

# HHIP, HDAC4, NCR3 and RARB polymorphisms affect fetal, childhood and adult lung function

To the Editor:

Impaired lung function, and consequent respiratory morbidity including asthma and chronic obstructive pulmonary disease, may have their origins in early life [1–3]. Genome-wide analysis studies (GWAS) have identified a number of single-nucleotide

polymorphisms (SNPs) in those of European ancestry that affect adult lung function, as measured by forced expiratory volume in 1 s (FEV<sub>1</sub>) and FEV<sub>1</sub>/forced vital capacity (FVC) ratio. 23 of these SNPs have directionally consistent effects on both FEV<sub>1</sub> and FEV<sub>1</sub>/FVC in children and adults [4].

**TABLE 1** Single-nucleotide polymorphism (SNP) code, target gene, chromosome and minor allele of the 23 analysed SNPs associated with adult lung function and previously showing directionally consistent effects in children, and SNPs and their target genes showing significant associations with lung function in infants along with the mean values of the relevant parameter according to the minor allele count

SNP	Gene	Chromosome	Minor allele	AA	Aa	aa
rs993925	TGFB2	1	T	55	57	22
rs12477314	HDAC4	2	T	87	39	5
rs1529672	RARB	3	C	93	38	0
rs1344555	MECOM	3	T	80	45	7
rs153916	SPATA9	5	T	46	66	18
rs6903823	ZKSCAN3/ZNF323	6	G	63	57	12
rs2857595	NCR3	6	G	76	52	0
rs2798641	ARMC2	6	T	95	37	3
rs7068966	CDC123	10	T	85	42	2
rs11001819	C10orf11	10	G	41	56	0
rs11172113	LRP1	12	T	51	64	18
rs1036429	CCDC38	12	T	38	66	0
rs12447804	MMP15	16	T	76	55	4
rs2571445	TNS1	2	G	51	62	23
rs10498230	PID1	2	T	105	26	2
rs2045517	FAM13A	4	T	45	65	26
rs10516526	GSTCD	4	G	117	18	0
rs17331332	NPNT	4	G	116	18	0
rs6823809	NPNT	4	T	66	59	11
rs1032296	HHIP	4	T	38	73	21
rs11100860	HHIP	4	G	50	68	18
rs11134779	ADAM19	5	G	53	64	16
rs2070600	AGER	6	T	113	20	0

  

SNP	Gene	Minor allele	Effect on infant lung function	Minor allele count	Mean	β	p-value
rs12477314 (downstream)	HDAC4	T	↑ compliance	0	47.4	0.07	0.02
				1	51.0		
				2	58.1		
rs12477314 (downstream)	HDAC4	T	↑ V <sub>max,FRC</sub>	0	136.3	0.18	0.02
				1	146.4		
				2	233.1		
rs2857595 (upstream)	NCR3	G	↓ respiratory rate	0	46.3	-0.06	0.04
				1	43.0		
				2	NA		
rs1529672 (intron)	RARB	C	↑ V <sub>max,FRC</sub>	0	133.1	0.20	0.03
				1	161.1		
				2	NA		
rs11100860 (upstream)	HHIP	T	↑ compliance	0	45.2	0.08	<0.001
				1	50.3		
				2	51.9		
rs1032296 (upstream)	HHIP	G	↓ compliance	0	51.8	-0.06	0.02
				1	47.5		
				2	46.7		

Frequency of major allele (A) and minor allele (a) homozygotes/heterozygotes in our study is also shown. Effect size is shown as the β-coefficient following logarithmic transformation and regression, along with the associated p-value. TGFB2: transforming growth factor β2; HDAC4: histone deacetylase 4; RARB: retinoic acid receptor β; MECOM: MDS1 and EVI1 complex; SPATA9: spermatogenesis-associated protein 9; ZKSCAN3: zinc finger with KRAB and SCAN domains 3; ZNF323: zinc finger protein 323; NCR3: natural cytotoxicity triggering receptor 3; ARM2: armadillo repeat-containing protein 2; CDC123: cell division cycle homologue 123; C10orf11: chromosome 10 open reading frame 11; LRP1: low-density lipoprotein receptor-related protein 1; CCDC38: coiled coil domain-containing protein 38; MMP15: matrix metalloproteinase 15; TNS1: tensin 1; PID1: phosphotyrosine interaction domain-containing protein 1; FAM13A: family with sequence similarity 13, member A; GSTCD: glutathione S-transferase, C-terminal domain-containing protein; NPNT: nephronectin; HHIP: hedgehog interacting protein; ADAM19: a disintegrin and metalloproteinase 19; AGER: advance glycosylation and end produce-specific receptor; V<sub>max,FRC</sub>: maximal expiratory flow at functional residual capacity; NA: not applicable (no subjects with two minor alleles).

During 1998–2002, the Southampton Women's Survey recruited 12,579 females pre-conception through their general practitioners [5]. By the end of 2003, there had been 1,973 babies born to these females, of which 147 had infant lung function measured between 5 and 14 weeks of age, according to previously published protocols [6] using raised volume/rapid compression techniques to measure maximal expiratory flow at functional residual capacity ( $V'_{max,FRC}$ ), FEV<sub>0.4</sub>, respiratory rate and compliance. DNA was obtained from cord blood samples or from buccal samples taken at the 6-yr follow-up. DNA from these 147 children was analysed for each of the 23 SNPs identified as above. These SNPs are detailed in table 1.

Linear regression was used to analyse the minor allele count for each SNP (either 0, 1 or 2) against logarithmically transformed and age-adjusted values for infant lung compliance, respiratory rate, FEV<sub>0.4</sub> and  $V'_{max,FRC}$ . Smoking in pregnancy, maternal body mass index, social class, birth weight, gestation and crown–rump length were analysed as potential confounding factors. The average n per group (0, 1 or 2 minor alleles) across all 23 SNPs was 71, 50 and 9, respectively, giving 80% power to detect a 3.7-mL·mmH<sub>2</sub>O<sup>-1</sup> change in compliance per increase in minor allele count.

Five SNPs, relating to four genes, showed significant associations with infant lung function (table 1). Hedgehog interacting protein (*HHIP*) had one SNP (rs11100860) that was associated with increased compliance ( $p < 0.001$ ) and one (rs1032296) associated with decreased compliance ( $p < 0.05$ ). Retinoic acid receptor  $\beta$  (*RARB*) (rs1529672) was associated with increased  $V'_{max,FRC}$  ( $p < 0.05$ ), the natural cytotoxicity triggering receptor 3 (*NCR3*) SNP (rs2857595) was associated with a lower respiratory rate ( $p < 0.05$ ), and the histone deacetylase 4 (*HDAC4*) SNP (rs12477314) was associated with both increased compliance and  $V'_{max,FRC}$  (both  $p < 0.05$ ). Table 1 summarises these findings. These effects were all directionally consistent with the previous GWAS.

*HHIP* is known to have a role in lung development through fibroblast growth factor 10 (*FGF10*) and its control of lung branching [7], while *RARB* regulates lung bud formation and branching through the Wnt pathway [8] with retinoic acid playing a central role in pre- and post-natal lung development in humans [9]. *HDAC4* and *NCR3* have uncertain roles in lung development, though the former may modulate epigenetic effects on lung function.

Branching of the lung occurs in the pseudoglandular phase and is complete by 16 weeks of gestation [10]; therefore, *RARB* and *HHIP* are likely to have their effects in the first trimester. Early branching is the primary determinant of resistance in normal lungs and, therefore, of compliance. This large airway function is reflected as FEV<sub>1</sub> and FEV<sub>1</sub>/FVC in later life; thus, there is a scientifically plausible link between these SNPs and lung function.

As there was *a priori* evidence of association between these SNPs and lung function, we have not corrected for the number of SNPs and lung function tests. However, even if a Bonferroni correction is applied (23 SNPs  $\times$  4 lung function measurements), the rs11100860 *HHIP* SNP remains significant. As the original GWAS was in similar populations to our cohort, we feel it reasonable to assume the key SNPs identified may be good proxy markers of the causal locus. It is also possible that the present study was underpowered to detect significant associations between infant lung function and the other SNPs tested.

We accept that small numbers and multiple testing are limitations of our study; however, these results may link early fetal lung development, through infant lung function, to adult lung function and respiratory morbidity in later life. This is an interesting starting point for identification of the mechanisms of fetal origins of lung function.

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**Statement of Interest:** A statement of interest for K.M. Godfrey can be found at [www.erj.ersjournals.com/site/misc/statements.xhtml](http://www.erj.ersjournals.com/site/misc/statements.xhtml)

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