

## A *DRD1* Polymorphism Predisposes to Lung Cancer among Those Exposed to Secondhand Smoke during Childhood

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### Abstract

Lung cancer has a familial component which suggests a genetic contribution to its etiology. Given the strong evidence linking smoking with lung cancer, we studied miRNA-related loci in genes associated with smoking behavior. *CHRNA*, *CHRN* gene families, *CYP2A6*, and *DRD1* (*dopamine receptor D1*) were mined for SNPs that fell within the seed region of miRNA binding sites and then tested for associations with risk in a three-stage validation approach. A 3'UTR (untranslated region) SNP in *DRD1* was associated with a lower risk of lung cancer among individuals exposed to secondhand smoke during childhood [OR, 0.69; 95% confidence interval (CI), 0.60–0.79;  $P < 0.0001$ ]. This relationship was evident in both ever (OR, 0.74; 95% CI, 0.62–0.88;  $P = 0.001$ ) and never smokers (OR, 0.61; 95% CI, 0.47–0.79;  $P < 0.0001$ ), European American (OR, 0.65; 95% CI, 0.53–0.80;  $P < 0.0001$ ), and African American (OR, 0.73; 95% CI, 0.62–0.88;  $P = 0.001$ ) populations. Although much remains undefined about the long-term risks associated with exposure to secondhand smoke and heterogeneity between individuals in regard to their susceptibility to the effects of secondhand smoke, our data show an interaction between an SNP in the 3'UTR of *DRD1* and exposure to secondhand smoke during childhood. Further work is needed to explore the mechanistic underpinnings of this SNP and the nature of the interaction between *DRD1* and exposure to secondhand smoke during childhood. *Cancer Prev Res*; 7(12); 1210–8. ©2014 AACR.

### Introduction

Though lung cancer was once considered a rare disease, it is now the leading cause of cancer-related deaths worldwide (1). Tobacco smoking is the main risk factor. The lifetime risk of developing lung cancer among smokers is approximately 16% in men, and 10% in women. These estimates are significantly lower for nonsmokers, 0.2% and 0.4%,

respectively. Exposure to environmental tobacco smoke is also a significant cause of lung cancer. The 2006 Report of the Surgeon General on *The Health Consequences of Involuntary Exposure to Tobacco Smoke* (2) concluded that there was sufficient evidence to infer a causal relationship between adult secondhand smoke (SHS) exposure and lung cancer incidence, whereas we and others have shown that exposure to SHS during childhood is associated with a higher risk of lung cancer in never smokers (3–5).

Apart from smoking, familial and segregation studies have shown that genetics also play a role in the etiology of lung cancer (6, 7). As not all smokers get lung cancer, it has been interesting to learn of several gene–environment interactions that modulate lung cancer risk. Among the most notable of these are a suite of polymorphisms in *CYP2A6*, the enzyme responsible for the metabolism of nicotine and other tobacco-specific carcinogens. *CYP2A6* SNPs that reduce the metabolism of nicotine have been associated with both smoking behavior and lung cancer incidence (8–10). In addition, several genome-wide association studies (GWAS) of lung cancer have identified a significant lung cancer susceptibility locus at cytoband 15q25, especially in early-onset smokers (9, 11, 12). SNPs in this region, which encodes subunits of the nicotinic acetylcholine receptors (nAChR), have been shown to modulate the physiologic response to nicotine, smoking behavior, and lung carcinogenesis (13). nAChRs are activated both by endogenous neurotransmitters and

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exogenous agents such as nicotine, which stimulates acetylcholine receptors in the ventral tegmental area causing the release of dopamine into the nucleus accumbens. Dopamine then activates dopamine receptors to mediate reward, and thus reinforcing the effects of nicotine (14). Gene–environment interactions with indoor air pollution, exposure to SHS during adulthood, and exposure to SHS during childhood have also been reported to modulate lung cancer risk (3, 15, 16). Because CYP2A6, nAChRs, and dopamine mediate sensitivity to nicotine, we hypothesized that variants in these genes could modulate lung cancer susceptibility via primary or secondhand exposure. Specifically, we focused on the 3'UTR (untranslated region) of these genes as this area has not been extensively studied in the past, and SNPs in this region have strong potential to modulate miRNA binding and protein levels (17). In addition, global deregulation of miRNAs has been observed in lung cancer, whereas specific miRNAs have been demonstrated to function as both oncogenes and tumor suppressors (18). miR21 and miR155, for example, are key miRNAs associated with poor outcome in lung cancer (19). Our study included an initial test population and two validation cohorts. We found that the rs686 polymorphism in *DRD1* is associated with risk of lung cancer in European Americans and African Americans and further identify a novel gene–environment interaction between this variant with exposure to SHS during childhood.

## Materials and Methods

### Patients

**NCI/MD case–control study.** Patients with histologically confirmed non–small cell lung cancer were recruited from seven hospitals in the greater metropolitan area of Baltimore, MD. Population controls were identified from the Department of Motor Vehicles, MD, and frequency matched to cases by age and gender. Written informed consent was obtained from all participants, and the study was approved by the Institutional Review Boards of the participating institutions. Inclusion criteria for this ongoing case–control study have been previously described (20). Never smokers were defined as those who smoked <100 cigarettes over their lifetime. Former smokers were defined as those who reported quitting smoking  $\geq 1$  year before the date of interview. Ethnicity and exposure to SHS were self-reported. All participants included in this study, 665 cases and 774 population controls, self-reported their race to be either European American or African American; no individuals of Hispanic ancestry were included (Table 1 and Supplementary Table S1).

**Mayo Clinic study.** Three hundred and twenty-one controls and 323 cases were used, all of whom were never smokers (Table 1 and Supplementary Table S1). Written informed consent was obtained from all participants at each of the participating institutions. A detailed explanation of the recruitment process has been reported previously (21). The study included predominantly European American participants (623/625).

**EXHALE study.** The Exploring Health, Ancestry, and Lung Epidemiology (EXHALE) study is a population-based case–control study. African American cases were identified through the Metropolitan Detroit Cancer Surveillance System, a participant in the National Cancer Institute's Surveillance, Epidemiology and End Results (SEER) program. African American controls were selected from volunteers, including friends of the cases, and through advertising. Controls were frequency matched to cases by 5-year age group, sex, and self-reported ethnicity. This study has been described previously (22). In total, 442 African American controls and 394 African American cases were included (Table 1 and Supplementary Table S1).

### SNP selection

SNPs in the 3'UTR of *CHRNA1*, *CHRNA2*, *CHRNA3*, *CHRNA4*, *CHRNA5*, *CHRNA6*, *CHRNA7*, *CHRNA8*, *CHRNA9*, *CHRNA10*, *CHRNA11*, *CHRNA12*, *CHRNA13*, *CHRNA14*, *CHRNA15*, *CHRNA16*, *CHRNA17*, *CHRNA18*, *CHRNA19*, *CHRNA20*, *CHRNA21*, *CHRNA22*, *CHRNA23*, *CHRNA24*, *CHRNA25*, *CHRNA26*, *CHRNA27*, *CHRNA28*, *CHRNA29*, *CHRNA30*, *CHRNA31*, *CHRNA32*, *CHRNA33*, *CHRNA34*, *CHRNA35*, *CHRNA36*, *CHRNA37*, *CHRNA38*, *CHRNA39*, *CHRNA40*, *CHRNA41*, *CHRNA42*, *CHRNA43*, *CHRNA44*, *CHRNA45*, *CHRNA46*, *CHRNA47*, *CHRNA48*, *CHRNA49*, *CHRNA50*, *CHRNA51*, *CHRNA52*, *CHRNA53*, *CHRNA54*, *CHRNA55*, *CHRNA56*, *CHRNA57*, *CHRNA58*, *CHRNA59*, *CHRNA60*, *CHRNA61*, *CHRNA62*, *CHRNA63*, *CHRNA64*, *CHRNA65*, *CHRNA66*, *CHRNA67*, *CHRNA68*, *CHRNA69*, *CHRNA70*, *CHRNA71*, *CHRNA72*, *CHRNA73*, *CHRNA74*, *CHRNA75*, *CHRNA76*, *CHRNA77*, *CHRNA78*, *CHRNA79*, *CHRNA80*, *CHRNA81*, *CHRNA82*, *CHRNA83*, *CHRNA84*, *CHRNA85*, *CHRNA86*, *CHRNA87*, *CHRNA88*, *CHRNA89*, *CHRNA90*, *CHRNA91*, *CHRNA92*, *CHRNA93*, *CHRNA94*, *CHRNA95*, *CHRNA96*, *CHRNA97*, *CHRNA98*, *CHRNA99*, and *CYP2A6* were initially identified and then evaluated for potential positioning within the seed region of a miRNA binding site using three web-based tools: Patrocles ([www.patrocles.org](http://www.patrocles.org)), PolymiRTS (<http://compbio.uthsc.edu/miRSNP/>), and SNPInfo (<http://snpinf.niehs.nih.gov/>; Supplementary Fig. S1). We excluded SNPs with a minor allele frequency <5% because of low statistical power. SNPs identified by 2 or more programs were included for further analysis. To increase the likelihood that we would select SNPs with biologic function, i.e., SNPs that affect RNA structure and thus alter miRNA–mRNA binding, we used RNAHybrid (<http://bibiserv.techfak.uni-bielefeld.de/rna-hybrid/>) to compare thermodynamic models for ancestral and variant alleles (Supplementary Table S2). An SNP in *DRD1* (rs686) previously related to nicotine dependence and in the seed region of binding by miR-504 (23, 24) was also included and genotyped for this study. This filtering process resulted in 3 SNPs for downstream analysis: rs686, rs4809294, and rs2292975. A flowchart detailing the SNP selection process is outlined in Supplementary Fig. S1. Genotyping methods are described in Supplementary Methods.

### Statistical analysis

We estimated per-allele ORs, 1df, using unconditional logistic regression with adjustment for potential confounding factors: current cigarette smoking status (ever/never), gender (male/female), age at diagnosis (continuous), exposure to SHS during childhood (no/yes), exposure to SHS during adulthood (no/yes), and pack-years of cigarette smoking (continuous), unless otherwise stated. We assessed whether the effect of rs686 on lung cancer risk varied over strata of exposure to SHS during childhood (i.e., effect modification; ref. 25) by adding a cross-product term to a logistic regression model adjusted for age, gender, cigarette smoking status, smoking exposure during childhood, smoking exposure during adulthood, and pack-years of smoking. To test whether these strata were significantly different, models with and without the cross-product term were compared using the likelihood ratio test.

**Table 1.** Characteristics of cases and controls from three studies

	NCI				Mayo Clinic				Wayne State				
	Controls	%	Cases	P	Controls	%	Cases	P	Controls	%	Cases	%	P
Age (mean ± SD)	67.2 ± 8.2		65.7 ± 10.4	0.002 0.364	61.8 ± 13.2		61.9 ± 13.2	0.923 0.962	62.8 ± 10.4		62.8 ± 10.3		0.42 0.725
Gender													
Male	398	51.4	326	49.0	87	27.1	87	26.9	210		192	47.5	48.7
Female	376	48.6	339	51.0	234	72.9	236	73.1	232		202	52.5	51.3
Smoking status				<0.0001				NA					<0.0001
Never	322	41.7	77	11.8	321	100	323	100	146		19	33.0	4.80
Ever	451	58.3	578	88.2	0	0	0	0	296		375	67.0	95.20
Race				0.340				0.998					NA
African American	314	40.6	253	38.1	1	0.3	1	0.3	422		394	100	100
European American	460	59.4	411	61.9	311	99.7	312	99.7	0		0	0	0
Pack-years (mean ± SD)	14.5 ± 21.0		39.2 ± 29.5	<0.0001				<0.0001	18.2 ± 21.2		37.1 ± 28.4		<0.0001
Childhood exposure				<0.0001				0.500					0.044
No	217	28.0	132	19.9	166	52.2	159	49.5	165		121	37.3	30.7
Yes	557	72.0	532	80.1	152	47.8	162	50.5	277		273	62.7	69.3
Adulthood exposure				<0.0001				0.004					0.454
No	403	52.1	211	31.7	139	43.7	105	32.7	151		125	34.2	31.7
Yes	371	47.9	545	68.3	179	56.3	216	67.3	291		269	65.8	68.3
Tumor histology													
Adenocarcinoma			309	51.8			211	65.3			134		34.0
Squamous			157	26.3			14	4.3			110		27.9
Large cell			119	19.9			19	5.9			51		12.9
Other			12	2.0			79	24.5			99		25.1

NOTE: Numbers in subcategories might not add total due to missing data.

To determine whether rs686 statistically interacted with childhood exposure to SHS, we tested for departure from additivity (26). Departure from additivity, or synergistic interaction, refers to a situation where the joint risk of rs686 and exposure to SHS during childhood are greater than would be expected from the joint risks of each factor (i.e., assuming independence). We tested for interaction with rs686 with reverse coding for the model given the inverse association with lung cancer risk (i.e., AA = 1, AG/GG = no) and the need for the exposed group to be at higher risk in such models (27). Four exposure groups were generated for the analysis: A = rs686 (AG/GG), exposure to SHS = no; B = rs686 (AG/GG), exposure to SHS = yes; C = rs686 (AA), exposure to SHS = no; D = rs686 (AA), exposure to SHS = yes. These groups were then compared in a single minimally adjusted (age, gender) logistic regression model and also a second fully adjusted model (age, gender, smoking status, pack-years of smoking). The output of each of these models was used to estimate two interaction statistics: interaction contrast ratio (ICR) and attributable proportion (AP). When the ICR and AP ≠ 0, there is evidence for departure from additivity (synergistic interaction). ICR is the excess risk due to interaction relative to the risk without either exposure. AP is the proportion of disease attributable to interaction among individuals with both exposures (26).

Analyses were performed using STATA version 12 software (STATA Corp). All statistical tests were two-sided.

**Results**

Three SNPs in *DRD1*, *CHRNA2*, and *CHRNA9* were identified as potential miRNA-modulating SNPs and successfully genotyped in the NCI-MD European American population (n = 316 controls; n = 319 cases). The minor allele frequencies for the three SNPs were as follows: rs686 (0.42), rs4809294 (0.05), rs2292975 (0.47). Of these, only rs686 was associated with lung cancer risk [OR, 0.72; 95% confidence interval (CI), 0.56–0.93; P = 0.011; n = 316 controls, n = 319 cases; Supplementary Table S3]. In an expanded analysis of the NCI-MD European American population (n = 665 cases, 774 controls; Table 1), we confirmed that the G allele of rs686 was associated with a lower risk of lung cancer after adjustment for age and gender (OR, 0.76; 95% CI, 0.62–0.93; P = 0.007). Because the effects of nicotine are mediated by dopamine release (14) and *DRD1* was previously associated with nicotine dependence (28), we reasoned that the relationship between *DRD1* and lung cancer would be confounded by smoking. Although adjustment of the model for smoking status and pack-years of smoking altered the size of the risk estimate, it did not significantly modify the relationship between the SNP and lung cancer risk (OR, 0.70; 95% CI, 0.55–0.88; P = 0.002; Table 2).

Our data indicated that the relationship between rs686 and lung cancer is independent of smoking behavior as an adult. To test this further, we analyzed a lung cancer case-control study of never smokers at Mayo Clinic (n = 309 controls, n = 319 cases). After adjustment for age and

**Table 2.** Association between rs686 and lung cancer risk stratified by exposure to SHS during childhood

	Unstratified				Unexposed to SHS during childhood				Exposed to SHS during childhood					
	Control	Case	OR	LCI-UCI	Control	Case	OR	LCI-UCI	P value <sup>a</sup>	Control	Case	OR	LCI-UCI	P value <sup>a</sup>
All	1,525	1,378	0.76	0.64–0.9	548	412	0.92	0.76–1.12	0.405 <sup>b</sup>	986	967	0.69	0.60–0.79	<0.0001 <sup>b</sup>
NCI-EA <sup>b</sup>	774	665	0.70	0.55–0.88	113	71	0.84	0.51–1.39	0.510 <sup>b</sup>	347	339	0.66	0.51–0.85	0.002 <sup>b</sup>
NCI-AA <sup>b</sup>	314	253	0.83	0.62–1.11	104	61	1.13	0.64–2.00	0.664 <sup>b</sup>	210	192	0.75	0.53–1.06	0.107 <sup>b</sup>
Mayo Clinic <sup>c</sup>	309	319	0.77	0.62–0.97	166	159	0.95	0.69–1.32	0.777 <sup>c</sup>	152	162	0.65	0.47–0.90	0.01 <sup>c</sup>
Wayne State <sup>b</sup>	442	394	0.89	0.72–1.1	191	121	1.28	0.87–1.87	0.214 <sup>b</sup>	277	273	0.74	0.57–0.96	0.025 <sup>b</sup>

Abbreviations: OR, odds ratio, 1 df test; LCI, lower confidence limit; UCI, upper confidence limit.  
<sup>a</sup>Adjusted for age, gender (male vs. female), smoking status (never/ever), pack-years of smoking.  
<sup>b</sup>Adjusted for age, gender (male vs. female), smoking status (never/ever), secondhand adult smoking exposure (no/yes), and pack-years.  
<sup>c</sup>Adjusted for age, gender (male vs. female), smoking exposure as an adult.

gender, we confirmed that the G allele rs686 was associated with lower risk of lung cancer (OR, 0.77; 95% CI, 0.62–0.97;  $P = 0.027$ ;  $n = 628$ ; Table 2). As rs686 appeared to be independent of smoking behavior as an adult, we asked whether rs686 was associated with risk of lung cancer among those exposed to SHS during adulthood and childhood. Data on SHS exposure during both of these periods were collected in the NCI-MD study. When we stratified our results by SHS exposure during adulthood, we did not observe an interaction (Supplementary Table S4); however, when we stratified our data based on SHS during childhood, we found that the relationship between rs686 and lung cancer risk was only observed among those exposed during childhood (OR<sub>(not exposed)</sub>, 0.84; 95% CI, 0.51–1.39;  $P = 0.510$ ;  $n = 284$ ; OR<sub>(exposed)</sub>, 0.66; 95% CI, 0.51–0.85;  $P = 0.002$ ;  $n = 686$ ; model adjusted for age, gender, smoking status, pack-years of smoking, and exposure to SHS during adulthood; Table 2). We confirmed this result in the Mayo Clinic Study of never smokers (OR<sub>(exposed)</sub>, 0.65; 95% CI, 0.47–0.90;  $P = 0.01$ ;  $n = 314$ ; OR<sub>(not exposed)</sub>, 0.95; 95% CI, 0.65–1.32;  $P = 0.777$ ;  $n = 325$ ; model adjusted for age, gender, and exposure to SHS during adulthood; Table 2). These data suggest that the relationship between rs686 and lung cancer risk is restricted to those exposed to SHS during childhood. The main effects of SHS exposure during childhood or adulthood and active smoking for all studies are shown in Supplementary Table S5. The relationship between the other two SNPs analyzed in this study with lung cancer, stratified by exposure to SHS during childhood, is presented in Supplementary Table S6.

The allele frequency of rs686 varies significantly across geographic regions. The ancestral allele, G, is highest among African populations. It decreases in European populations and is almost completely lost in Asian populations. We therefore asked whether the association between rs686, lung cancer risk, and exposure to SHS during childhood is also found in populations of African descent. The NCI-MD case-control study is an ongoing study that also recruits African Americans. We initially genotyped rs686 in a relatively small sample set comprising 314 controls and 253 cases (size limited by sample availability). Although we did not observe a significant association (Table 2), the direction of the observation was the same as that observed in European Americans smokers (OR<sub>(exposed)</sub>, 0.75; 95% CI, 0.53–1.06;  $P = 0.107$ ,  $n = 402$ ; OR<sub>(not exposed)</sub>, 1.13; 95% CI, 0.64–2.00;  $P = 0.664$ ;  $n = 165$ ; model adjusted for age, gender, and exposure to SHS during adulthood; Table 2). We therefore leveraged a larger sample of African Americans from the EXHALE study at Wayne State University that had greater power. In this analysis, we again validated the association between rs686-G with lung cancer risk only among individuals exposed to SHS during childhood (OR<sub>(not exposed)</sub>, 1.28; 95% CI, 0.87–1.87;  $P = 0.214$ ;  $n = 286$ ; OR<sub>(exposed)</sub>, 0.74; 95% CI, 0.57–0.96;  $P = 0.025$ ;  $n = 550$ ; model adjusted for age, gender, smoking status, pack-years of smoking, and exposure to SHS during adulthood). Collectively, these results show that rs686-G is associated with a lower risk of lung cancer in both African Americans

and European Americans (EAs), never smokers and ever smokers, and that the relationship is only evident among individuals exposed to SHS during childhood.

Because rs686 appeared to be associated with lung cancer risk only among those exposed to SHS during childhood, we tested whether there was a synergistic additive interaction (26) between rs686 and SHS exposure during childhood or whether the effect of rs686 was significantly modified by SHS exposure. As shown in Supplementary Table S7, we did not find evidence for synergistic interaction; however, using a  $\chi^2$  test to assess heterogeneity in the ORs among those exposed and not exposed to SHS during childhood, we found statistical evidence that childhood exposure was an effect-modifier of the relationship between rs686 and lung cancer risk ( $P = 0.002$ ,  $n = 2,919$ ).

In a pooled analysis of the three studies ( $n = 2,919$ ), rs686-G was associated with a 29% decrease in lung cancer risk among those exposed to SHS during childhood (OR<sub>(not exposed)</sub>, 1.01; 95% CI, 0.83–1.24;  $P = 0.891$ ;  $n = 952$ ; OR<sub>(exposed)</sub>, 0.71; 95% CI, 0.62–0.82;  $P < 0.0001$ ;  $n = 1,945$ ; Table 3). The association remained significant after additional adjustment for age at smoking initiation (OR<sub>(exposed)</sub>, 0.74; 95% CI, 0.62–0.88;  $P = 0.001$ ;  $n = 1,266$ ). Among the pooled groups, the association between the SNP and risk of lung cancer among those exposed to SHS remained consistent among European Americans, African Americans, ever smokers, never smokers, males, and females (Table 3). In support of the observation of risk among never smokers and ever smokers, we found that rs686 was associated with risk of both adenocarcinoma and squamous cell carcinoma (Table 4). Notably, this significant association was again only observed following stratification by exposure to secondhand tobacco smoke during childhood (Table 4).

## Discussion

In this three-stage candidate pathway analysis of miRNA-related SNPs, we asked whether SNPs that modulate miRNA binding in smoking-associated genes were associated with lung cancer risk. We acknowledge that not all 3'UTR SNPs will be miRNA-disrupting alleles; however, we identified, and replicated, one such SNP, rs686, in *DRD1*.

A novel finding in our study is that the G allele of rs686 is associated with a lower risk of lung cancer among individuals exposed to SHS during childhood. Studies with data on SHS exposure, particularly during childhood, are rare. However, we were able to test, and validate, this key observation in three studies. The relationship was evident in both ever smokers and never smokers. Although many susceptibility loci, such as the Chr15q24 locus, are only found in smokers, some loci, such as the TERT locus (9, 11, 12, 29–31), are associated with risk of lung cancer in both never and ever smokers, suggesting that both diseases are likely to share some common molecular mechanisms. We also demonstrated cross-population convergence of the association as we replicated our observation in both African Americans and EAs. We attempted to demonstrate further convergence

**Table 3.** Pooled analysis of the association between rs686 and lung cancer risk stratified by exposure to environmental tobacco smoke during childhood

	Unexposed to SHS during childhood					Exposed to SHS during childhood				
	Control	Case	OR	LCI-UCI	P value	Control	Case	OR	LCI-UCI	P value
All <sup>a</sup>	542	410	1.01	0.83–1.24	0.891	980	965	0.71	0.62–0.82	<0.0001
European American <sup>b</sup>	269	223	0.90	0.68–1.18	0.449	488	493	0.65	0.53–0.80	<0.0001
African American <sup>c</sup>	269	182	1.17	0.87–1.57	0.311	488	466	0.73	0.62–0.88	0.001
Ever smokers <sup>d</sup>	202	219	1.17	0.86–1.57	0.311	545	733	0.74	0.62–0.88	0.001
Never smokers <sup>e</sup>	340	190	0.91	0.69–1.21	0.513	434	223	0.61	0.47–0.79	<0.0001
Male <sup>f</sup>	322	238	1.13	0.86–1.47	0.391	507	532	0.70	0.58–0.86	<0.0001
Female <sup>f</sup>	220	172	0.87	0.63–1.19	0.381	473	433	0.71	0.58–0.87	0.001

Abbreviations: OR, odds ratio, 1df test; LCI, lower confidence limit; UCI, upper confidence limit.

<sup>a</sup>Adjusted for age, gender (male/female), race (African American/EA), study (NCI-MD/Mayo Clinic/Wayne State), smoking status (never/ever), smoking exposure as an adult, and pack-years of smoking.

<sup>b</sup>Adjusted for age, gender (male/female), smoking status (never/ever), study (NCI-MD/Mayo Clinic), smoking exposure as an adult, and pack-years of smoking.

<sup>c</sup>Adjusted for age, gender (male/female), smoking status (never/ever), study (NCI-MD/Wayne State), smoking exposure as an adult, and pack-years of smoking.

<sup>d</sup>Adjusted for age, gender (male/female), race (African American/EA), pack-years of smoking, study (NCI-MD/Mayo Clinic/Wayne State), SHS exposure as an adult, and pack-years of smoking.

<sup>e</sup>Adjusted for age, gender (male/female), race (African American/EA), study (NCI-MD/Mayo Clinic/Wayne State), SHS exposure as an adult.

<sup>f</sup>Adjusted for age, race (African American/EA), smoking status (never/ever), study (NCI-MD/Mayo Clinic/Wayne State), smoking exposure as an adult, and pack-years of smoking.

in an Asian population, but the frequency of the G allele is <2%. This SNP, or any *DRD1* SNPs, has not been identified in GWAS of lung cancer to our knowledge, which could question the strength of our findings. However, the key result in our study is the relationship between rs686 with exposure to SHS during childhood. As data about childhood exposure to SHS are not collected in many case-control studies, or reported in GWAS of lung cancer, it likely explains why this association has not been uncovered previously.

If the statistical interaction between rs686 and childhood exposure to SHS reflects a biologic interaction, then one

might expect to see a stronger association among smokers, while if anything, the effect seems to be stronger in never smokers. However, because we did not observe an association between rs686 and SHS exposure as an adult, we speculate that exposure during childhood, a window of time during which there is a heightened sensitivity to both the acute and chronic toxic effects of environmental exposures (32, 33). Epidemiologic and experimental studies show that this increased sensitivity translates to a differential effect on cancer risk and outcomes (33–36). Indeed, a recent Surgeon's General report concluded that children exposed to parental smoke have higher risk of lower respiratory tract

**Table 4.** Association between rs686 and lung cancer risk stratified by histology

Genotype	Adenocarcinoma			Squamous cell carcinoma		
	OR	LCI-UCI	P value	OR	LCI-UCI	P value
rs686	0.72	0.63–0.73	<0.0001	0.85	0.71–1.03	0.093

  

	Exposed to SHS during childhood			Exposed to SHS during childhood		
	OR	LCI-UCI	P value	OR	LCI-UCI	P value
rs686	0.68	0.60–0.80	<0.0001	0.76	0.61–0.94	<b>0.013</b>

Abbreviations: OR, odds ratio, 1df test; LCI, lower confidence limit; UCI, upper confidence limit.

Note: Analyses adjusted for age, gender (male vs. female), smoking status (never/ever), smoking exposure as an adult, and pack-years of smoking.

illnesses (2), and studies of long-term exposures starting at different time points in the life-course have shown that the earlier the exposure is encountered, the greater the tumor incidence that ensues (37). Interestingly, several recent studies also point to a role for prenatal and early-life exposures in the modulation of *DRD1* expression and function later in life (38, 39). As to how the pathobiologic memory of an early-life exposure is maintained into adult life is largely unknown, but epigenetic modifications are one possibility (40–42). Recent evidence shows that nicotine exposure acetylates the *DRD1* promoter and increases *DRD1* expression (43), suggesting that the effect modification between *DRD1* and childhood exposure to SHS we observed could reflect a direct biologic relationship.

It was surprising to us to find that an allele previously associated with nicotine dependence (28, 44) was significantly associated with a lower risk of lung cancer. However, we did not find an association between the SNP and cigarettes per day in either the NCI-MD or Wayne State studies (Supplementary Fig. S2). In addition, the observation that rs686 was associated with cancer risk in never smokers and in ever smokers after adjustments for smoking in terms of status, pack-years, and age at smoking initiation supports the contention that the association with lung cancer could be independent of, or in addition to, any relationship with cigarette smoking behavior as an adult. Our finding that the SNP is associated with risk of both adenocarcinoma and squamous cell carcinoma, albeit only after stratification by exposure to secondhand tobacco as a child, further supports this argument.

It is possible that dopamine, or *DRD1*, has tumor suppressive functions (45, 46). However, as dopamine cannot cross the blood–brain barrier, logic suggests that the relationship is somehow mediated outside of the central nervous system. *DRD1* is expressed peripherally and is associated with immune function (47–49). Indeed, some of the most interesting literature suggesting that the dopamine axis plays a role in cancer comes from epidemiologic studies that highlight an inverse link between cancer incidence and neurologic disorders, such as Parkinson disease, schizophrenia, and Alzheimer disease. Among these patient groups, which are characterized at least in part by aberrant dopamine signaling (50), there are reduced rates of cancer, including lung cancer (51–54). Interestingly, increased rates of smoking and other risk factors have been described in these patient populations, despite their reduced rates of cancer (55). Two other recent studies also point to a potential tumor suppressive role of dopamine in cancer: A dopamine receptor antagonist was identified as a selective agent that eradicates cancer stem cells (56), and a drug repositioning approach identified tri-cyclic antidepressants as selective agents for the treatment of small cell lung cancer (57). Both approaches employed unbiased screens for effective agents. If the relationship between dopamine and cancer is independent of smoking, as suggested by the results of this study, it is possible that one mechanism could involve T- and B-cell function, given the strong relationship between inflammation and lung cancer (58)

and inflammation and dopamine (47, 48, 59). However, extended functional studies will be needed to address these possibilities and a potential role for *DRD1* as a tumor suppressor in lung cancer.

The rs686 polymorphism represents a base change in the noncoding 3'UTR of *DRD1*. Work by Huang and colleagues (24, 28) suggests that rs686 disrupts miR-504 binding and results in allelic-specific expression of *DRD1*; however, it is unclear how or where this interaction might take place in relation to lung cancer. It is possible that rs686 is a marker allele, as opposed to a causative allele. In this regard, the entire *DRD1* gene is contained in a haplotype block that places rs686 in close linkage disequilibrium with rs4532 in the 5'UTR of *DRD1*. The possibility that transcriptional regulation through this site is driving the interaction cannot be dismissed.

Our study has several strengths and limitations. We only focused on SNPs that modulated 3'UTR sites, and miRNAs are known to also bind to coding regions. In addition, the initial gene selection was based on a candidate approach, including cytochrome p450, dopamine receptor, and nicotinic acetylcholine receptor genes. As such, this is not an exhaustive study of the association between miRNA-modulating SNPs, smoking behavior-associated genes, and lung cancer. However, we replicated our key findings in three studies, which strengthen the validity and interpretation of our results. Another limitation is the potential for recall bias about childhood exposures. However, as the exposure window in question in our study was during childhood, this was not possible. Of note, however, previous studies of adult nonsmokers and children comparing exposure biomarkers with self-reported data indicated that these exposure data are likely to be legitimate (60). In addition, the mean age at diagnosis was 65 years. Given that smoking prevalence rates among men and women in the 1950s to 1970s (i.e., the period when most of our population would have been children) ranged between 40% and 60%, this makes our data on childhood exposure consistent with these trends (54% of controls reported exposure to SHS during childhood). Moreover, the validation of our work in three studies further limits the likelihood that recall bias may have confounded our analysis. Finally, it is possible that the selection of controls from the Department of Motor Vehicles in the NCI-MD study could introduce a bias based on socioeconomic factors. The prevalence of SHS exposure can be higher among children living in poverty and among those whose parents had less than 12 years of education (61). Therefore, we also adjusted our model for education level, income at the time of diagnosis, and income in 1980. These data were only available for the NCI-MD study; however, the adjustments did not alter the relationship between rs686 and risk of lung cancer ( $OR_{(exposed)}$ , 0.66; 95% CI, 0.48–0.90;  $P = 0.008$ ;  $OR_{(not\ exposed)}$ , 0.92; 95% CI, 0.46–1.86;  $P = 0.825$ ).

Although studying susceptibility variants can extend our understanding of the etiology of disease, it can also help to elucidate the underlying process of carcinogenesis and provide clues for cancer prevention and treatment. Previous

epidemiologic evidence linking various neurologic disorders with lower rates of cancer, combined with our data linking *DRD1* with cancer, suggests that unraveling the connection between lung cancer and the dopamine pathway will lead to a new and significant impact on our understanding of lung carcinogenesis.

#### Disclosure of Potential Conflicts of Interest

J. Jen reports receiving a commercial research grant for research in circulating tumor cells unrelated to the current project. No potential conflicts of interest were disclosed by the other authors.

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