

# Interactive effect between ATPase-related genes and early-life tobacco smoke exposure on bronchial hyper-responsiveness detected in asthma-ascertained families

Marie-Hélène Dizier, Patricia Margaritte-Jeannin, Lucile Pain, Chloé Sarnowski, Myriam Brossard, Hamida Mohamdi, Nolwenn Lavielle, Marie-Claude Babron, Jocelyne Just, Mark Lathrop, et al.

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1 **Interactive effect between ATPase-related genes and early-life tobacco smoke**  
2 **exposure on bronchial hyper-responsiveness detected in asthma-ascertained**  
3 **families**

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32

33 **Running title:**

34 ATP genes and early-life smoking exposure in BHR

35

36 **Key messages:**

37 What is the key question?

38 Could genes belonging to ATP-related pathways interact with exposure to early-life

39 tobacco smoke exposure on bronchial hyper-responsiveness?

40

41 What is the bottom line?

42 Gene x Environment interaction analyses with ATP-related genes allowed to identify

43 promising candidate genes, ATP8A1 and ABCA1, interacting with early-life tobacco

44 smoke exposure in bronchial hyper-responsiveness susceptibility.

45

46 Why read on?

47 The present study highlights that Gene x Environment interaction analyses under a

48 pathway-based strategy can greatly contribute to the identification of novel genes

49 involved in complex disease as bronchial hyper-responsiveness.

50

51 **ABSTRACT**

52 Background: A positional cloning study of bronchial hyper-responsiveness (BHR) at the  
53 17p11 locus in the French Epidemiological study on the Genetics and Environment of  
54 Asthma (EGEA) families showed significant interaction between early life  
55 environmental tobacco smoke (ETS) exposure and genetic variants located in *DNAH9*.  
56 This gene encodes the heavy chain subunit of axonemal dynein, which is involved with  
57 adenosine triphosphate (ATP) in the motile cilia function.

58 Our goal was to identify genetic variants at other genes interacting with ETS in BHR by  
59 investigating all genes belonging to the “*ATP-binding*” and “*ATPase activity*” pathways  
60 which include *DNAH9*, are targets of cigarette smoke and play a crucial role in the  
61 airway inflammation.

62 Methods: Family-based interaction tests between ETS exposed *versus* unexposed BHR  
63 siblings were conducted in 388 EGEA families. Twenty SNPs showing interaction  
64 signals ( $P \leq 5.10^{-3}$ ) were tested in the 253 Saguenay-Lac-Saint-Jean (SLSJ) families.

65 Results: One of these SNPs was significantly replicated for interaction with ETS in  
66 SLSJ families ( $P=0.003$ ). Another SNP reached the significance threshold after  
67 correction for multiple testing in the combined analysis of the two samples ( $P=10^{-5}$ ).

68 Results were confirmed using both a robust log-linear test and a gene-based interaction  
69 test.

70 Conclusion: The SNPs showing interaction with ETS belong to the *ATP8A1* and *ABCA1*  
71 genes, which play a role in the maintenance of asymmetry and homeostasis of lung  
72 membrane lipids.

73

74 **Key words:** BHR, FBAT, ETS, GxE interaction, ATP, asthma

75 Key message: *ATP8A1* and *ABCA1* genes interact with early-life tobacco smoke  
76 exposure in BHR in asthma-ascertained families.

77

78

## 79 INTRODUCTION

80 Bronchial hyper-responsiveness (BHR) is both a feature and an important risk factor for  
81 asthma [1]. The susceptibility genes for asthma and BHR [2], identified to date, account  
82 for a relatively small proportion of the genetic component of these phenotypes [3]. As  
83 asthma and BHR are complex diseases which result from both genetic and  
84 environmental factors, the effect of genetic factors may be missed if they are tested  
85 individually, i.e. by ignoring gene by environment (GxE) interactions. Furthermore,  
86 taking into account the biological function shared by genes or pathways they are  
87 involved in may help discovering new genes [4].

88 Maternal smoking during pregnancy and early life environmental tobacco smoke (ETS)  
89 exposure are well-known risk factors for asthma and BHR [5]. Gene x ETS interaction  
90 underlying susceptibility to asthma and asthma-related phenotypes have been evidenced  
91 by positional cloning studies which detected *PCDHI* (protocadherin 1) and *ADAM33*  
92 (ADAM metallopeptidase domain 33) genes [6, 7, 8], by association studies with  
93 candidate genes including *ADRB2* ( $\beta$ 2-adrenergic receptor) [9], and by interaction  
94 analysis with genetic variants at the 17q12-21 locus discovered by the first asthma  
95 GWAS [10, 11]. More recently, a meta-analysis of genome-wide interaction studies  
96 (GEWIS) for childhood asthma [12] suggested interaction between ETS exposure and  
97 *PACRG* (Parkin coregulated) - a gene having a role in motile cilia function.

98 In the French Epidemiological study on the Genetics and Environment of Asthma  
99 (EGEA) families, we previously performed a positional cloning study in the 17p11  
100 region that showed interactive effect between ETS and *DNAH9* (Dynein, Axonemal,  
101 Heavy Chain 9) [13, 14] genetic variant on BHR. This gene encodes the heavy chain  
102 subunit of axonemal dynein, a component responsible for cilia mobility. Interestingly, a

103 recent study of atopy, another asthma-related phenotype, showed significant interaction  
104 between *DNAH5*, a gene of the same family as *DNAH9*, and *ADGRV1* (adhesion G  
105 protein-coupled receptor V1), both genes being involved in ciliary function [15].  
106 Overall, these findings suggest that ciliary dysfunction may represent a novel  
107 mechanism underlying asthma-related phenotypes.

108 The heavy chain subunit of axonemal dynein contains all of the elements that are  
109 needed to convert the energy into movement though a process in which dynein,  
110 adenosine triphosphate (ATP) binding and ATP hydrolysis are involved [16, 17, 18].  
111 Interestingly, in asthmatic patients, ATP was shown to be accumulated in the airways  
112 and to trigger HRB, suggesting an important role played by ATP in the airway  
113 inflammation [19]. Moreover, ATP-binding cassette (ABC) transporters were  
114 implicated in pulmonary lipid homeostasis and inflammation, indicating a crucial and  
115 protective role in lung [20].

116 Smoking and exposure to cigarette smoke have been shown to affect the number and  
117 function of human bronchial cilia [18, 21], while a significant loss of Na,K-ATPase  
118 activity was observed in human lung cell lines exposed to cigarette smoke [22] and in  
119 platelet membrane in cigarette smokers compared to controls [23].

120

121 In the present study, we hypothesized that genes belonging to *ATPase activity*” and  
122 “*ATP binding*” pathways, the two ATP-related pathways that include *DNAH9*, may also  
123 interact with exposure to ETS in BHR. We tested for interaction all genes of these two  
124 pathways using the discovery sample of 388 French EGEA families, ascertained  
125 through asthmatic probands. We first applied FBAT (Family-Based Association Test)  
126 [24] homogeneity test between exposed *versus* unexposed BHR siblings to detect

127 interactions for SNPs located in the genes belonging to the two pathways. Replication  
128 of results was sought in an independent sample of 253 French-Canadian asthma-  
129 ascertained families. We also validated our results by using another SNP x E interaction  
130 test based on log-linear modeling case-parent triads [25], and finally by gene-based  
131 interaction analysis.

132



## 133 MATERIAL AND METHODS

### 134 Discovery sample

135 The EGEA study and inclusion criteria have been described in detail previously [26].  
136 The EGEA family sample consisted of 388 French nuclear families that included 253  
137 families ascertained through offspring with asthma (one offspring proband in 90% of  
138 families and two offspring probands in the remainder) and 135 families ascertained  
139 through one parent with asthma. Ethical approval was obtained from the relevant  
140 institutional review board committees (Cochin Port-Royal Hospital and Necker-Enfants  
141 Malades Hospital, Paris). Written informed consent was signed by all participants or by  
142 kin or guardians of the minors/children.

143 The BHR phenotype was defined according to the results of the methacholine bronchial  
144 challenge test, as done previously [13, 14]. Participants who had a fall in their baseline  
145 FEV<sub>1</sub> (forced expiratory volume in 1s)  $\geq 20\%$  at  $\leq 4$  mg/ml of methacholine (PD20) had  
146 BHR while participants that did not show a fall in FEV<sub>1</sub> did not have BHR. The  
147 protocol of the methacholine challenge test has been described in detail elsewhere [26].  
148 The ETS exposure in early-childhood was defined, as previously [10, 13, 14] through  
149 questionnaires: 1) for an adult, by a positive answer to the question: "*Did your mother*  
150 *or your father smoke during your early-childhood?*", 2) for a child, by a positive answer  
151 to the question asked to the child's mother (or father): "*Did you or the father (or the*  
152 *mother) of your child smoke when your child was less than 2 years old?*". We did not  
153 use information on *in-utero* exposure to tobacco-smoke since all mothers who smoked  
154 during pregnancy continued to smoke during the early childhood of their offspring.

155

156

157 **Replication study**

158 The Saguenay-Lac-Saint-Jean (SLSJ) asthma study comprised 253 French-Canadian  
159 multigenerational families ascertained through two probands with asthma [27].  
160 Inclusion criteria of probands have been described previously [27]. The SLSJ local  
161 ethics committee approved the study, and all subjects gave informed consent.  
162 The BHR (PD20) phenotype and ETS exposure were defined in SLSJ in an identical  
163 manner as in the EGEA study.

164

165 **Genotyping**

166 The EGEA subjects were genotyped using Illumina 610 Quad array (Illumina, San  
167 Diego, CA) at the Centre National de Génomique (CNG, Evry, France), as part of the  
168 European Gabriel consortium asthma GWAS [28]. Stringent quality control criteria, as  
169 detailed previously [28], were used to select both individuals and genotyped SNPs for  
170 analysis. For this study, we selected from the Gene Ontology (GO) database  
171 (<http://amigo.geneontology.org/>) 296 genes belonging to both molecular functions  
172 “ATPase binding” (GO: 0005524) and “ATPase activity” (GO: 0016887) and the  
173 corresponding 4,252 SNPs located within these genes (see Supplementary Table S1).

174 The SLSJ sample was also genotyped at CNG using the Illumina 610 Quad array. The  
175 same quality control criteria for individuals and SNPs as those used for EGEA were  
176 applied to this dataset.

177

178 **Statistical analysis**

179 GxE interaction analysis using FBAT-homogeneity test

180 *Analysis of the EGEA discovery sample*

181 Analyses were conducted using the FBAT approach [24], which tests for association in  
182 presence of linkage. We assumed an additive genetic model and used the option for an  
183 empirical estimator of the variance [29], which makes the association test robust to the  
184 dependency between siblings and allows use of all siblings in a family. FBAT was  
185 applied separately to ETS exposed and unexposed siblings. We searched for SNP x ETS  
186 interaction by testing homogeneity of FBAT association results between ETS exposed  
187 and unexposed [30]. Note that after exclusion of SNPs leading to insufficient sample  
188 size (<30) of informative families for FBAT analyses in the EGEA sample, only 4,112  
189 SNPs belonging to only 266 genes were analysed.

190

#### 191 *Replication analysis with the SLSJ sample*

192 SNPs showing interaction signals ( $P \leq 5 \times 10^{-3}$ ) in the EGEA sample were followed-up in  
193 the SLSJ sample. The arbitrary threshold of  $5 \cdot 10^{-3}$  was chosen to obtain both a strong  
194 indication of association and a reasonable number of SNPs (here 20, see results) tested  
195 in the replication dataset. For replication study of these SNPs detected in EGEA, both  
196 analysis in SLSJ and combined analysis in EGEA and SLSJ were conducted.

197 First, analyses were conducted in SLSJ and results were declared as significant if they  
198 meet the Bonferroni corrected significance  $P$ -threshold applied to the  $M_{\text{eff}}$  (effective  
199 number of independent tests after discarding dependence due to Linkage Disequilibrium  
200 (LD) between the SNPs) [31] calculated from the 20 SNPs tested in SLSJ. The  $M_{\text{eff}}$   
201 was estimated to 15 and thus the significance  $P$ -threshold equal to  $3 \cdot 10^{-3}$ .

202 Second, combined FBAT analysis of the EGEA and SLSJ samples was conducted,  
203 separately in ETS exposed and unexposed siblings using the Stouffer's  $Z$ -score method,  
204 and homogeneity test was applied between exposed vs unexposed siblings to the

205 combined results. The results of this combined analysis are not independent from the  
206 results obtained in EGEA. We thus declared results as significant if they meet the  
207 significance  $P$ -threshold ( $P=2.10^{-5}$ ), calculated after correction for multiple tests by the  
208 Bonferroni correction applied to the Meff (2500) estimated from the total number of  
209 SNPs tested in EGEA.

210

#### 211 *Validation analysis using Umbach and Weinberg method*

212 In order to validate the significant interactions found with the FBAT homogeneity test,  
213 we applied, the log-linear modeling approach for testing interaction in triads (case and  
214 parents), as proposed by Umbach and Weinberg (UW) [25], to the pooled sample of  
215 EGEA and SLSJ. This approach allows adjusting on the genotypic parental mating of  
216 each sibling and thus avoids bias due to population stratification. A different  
217 distribution of parental genotypic matings between exposed *versus* unexposed siblings,  
218 due to population stratification, may lead to different transmission probabilities in the  
219 two groups and consequently to false detection of interaction. FBAT is less robust  
220 because it only adjusts for the genotypic parental distribution within the exposed and  
221 unexposed groups of siblings. However, the UW method is less powerful than FBAT  
222 because it can be applied to only one sib per family. The log-linear analysis was  
223 conducted using the youngest siblings for whom the information on ETS exposure was  
224 the closest in time with respect to BHR occurrence and thus the less influenced by a  
225 potential recall bias. The analysis was also performed by considering the oldest siblings,  
226 but similar results were obtained and are thus not presented.

227 As for FBAT analysis, all UW analyses assumed an additive genetic model and the  
228 same correction for multiple testing was applied, *i.e.* Bonferroni correction applied to  
229 the Meff of 2,500.

230

### 231 *Gene-based analysis*

232 For each of the 266 genes, interactions with ETS exposure in BHR were also  
233 investigated at the gene level by using the versatile gene-based test (VEGAS) [32] .  
234 The gene-based statistic was defined as the best SNP test statistic (or min  $P$  value) using  
235 the results of FBAT-homogeneity tests in the combined analysis of EGEA and SLSJ  
236 samples. Empirical  $P$ -value of the gene-based statistic was computed through Monte-  
237 Carlo simulations using the linkage-disequilibrium pattern of HapMap CEU reference  
238 sample. The empirical  $P$ -values were adjusted for multiple testing using the Bonferroni  
239 correction (significance  $P$ -threshold= $0.05/266=2.10^{-4}$ ).

240

### 241 *Expression Quantitative Trait loci (eQTL) analysis, functional annotation and* 242 *chemical-gene/protein interactions*

243 We investigated whether the SNPs (or their proxies,  $r^2 \geq 0.8$ ) found to interact with ETS  
244 were cis-expression quantitative trait loci (cis-eQTLs). We used the GTEx browser  
245 (<http://www.gtexportal.org/home/>) [33], that includes e-QTL data from many tissues.  
246 Functional annotations of these SNPs (or proxies) were done using the HaploReg tool  
247 (<http://www.broadinstitute.org/mammals/haploreg/haploreg.php>). HaploReg annotates  
248 SNPs in terms of co-localization with regulatory elements, such as promoter and  
249 enhancer marks, DNase I hypersensitivity sites, and transcription factor (TF) and

250 protein binding sites, based on ROADMAP and ENCODE (ENcyclopedia Of DNA  
251 Elements) data.

252 Furthermore, curated [chemical–gene interactions|chemical–disease|gene–disease] data  
253 were retrieved from the Comparative Toxicogenomics Database (CTD) [34], MDI  
254 Biological Laboratory, Salisbury Cove, Maine, and NC State University, Raleigh, North  
255 Carolina. World Wide Web, (URL: <http://ctdbase.org/>). [May, 2018]. CTD is a robust,  
256 publicly available database that aims to advance understanding about how  
257 environmental exposures affect human health. It provides manually curated information  
258 about chemical–gene/protein interactions, chemical–disease and gene–disease  
259 relationships.

260

261

262 **RESULTS**263 **Data description**

264 The characteristics of genotyped siblings having BHR in EGEA and SLSJ families are  
265 shown in Table 1.

266 Table 1: Phenotypic features of genotyped siblings having BHR in EGEA and SLSJ  
267 asthma-ascertained families  
268

	EGEA	SLSJ
N siblings	304	145
Age, years, mean (SD)	16.1 (8.1)	20.3 (10.3)
Sex, n (%) women	132 (43.4)	76 (52.4)
Asthma, n (%)	181 (59.5)	138 (95.2)
Age at asthma onset, years, mean (SD)	7.4 (7.7)	9.4 (9.3)
Allergic sensitization*, n (%)	228 (76.0)	121 (85.8)
ETS** exposure, n (%)	176 (57.9)	93 (64.1)

269 \*: allergic sensitization: a positive response of skin prick test to at least one allergen.

270 \*\*: ETS: Environmental tobacco smoke.

271

272 Three hundreds and four siblings (from 189 families) had BHR in EGEA and 145 (from  
273 120 families) in SLSJ. They were younger in EGEA than in SLSJ with respective mean  
274 ages equal to 16.1 and 20.3 years ( $P < 10^{-4}$ ). The proportion of siblings with allergic  
275 sensitization was similar in the two datasets (76% in EGEA and 86% in SLSJ), while  
276 the proportion of asthmatics was higher in SLSJ (95%) than in EGEA (60%) ( $P < 10^{-4}$ ).  
277 The proportion of female was similar in the two datasets (43% in EGEA and 52% in  
278 SLSJ). The mean age at onset of asthma was slightly lower in EGEA (7.4) than in SLSJ  
279 (9.4) ( $P = 0.05$ ). Finally, the proportion of exposed siblings was similar in EGEA and in  
280 SLSJ (58% *versus* 64% respectively).

281 **Analysis of Gene x ETS interactions using FBAT-homogeneity test**

282 The results in the EGEA, SLSJ, and combined samples are shown in Table 2 (for more  
283 details see Supplementary Table S2).

284 Table 2: Results of FBAT-homogeneity test in the EGEA and SLSJ samples for SNPs  
285 detected in EGEA with  $P \leq 5.10^{-3}$ .

						EGEA	SLSJ	EGEA+SLSJ#
<b>Chr</b>	<b>SNP</b>	<b>Gene</b>	<b>Location</b>	<b>Position*</b> <b>(kb)</b>	<b>MAF**</b>	<b>P</b>	<b>P</b>	<b>P</b>
1	rs10924249	KIF26B	flanking_3UTR	243837	0.18	0.004	0.302	0.059
2	rs6736802	KIF5C	flanking_5UTR	149566	0.43	0.002	0.320	0.056
2	rs6435220	KIF5C	flanking_5UTR	149569	0.31	0.003	0.659	0.032
4	rs1460354	ATP8A1	Intron	42266	0.22	0.001	0.115	6.0E-04
4	rs13124088	ATP8A1	Intron	42280	0.20	0.005	0.227	0.004
<b>4</b>	<b>rs17448506</b>	<b>ATP8A1</b>	<b>Intron</b>	<b>42343</b>	<b>0.27</b>	<b>1.7E-05</b>	<b>0.133</b>	<b>1.2E-05</b>
6	rs160666	WRNIP1	flanking_3UTR	2719	0.32	0.003	0.398	0.041
8	rs2279444	KIF13B	Intron	29053	0.15	0.005	0.400	0.006
<b>9</b>	<b>rs2253304</b>	<b>ABCA1</b>	<b>Intron</b>	<b>106658</b>	<b>0.27</b>	<b>0.004</b>	<b>0.003</b>	<b>6.1E-05</b>
9	rs2253182	ABCA1	Intron	106659	0.27	0.004	0.005	9.2E-05
9	rs2253175	ABCA1	Intron	106660	0.27	0.004	0.004	7.2E-05
9	rs2253174	ABCA1	Intron	106660	0.27	0.004	0.004	7.2E-05
9	rs2230805	ABCA1	Coding	106663	0.25	0.005	0.017	2.0E-04
11	rs762667	MYO7A	Coding	76546	0.38	0.002	0.446	0.003
16	rs2914819	ATP2C2	Intron	83026	0.19	0.003	0.353	0.0018
17	rs7225157	DNAH9##	Intron	11621	0.17	8.1E-04	0.038	6.8E-05
18	rs12458154	ATP9B	Intron	75187	0.28	0.002	0.551	0.0047



20	rs6067867	ATP9A	Intron	49698	0.46	0.005	0.376	0.0056
20	rs6067892	ATP9A	Intron	49731	0.47	0.002	0.410	0.0036
20	rs1475670	ATP9A	Intron	49777	0.50	0.004	0.058	7.0E-04

286 \*: SNP position in kilobase (dbSNP, build 37.1)

287 \*\*: estimated in EGEA

288 #: combined analysis of the EGEA and SLSJ samples using the Stouffer's Z-score  
289 method

290 ##: previously detected by our positional cloning [14]

291 Significant results are in bold

292

293 FBAT-homogeneity test in EGEA detected 20 SNPs (at the level of  $P \leq 5.10^{-3}$ ), for

294 which replication study was then conducted. The analysis in SLSJ detected a significant

295 association ( $P=3.10^{-3}$ ) with one of these SNPs, rs2253304 which is located in *ABCA1*

296 intron. The combined analysis of the two EGEA and SLSJ samples detected another

297 SNP, rs17448506 which is located in *ATP8A1* intron, and reached the significance

298 threshold for interaction with ETS ( $P=10^{-5}$ ). The SNP rs2253304 was also the second

299 top signal in the combined analysis ( $P=6.10^{-5}$ ).

300 At both SNPs, there was a "Flip-Flop" interaction effect (i.e. an inverse effect

301 depending on exposure): the C allele (*versus* T allele) of rs17448506 was positively

302 associated with BHR in ETS-exposed siblings and negatively in ETS-unexposed

303 siblings, while G allele (*versus* A allele) of rs2253304 was positively associated with

304 BHR in ETS-exposed siblings and negatively in ETS-unexposed siblings.

305

### 306 **Validation analysis using Umbach and Weinberg method**

307 For the two SNPs retained by the analyses based on FBAT homogeneity test

308 (rs17448506 and rs2253304), results of UW analysis in the pooled EGEA and SLSJ

309 samples are presented in Table 3.

310 Table 3: Results with UW in the pooled sample of EGEA and SLSJ for SNPs detected  
 311 by FBAT-homogeneity test:

312

Chr	SNP	Gene	Location	Position * (kb)	MAF	<i>P</i>
4	rs17448506	ATP8A1	intron	42343	0.27	9.0E-04
9	rs2253304	ABCA1	intron	106658	0.27	5.0E-04

313 \*: SNP position in kilobase (dbSNP, build 37.1)

314

315 Both SNPs showed quite strong signals of interaction ( $P \leq 10^{-3}$ ) with the UW method,  
 316 although they did not reach the significance threshold of  $2 \times 10^{-5}$ .

317

### 318 Gene-based analysis

319 Results by the gene-based test using the combined results of EGEA and SLSJ were  
 320 given for all 266 genes in Supplementary Table S3. *ATP8A1* and *ABCA1* were the first  
 321 and third top genes, respectively, interacting with ETS exposure in BHR that were  
 322 detected ( $P=3.10^{-4}$  and  $P=3.10^{-3}$ , respectively). Only the *P*-value for *ATP8A1* was close  
 323 to the significance threshold of  $2.10^{-4}$  adjusted for multiple testing. The second top gene  
 324 was *ATP9B* and the 4<sup>th</sup> top gene *DNAH9*.

325

### 326 eQTL, Functional Annotations and Chemical–Gene/Protein Interactions

327 No eQTL was found among the SNPs (or proxies) interacting with ETS at *ATP8A1* and  
 328 *ABCA1* loci. Using the functional annotation tool HaploReg-v4.1, we found that both  
 329 SNPs map to enhancer and promoter histone marks and that rs2253304 and its proxies  
 330 map to DNase hypersensitivity sites, notably in fetal lung fibroblasts cell line, Lung  
 331 Carcinoma Cell Line and Lung Fibroblast Primary Cells. They also map to binding sites

332 of many transcription factors including the redox-sensitive nuclear factor (NF)-kappaB  
333 (NF-κB) for rs17448506 and the Histone Deacetylase 2 (HDAC2), Activator Protein 1  
334 (AP-1), Smad and STAT for rs2253304 and proxies.

335 Further, from the Comparative Toxicogenomics Database, we found that tobacco smoke  
336 pollution and soot have been reported to modify the expression of *ATP8A1* and *ABCA1*  
337 mRNA (see Table S4). We also found that air pollutant exposures known to contain  
338 compounds with irritant properties such as in tobacco smoke modified the expression of  
339 *ABCA1* (see Table S4).

340

## 341 **DISCUSSION**

342 This study identified genetic variants at two novel loci, in chromosomes 4 and 9,  
343 interacting with ETS exposure in BHR. After a selection of SNPs showing signal of  
344 interaction with ETS in EGEA, interaction was significantly replicated in SLSJ for a  
345 first SNP intronic to *ABCA1* gene. Significant interaction with ETS was detected for a  
346 second SNP intronic to *ATP8A1* gene in the combined analysis of EGEA and SLSJ  
347 samples. Furthermore, in the gene-based analysis, *ATP8A1* and *ABCA1* were among the  
348 three top genes interacting with ETS exposure, this interaction being very close to the  
349 significance level for *ATP8A1*.

350 Most of previous interaction studies of genetic variants with ETS on BHR or asthma  
351 risk had difficulties to show significant interaction and/or replication in independent  
352 samples [6, 12, 35]. Indeed, replication of GxE interaction is much more difficult to  
353 achieve than replication of single SNP association. It is well-recognized that interaction  
354 tests have low power. Moreover, replication of interaction is affected by heterogeneity  
355 not only in the outcome but also in exposure definition of the participating studies. The  
356 distribution of exposure may also differ across populations and therefore change the  
357 potential to identify the interaction. It is well-known that ETS is influenced by  
358 socioeconomic position and generation effect. Tobacco use seems to be almost  
359 universally more prevalent in low socioeconomic groups than in high socioeconomic  
360 groups [36]. Over the last ten years, the prevalence of ETS exposure at home among  
361 children and the percentage of children whose parents smoke has declined in several  
362 industrialized countries [37]. Difference in the distribution of ETS may thus result in  
363 different relationships among the gene, environment and disease. It was difficult to find  
364 replication samples that showed consistent definitions of BHR and ETS exposure and

365 similar distribution of ETS exposure with those of the EGEA discovery sample. Only  
366 one replication sample from the SLSJ study showed similarities with EGEA in terms of  
367 ascertainment through asthmatic subjects, definition of both BHR and ETS, distribution  
368 of ETS and genotype information available in parents and siblings. To keep reasonable  
369 the number of tests and then limit the problem of low power of interaction test, we  
370 examined only SNPs located within gene boundaries. Even if SNPs lying at some  
371 distance upstream and downstream from the gene are often considered, the choice of  
372 that distance is not obvious.

373 Nevertheless, we were able to identify two SNPs, with significant evidence for  
374 interaction with ETS. These results were confirmed by the UW approach, which is more  
375 robust although less powerful than FBAT as described above in the methods section.

376 Our study relies on an original strategy to select and enlarge a list of candidate genes.  
377 Supported by biological knowledge, we think our pathway selection approach allows a  
378 good tradeoff between GEWIS and candidate gene approaches, and offers the  
379 possibility to identify new genes as we previously showed [4]. We cannot exclude that  
380 our selection may lose a number of relevant genes that are not targeted by our analysis.

381 In particular, we choose the stringent option to investigate genes, which similarly to  
382 *DNAH9*, belong simultaneously to the two ATP-related pathways. We thus used the  
383 intersection and not the union of these two pathways. Advantage of this strategy was to  
384 limit the number of SNPs to be tested, leading to a reduction of the multiple testing  
385 burden and to a gain of power. Furthermore, after the analysis in the discovery sample  
386 (EGEA), we used two different replication analyses of top EGEA results: first analysis  
387 in the SLSJ sample, and then a combined analysis in the two samples (EGEA and  
388 SLSJ). Although these two types of analyses are not independent (indeed combined

389 analysis of EGEA and SLSJ included SLSJ results), they led to detect two different  
390 genes, that appear both interesting. Note that the *DNAH9* gene evidenced by our  
391 previous positional cloning study [14] was also detected in the present study, ranked as  
392 the third top SNP and as the 4<sup>th</sup> top gene, although results did not reach significance.

393 To our knowledge, none of our findings has been previously reported by published  
394 GWAS (GWAS-Catalog of Published Genome-Wide Association Studies,  
395 <http://genome.gov/gwastudies>), or by GEWIS for asthma, BHR or lung function.

396 Although a few G x ETS interaction studies [16, 18] have been published for BHR to  
397 date, neither the *ATP8A1* nor the *ABCA1* genes have been mentioned.

398 The *ATP8A1* gene codes for a putative aminophospholipid transporting enzyme which  
399 helps to maintain phospholipid asymmetry in cell membranes [38]. Recently, in non-  
400 small-cell lung cancer, *ATP8A1* was found to be a novel direct target of miR-140-3p  
401 [39], a small noncoding RNA molecule known to regulate gene expression, and that  
402 may contribute substantially to airway epithelium abnormalities [40]. Moreover,  
403 exposure of rats to cigarette smoke causes extensive alterations in miRNA expression of  
404 the miR-140 family in the lung [41]. The *ABCA1* gene encodes a transport protein  
405 known to participate to the maintenance of lung lipid homeostasis by interacting with  
406 the apolipoprotein A-I (apoA-I), and which expression and function are affected by  
407 smoking [42]. The critical role of ABCA1 in lung inflammation was evidenced from  
408 murine knockout models [20] and a recent review reported that the apoA-I/ABCA1  
409 pathway was involved in the modulation of the function of airway structural cells, and  
410 associated with neutrophilic airway inflammation and airway hyperresponsiveness [43].  
411 Furthermore, rs17448506 located in *ATP8A1* and rs2253304 in *ABCA1* are both intronic  
412 variants, and map near regulatory elements and transcription factor binding sites

413 include that of NF-kappaB, an important participant in a broad spectrum of  
414 inflammatory networks that regulate cytokine activity in airway pathology [44]. Lastly,  
415 tobacco smoke pollution and soot have been reported to modify the expression of  
416 *ATP8A1* and *ABCA1* mRNA.

417 Interestingly, some of the previous genes detected to interact with ETS in BHR, belong  
418 to or interact experimentally with genes belonging to the “*ATPase activity*” or “*ATP*  
419 *binding*” pathways. Among them, the *ADRB2* gene [9] belongs to the “*ATPase activity*”  
420 pathway. The *PCDH1* gene [6] was shown to interact with *ABCA2* and *ATF7IP* genes,  
421 which both belong to “*ATP binding*” and/or “*ATPase activity*” pathways. Similarly the  
422 *PACRG* and the *EPB41L3* genes [12] were also shown to interact with numerous genes  
423 belonging to “*ATP binding*” and/or “*ATPase activity*” pathways. Overall, all these data  
424 suggest that *ATP8A1* and *ABCA1* may play a role in BHR in relationship with early  
425 tobacco smoke exposure.

426 In conclusion, the present study highlights that G x E interaction analyses under a  
427 pathway-based strategy allowed to identify promising candidate genes interacting with  
428 ETS exposure in BHR susceptibility. Further confirmation of the interaction of *ATP8A1*  
429 and *ABCA1* with ETS exposure as well as functional studies are needed to bring greater  
430 insight into the role of these genes in BHR. Our study suggest that the two pathways are  
431 promising to be further explored in the search of more effective therapies for  
432 inflammatory lung diseases, especially for BHR that is a feature and an important risk  
433 factor for asthma.

434

435 **COMPETING INTERESTS**

436 ‘None declared’

437

438 **CONTRIBUTORSHIP STATEMENT**

439 MHD and RN conducted the design. MHD and PMJ performed data analysis, N. MHD  
440 and RN interpreted the findings and drafted the initial version of the manuscript. JJ, CL,  
441 ML, FD, EB and MHD contributed to the data acquisition. FD and EB revised the  
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484

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