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Transcriptome-wide and differential expression network analyses of childhood asthma in nasal epithelium

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Capsule Summary:

In a transcription-wide association study of nasal epithelium, we identify novel and previously reported susceptibility genes for atopic asthma in children and show that gene co-expression networks differ markedly between children with and without atopic asthma.

Keywords

Airway epithelium; TWAS; atopic asthma; childhood asthma; gene network analysis

To the Editor:

Asthma affects ~7 million children in the U.S., where ~11–13% of children report respiratory or skin allergies. Genetic variants identified in large genome-wide association

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studies explain only a modest proportion of asthma risk, suggesting a substantial contribution of environmental exposures –which could alter the expression of susceptibility genes, ultimately leading to asthma pathogenesis.

Gene expression in nasal airway epithelium is well correlated with that in bronchial epithelium. Environmental stimuli such as pollutants and allergens could modify the epigenetic and transcriptomic characteristics of airway epithelium, leading to abnormal immune responses and asthma. We recently identified >7,000 CpGs associated with atopic asthma in an epigenome-wide association study of nasal epithelium in Puerto Rican children[1], and a recent meta-analysis of airway epithelial gene expression identified 1,273 differentially expressed genes (DEGs) in asthma.[2] Here, we report a transcriptome-wide study of nasal epithelium and atopic asthma in Puerto Rican children, with replication in three separate cohorts.

Recruitment and procedures for the Epigenetic Variation and Childhood Asthma in Puerto Ricans (EVAPR) study, a case-control study of asthma in subjects aged 9–20 years, have been previously described.[1] Detailed methods are found in the Online Repository. For this analysis, cases (n=157) had atopic asthma, defined as a doctor's diagnosis of asthma, ≥1 episode of wheezing in the previous year, and atopy (≥1 positive IgE to aero-allergens). Controls (n=101) had neither asthma nor atopy. RNA from nasal specimens was sequenced using 75-bp paired-end reads at 80M reads/sample, reads were aligned to reference genome (hg 19), and transcripts-per-kilobase-million (TPM) were used as proxy for gene expression. After QC, 18,311 genes were retained for analysis. DEGs were identified by negative binomial regression in DESeq2 adjusted for age, sex, sequencing plate, sample sorting protocol, and principal components from genotypic data. Significance was defined as false discovery rate (FDR)-corrected P-value<0.01. Replication (P-value<0.05 and effect direction concordant with EVAPR) was attempted in three independent datasets.[3–5] Gene co-expression analysis was performed using SILGGM.[6]

Compared to controls (Table E1), cases had higher total IgE (mean 372 IU/mL vs 42 IU/mL). We found 6,058 DEGs (Figure 1A; 3,418 over-expressed and 2,640 under-expressed in atopic asthma). Of those, 458 had expression levels ≥1.5-fold times higher in cases, and 227 showed expression ≥1.5-fold times higher in controls. Table 1 shows the top 50 DEGs (FDR $P=2.78\times10^{-18}$ to 2.08×10^{-60}), including *CST1, CST2, CST4, NTRK2, CDH26, CCL26, POSTN, TPSAB1, CLCA1, ALOX15, ITLN1, CPA3*, and other biologically relevant genes. While most enriched pathways (P-values=0.048 to 1.15×10^{-7}, see Figure E1) were related to immune system regulation (including antigen presentation, leukocyte extravasation, T_H1 and T_H2 activation, and granulocyte adhesion and diapedesis), a few were related to the biosynthesis of heparan, chondroitin, and dermatan sulfate (P-values=0.022 to 7.76×10^{-4}). Upstream regulatory analysis predicted activation of the IL-13 pathway ($P=6.5\times10^{-14}$; Figure E2); indeed, *IL13* was over-expressed in EVAPR cases (FDR $P=2.24\times10^{-10}$). String-db interaction analysis[7] showed significant enrichment, with 179 connections among the top 200 DEGs ($P=4.88\times10^{-15}$; Figure E3). Literature database analysis yielded 100 publications containing ≥4 of our top genes (FDR P=0.022 to 6.17×10^{-7}; Table E2); most of them related to asthma, atopy, eosinophilic esophagitis, eosinophils, mast cells, or T_H2 cytokines. We also evaluated the association between gene expression and methylation (Table E3): 26 of our top

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50 DEGs were also eQTMs (CpG/gene pairs where DNA methylation is inversely associated with gene expression) in which both methylation and expression were associated with atopic asthma in EVAPR –including *CDH26, CCL26, CPA3, MS4A2, ALOX15, NTRK1* and *NTRK2*.[8]

We replicated our top findings in three datasets (Table E1): 40 of the top 50 genes replicated in ≥1 cohort (combined $P=4.08\times10^{-18}$ to 2.93×10^{-79}, Table 1), and 11/50 replicated in all three. Replication rates were higher in pediatric than in adult data: 35/49 (71.4%) of available top-50 DEGs replicated using data from Giovannini-Chami (GSE19187),[4] as did 20/24 (83.3%) in the pediatric data from Yang (GSE65205);[5] compared to 21/48 (43.8%) from the study in adults by Yang (GSE104472).[3] Of the 6,058 DEGs in EVAPR, 1,318 (21.8%) replicated in ≥1 dataset: 684 (51.9%) in GSE19187, 747 (56.7%) in GSE65205, and 276 (20.9%) in GSE104472. We also replicated the top results from previous studies on transcriptome-wide gene expression in nasal epithelium and asthma (Tables E4–E6).[3–5,9]

Co-expression network analysis of the top 200 DEGs showed marked differences (Figure E4), indicating that the way these genes are connected (co-expressed) with each other also differs between atopic asthma and controls. The degree of connectivity (the number of genes with which each DEG is co-expressed) was significantly higher in cases (Figure E4; Kolmogorov-Smirnov $P=5.23\times10^{-14}$): almost 100% of DEGs connected to ≤2 others among controls, while among cases ~50% of DEGs connected to ≥2 others. We identified 17 gene "hubs" (those connected to ≥4 other genes in the network) in cases, including *POSTN, BRD4, DOK1, ELOVL5, FA2H, GCNT3, and SEC14L1* (Figure 1B, Table E7). Of those, 16 were significant in the pediatric cohorts and only 4 in the adult data (Table E8). There were no gene "hubs" among controls. Moreover, we found 194 gene pairs whose co-expression was significantly different in cases vs controls (Table E9); e.g., *POSTN* and *CTSG* were co-expressed in cases ($P=4.87\times10^{-4}$) but not in controls (P=0.99), with a significant difference between groups (P=0.013). While connectivity distributions can depend on sample size, differences between cases and controls remained significant when we performed sensitivity analyses randomly selecting 101 cases to match the number of controls (Table E10).

Finally, we evaluated the ability of DEGs to predict atopic asthma in EVAPR using panels based on the top P-values, largest expression differences, or connectivity (Figure 1C; n=17 genes in each panel, to match the number of gene "hubs"): these panels achieved areas under the curve (AUC) of ~0.89–0.92, sensitivity ~0.80–0.85, specificity ~0.83–0.91, PPV ~0.88–0.93, NPV ~0.74–0.79, and overall accuracy of 82%–86% (Table E11). Replication results are shown in Table E11 and Figure E5.

To our knowledge, this is the first study to report both individual-gene and network-level differences in gene expression from nasal epithelium in childhood asthma. We identified biologically relevant DEGs –including genes previously reported in asthma or other atopic diseases– as well as several novel genes. Many top DEGs were eQTMs,[1] with methylation inversely associated with expression and both associated with atopic asthma. As expected, the majority of top genes are related to atopy and immune pathways, but some are related to epithelial barrier processes (e.g., NTRK2 has been implicated in epithelial-mesenchymal transition dysfunction in asthma, while CDH26 regulates airway epithelial cell structure and

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polarity).12 Interestingly, enriched pathways also included the biosynthesis of glycosaminoglycans that can participate in fibroblast activation in response to injury/inflammation.

We report a larger number of DEGs than a recent meta-analysis,[2] which pooled data from eight studies (two on pediatric nasal samples and six on adult bronchial samples) that used different platforms. EVAPR participants all met the same inclusion criteria and underwent uniform phenotyping and RNA sequencing protocols. We hypothesize that this allowed us to detect a larger number of significant signals, which nonetheless were statistically robust and largely replicated in independent datasets from different racial/ethnic and environmental backgrounds. We report higher replication rates using data from pediatric cohorts compared to adults, which suggests that many asthma DEGs vary with age.

Beyond the traditional individual-gene approach, we show that transcriptomic networks are quite different in atopic asthma. We identify “hub” genes that are biologically relevant and highly co-expressed with several others and may represent important novel targets for further exploration in functional and experimental studies. Taken together, our findings suggest a complex interplay between epithelial integrity, immune regulation, and response to injury and inflammation. Finally, we show that a small number of DEGs can achieve high accuracy in identifying subjects with atopic asthma. If replicated in longitudinal studies, our findings may yield novel insights and promising biomarkers.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Declaration of Funding and Conflicts of Interest:

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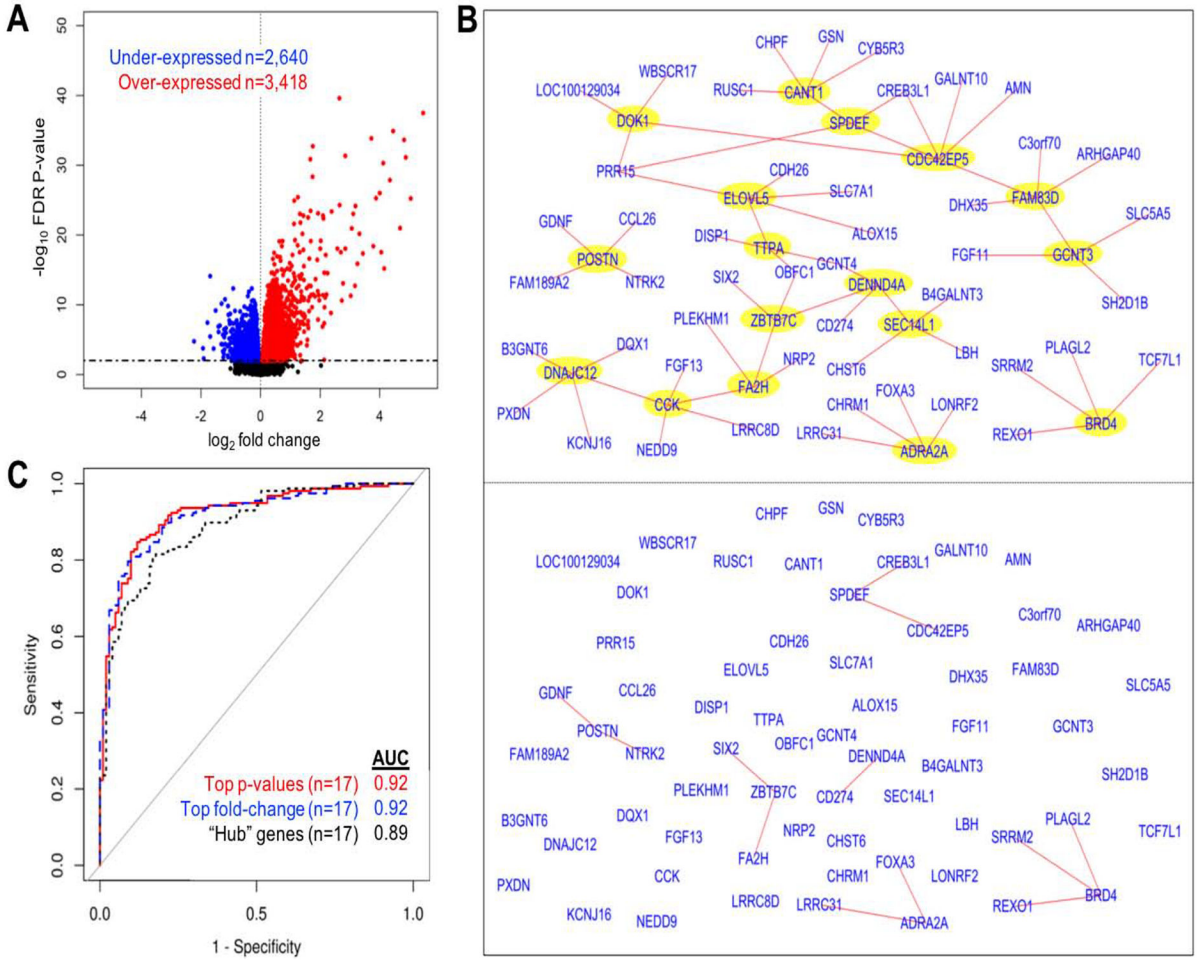

Figure 1 –. Transcriptome-wide association study (TWAS) of atopic asthma in nasal epithelium

A) Volcano plot showing differential gene expression in nasal epithelium between cases and controls. *CST1* (P-value 2.08×10^{-60}) and *CLCA1* ($\log_2$ fold change 8.14) not shown. **B)** Hub-based sub-network in cases (top) and controls (bottom). Hubs are genes with connected to ≥4 co-expressed genes. Only hub genes in cases and their direct connections are shown. In controls no genes had ≥4 connections. **C)** Prediction analysis of using three panels of top genes (by P-value, by $\log_2$-fold change, or by "hub" genes). Each n=17 (based on the number of "hub" genes identified) to ensure an equal number of predictors. AUC: Area under the receiver-operating characteristic (ROC) curve.

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Table 1 –

Top 50 differentially expressed genes (DEGs) in atopic asthma

Gene	EVAPR			GSE19187		GSE65205		GSE104472		Combined P-value[a]
	Fold-change	P-value	FDR P-value	Fold-change	P-value	Fold-change	P-value	Fold-change	P-value	
CST1 *	79.00	1.14×10^{-64}	2.08×10^{-60}	145.96	1.21×10^{-12}	10.82	1.45×10^{-08}	140.83	6.39×10^{-06}	2.93×10^{-79}
CLCA1	282.24	1.40×10^{-47}	1.28×10^{-43}	3.23	7.96×10^{-03}	n/a	n/a	13.65	5.03×10^{-04}	3.22×10^{-45}
NTRK2 *	6.24	4.27×10^{-44}	2.60×10^{-40}	2.68	1.20×10^{-05}	2.07	1.67×10^{-06}	2.01	0.014	2.14×10^{-47}
FETUB	43.82	7.54×10^{-42}	3.45×10^{-38}	4.67	8.81×10^{-05}	n/a	n/a	35.18	6.90×10^{-07}	1.29×10^{-44}
CPA3 *	21.77	3.43×10^{-39}	1.26×10^{-35}	6.01	2.19×10^{-06}	3.19	1.43×10^{-07}	6.34	4.91×10^{-04}	5.25×10^{-46}
GATA2	13.14	4.45×10^{-38}	1.36×10^{-34}	1.12	0.14	1.50	6.87×10^{-04}	4.85	0.018	3.03×10^{-35}
ITLN1 *	28.11	8.68×10^{-38}	2.27×10^{-34}	8.48	5.00×10^{-05}	4.79	1.57×10^{-05}	8.98	5.49×10^{-03}	1.87×10^{-40}
CDH26 *	3.37	8.55×10^{-37}	1.96×10^{-33}	3.05	3.16×10^{-05}	2.03	3.23×10^{-05}	2.23	1.86×10^{-03}	6.83×10^{-40}
CCL26 *	7.16	2.15×10^{-35}	4.38×10^{-32}	2.00	1.32×10^{-03}	2.24	4.47×10^{-04}	9.74	4.48×10^{-04}	1.67×10^{-36}
CST2	29.25	4.02×10^{-35}	7.37×10^{-32}	4.27	2.27×10^{-07}	n/a	n/a	92.64	3.25×10^{-06}	2.75×10^{-40}
C3orf70	3.18	8.30×10^{-35}	1.38×10^{-31}	1.24	0.018	n/a	n/a	1.32	0.34	2.53×10^{-30}
TPSAB1 *	17.36	3.27×10^{-34}	4.98×10^{-31}	2.10	3.25×10^{-04}	2.66	5.40×10^{-06}	4.82	2.50×10^{-03}	3.32×10^{-37}
CISH	3.34	3.02×10^{-32}	4.26×10^{-29}	1.48	2.56×10^{-04}	n/a	n/a	2.00	0.26	8.20×10^{-30}
CLC	20.29	9.83×10^{-32}	1.29×10^{-28}	3.00	7.33×10^{-05}	n/a	n/a	1.80	0.32	8.69×10^{-30}
TPSB2	15.97	7.98×10^{-30}	9.74×10^{-27}	2.21	2.43×10^{-04}	n/a	n/a	n/a	n/a	1.64×10^{-28}
AL0X15 *	2.38	3.37×10^{-29}	3.85×10^{-26}	1.74	2.61×10^{-04}	2.13	1.49×10^{-06}	1.62	0.046	6.86×10^{-32}
MS4A2	14.65	4.86×10^{-29}	5.23×10^{-26}	1.93	1.06×10^{-04}	n/a	n/a	3.82	3.65×10^{-03}	5.52×10^{-29}
TPSG1	32.78	5.95×10^{-29}	6.06×10^{-26}	0.94	0.23	1.08	0.42	0.92	0.79	1.77×10^{-22}
CEP72	2.19	1.26×10^{-28}	1.22×10^{-25}	1.27	9.47×10^{-03}	1.38	4.74×10^{-04}	0.87	0.75	2.43×10^{-26}
SLC5A5	6.26	5.54×10^{-28}	5.07×10^{-25}	2.79	2.14×10^{-03}	n/a	n/a	2.38	0.21	4.74×10^{-25}
POSTN †	9.10	7.69×10^{-28}	6.70×10^{-25}	13.93	6.82×10^{-07}	n/a	n/a	5.63	5.33×10^{-04}	7.48×10^{-31}
MY015A	3.20	4.14×10^{-27}	3.44×10^{-24}	1.02	0.78	n/a	n/a	1.66	0.11	4.72×10^{-22}
HS3ST4	5.22	5.19×10^{-27}	4.13×10^{-24}	0.96	0.58	n/a	n/a	3.35	8.88×10^{-03}	3.88×10^{-23}
PRB2	87.44	7.05×10^{-27}	5.38×10^{-24}	1.23	0.13	n/a	n/a	5.06	0.010	1.32×10^{-23}
LOC100507472	3.80	1.07×10^{-26}	7.87×10^{-24}	n/a	n/a	n/a	n/a	0.47	0.34	1.49×10^{-22}

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Gene	EVAPR			GSE19187		GSE65205		GSE104472		Combined P-value[a]
	Fold-change	P-value	FDR P-value	Fold-change	P-value	Fold-change	P-value	Fold-change	P-value	
PCSK6 *	2.50	1.35×10^{-26}	9.28×10^{-24}	1.39	1.06×10^{-03}	1.25	4.52×10^{-04}	1.81	0.039	1.08×10^{-26}
NTRK1	8.60	1.37×10^{-26}	9.28×10^{-24}	1.11	0.036	n/a	n/a	2.54	1.70×10^{-03}	1.15×10^{-24}
WBSCR17	4.27	2.54×10^{-26}	1.66×10^{-23}	1.40	7.63×10^{-03}	n/a	n/a	2.10	0.26	5.87×10^{-23}
CCBL1	2.70	2.78×10^{-26}	1.75×10^{-23}	1.68	2.99×10^{-03}	1.31	2.65×10^{-03}	1.24	0.64	4.16×10^{-24}
AN01	3.01	5.10×10^{-26}	3.11×10^{-23}	2.35	2.12×10^{-05}	1.65	1.31×10^{-06}	1.37	0.25	1.70×10^{-29}
PTGDR2	4.30	7.09×10^{-26}	4.19×10^{-23}	0.99	0.89	n/a	n/a	1.51	0.43	2.29×10^{-20}
ABO	2.52	3.05×10^{-25}	1.74×10^{-22}	1.18	0.078	1.02	0.89	1.24	0.35	1.18×10^{-19}
CMYA5 *	2.17	4.46×10^{-25}	2.47×10^{-22}	2.07	6.43×10^{-06}	1.26	9.23×10^{-04}	1.85	7.76×10^{-03}	7.87×10^{-28}
CST4	25.58	1.89×10^{-24}	1.02×10^{-21}	1.03	0.66	n/a	n/a	n/a	n/a	3.35×10^{-20}
GCSAML	8.33	2.08×10^{-24}	1.09×10^{-21}	1.12	0.090	n/a	n/a	0.99	0.89	1.17×10^{-19}
CDK15	9.97	1.28×10^{-23}	6.50×10^{-21}	1.03	0.59	n/a	n/a	1.47	0.093	4.53×10^{-19}
SLC24A3	2.64	1.32×10^{-23}	6.52×10^{-21}	1.06	0.45	1.48	8.76×10^{-04}	2.06	0.22	1.74×10^{-20}
GCNT4	2.23	1.09×10^{-22}	5.24×10^{-20}	2.70	7.57×10^{-05}	n/a	n/a	2.31	0.20	1.23×10^{-21}
PTCHD4	4.05	1.40×10^{-22}	6.58×10^{-20}	1.11	0.28	n/a	n/a	2.27	0.17	3.54×10^{-18}
SLC7A1	1.67	1.60×10^{-22}	7.34×10^{-20}	1.66	1.69×10^{-04}	1.24	2.92×10^{-03}	0.94	0.88	1.14×10^{-21}
ST18	3.21	1.64×10^{-22}	7.34×10^{-20}	1.26	2.27×10^{-03}	n/a	n/a	1.24	0.26	5.94×10^{-20}
SLC45A4	1.55	1.79×10^{-22}	7.79×10^{-20}	1.30	2.54×10^{-03}	1.20	5.45×10^{-03}	1.21	0.19	6.56×10^{-21}
DQX1	2.37	6.88×10^{-22}	2.93×10^{-19}	1.37	0.037	1.23	0.079	1.47	0.074	1.49×10^{-18}
GSN *	1.64	9.39×10^{-22}	3.86×10^{-19}	1.53	3.44×10^{-05}	1.53	4.74×10^{-06}	1.96	1.35×10^{-03}	5.38×10^{-27}
LGALS12	13.75	9.48×10^{-22}	3.86×10^{-19}	1.28	0.023	n/a	n/a	1.77	0.19	1.99×10^{-18}
HRH4	3.99	2.25×10^{-21}	8.87×10^{-19}	1.72	0.011	n/a	n/a	1.13	0.37	4.08×10^{-18}
KCNJ16	5.97	2.28×10^{-21}	8.87×10^{-19}	1.70	0.011	1.63	5.82×10^{-04}	1.91	0.36	5.90×10^{-20}
TAL1	7.16	2.37×10^{-21}	9.04×10^{-19}	0.94	0.38	1.16	0.060	1.06	0.88	3.05×10^{-16}
SLC9B2	2.70	3.50×10^{-21}	1.31×10^{-18}	2.72	3.66×10^{-04}	n/a	n/a	3.80	0.13	8.51×10^{-20}
CTSG	16.51	7.74×10^{-21}	2.78×10^{-18}	1.15	0.094	2.38	7.16×10^{-08}	4.47	1.44×10^{-03}	1.35×10^{-24}

EVAPR analysis adjusted for age, sex, and genotypic principal components. GSE19187, GSE65205, and GSE104472 models adjusted for gender and age. Replication defined as P-value <0.05 and effect in the same direction as in EVAPR. **Bold**: Replicated in all available cohorts.

[a]Fisher combined P-values.

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* Replicated in all three cohorts.

† Gene also a "hub" gene in the differential gene network analysis.

n/a: Not available.