Genome-wide association study of smoking behaviours in patients with COPD

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ABSTRACT

Background Cigarette smoking is a major risk factor for chronic obstructive pulmonary disease (COPD) and COPD severity. Previous genome-wide association studies (GWAS) have identified numerous single nucleotide polymorphisms (SNPs) associated with the number of cigarettes smoked per day (CPD) and a dopamine beta-hydroxylase (DBH) locus associated with smoking cessation in multiple populations.

Objective To identify SNPs associated with lifetime average and current CPD, age at smoking initiation, and smoking cessation in patients with COPD.

Methods GWAS were conducted in four independent cohorts encompassing 3441 ever-smoking patients with COPD (Global Initiative for Obstructive Lung Disease stage II or higher). Untyped SNPs were imputed using the HapMap (phase II) panel. Results from all cohorts were meta-analysed.

Results Several SNPs near the HLA region on chromosome 6p21 and in an intergenic region on chromosome 2q21 showed associations with age at smoking initiation, both with the lowest p = 2 × 10−7. No SNPs were associated with lifetime average CPD, current CPD or smoking cessation with p < 10−6.

Nominally significant associations with candidate SNPs within cholinergic receptors, nicotinic, alpha 3/5 (CHRNA3/CHRNA5; eg, p = 0.00011 for SNP rs1051730) and cytochrome P450, family 2, subfamily A, polypeptide 6 (CYP2A6; eg, p = 2.78 × 10−6 for a non-synonymous SNP rs1801272) regions were observed for lifetime average CPD, however only CYP2A6 showed evidence of significant association with current CPD. A candidate SNP (rs3025343) in DBH was significantly (p = 0.015) associated with smoking cessation.

Conclusion The authors identified two candidate regions associated with age at smoking initiation in patients with COPD. Associations of CHRNA3/CHRNA5 and CYP2A6 loci with CPD and DBH with smoking cessation are also likely of importance in the smoking behaviours of patients with COPD.

INTRODUCTION

Chronic obstructive pulmonary disease (COPD) is a common, genetically complex disease caused, and accelerated in its progression, predominantly by tobacco smoking. High smoking intensity, likely related at least in part to nicotine addiction, increases the risk of developing COPD. Although many patients quit smoking after they are diagnosed with COPD, some continue to smoke, placing them at high risk for continued disease progression.

Smoking behaviours, such as age at smoking initiation, smoking cessation, and number of cigarettes smoked per day (CPD), are partially genetically determined and have substantial heritability.1–4 Numerous loci and candidate genes have been suggested to contain genetic markers affecting smoking behaviours using genome-wide linkage scans5 and genome-wide association study (GWAS) approaches.6–7 Recent GWAS have identified loci associated with smoking cessation (dopamine beta-hydroxylase (DBH) on chromosome 9q34) and CPD (eg, cholinergic nicotinic receptors locus on chromosome 15q25 and cytochrome P450, family 2, subfamily A, polypeptide 6 (CYP2A6) locus on chromosome 19q13) in multiple populations.8–11 although GWAS of smoking behaviours specifically of patients with COPD have not been reported. Interestingly, the same single nucleotide polymorphisms (SNPs) in the 15q25 locus were previously associated with development of COPD,12 but the role of this locus in smoking behaviours in patients with COPD and whether the sole effect of this locus on COPD susceptibility relates to smoking behaviour remain unclear.

Because of their typically heavy lifetime smoking exposures, potentially related to (at least in part) enrichment in genetic variants responsible for nicotine addiction, patients with COPD can be considered as a unique population for studying smoking behaviours. However, diagnosis and...
further progression of COPD are likely to modify smoking status (ie, increased efforts to quit smoking) and smoking intensity (eg, reduction of CPD). Identifying genetic factors involved in smoking cessation is of special importance in clinical practice, since quitting smoking may reduce subsequent loss of lung function in patients with COPD. Smoking cessation results in an improvement of respiratory symptoms in patients with COPD, and is associated with reduced mortality due to COPD. Another smoking-related phenotype, age at smoking onset, correlates with nicotine dependence in adulthood and mortality due to COPD. Taken together, it is of special interest to search for markers associated with smoking cessation and smoking status among patients with COPD. Likewise, it is of interest to assess whether SNPs, regarded as established genetic determinants of smoking cessation and CPD in other populations, associate with these traits in patients with COPD as well. Identification and description of such genetic variations may have significant consequences on future, targeted therapy aiming to reduce smoking among patients with COPD.

The aim of the current study was to identify SNPs associated with age at smoking initiation, smoking cessation, and lifetime average CPD among patients with COPD, using GWAS in four independent cohorts: National Emphysema Treatment Trial (NETT), Evaluation of COPD Longitudinally to Identify Predictive Surrogate End-points (ECLIPSE), GenKOLS cohort from Bergen, Norway, and COPDGene. The authors additionally hypothesised that a subset of smoking behaviour genetic determinants in other population samples would influence smoking behaviour in patients with COPD.

### METHODS

#### Subjects and phenotypes

Ever-smoking, Caucasian patients with at least moderate COPD (Global Initiative for Obstructive Lung Disease stage II or higher) from four independent cohorts (NETT, ECLIPSE, GenKOLS cohort from Bergen, Norway, and COPDGene (first 1000 subjects)) were studied (table 1). In total 3441 patients had at least one (out of four) non-missing, smoking-related phenotype (table 1). All phenotypes were self-reported using either a Case Report Form (smoking status and the lifetime average CPD in the ECLIPSE cohort) or modified versions of the American Thoracic Society/Division of Lung Diseases Respiratory Disease Questionnaire. Because current smokers were not eligible for the NETT study, this cohort did not contribute to the analyses on smoking cessation and current CPD.

#### Genotyping and quality control

Different genotyping chips from Illumina (San Diego, California, USA) were used (table 1). Quality control (QC) steps were previously described in detail for the NETT, Norwegian and ECLIPSE cohorts, and were applied to the COPDGene study as well. Briefly, QC steps consisted of filtering SNPs based on missing call rates (>5%) and Hardy-Weinberg Equilibrium deviation (p<10^-8), and filtering patients based on genotyping call rate (<95%), sex discrepancy, unexpected relatedness (FLINK phat cut-off of 0.125), and ethnicity. Removal of cases that were outliers for genetic ancestry was performed based on principal components analysis in cases only. In the primary analysis, untyped markers were imputed using 120 founder Caucasian

### Table 1 Characteristics of patients with chronic obstructive pulmonary disease (COPD) and smoking-related phenotypes studied

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>NETT n = 362*</th>
<th>Norway n = 851*</th>
<th>ECLIPSE n = 1734*</th>
<th>COPDGene n = 494*</th>
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<td></td>
<td></td>
<td></td>
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<tr>
<td><strong>Phenotype studied</strong></td>
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<tr>
<td>Age at smoking initiation</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Mean (SD)</td>
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<td>18.7 (5.1)</td>
<td>16.9 (4.4)</td>
<td>16.8 (4.4)</td>
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<td>851</td>
<td>1690</td>
<td>494</td>
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<td>0.997</td>
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<td>Lifetime average CPD</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean (SD)</td>
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<td>15.7 (7.8)</td>
<td>25.5 (12.4)</td>
<td>27.6 (11.8)</td>
</tr>
<tr>
<td>Number of patients with non-missing phenotype</td>
<td>361</td>
<td>851</td>
<td>1734</td>
<td>494</td>
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<tr>
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<td>Current smokers, n (%)</td>
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<td>404 (47.5)</td>
<td>610 (35.3)</td>
<td>150 (30.6)</td>
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<td>Former smokers, n (%)</td>
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<td>1120 (64.7)</td>
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<td>0.995</td>
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<tr>
<td>Mean (SD)</td>
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<td>15.6 (10.8)</td>
<td>18.4 (12.4)</td>
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</tr>
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<td>1.005</td>
<td>0.997</td>
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</table>

*Calculated for patients with at least one non-missing phenotype.
†For patients with reported current CPD >0.
CPD, number of cigarettes smoked per day; ECLIPSE, Evaluation of COPD Longitudinally to Identify Predictive Surrogate End-points; FEV₁, forced expiratory volume in 1 s; FVC, forced vital capacity; NETT, National Emphysema Treatment Trial.
(Centre d’Etude du Polymorphisme Humain (Utah residents with ancestry from northern and western Europe) (CEU)) haplotypes from HapMap reference panel (phase II) and, as a secondary analysis, using 1000 Genomes Project data. We limited our analysis to SNPs genotyped/imputed in at least two cohorts, with imputation r^2 coefficient ≥0.3 (for imputed SNPs only). Overall, approximately 2.5 and 6.3 million SNPs per phenotype were analysed using the reference HapMap Project and 1000 Genomes Project panels, respectively.

**Association analysis of candidate SNPs**

We extracted candidate SNPs achieving genome-wide significance in the previous studies on smoking cessation and CPD. Following previous GWAS, we additionally extracted two SNPs from CYP2A6 (rs1801272 (Leu160His)) and cholinergic receptor, nicotinic, alpha 5 (CHRNA5, rs883765) based on their biological function. Since a candidate SNP from the DBH locus and most of the candidate SNPs from the CYP2A6 locus were imputed in all cohorts, we searched for the best proxy SNP genotyped in at least three of the cohorts.

**Statistics**

According to Box-Cox transformation that identified approximately the best transformation of dependent variables, which could be applied to all cohorts, we studied log2-transformed age at smoking initiation and lifetime average CPD, and the square root of the current CPD. Regression models were run under an additive model for SNPs, while adjusting for potential confounders (see online supplementary material for details). A fixed effect model was used for all meta-analyses. Effect allele was defined as the one associated with later age at smoking initiation, higher CPD or higher odds for smoking cessation. Meta-analytic p < 5 × 10^{-4} was considered as genome-wide significant; 5 × 10^{-4} ≤ p < 5 × 10^{-7} was interpreted as a suggestive association in the genome-wide panel with p < 0.05 as a suggestive association for candidate SNPs.

**Software**

Box-Cox transformations were performed with MASS package, while lambda inflation factors were calculated with GenABEL package in R (V2.10.1). SNP imputation was performed with MACH (V1.0.1). Principal components, reflecting genetic structure of each study population, were calculated and analysed with the EIGENSOFT package (V2.0). Genetic association analyses and meta-analyses were run with PLINK (V1.0.7), SNAP (V2.2) was used to search for proxy SNPs (r^2 ≥0.8) using the CEU HapMap phase II panel and to assess linkage disequilibrium (LD) coefficients in 1000 Genomes Project data. SNP/gene annotations and regional association plots were created with LocusZoom (V1.1; human genome build hg18).

**RESULTS**

**Age at smoking initiation**

Analyses in the individual cohorts were adjusted for sex and principal components for genetic ancestry. In total, the meta-analysis included 5397 patients for the age at smoking initiation phenotype. Lambda inflation factors were between 0.986 and 1.019 for individual cohorts (table 1), and 1.002 for meta-analytic p values (see online figure S1 for a Q-Q plot of meta-analysis). No SNPs showed meta-analytic association p values below the genome-wide significance level. Numerous SNPs in the intergenic region on chromosome 2q21 and in the region between BCL2-antagonist/killer 1 (BALK) and zinc finger and

**Lifetime average CPD**

Analyses in single cohorts were adjusted for sex, age and principal components for genetic ancestry. In total, the meta-analysis included 3440 patients for the lifetime average CPD phenotype. Lambda inflation factors were between 0.996 and 1.018 for individual cohorts (table 1), and 1.019 for meta-analytic p values (see online figure S2 for a Q-Q plot of meta-analysis). Thirteen SNPs were associated with lifetime average CPD.
CPD with meta-analytic $p<10^{-5}$, however, no SNPs showed association with meta-analytic $p<10^{-6}$ (table 2).

Candidate SNPs from the cholinergic nicotinic receptors locus on chromosome 15q25 (rs578776, rs588765, rs5034191, rs1051750 and rs16996968) were significantly ($p<0.05$) associated with lifetime average CPD with the same direction of effect as seen in previous GWAS on CPD (table 2). The synonymous rs1051750 SNP was the top associated SNP in this locus (figure 2).

Four candidate SNPs (rs7251570, rs4105144, rs1801272 and rs12461383) in the CYP2A6 locus on chromosome 19q13 were significantly ($p<0.05$) associated with lifetime average CPD with the same direction of effect as seen in previous GWAS on CPD (table 2). A non-synonymous SNP (rs1801272) was the second most significantly associated SNP in this locus (figure 2; table 2). There is, at most, a moderate level of LD between these four SNPs according to the Hapmap phase II panel ($r^2=0.6$ and $D'\approx0.84$; see online figure S3). Analysis of proxy SNPs that were genotyped in at least three cohorts was performed. Analysis of rs8102683 (genotyped in the NETT, ECLIPSE and Norwegian cohorts, and imputed in COPDGene) that is a proxy for rs4105144 ($r^2=0.87$), and rs7251418 (genotyped in all cohorts) that is a proxy for rs7251570 ($r^2=0.81$) confirmed the associations observed ($p=4.65\times10^{-8}$ (B=0.074 for the ‘C’ effect allele; $I^2=0$) and $p=0.0024$ (B=0.054 for the ‘G’ effect allele; $I^2=0$), respectively). No genotyped proxy SNPs could be found for rs12461383 and rs1801272 SNPs. We did not replicate, with a nominal $p<0.05$, associations between SNPs in 7p14, 8p11 and 10q23 loci, reported in previous GWAS on CPD in our analysis on lifetime average CPD (see online table S2).

Smoking cessation

Analyses in single cohorts were adjusted for age, percentage of predicted forced expiratory volume in 1 s ($FEV_1$) and principal components summarising genetic ancestry. In total, the meta-analysis included 1164 patients who were current smokers (defined as ‘no’ for smoking cessation) and 1907 patients who were former smokers (defined as ‘yes’ for smoking cessation). Lambda inflation factors were between 0.995 and 1.000 for individual cohorts (table 1), and 0.998 for meta-analytic $p$ values (see online figure S4 for a Q–Q plot of meta-analysis). No SNPs showed an association with meta-analytic $p<10^{-6}$ (table 3). Candidate SNP rs9025343 in the DBH locus showed nominally significant association with smoking cessation with the same direction of effect as seen in recent GWAS, yet with substantial heterogeneity between studies (table 3). SNP rs9025316, a proxy for rs9025343 ($r^2=0.94$), was genotyped in all cohorts and confirmed this association ($p=0.002$, OR=1.32 for the ‘T’ effect allele; $I^2=18$).

Current CPD

Analyses were adjusted for sex, age, percentage of predicted $FEV_1$, and principal components for genetic ancestry. In total, the meta-analysis included 1113 patients who were current smokers for the current CPD phenotype. Lambda inflation factors were between 0.995 and 1.005 for individual cohorts (table 1), and 1.010 for meta-analytic $p$ values (see online figure S5 for a Q–Q plot of meta-analysis). No SNPs showed a meta-analytic association with $p<10^{-6}$ (table 4). Among candidate SNPs, rs12461383 from the CYP2A6 locus was significantly
associated with current CPD with the same effect direction compared with previous GWAS on CPD (table 4). Candidate SNPs rs1801272 and rs7251570 showed a borderline significant association with the same effect direction compared with previous GWAS on CPD (table 4). We did not replicate, at a nominal p<0.05, associations between SNPs in 7p14, 8p11 and 10q23 loci reported in previous GWAS on CPD (online table S3).

**Analyses of SNPs imputed with 1000 Genomes Project data**

Analysis of all phenotypes using SNP genotypes imputed using the 1000 Genomes Project revealed 20 additional associations below the suggestive genome-wide significance level (see online table S4). SNP rs9394152 in the 6p21 locus was the most significantly associated SNP with the age at smoking initiation (meta-analytic \( p = 6.55 \times 10^{-5} \)) and, similarly to the majority of SNPs associated with this phenotype below the suggestive genome-wide significance level, was characterised by high \( (\geq 0.96) \), cohort-specific imputation \( r^2 \) coefficients (see online table S4). We observed novel associations of three SNPs with the lifetime average CPD; the most significantly associated SNP rs28675338 \( (r^2 = 0.07 \text{ and } D'=1.00 \text{ to } rs1051730 \text{ according to } 1000 \text{ Genomes Project Data}) \) maps to the 15q25 locus. We also found one SNP associated with smoking cessation, with metanalytic \( p < 5 \times 10^{-7} \) (see online table S4). Because cohort-specific, imputation \( r^2 \) coefficients of the four SNPs, associated with lifetime average CPD and smoking cessation below the suggestive genome-wide significance level, were rather modest (range 0.35–0.64; see online table S4), the observed associations certainly require additional confirmation and should be interpreted with caution. The three SNPs associated with current CPD with meta-analytic \( p < 5 \times 10^{-7} \) map to regions on chromosomes two and three (see online table S4), which were already ranked as top loci using the HapMap II reference panel (table 4).

**DISCUSSION**

Cigarette smoking is the most important environmental risk factor for COPD, and smoking cessation is the most important therapeutic intervention to prevent its progression. Our current study identified two loci on chromosomes 2q21 and 6p21 as candidates for containing genes influencing age at smoking initiation in patients with COPD, both showing suggestive levels of genome-wide significance. Furthermore, this study confirmed that certain SNPs in the cholinergic nicotinic receptor locus on chromosome 15q25 and SNPs in the CYP2A6 locus on chromosome 19q15 were associated with CPD in patients with COPD. Of importance, we additionally confirmed in patients with COPD the previously reported association of a marker (rs3025345) in the DBH locus with smoking cessation.

The two loci mapping to chromosomes 2q21 and 6p21 showed evidence of association with age at smoking initiation at a suggestive genome-wide significance level, using both HapMap II and 1000 Genomes projects reference imputation panels. The association peaks found here do not localise within any known genes, suggesting that distant regulation of yet unidentified target genes may be involved. SNPs from chromosome 6p21 are located close to the human leucocyte antigen locus, and ZBTB9 and BAK1 are the closest genes to the association peak. The BAK1 gene, encoding a proapoptotic protein, has been previously associated by GWAS with testicular germ cell tumours37 and platelet number.38 Yet SNPs identified in these studies do not correlate, in terms of LD, with top SNPs from our age at smoking initiation GWAS.

Analysis of candidate SNPs, with respect to the lifetime average CPD, revealed that the majority of those SNPs in the CHRNA3/CHRNA5 (15q25) and CYP2A6 (19q13) regions significantly associated with this trait showed the same direction of effect described previously.8–11 26 However, SNPs from the 7p14, 8p11 (CHRN83/CHRNA6 locus) and 10q23, as well as some SNPs from the CYP2A6 and CHRNA3/CHRNA5 loci, were not replicated in the current study with a nominal significance threshold. This may be caused by effect sizes that are too small to be detected in our populations or potentially to different genetic determinants of smoking behaviours within patients with COPD.


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**Figure 2** Regional association plots of the candidate loci centered on CHRNA3 (top) and CYP2A6 (bottom) and their associations with lifetime average number of cigarettes smoked per day. Dots correspond to meta-analysed SNPs. Colour of dots corresponds to \( r^2 \) (linkage disequilibrium (LD) coefficient in the HapMap II CEU population; grey dots correspond to SNPs with missing LD information) relative to the most significantly associated SNP in the region (depicted with diamond) that is, rs1051730 in the CHRNA3 (top figure) and rs1496402 (bottom figure; the second top SNP in this region is a non-synonymous (Leu160His) rs1801272 SNP in the CYP2A6). Chr, chromosome; CHRNA3, cholinergic receptor, nicotinic, alpha 3; CYP2A6, cytochrome P450, family 2, subfamily A, polypeptide 6.

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**Analyses of SNPs imputed with 1000 Genomes Project data**

Analysis of all phenotypes using SNP genotypes imputed using the 1000 Genomes Project revealed 20 additional associations...
from the dopamine beta-hydroxylase (DBH) locus identified by previous genome-wide association studies (GWAS) on smoking cessation by the Tobacco Genetics Consortium. Importantly, the effect sizes of replicated SNPs from this region are similar to most of those from the CYP2A6 locus in our study, which contrasts with recent GWAS where bigger effect sizes were seen for the former locus. Additionally, variations in the CHRNA3/CHRNA5 loci are similar to most of those from the CYP2A6 locus in our study, which contrasts with recent GWAS where bigger effect sizes were seen for the former locus.

We speculate that this might be due to between-study differences in general (eg, educational status or peer smoking) or those previously reported, suggesting larger COPD cohorts are required to establish significance of independent SNPs/haplotypes in this region.

### Table 3

<table>
<thead>
<tr>
<th>Chr</th>
<th>Top SNP</th>
<th>Nearest gene within 50 kb</th>
<th>Effect/Non-effect allele</th>
<th>OR</th>
<th>p</th>
<th>I²</th>
<th>Q stat.</th>
<th>N/Nimp</th>
<th>Freq.</th>
<th>Effect direction consistent with previous GWAS</th>
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Analyses were adjusted for age, % of predicted forced expiratory volume in 1 s (FEV₁) and principal components for genetic ancestry. Patients who were current smokers were considered as 'controls', while patients who were former smokers were considered as 'cases'.

N/Nimp, number of studies contributing to the meta-analysis/number of studies in which SNP was imputed; I², heterogeneity index; Q stat., p value for Q statistic; p, p value from the fixed effect meta-analysis; Freq., effect allele frequency in 3441 patients with at least one non-missing phenotype from four cohorts studied; Chr., chromosome; B, regression coefficient; UTR, untranslated region; CHRNA3/CHRNA5, cholinergic receptors, nicotinic, alpha 3/5; CYP2A6, cytochrome P450, family 2, subfamily A, polypeptide 6.

### Table 4

<table>
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<td>rs12615264</td>
<td>SOC5 (3' region)</td>
<td>T/G</td>
<td>0.644</td>
<td>3.46×10⁻⁶</td>
<td>0</td>
<td>0.38</td>
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<td>rs11682595</td>
<td>SOC5 (3' region)</td>
<td>T/G</td>
<td>0.642</td>
<td>3.49×10⁻⁶</td>
<td>0</td>
<td>0.41</td>
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<td>SOC5 (3' region)</td>
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<td>3.58×10⁻⁶</td>
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<td>4.66×10⁻⁶</td>
<td>49</td>
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<td>0.289</td>
<td>4.90×10⁻⁶</td>
<td>51</td>
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<td>4.99×10⁻⁶</td>
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<td>5.21×10⁻⁶</td>
<td>53</td>
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<td>7.71×10⁻⁶</td>
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<td>rs1051730</td>
<td>CHRNA3 (exon, Tyr215Thr)</td>
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<td>0.009</td>
<td>0.951</td>
<td>32</td>
<td>0.23</td>
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<td>CHRNA5 (exon, Asp398Asn)</td>
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<td>0.963</td>
<td>30</td>
<td>0.24</td>
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<td>AGPD1 (intron)</td>
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<td>0.006</td>
<td>0.914</td>
<td>5</td>
<td>0.35</td>
<td>3/0</td>
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<td>0.153</td>
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<td>0.388</td>
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<td>E2NL2 (intron)</td>
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<td>0.930</td>
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<td>0.590</td>
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<td>0.62</td>
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Analyses were adjusted for sex, age, % of predicted forced expiratory volume in 1 s (FEV₁) and principal components for genetic ancestry. Patients who were current smokers were considered as ‘controls’, while patients who were former smokers were considered as ‘cases’.

N/Nimp, number of studies contributing to the meta-analysis/number of studies in which SNP was imputed; I², heterogeneity index; Q stat., p value for Q statistic; p, p value from the fixed effect meta-analysis; Freq., effect allele frequency in 3441 patients with at least one non-missing phenotype from four cohorts studied; Chr., chromosome; B, regression coefficient; UTR, untranslated region; CHRNA3/CHRNA5, cholinergic receptors, nicotinic, alpha 3/5; CYP2A6, cytochrome P450, family 2, subfamily A, polypeptide 6.
COPD-specific (eg, reporting lifetime average CPD which may be influenced by severity of disease) characteristics.

Analysis of current CPD, which was much less powered than lifetime CPD because of a lower number of patients, was still able to detect some evidence of association with markers near CYP2A6, yet not for those located in the CHRNA3/CHRNA5 region. CYP2A6 is an enzyme primarily responsible for conversion of nicotine to cotinine in the liver, and rs1801727 (Leu160His) codes for the CYP2A6*2 allele, which inactivates the enzyme.41 This SNP showed the largest effect size on both current and lifetime average CPD among all analysed candidate SNPs in the region. Leu160His is in LD (D’=1.0) with other SNPs that were replicated in the CYP2A6 locus. This agrees with previous GWAS and suggests that the rs1801727 SNP may be a true causative variant, while the other associations observed may be due to partial tagging by this SNP.8 Importantly, we show that the genotyped proxy SNPs in the CYP2A6 locus confirmed our analysis on imputed SNPs with respect to lifetime average CPD. The lack of convincing association for the proxy SNP rs7251418 with current CPD may be explained by the relatively smaller sample size in this analysis, and incomplete LD between the target and the proxy SNPs. Previous GWAS suggested that other genes may be associated with CPD in the 19q13 region, yet we observed no nominally significant associations for EGLN2, RAB4B and CY2B6.

Analysis of smoking cessation did not reveal any loci associated below the suggestive significance level, and it showed that the previously reported10 association between rs3025545 in the DBH locus can be replicated in patients with COPD with a nominal significance threshold. DBH is a plausible candidate gene for smoking cessation because it participates in the metabolism of dopamine. This neurotransmitter is released from neurons in response to nicotine,7 and is an important mediator of addiction behaviours such as smoking. The rs3025345 SNP that we extracted showed a substantial heterogeneity in this effect, which may reflect the between-study differences in factors such as use of nicotine replacement therapy or socioeconomic status. Interestingly, the best proxy SNP rs3025516 (genotyped in all cohorts) showed a more pronounced effect with a somewhat smaller heterogeneity index compared with the rs3025345.

Our study possesses several limitations, and some of them are typical for many GWAS. For example, the size of the current study may have been too small to detect associations at a genome-wide significance level. Phenotypes studied are genetically complex and are likely determined by many genes of modest effects, which makes them difficult to detect with genome-wide significance for the currently studied sample size. It is worth noting that the much larger Tobacco and Genetics consortium did not identify any genome-wide significant associations for age at smoking initiation in patients with COPD. We showed that variation in the CHRNA3/CHRNA5 locus on chromosome 15q25 locus and the CYP2A6 locus on chromosome 19q13 were associated with lifetime average CPD among patients with COPD. The latter gene may play a significant role in the current smoking intensity among patients with COPD. Future studies in larger populations will be required to determine the overlap between genetic determinants of smoking behaviour in the general population and in patients with COPD.

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