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

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To the Editor;

Impaired lung function, and consequent respiratory morbidity including asthma and chronic obstructive pulmonary disease (COPD), 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 FEV<sub>1</sub> and FEV<sub>1</sub>/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].

During 1998-2002, the Southampton Women's Survey (SWS) recruited 12,579 women pre-conception through their general practitioners[5]. By the end of 2003 there had been 1973 babies born to these women, 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 V'maxFRC, FEV<sub>0.4</sub>, respiratory rate and compliance. DNA was obtained from cord blood samples or from buccal samples taken at the 6 year follow-up. DNA from these 147 children were analysed for each of the 23 SNPs identified as above. These SNPs are detailed in supplementary 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'maxFRC. Smoking in pregnancy, maternal BMI, 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 3.7ml/mmH<sub>2</sub>O change in compliance per increase in minor allele count.

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Five SNPs, relating to four genes, showed significant associations with infant lung function (Table I). 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  $\beta$  (RAR $\beta$ ) (rs1529672) was associated with increased V'maxFRC ( $p < 0.05$ ), 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'maxFRC (both  $p < 0.05$ ). Table 1 summarises these findings. These effects were all directionally consistent with the previous GWAS analysis.

HHIP is known to have a role in lung development through fibroblast growth factor 10 (FGF10) and its control of lung branching[7], whilst RAR $\beta$  regulates lung bud formation and branching through the Wnt pathway[8] with retinoic acid playing a central role in pre- and postnatal 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 RAR $\beta$  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 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 had been applied (23 SNPs x 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 we are underpowered to detect significant associations between infant lung function and the other SNPs tested.

We accept that small numbers and multiple testing are limitations; 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.

## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

## References

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**Table 1**

Single nucleotide polymorphisms (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, n/a indicates there were no subjects with 2 minor alleles. Effect size is shown as beta co-efficient following log transformation and regression, along with associated p value. Histone deacetylase 4 (HDAC4), natural cytotoxic receptor 3 (NCR3), retinoic acid receptor beta (RAR $\beta$ ), hedgehog interacting protein (HHIP).

SNP	Gene	Minor Allele	Effect on Infant Lung Function	Minor allele count	Mean	Beta	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</sub> FRC	0	136.3	0.18	0.02
				1	146.4		
				2	233.1		
rs2857595 (upstream)	NCR3	G	↓ RR	0	46.3	-0.06	0.04
				1	43.0		
				2	n/a		
rs1529672 (intron)	RAR $\beta$	C	↑ V <sub>max</sub> FRC	0	133.1	0.20	0.03
				1	161.1		
				2	n/a		
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		