted in CYP2A6 activity in Native Hawaiians. In all ethnic groups, our most significant SNP (rs56113850) entered the stepwise regression model with level $P < 0.001$ explaining from 3.4% (in Japanese Americans) to 18.4% (in Latinos) of the variability of CYP2A6 activity in each group. Further, this was the only SNP in the ethnic-specific analyses that was significantly associated with CYP2A6 activity at the genome-wide level in all ethnic groups.

We next tested the associations of the SNPs affecting CYP2A6 activity in the MEC smokers with lung cancer risk in TRICL. Characteristics of the TRICL participants are presented in Supplementary Table S3. Of the 226 overlapping SNPs, 186 (81%) were also directionally consistent in the TRICL dataset, meaning that the allele associated with increased CYP2A6 activity in MEC had a lung cancer odds ratio > 1.0 in the TRICL data. In an analysis of the TRICL GWAS data adjusted for age, sex, country (if applicable), and PCs, 6 among the 226 SNPs tested were globally significantly associated with lung cancer at $P < 5 \times 10^{-8}$ (Figs. 2 and 3; Supplementary Table S2); all six of these variants were also found to be strongly associated with levels of CYP2A6 activity in the MEC GWAS and with a direction that was consistent with the expected effect on lung cancer risk (Table 3). We note all six of these SNPs are highly correlated with each other among Whites with correlations above 0.83. The Q-Q plot indicates that this region as a

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Table 2. List of SNPs that enter stepwise regression for association with CYP2A6 activity in the MEC smokers while keeping TNE, BMI, age, sex, race, and PCs in the model

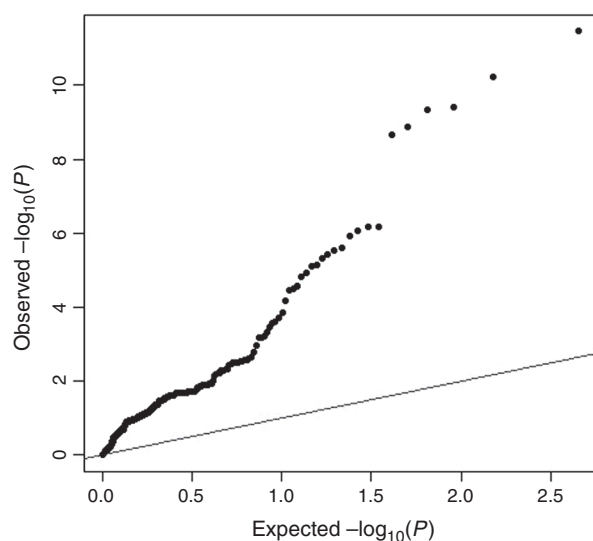
CHR	SNP	BP	Risk_Allele ^a	Ref_Allele ^b	BETA ^c	P ^d
19	rs56113850	41353107	T	C	-0.3644	1.19E-50
19	rs113029345	41370176	C	T	0.3592	1.26E-41
19	rs76935404	41419294	T	C	0.2489	1.09E-25
19	rs10425738	41417727	G	A	-0.2425	1.46E-24
19	rs11878604	41333284	C	T	-0.276	6.75E-24
19	rs7247903	41372475	G	A	-0.3222	1.12E-21
19	rs2316205	41346768	C	T	0.1786	4.24E-14
19	rs4079366	41384675	T	C	-0.1854	7.81E-14
19	rs73931391	41407874	G	A	-0.5852	1.88E-12
19	rs2545770	41324180	A	C	-0.2012	3.98E-11
19	rs185308415	41317179	G	A	-0.3344	2.92E-09
19	rs76617915	41538078	A	G	-0.6151	2.12E-08
19	rs7507400	41330179	T	G	-0.1679	3.68E-08

^aRisk_Allele, allele used for association testing.^bRef_Allele, reference allele.^cBETA, effect estimate per risk allele carried when MEC GWAS has been adjusted for age, sex, TNE, BMI, race, and PCI-PC10.^dP, MEC GWAS P value that has been adjusted for age, sex, TNE, BMI, race, and PCI-PC10.

whole is associated with lung cancer with a greater strength of association than expected by chance (Figs. 2 and 3). By far, the strongest association for lung cancer risk was with rs35755165 at $P = 3.45 \times 10^{-12}$ (Table 3). This SNP was also significantly associated with CYP2A6 activity levels at $P = 6.16 \times 10^{-15}$. Likewise, rs56113850 (the strongest single SNP predictor of CYP2A6 activity) was the second strongest predictor of lung cancer risk and was in modest linkage disequilibrium (LD) with the top SNP associated with lung cancer rs35755165 ($r^2 = 0.47$). No other SNP in the region, beyond the 226 SNPs of interest, was associated with lung cancer in TRICL with a P value less than 4.6×10^{-8} . When the TRICL analysis was restricted to ever smokers and additionally adjusted for smoking status and pack-years, the six significant SNPs were no longer as strongly associated; and only two variants remained nominally significant. The most significant association was with rs113029345 at $P = 0.039$ (Table 3). When the analysis was stratified by lung cancer cell type, the P values

were lower for all SNPs for both adenocarcinoma and squamous cell carcinoma (Supplementary Table S4). For squamous cell carcinoma, the lowest P value (0.006) was observed with rs113029345. As expected, an analysis restricted to never smokers did not yield any significant association for these six SNPs (all P's > 0.35; data not shown).

In the MEC smokers, we were able to impute (info score ≥ 0.7) the following "functional" variants previously reported to be associated with CYP2A6 activity (38): rs1137115 (*1A), rs1801272 (*2), rs28399433 (*9), rs28399435 (*14), rs28399454 (*17), rs28399468 (*8), rs5031016 (*7), rs61663607 (*1H), and the recently reported functional SNP rs4803381 (also denoted rs150298687) by Bergen and colleagues (39). We also considered two deletions, CYP2A6*4 and CYP2A6*12, that were genotyped separately using TaqMAN assay CYP2A6-Hs07545274_cn and CYP2A6-Hs07545275_cn, respectively (40). Among Whites, we found two of the previously reported functional variants to be in LD with the TRICL top SNP (rs35755165) and the MEC smokers top SNP (rs56113850). The functional variants rs1137115 (CYP2A6*1A) and rs4803381 were in modest LD with rs35755165 in Whites ($r^2 = 0.37$ and 0.46 , respectively; Supplementary Table S5). Likewise, rs1137115 (CYP2A6*1A) and rs4803381 were also correlated with rs56113850 among Whites ($r^2 = 0.47$ and 0.62 , respectively). We conducted a conditional analysis on our top variants, rs56113850 (for MEC) and rs35755165 (for TRICL), conditioning on each of the nine known functional CYP2A6 variants and two deletions. For rs56113850, when conditioning on either rs28399433 (*9) or rs4803381, the strength of the association with CYP2A6 activity was weakened slightly (from $P = 1.19 \times 10^{-50}$ to $P = 1.32 \times 10^{-38}$ and 2.61×10^{-36} , respectively). For rs35755165, adjusting for rs4803381 had the greatest impact on the significance of the association with CYP2A6 activity (P reduction from 3.22×10^{-9} to 1.71×10^{-6}). We performed a similar conditional analysis for lung cancer risk in the TRICL data (using GCTA based on summary statistics; ref. 41) conditioning on each of the four functional variants (rs4803381, rs1137115, rs28399433, and rs61663607) and found that both rs56113850 and rs35755165 remained strongly statistically significant, with the greatest effects noted when conditioning on rs4803381 ($P = 3.95 \times 10^{-8}$, for rs35755165, and $P = 9.32 \times 10^{-7}$ for rs56113850).

**Figure 2.**

Q-Q plot of observed and expected $-\log_{10}$ -transformed P values of associations with lung cancer risk in the TRICL study near the CYP2A6 gene.

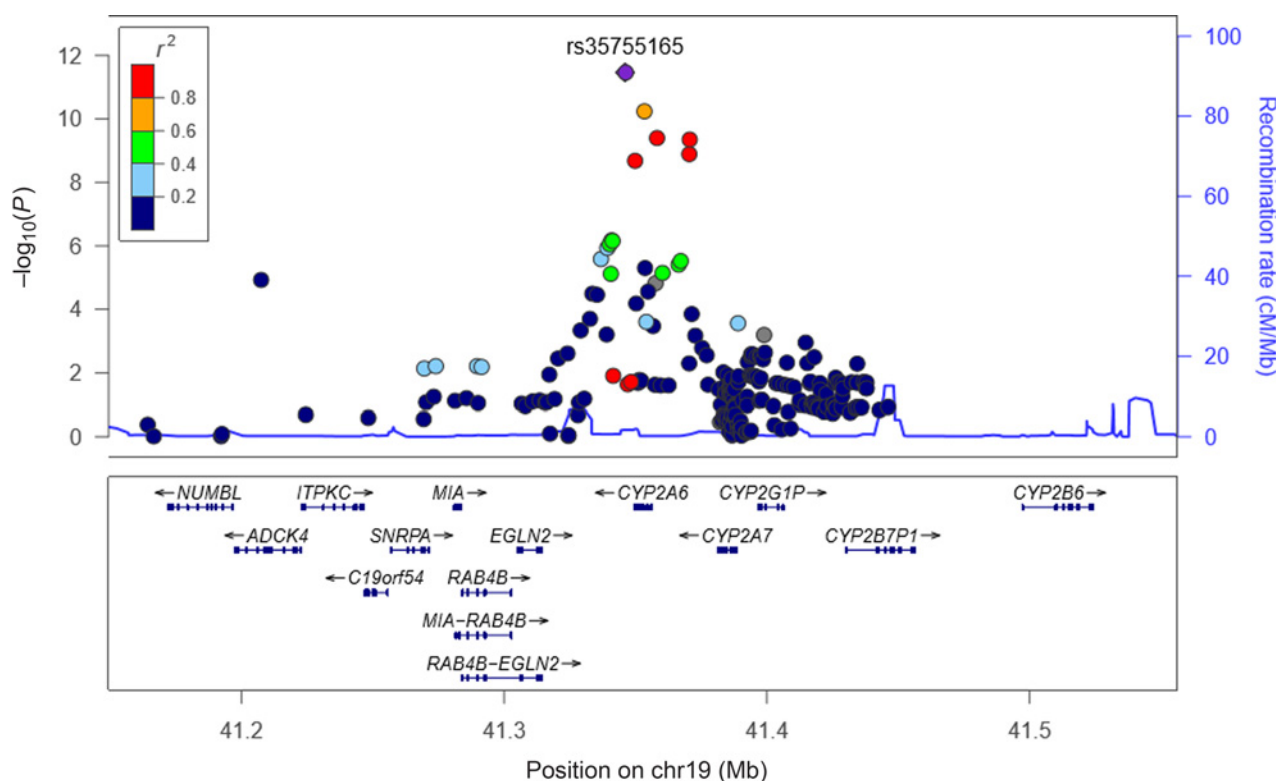


Figure 3. LocusZoom plot of 19q13.2 in the TRICL study, with European LD values.

Discussion

In a multiethnic population of smokers participating in the MEC Biospecimen Sub-Cohort, we identified a large number of variants in the *CYP2A6* region that were associated at the genome-wide significance level with *CYP2A6* activity (measured by the ratio of total 3-hydroxycotinine to cotinine). We

also found that *CYP2A6* activity was significantly correlated with an increased uptake of nicotine, as measured by TNE, supporting the hypothesis that a greater *CYP2A6* activity has the effect of making smokers smoke more extensively. When we examined the association of these variants on lung cancer risk in the large TRICL GWAS dataset, we found that the vast

Table 3. The six overlapping globally significant associations ($P < 5E-8$) with lung cancer risk in TRICL and with *CYP2A6* activity in MEC

CHR	SNP	BP	Gene ^a	Type ^b	Risk Allele_	Ref Allele_	Beta_TRICL ^e	SE_TRICL ^f	P_TRICL ^g	P_TRICL ^h	Beta_MEC ⁱ	SE_MEC ^j	P_MEC ^k
					TRICL ^c	TRICL ^d							
19	rs35755165	41345989	RAB4B-EGLN2, CYP2A6	Intergenic	G	A	0.1462	0.021	3.45E-12	0.292	0.1858	0.0236	6.16E-15
19	rs56113850	41353107	CYP2A6	Intronic	T	C	-0.1369	0.0209	5.78E-11	0.279	-0.3644	0.0237	1.19E-50
19	rs57837628	41357910	CYP2A6, CYP2A7	Intergenic	A	G	-0.1317	0.0211	4.01E-10	0.145	-0.3237	0.0251	6.84E-37
19	rs12461383	41370338	CYP2A6, CYP2A7	Intergenic	C	G	-0.1332	0.0214	4.48E-10	0.092	-0.3275	0.0256	4.23E-36
19	rs113029345	41370176	CYP2A6, CYP2A7	Intergenic	C	T	0.1319	0.0217	1.29E-09	0.039	0.3592	0.026	1.26E-41
19	rs8192733	41349550	CYP2A6	UTR3	C	G	0.1283	0.0214	2.10E-09	0.043	0.1368	0.0245	2.78E-08

^aGene, nearest gene designation.

^bType, SNP/variant classification.

^cRisk Allele_TRICL, allele used for association testing in TRICL study.

^dRef Allele_TRICL, reference allele in TRICL study.

^eBETA_TRICL, effect estimate per risk allele carried when TRICL GWAS has been adjusted for age, sex, country (if applicable), and PCs.

^fSE_TRICL, standard error, when TRICL GWAS has been adjusted for age, sex, country (if applicable), and PCs.

^gP_TRICL, GWAS *P* value has been adjusted for age, sex, country (if applicable), and PCs.

^hP_TRICL, GWAS *P* value has been adjusted for age, sex, country (if applicable), PCs, smoking status, and pack-years.

ⁱBETA_MEC, effect estimates per allele carried when MEC GWAS has been adjusted for age, sex, TNE, BMI, race, and PCs.

^jSE_MEC, standard error, when MEC GWAS has been adjusted for age, sex, TNE, BMI, race, and PCs.

^kP_MEC, GWAS *P* value has been adjusted for age, sex, TNE, BMI, race, and PCs.

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majority of their individual effects were directionally consistent and associated with an increased lung cancer risk, suggesting that smokers with a high CYP2A6 activity genotype were at greater risk of lung cancer. Indeed, a subset of six variants that were strongly associated with CYP2A6 activity in the MEC was also globally significantly associated with lung cancer risk in TRICL, with effects that were directionally consistent in the two studies.

Overall, the data presented here provide strong evidence for an association of specific CYP2A6 variants with lung cancer risk and that this association is primarily due to an influence on smoking behavior rather than a direct effect on susceptibility to lung cancer. We observed that the six SNPs that were globally associated with lung cancer risk in the TRICL GWAS without adjusting for smoking remained only marginally significant after adjustment for smoking status and pack-years. The smallest *P* value was 0.039 after adjustment for smoking status and pack-years, although for squamous cell carcinoma, the lowest *P* value was smaller (0.006). We interpret this, like similar data showing that smokers with the *CHRNA5* variant uptake more nicotine and carcinogens per cigarette (6), as suggesting that, in epidemiologic studies, residual confounding by the effect of smoking remains when adjusting lung cancer risk estimates for cigarettes per day or pack-years. Accordingly, markers of CYP2A6 activity may be useful, along with *CHRNA5* genotype, in predicting risk of lung cancer among smokers, over and beyond the exposure information captured through standard smoking history.

We are the first to show with GWAS data that this region is associated with risk of lung cancer, due evidently to its influence on nicotine metabolism as measured by the CYP2A6 activity ratio. CYP2A6 is a member of the cytochrome P450 super family involved in the metabolism of xenobiotics. It is the primary metabolizing enzyme for nicotine, and it has been found to account for 75% of nicotine metabolism via C-oxidation (7). Genetic variants in this gene may influence lung cancer risk by modifying nicotine metabolism, and therefore smoking behavior with specific alleles either increasing or decreasing smoking dose and exposure to tobacco lung carcinogens (Fig. 1; refs. 6, 42, 43). However, it should be noted that CYP2A6 variants may also affect bioactivation of the tobacco-specific lung carcinogen, 4-(methyl-nitrosamino)-1-(3-pyridyl)1-butanone (NNK; refs. 13, 44). Candidate-gene studies have shown that among Asians, CYP2A6*4, the whole gene deletion, which has been associated with little to no CYP2A6 enzymatic activity, is associated with a decreased risk of lung cancer (11–13, 45, 46). In a study in Whites (47), it was found that a genetic risk score including CYP2A6*2, *4, *9, and *12 was weakly associated with an increased lung cancer risk [wild-type metabolizers vs. reduced metabolizers-referent; OR = 1.26; 95% confidence interval (CI), 0.90–1.76; *P* = 0.180]. Among light smokers, the association with lung cancer reached statistical significance (OR = 1.60; 95% CI, 1.03–2.49; *P* = 0.036; ref. 47).

A recently published GWAS and a meta-GWAS reported that rs56113850 was globally associated with nicotine metabolism (48, 49). Of these, in our study, only rs56113850 was strongly associated with both CYP2A6 activity levels and lung cancer risk, whereas rs113288603 and esv2663194 (CYP2A6 *12) were also associated with CYP2A6 activity, but were not strongly associated with lung cancer.

In examining the relationship of our strongest CYP2A6 activity and lung cancer GWAS hits (rs56113850 and rs35755165) with functional variants previously reported to be associated with

CYP2A6 activity that were imputed in both TRICL and MEC, we further considered rs4803381, an SNP found to be associated with reduced nicotine metabolism in a two-stage meta-analysis study by Bergen and colleagues (39). When adjusting for each of these imputed functional variants, our top two SNPs (rs56113850 and rs35755165) remained significantly associated with CYP2A6 activity (all *P* values remained $<5.8 \times 10^{-8}$). Among the significant functional variants, rs4803381, previously found to be correlated with various functional CYP2A6 haplotypes (50), had the greatest influence on our findings with CYP2A6 activity. The level of significance for both top hits rs56113850 and rs35755165 decreased somewhat when conditioning on rs4803381. When performing similar conditional analyses for lung cancer risk in the TRICL data, we found that both rs56113850 and rs35755165 remained strongly statistically significant when conditioning on any of the same four functional variants, with the greatest effects also noted when conditioning on rs4803381.

We were unable to clearly identify a single, or group of, CYP2A6 functional variants that entirely explained our findings. This may be related to the limitations of the commercial GWAS arrays, which do not systematically include coverage of copy-number variants and translocations. However, considering the additional copy-number genotyping conducted on the MEC smokers (40), we found that conditioning on CYP2A6*4 or *12 only moderately weakened our SNP findings, suggesting that the associations of rs56113850 and rs35755165 with CYP2A6 activity are independent of the whole or partial gene deletion, respectively. We note that the high sequence homology across CYP2A6, CYP2A7, and CYP2A13 may result in genotyping misclassification for these variants. Indeed, a comparison between the same SNPs genotyped with TaqMan assays and genotyped on the Illumina commercial array or imputed from data using commercial array data in the MEC smokers data showed only a moderate correlation (r^2 range = 0.62 to 0.81; ref. 40). This all suggests that while rs56113850 and rs35755165 may be linked with one or more functional variants, due to the inherent difficulty in genotyping this region, the causal variants cannot be clearly identified at this time.

The present study comprises of the largest GWAS of CYP2A6 activity and the largest lung cancer GWAS dataset assembled to date. Limitations include our inability to genotype for all of the copy number variants in CYP2A6 that are known to affect CYP2A6 activity, as well as our current inability to conduct lung cancer analyses in populations other than of European ancestry.

In summary, these GWAS studies provide strong support to the long-standing hypothesis that CYP2A6 activity levels modulate lung cancer risk via modulation of smoking levels. We identified specific CYP2A6 variants associated with both CYP2A6 activity (a measure we found correlated to smoking dose) and lung cancer risk, supporting the hypothesis that a greater CYP2A6 activity causes smokers to smoke more extensively and be exposed to higher levels of carcinogens, resulting in an increased risk for lung cancer. From our data, both CYP2A6 activity and CYP2A6 genotype appear to capture additional exposure information, compared with smoking history. Because of the difficulty in genotyping the high-homology region that includes CYP2A6, CYP2A6 activity is expected to be a stronger risk predictor than CYP2A6 genotype. In addition to identifying the exact causal variants, studies are needed to formally test whether CYP2A6 activity and genotype improve current lung cancer risk prediction models for possible application in the context of low-dose computerized tomography screening.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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Novel Association of Genetic Markers Affecting CYP2A6 Activity and Lung Cancer Risk

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