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Genetic Variants Associated with the Risk of Chronic Obstructive Pulmonary Disease with and without Lung Cancer

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Abstract

Chronic Obstructive Pulmonary Disease (COPD) is a strong risk factor for lung cancer. Published studies regarding variations of genes encoding glutathione metabolism, DNA repair, and inflammatory response pathways in susceptibility to COPD were inconclusive.

We evaluated 470 single nucleotide polymorphisms (SNPs) from 56 genes of these 3 pathways in 620 cases and 893 controls to identify susceptibility markers for COPD risk, using existing resources. We assessed SNP- and gene-level effects adjusting for sex, age, and smoking status. Differential genetic effects on disease risk *with* and *without* lung cancer were also assessed; cumulative risk models were established.

Twenty-one SNPs were found to be significantly associated with risk of COPD ($P < 0.01$); gene-based analyses confirmed 2 genes (*GCLC* and *GSS*) and identified 3 additional (*GSTO2*, *ERCC1*, and *RRM1*). Carrying 12 high-risk alleles may increase risk by 2.7-fold; 8 SNPs altered COPD risk *with* lung cancer 3.1-fold, and 4 SNPs altered the risk *without* lung cancer 2.3-fold.

Our findings indicate that multiple genetic variations in the 3 selected pathways contribute to COPD risk through *GCLC*, *GSS*, *GSTO2*, *ERCC1*, and *RRM1* genes. Functional studies are

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Conflicts of Interest

None of the authors have any conflicts of interest.

needed to elucidate the mechanisms of these genes in the development of COPD, lung cancer, or both.

Keywords

Chronic Obstructive Pulmonary Disease; Glutathione Metabolism Pathway; DNA Repair Pathway; Inflammatory Response Pathway

Introduction

Chronic Obstructive Pulmonary Disease (COPD including emphysema and/or chronic bronchitis), characterized by airflow limitation that is not fully reversible, has been a major and independent risk factor for lung cancer (1-3). Although cigarette smoking is a major risk factor for COPD, very similar to lung cancer, only a minority of smokers develops the disease (4), indicating additional risk factors being involved. It is important to identify the role of genetic susceptibility (5), particularly the common and disparate effects on the risk of COPD *with* and *without* lung cancer. Evidence for genetic susceptibility in COPD risk has been derived from family studies (6-8). A well-established genetic predictor for COPD is α_1 -antitrypsin deficiency status (9), with 1–2% of COPD patients having inherited α_1 -antitrypsin deficiency (10). Genomic variations of genes participating in the toxin metabolism, DNA repair, and inflammatory response pathways have been implicated in the pathogenesis of COPD (2, 11-18). Genes in the glutathione pathway are highly polymorphic and many are correlated with enzyme activities of the pathway and may alter susceptibility in individuals exposed to hazardous environments, such as cigarette smoking (19). The DNA repair system plays a critical role in protecting the genome from insults caused by hazardous environments (2). Polymorphisms in DNA repair genes, which affect the normal protein activity, may alter the efficiency of DNA repair processes and lead to genetic instability and increased COPD risk (12, 20). Persistent inflammatory responses to environmental exposures, including microbial agents, may have a role in COPD pathogenesis through a complex network of signaling molecules (21). Genetic variants in the inflammatory response pathway may perturb the balance of the network and lead to COPD.

Common etiologic and pathogenetic pathways leading to COPD and lung cancer have been well accepted (1, 2, 22, 23) and is a pressing challenge in understanding the biological mechanisms linking the two diseases. The importance of identifying genetic markers is at least three-fold: linking DNA sequence change to functional alterations, leading to more in-depth mechanistic investigations, and easy-access DNA to test in practice. Although numerous candidate gene and pathway based studies exist on lung cancer and COPD risks, only a few have considered both phenotypes (24-28). Four genome-wide association studies (GWAS) have identified candidate genes and genomic loci for lung cancer at chromosomes 5p15.33, 15q25.1, 6p21.33, and 13q31.3; three GWAS on COPD risk or lung function pointed to 2q35, 4q22, 4q24, 4q31, 5q33, 6p21, and 15q23 (29-35). Three of the four GWAS on lung cancer were primarily performed in smokers but none considered COPD. Moreover, results from the candidate gene approach provided further evidence that COPD should be considered when linking genetic markers to lung cancer risk (5, 22, 23). In our study, we comprehensively explored the potential genetic effects of the glutathione (GSH) metabolism, DNA repair, and inflammatory response pathways on COPD risk by using haplotype tagging single nucleotide polymorphisms (htSNPs or SNPs) using multi-level analytic strategies in a relatively large set of United States' white cases and controls with European ancestry. Importantly, we evaluated the common and unique genetic variations in risk of COPD *with* and *without* lung cancer.

Methods and Materials

Study Subjects

As a part of the Mayo Clinic Epidemiology and Genetics of Lung Cancer Program, initiated in 1997, all patients with pathologically diagnosed primary lung cancer, with or without COPD, have been prospectively recruited (9). Community residents, with or without COPD were identified and enrolled within the same time period of cases' recruitment, having had a general medical examination and a leftover blood sample from routine clinical tests (36). There are two sets of COPD cases. The first set is lung cancer cases with COPD, and the second set is community residents with COPD. Never smokers were defined as having smoked fewer than 100 cigarettes during their lifetimes (cigar or pipe smokers were excluded from the never smokers). Former smokers were defined as having quit smoking six months or longer before the date of diagnosis (cases) or enrollment (controls).

The diagnosis of COPD was based on symptoms (cough, sputum production, and/or dyspnea) and spirometry, confirming non-reversible airflow limitation (3, 37). We extracted medical record information on all subjects who had a confirmed diagnosis of COPD prior to lung cancer diagnosis (COPD *with* lung cancer) and gathered information by study questionnaires from enrolled community residents who reported a physician-diagnosed history of COPD (COPD *without* lung cancer). The control group was comprised of community residents who had neither COPD history nor lung cancer (9, 33). To minimize ethnic background heterogeneity, we restricted our analysis to the U.S. European descendants. In total, 620 COPD cases and 893 controls were included in this study. Of the COPD cases, 432 developed lung cancer after suffering from COPD, and 188 were free of lung cancer.

SNP Selection and Genotyping

We selected 56 genes, 29 from the GSH metabolic pathway (19), 20 from the DNA repair pathway, and 7 from the inflammatory response pathway following a review of the literature that reported an association with lung cancer. HapMap htSNPs were selected based on HapMap data of 60 unrelated Caucasian (CEU) subjects (Release 22/Phase II on NCBI B36) using Haploview (<http://www.broad.mit.edu/mpg/haploview>). Four hundred seventy htSNPs, 267 from GSH, 152 from DNA repair, and 51 from inflammation pathways, were genotyped in Mayo Clinic's Technology Center Genotyping Shared Resource of the using a custom-designed Illumina GoldenGate 480-SNP panel. Quality assessment was conducted in multiple steps as described previously(16). Excluded were SNPs with a call rate less than 95%, Hardy-Weinberg P-values less than 0.0001, or a minor allele frequency less than 0.01.

Statistical Analysis

We first performed unconditional logistic regression analysis adjusting for age, sex, and smoking status under additive, dominant, and recessive genetic models. We then performed a Fisher's combination test of *P*-values that were assumed independent (38, 39). This test follows a Chi-squared (χ^2) distribution with a degree of freedom equal to 2-fold the number of haplotype tagging single nucleotide polymorphisms (htSNPs) within the gene, assuming linkage disequilibrium between the SNPs is less than 0.2 (40). We also performed stratified analyses by subjects' lung cancer status. To determine the cumulative effects of the statistically significant htSNPs on COPD risk, we modeled total number of risk alleles as a categorical variable and a continuous variable (41). All tests were two-tailed, and the significance threshold was set at less than 0.01. We chose not to take conventional multiple comparison approaches that treats all SNPs are independent of each other. All analyses were carried out using SAS, Version 9.2 (SAS Institute, Inc., Cary, NC) and R software.

Results

SNP-based analysis results

Among the 470 htSNPs selected for genotyping, 405 passed quality assessment and were used in the analyses (see Supplementary Appendix, Table E1). Table 1 provides demographic and clinical characteristics of the COPD cases and controls; age, sex, smoking status, and pack-years were found significantly different ($P < 0.01$). Since smoking status and pack-years are surrogate to each other, we included only smoking status, age, and sex in further multivariable logistic regression models.

Among the 405 SNPs, 21 SNPs in 12 genes were found to be significant; 13 of the 21 SNPs are from 7 genes in GSH pathway (*ABCC1*, *ABCC2*, *ABCC3*, *ABCC4*, *GCLC*, *GSS*, and *GSTP1*), 7 from 4 genes in the DNA repair pathway (*ERCC2*, *MSH3*, *PARP*, and *XPA*), and 1 from the *PTGS2* gene in the inflammatory response pathway (Table 2). The detailed SNP-based association results under the additive, dominant, and recessive genetic models using the complete dataset and the stratified dataset for lung cancer status are described in the Supplementary Appendix, Tables E2-E3.

Twelve htSNPs from 8 genes (*ABCC1*, *ABCC2*, *ABCC3*, *ABCC4*, *GCLC*, *GSTP1*, *GSS*, and *ERCC2*) showed significant associations with COPD in the whole dataset ($0.0016 < p < 0.0098$); four htSNPs from four genes (*ABCC1*, *ABCC2*, *GSTP1*, and *MSH3*) were significant ($0.00819 < p < 0.00969$) in the subset of COPD *with* lung cancer; and eight htSNPs from five genes (*ABCC4*, *PARP*, *MSH3*, *XPA*, and *PTGS2*) were significant in the subset of COPD *without* lung cancer, ($0.00858 < p < 0.0016$). Specifically, two htSNPs from the ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (*ABCC4*) gene were significant in both the whole dataset and the subset of COPD *without* lung cancer; and one htSNP from the glutathione S-transferase pi 1 (*GSTP1*) gene was strongly associated with COPD in both the whole dataset and the subset of COPD *with* lung cancer.

Gene-based analysis results

Although included in this study were all 56 htSNPs selected from the HapMap data of CEU subjects, only 52 genes with more than one htSNP each could be tested in the gene-based association analyses. Five of the 52 genes were found to be significantly associated with COPD (*GCLC*, *GSS*, *GSTO2*, *ERCC1*, and *RRM1*), as shown in Table 3. Glutamate-cysteine catalytic subunit (*GCLC*) from the GSH metabolism pathway showed a very strong association with COPD in all three data sets ($P < 0.001$); Glutathione s-transferase omega 2 (*GSTO2*) was significant in both the whole dataset and the subset of COPD *with* lung cancer ($P = 0.003$ and 0.001 , respectively); Glutathione synthetase (*GSS*) and excision repair cross-complementing rodent repair deficiency complementation group 1 (*ERCC1*) were significant in the subset of COPD *without* lung cancer ($P = 0.0001$ and 0.008 , respectively); and ribonucleotide reductase M1 (*RRM1*) was only associated with COPD in the combined dataset ($P < 0.01$).

Cumulative risk assessment

Table 4 presents the estimated cumulative risk for multiple independent high-risk htSNPs is presented: there are 24 maximum high-risk alleles. Overall, regardless of lung cancer status, individuals carrying 10 to 12 high-risk alleles had a 62% increased risk of developing COPD compared to individuals who carried less than 10 high-risk alleles (OR=1.62, 99% CI= 1.06-2.49, $P=0.004$); those carrying more than 12 high-risk alleles had a nearly 3-fold increased risk compared to individuals carrying less than 10 high-risk alleles (OR=2.73, 99% CI= 1.72-4.34, $P < 0.001$). The per-allele risk assessment demonstrated that, on average, each risk allele contributed a 21% increased risk of developing COPD (OR=1.21, 99%

CI=1.12-1.30, $P<0.001$). The estimated cumulative effect of the number of high-risk alleles for COPD, separately *with* or *without* lung cancer, are also presented in Table 4.

Figure 1 illustrates models for predicting the risk (or probability of developing) COPD in different strata by sex and smoking status, *with* and *without* lung cancer by age. Panels A and B show prediction curves of COPD risk for females and males *without* lung cancer, and panels C and D for females and males *with* lung cancer, respectively.

Discussion

We systematically evaluated associations of COPD risk with a full range of known polymorphisms in the glutathione metabolism, DNA repair, and inflammatory response pathways. We found that 21 SNPs in 12 genes (*ABCC1*, *ABCC2*, *ABCC3*, *ABCC4*, *GCLC*, *GSTP1*, *GSS*, *ERCC2*, *MSH3*, *XPA*, *PARP*, and *PTGS2*) were significantly associated with risk of COPD after adjusting for age, sex, and smoking status; 13 of the 21 SNPs were from 7 genes in the GSH metabolic pathway, 7 SNPs from 4 genes in the DNA repair pathway, and one from an inflammatory response gene. After stratifying COPD cases into subgroups *with* and *without* lung cancer, 4 htSNPs from 3 genes were significant in COPD *with* lung cancer, and 8 htSNPs from 5 genes were significant in COPD *without* lung cancer. These findings indicate that COPD and lung cancer share common susceptibility genes (i.e., *ABCC4*, and *PTGS2*), as well as hold independent susceptibility genes, i.e., *ABCC1*, *ABCC2*, *GSTP1*, and *MSH3*; the maximal sample size in the whole study dataset had improved statistic power to detect susceptibility loci for COPD, which could not be found in either sub-dataset.

Through a 52-gene based analysis using Fisher's combination test, 2 genes, *GCLC* and *GSS*, remained significant; an additional three genes, *GSTO2*, *ERCC1*, and *RRM1*, were also found to be strongly associated with COPD. The gene-based approach jointly considered all common variations of tagging single nucleotide polymorphisms (tagSNPs) within a candidate gene to capture all of the potential risk-conferring variations of the given gene, which improved the robustness of an identified association. However, the finding that a significant association was observed only from the SNP-based test but was not in the whole gene-based analysis for several genes (*ABCC1*, *ABCC2*, *ABCC3*, *ABCC4*, *GSTP1*, *ERCC2*, *MSH3*, *XPA*, *PARP*, and *PTGS2*) does not rule out their involvement in the etiology of COPD. Consistent with findings from other studies, our stratified analyses indicated that COPD and lung cancer have shared and independent susceptibility genes, which could serve as evidence for uncovering the common and unique mechanisms between COPD and lung cancer(2, 25, 26, 42-44) .

GSH holds an important role in protecting lung epithelial cells from injury and inflammation following a variety of insults, and is the most abundant antioxidant expressed in the lung resulting from the GSH metabolism pathway. *GCLC*, *GSS*, and *GSTO2* are genes dominating the synthesis, modification, and activation of GSH. *GCLC*, the γ -glutamylcysteine synthetase heavy subunit controlling the important rate-limiting step in GSH synthesis (45). Multiple genetic variants in the *GCLC* gene may induce a different level of GSH production, altering the antioxidant capacity of airway cells and leading to increased susceptibility to COPD and/or lung cancer. Four of the 13 tested htSNPs in the *GCLC* gene showed significant associations with COPD and, the gene-based analysis found even a stronger association, indicating that multiple independent *GCLC* variants multiplicatively confer risk to COPD.

Glutathione synthetase (*GSS*), the key enzyme for GSH synthesis, plays an important role in defending the lung cell against reactive oxygen species (46, 47). The COPD-associated

htSNP, rs6088659, is located in intron 1 of the *GSS* gene, which may be in strong linkage disequilibrium (LD) with an alternative splicing variant, causing differential alternative splicing of the *GSS* gene. Glutathione S-transferase omega 2 (*GSTO2*) is a new yet important member of the gene superfamily of multifunctional enzymes that catalyze the conjugation of GSH with electrophilic substrates (48). Variation in *GSTO2* may affect the catalytic activity of the rate-limiting step in arsenic biotransformation in humans (49). We detected a strong association of the *GSTO2* gene with COPD *with* lung cancer, indicating that *GSTO2* may be critical for developing cancer among COPD patients.

The excision repair cross-complementing rodent repair deficiency complementation group 1 gene (*ERCC1*) and ribonucleotide reductase M1 (*RRM1*) are two important genes in the DNA repair pathway. *ERCC1*, a structure-specific DNA repair endonuclease responsible for the 5' incision, has a key role in the removal of adducts from genomic DNA (50, 51). *RRM1*, a gene encoding the regulatory subunit of ribonucleotide reductase, influences cell survival and is an inhibitor of cell proliferation and suppresses cell migration and invasion by reducing the phosphorylation of focal adhesion kinase (52, 53). The expression levels of *RRM1* and *ERCC1* are significantly correlated (51, 53), and we found that *ERCC1* was significantly associated with COPD *without* lung cancer and that *RRM1* showed significance with all COPD, implying that *ERCC1* may have a more important role in COPD etiology than in lung cancer etiology; whereas, *RRM1* may affect both COPD and lung cancer susceptibility.

To appreciate the cumulative effects of multiple variants in different genes, we constructed a series of cumulative risk prediction models for COPD based on multiple high-risk htSNP combinations, serving as a translational portal of our study findings into potential clinical, basic science, and public health applications: first is risk prediction for COPD *without* or COPD *with* lung cancer; second is evidence for unique and common genes in COPD *with* and *without* further developing lung cancer, and third is relative importance of genetic versus environmental risk factors in developing COPD, *with* or *without* lung cancer. Noted is the impact of current and former smoking status, where the risk of COPD *without* lung cancer is lower in former smokers than in current smokers, the risk of COPD *with* lung cancer is virtually the same between the two smoking groups. This finding reiterates the benefits of smoking cessation in reducing COPD risk, which may also reduce the lung cancer risk.

Strengths of this study are summarized as follows: (1) Sample size is reasonably large from a single institution with a relatively recent patient population. (2) Phenotype of COPD is reliable, with diagnosis verified by medical records. (3) Gene and SNP selections are comprehensive, current or based on previously reported disease associations. Full htSNPs within each of these genes were used for capturing the genetic variation information. (4) Statistical analyses are comprehensive. Genetic association tests and replications should take place at the gene level because genes are the functional unit of the human genome; the positions, sequence, and function of genes are highly consistent across diverse human populations. In addition, gene-based replication implies that each population will be studied using their own allele frequencies and LD structure and should therefore overcome many of the problems of non-replication due to population differences in genetic structure. (5) A COPD risk prediction model was constructed to demonstrate the utilities of genetic markers and clinic information to achieve the goal of translational medicine. Finally, cross-validations between prediction models developed by independent research teams, e.g. Young et al, would accelerate this goal (44).

One disadvantage of using the existing resources as in our study design, specifically when involving a defined population or community is the incomplete diagnostic data for virtually

any diseases, particularly for diseases that could be undiagnosed or underdiagnosed due to a lack of significant and specific symptoms. One exception is the clinical definition of chronic bronchitis, which requires mainly patients' report on the presence of cough and sputum production for at least three months *and* for two consecutive years (37). Recognizing the low reliability of self-reported physician-diagnosed chronic bronchitis (54), we explicitly required in our study an answer to the clinical diagnosis of this disease from individuals who reported a physician-diagnosed chronic bronchitis. The specific question is, "Have you had an episode of cough and sputum production lasting 3 or more months for two consecutive years?" With regard to emphysema and lung cancer, our team recently published a study (55) demonstrating that clinical assessment, i.e., relying on either medical records or subjects-reported physician-diagnosed emphysema, has a fairly low sensitivity yet high specificity on detecting anatomic emphysema compared to that characterized by CT. Two implications to the current study are (1) underdiagnosing emphysema has been inevitable unless adequate resolution CT-scans were radiologically evaluated for the purpose of such specific diagnosis, and (2) as a consequence, most studies that attempted to estimate the burden of emphysema could only estimate the "physician-diagnosed" emphysema. Therefore, we had decided not to use the CT-scan-diagnosed emphysema or PFT (pulmonary function test) values that were available for virtually all subjects with lung cancer but only available for selected subjects without lung cancer, regardless of COPD phenotypes.

We acknowledge three additional limitations that need to be addressed in future studies: First, the limited sample size of the never smoker subgroup prohibited us to conduct stratified analyses by smoking status. Second, the number of COPD cases without lung cancer is small and therefore subject to chance findings. Third, because this is a systematic replication study of previously reported candidate or risk-bearing pathways, we did not use the convergent Bonferroni correction method for correction of multiple comparisons but used a stringent *P*-value threshold of 0.01. Considering the deficiency of our study design, we emphasized that our results are preliminary and calling for more rigorously-designed validation studies.

In summary, our results provide additional evidence supporting associations of COPD with variations in *GCLC*, *GSS*, *GSTO2*, *ERCC1*, and *RRM1* genes using individual htSNPs and combinational multi-locus analyses, confirming that genetic variations in the glutathione metabolic and DNA repair pathways indeed contribute to COPD risk in an U.S. European Ancestry population. Future studies should take systems genomic approaches to identify causative genetic variants, characterizing their functions, and assessing their common and unique relationship with COPD as well as lung cancer. The high-risk alleles identified may be used for risk prediction, early diagnosis, and proactive prevention of COPD as well as lung cancer.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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ABBREVIATIONS

ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1
ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2
ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4
CEU	Caucasian
COPD	Chronic obstructive pulmonary disease
ERCC1	Excision repair cross-complementing rodent repair deficiency complementation group 1
ERCC2	Excision repair cross-complementing rodent repair deficiency, complementation group 2
GCLC	Glutamate-cysteine catalytic subunit
GSH	Glutathione
GSS	Glutathione synthetase
GSTO2	Glutathione s-transferase omega 2
GSTP1	Glutathione S-transferase pi 1
GWAS	Genome-wide association study
htSNPs	Haplotype tagging single nucleotide polymorphisms
LD	Linkage disequilibrium
MSH3	MutS homolog 3
PARP	Poly-(ADP-ribose) polymerase
PTGS2	Prostaglandin-endoperoxide synthase 2
RRM1	Ribonucleotide reductase M1
SNP	Single nucleotide polymorphism
tagSNP	Tagging single nucleotide polymorphism
χ^2	Chi-squared
XPA	Xeroderma pigmentosum, complementation group A

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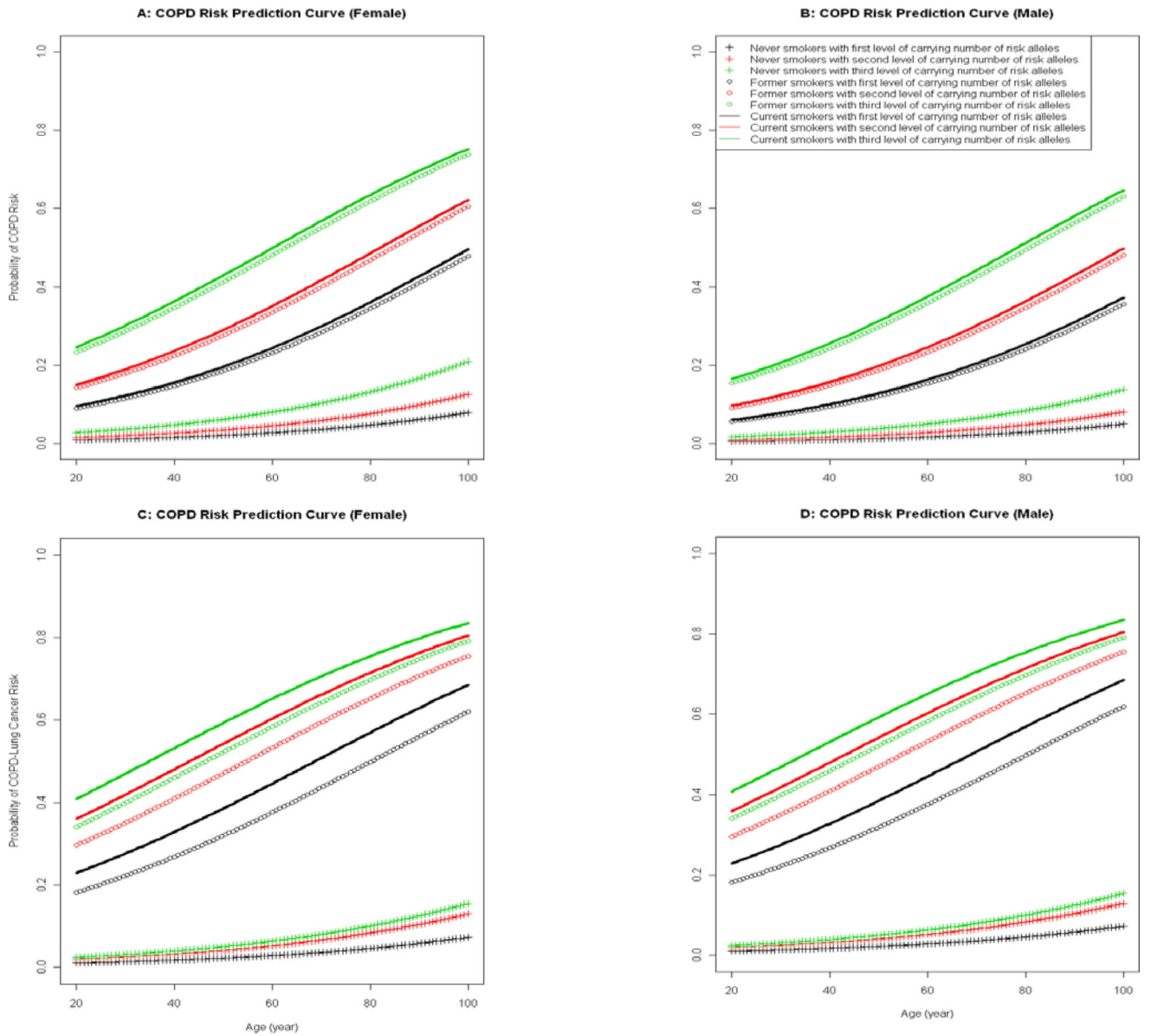


Figure.
 Predicting Risk of COPD with and without Lung Cancer:
 A: COPD Risk Prediction Curve (Female)
 B: COPD Risk Prediction Curve (Male)
 C: COPD Risk Prediction Curve (Female)
 D: COPD Risk Prediction Curve (Male)

Table 1

Demographic and Clinic Characteristics

Characteristics	Number of COPD Cases (%)		Total N=620	Number of Controls (%) (Without COPD and Lung Cancer) N=893	P-value ^a	P-value ^b	P-value ^c	P-value ^d
	With Lung Cancer N=432	Without Lung Cancer N=188						
Sex								
Male	240(55.56%)	82(43.62%)	322(51.94%)	348(38.97%)	0.008	<0.001	0.271	<0.001
Female	192(44.44%)	106(56.38%)	298(48.06%)	545(61.03%)				
Age± SD (year)	66.99± 8.54	67.27± 9.67	67.08± 8.89	64.97± 9.97	0.731	<0.001	0.004	<0.001
Smoking Status								
Never	31(7.18%)	29(15.43%)	60(9.67%)	564(63.16%)				
Former	217(50.23%)	94(50.00%)	311(50.16%)	195(21.84%)	0.004	<0.001	<0.001	<0.001
Current	184(42.59%)	65(34.57%)	249(40.16%)	134(15.01%)				
Pack-years								
0 & never smoker	31 (7.18%)	33 (17.55%)	64 (10.32%)	570 (63.83%)				
1-20	29 (6.71%)	15 (7.98%)	44 (7.10%)	32 (3.58%)	<0.001	<0.001	<0.001	<0.001
21-40	75 (17.36%)	43 (22.87%)	118 (19.03%)	121 (13.55%)				
> 40	297 (68.75%)	97 (51.60%)	394 (63.55%)	170 (19.04%)				

^a P-value for the comparison between COPD cases with lung cancer and COPD cases without lung cancer.

^b P-value for the comparison between COPD cases with lung cancer and controls.

^c P-value for the comparison between COPD cases without lung cancer and controls.

^d P-value for the comparison between all COPD cases and controls.

Table 2

Significant Results in Single SNP Analysis Adjusting for Clinical Variables

Pathway	Gene	RS ID	Most Significant Results in Three Genetic Models: Odds Ratio (99% Confidence Interval) and P-Value			
			Whole Case-Control Dataset	COPD Patients without Lung Cancer and Healthy Control Dataset	COPD Patients with Lung Cancer and Healthy Control Dataset	Minimum P Value
GSH	ABCC1	rs16967755	1.51(1.08 -2.10)	1.50(0.95 -2.38)	1.45(1.00 -2.10)	1.60×10 ⁻³
GSH	ABCC4	rs7324283	1.60×10 ⁻³	2.36×10 ⁻²	1.01×10 ⁻²	1.60×10 ⁻³
GSH	GCLC	rs12524550	1.90(1.07 -3.37)	2.40(1.17 -4.91)	1.58(0.83 -3.04)	3.54×10 ⁻³
GSH	GCLC	rs2100375	3.93×10 ⁻³	1.60×10 ⁻³	6.88×10 ⁻²	3.66×10 ⁻³
GSH	GCLC	rs8075406	2.42(1.11 -5.28)	2.60(0.92 -7.34)	2.11(0.91 -4.90)	4.88×10 ⁻³
GSH	ABCC3	rs1729786	3.54×10 ⁻³	1.79×10 ⁻²	2.28×10 ⁻²	5.67×10 ⁻³
GSH	ABCC4	rs1729786	0.75(0.58 -.97)	0.33(0.10 -1.04)	0.78(0.58 -1.03)	6.26×10 ⁻³
GSH	GCLC	rs542914	3.66×10 ⁻³	1.25×10 ⁻²	2.29×10 ⁻²	7.01×10 ⁻³
GSH	GCLC	rs4712035	0.70(0.50 -.97)	0.65(0.41 -1.02)	0.70(0.48 -1.01)	8.19×10 ⁻³
GSH	GSTP1	rs1138272	4.88×10 ⁻³	1.45×10 ⁻²	1.17×10 ⁻²	8.80×10 ⁻³
GSH	ABCC2	rs717620	1.61(1.01 -2.56)	1.43(1.03 -2.00)	1.59(0.94 -2.70)	9.22×10 ⁻³
GSH	GSS	rs6088659	8.91×10 ⁻³	5.67×10 ⁻³	2.29×10 ⁻²	9.34×10 ⁻³
GSH	ABCC2	rs2756109	0.78(0.62 -.99)	0.80(0.58 -1.11)	0.78(0.60 -1.02)	9.69×10 ⁻³
GSH	ABCC1	rs215100	6.26×10 ⁻³	7.70×10 ⁻²	1.68×10 ⁻²	
GSH	GCLC	rs4712035	1.37(1.01 -1.86)	1.38(0.86 -2.21)	1.36(0.97 -1.90)	
GSH	GSTP1	rs1138272	7.01×10 ⁻³	8.41×10 ⁻²	1.76×10 ⁻²	
GSH	ABCC2	rs717620	0.64(0.41 -1.00)	0.76(0.42 -1.36)	0.60(0.36 -.99)	
GSH	GSS	rs6088659	9.80×10 ⁻³	2.20×10 ⁻¹	8.19×10 ⁻³	
GSH	ABCC2	rs2756109	1.28(0.96 -1.72)	1.87(0.57 -6.12)	1.39(1.01 -1.94)	
GSH	ABCC1	rs215100	2.77×10 ⁻²	1.74×10 ⁻¹	8.80×10 ⁻³	
GSH	ABCC2	rs2756109	0.29(0.09 -.99)	0.39(0.07 -2.06)	0.23(0.05 -1.01)	
GSH	ABCC2	rs2756109	9.22×10 ⁻³	1.47×10 ⁻¹	1.06×10 ⁻²	
GSH	ABCC2	rs2756109	0.79(0.62 -1.00)	0.69(0.43 -1.11)	0.80(0.61 -1.04)	
GSH	ABCC1	rs215100	9.34×10 ⁻³	4.35×10 ⁻²	2.55×10 ⁻²	
GSH	ABCC1	rs215100	0.65(0.38 -1.12)	0.65(0.30 -1.41)	0.76(0.58 -1.00)	
GSH	ABCC1	rs215100	3.99×10 ⁻²	1.52×10 ⁻¹	9.69×10 ⁻³	

Pathway	Gene	RS ID	Most Significant Results in Three Genetic Models: Odds Ratio (99% Confidence Interval) and P-Value				Minimum P Value
			Whole Case-Control Dataset	COPD Patients without Lung Cancer and Healthy Control Dataset	COPD Patients with Lung Cancer and Healthy Control Dataset		
DNA	MSH3	rs12513549	4.04(0.72 -22.80)	8.68(1.36 -55.26)	1.35(0.89 -2.05)	2.63×10⁻³	
			3.75×10 ⁻²	2.63×10⁻³	6.64×10 ⁻²		
DNA	XPA	rs1800975	0.85(0.62 -1.18)	0.60(0.38 -0.94)	0.99(0.69 -1.42)	3.33×10⁻³	
			2.05×10 ⁻¹	3.33×10⁻³	9.26×10 ⁻¹		
DNA	PARP	rs11842915	1.26(0.93 -1.69)	1.53(1.02 -2.28)	1.14(0.77 -1.68)	6.43×10⁻³	
			4.79×10 ⁻²	6.43×10⁻³	3.81×10 ⁻¹		
DNA	×10RCC2	rs3916874	1.31(1.01 -1.70)	1.56(1.00 -2.46)	1.28(0.96 -1.71)	7.40×10⁻³	
			7.40×10⁻³	1.08×10 ⁻²	2.63×10 ⁻²		
DNA	MSH3	rs33013	0.72(0.52 -1.00)	0.80(0.51 -1.26)	0.69(0.48 -0.99)	8.42×10⁻³	
			1.01×10 ⁻²	2.11×10 ⁻¹	8.42×10⁻³		
DNA	MSH3	rs12522132	2.17(0.58 -8.09)	4.49(1.03 -19.52)	1.22(0.83 -1.82)	8.54×10⁻³	
			1.31×10 ⁻¹	8.54×10⁻³	1.86×10 ⁻¹		
DNA	MSH3	rs2897298	2.28(0.62 -8.32)	4.48(1.03 -19.47)	1.21(0.81 -1.79)	8.58×10⁻³	
			1.03×10 ⁻¹	8.58×10⁻³	2.17×10 ⁻¹		
Inflammation	PTGS2	rs689470	2.26(0.96 -5.36)	3.02(1.05 -8.71)	1.96(0.72 -5.32)	7.03×10⁻³	
			1.47×10 ⁻²	7.03×10⁻³	8.41×10 ⁻²		

Table 3

Significant Results Adjusting for Clinical Variables in Gene-Based Analysis

Pathway	Gene	Number of SNPs Tested	Minimum P Value in Three Genetic Models			Minimum P Value
			Whole Case-Control Dataset	COPD Patients without Lung Cancer and Healthy Control Dataset	COPD Patients with Lung Cancer and Healthy Control Dataset	
GSH	GCLC	13	4.04×10^{-7}	1.81×10^{-4}	7.16×10^{-4}	4.04×10^{-7}
GSH	GSS	7	3.61×10^{-2}	1.14×10^{-4}	1.75×10^{-2}	1.14×10^{-4}
GSH	GSTO2	6	3.30×10^{-3}	5.05×10^{-1}	1.06×10^{-3}	1.06×10^{-3}
DNA	×IORCCI	5	5.26×10^{-1}	8.11×10^{-3}	8.28×10^{-1}	8.11×10^{-3}
DNA	RRMI	6	9.66×10^{-3}	2.09×10^{-2}	8.71×10^{-2}	9.66×10^{-3}

Table 4
 Cumulative Risk Prediction Model for COPD Based on Multiple Independent High Risk HtSNP Combination

Number of Risk Alleles	Number of COPD Cases	Number of Healthy Controls	OR	S×10	Z	P-value
1. Whole Case-Control Dataset(12 risk htSNPs included)						
First Level: [0,9]	99	219	1.00(reference)			
Second Level: [10,12]	280	424	1.62	0.17	2.91	3.60×10^{-3}
Third Level: [13,24]	241	250	2.73	0.18	5.61	2.07×10^{-8}
Per-allele risk (trend test)			1.21	0.03	6.71	1.95×10^{-11}
2. COPD Patients without Lung Cancer and Healthy Control Dataset (8 risk htSNPs included)						
First Level: [0,2]	30	247	1.00(reference)			
Second Level: [3,5]	108	496	1.67	0.24	2.19	2.83×10^{-2}
Third Level: [6,16]	50	150	3.08	0.28	4.08	4.60×10^{-5}
Per-allele risk (trend test)			1.25	0.05	4.76	1.94×10^{-6}
3. COPD Patients with Lung Cancer and Healthy Control Dataset (4 risk htSNPs included)						
First Level: [0,4]	124	324	1.00(reference)			
Second Level: [5,6]	264	509	1.89	0.15	4.19	2.81×10^{-5}
Third Level: [7,8]	44	60	2.32	0.27	3.10	1.94×10^{-3}
Per-allele risk (trend test)			1.30	0.06	4.44	9.16×10^{-6}