Functional Genetic Variation in NFKBIA and Susceptibility to Childhood Asthma, Bronchiolitis, and Bronchopulmonary Dysplasia


*J Immunol* 2013; 190:3949-3958; Prepublished online 13 March 2013;
doi: 10.4049/jimmunol.1201015
http://www.jimmunol.org/content/190/8/3949

Supplementary Material
http://www.jimmunol.org/content/suppl/2013/03/13/jimmunol.1201015.DC1

References
This article cites 60 articles, 17 of which you can access for free at:
http://www.jimmunol.org/content/190/8/3949.full#ref-list-1

Subscription
Information about subscribing to *The Journal of Immunology* is online at:
http://jimmunol.org/subscription

Permissions
Submit copyright permission requests at:
http://www.aai.org/About/Publications/JI/copyright.html

Email Alerts
Receive free email-alerts when new articles cite this article. Sign up at:
http://jimmunol.org/alerts

*The Journal of Immunology* is published twice each month by The American Association of Immunologists, Inc., 1451 Rockville Pike, Suite 650, Rockville, MD 20852
Copyright © 2013 by The American Association of Immunologists, Inc. All rights reserved.
Print ISSN: 0022-1767 Online ISSN: 1550-6606.
Functional Genetic Variation in \textit{NFKBIA} and Susceptibility to Childhood Asthma, Bronchiolitis, and Bronchopulmonary Dysplasia


Respiratory diseases are the most frequent chronic illnesses in babies and children. Although a vigorous innate immune system is critical for maintaining lung health, a balanced response is essential to minimize damaging inflammation. We investigated the functional and clinical impact of human genetic variants in the promoter of \textit{NFKBIA}, which encodes IkBa, the major negative regulator of NF-kB. In this study, we quantified the functional impact of \textit{NFKBIA} promoter polymorphisms (rs3138053, rs2233406, and rs2233409) on promoter-driven protein expression, allele-specific and total \textit{NFKBIA} mRNA expression, IkBa protein expression, and TLR responsiveness; mapped innate immune regulatory networks active during respiratory syncytial virus infection, asthma, and bronchopulmonary dysplasia; and genotyped and analyzed independent cohorts of children with respiratory syncytial virus infection, asthma, and bronchopulmonary dysplasia. Genetic variants in the promoter of \textit{NFKBIA} influenced \textit{NFKBIA} gene expression, IkBa protein expression, and TLR-mediated inflammatory responses. Using a systems biology approach, we demonstrated that \textit{NFKBIA}/IkBa is a central hub in transcriptional responses of prevalent childhood lung diseases, including respiratory syncytial virus infection, asthma, and bronchopulmonary dysplasia. Finally, by examining independent pediatric lung disease cohorts, we established that this immunologically relevant genetic variation in the promoter of \textit{NFKBIA} is associated with differential susceptibility to severe bronchiolitis following infection with respiratory syncytial virus, airway hyperresponsiveness, and severe bronchopulmonary dysplasia. These data highlight the importance of negative innate immune regulators, such as \textit{NFKBIA}, in pediatric lung disease and begin to unravel common aspects in the genetic predisposition to bronchopulmonary dysplasia, bronchiolitis, and childhood asthma. The Journal of Immunology, 2013, 190: 3949–3958.

The most common chronic illnesses in children and babies are those of the respiratory system (1). Many of these serious childhood lung diseases are caused by infection and inflammation, including asthma, viral bronchiolitis, and bronchopulmonary dysplasia (BPD). The innate immune system plays a vital role in protecting our lungs but in many ways can be considered a double-edged sword that must be tightly regulated to minimize lung-damaging inflammation. Recent years have witnessed an explosion of interest in the innate immune system; nevertheless, most attention has focused on the elements involved in activation of the system, whereas negative regulators and modulators of innate immunity have received much less scrutiny.

*Department of Pediatrics, British Columbia Children’s Hospital and Child & Family Research Institute, University of British Columbia, Vancouver, British Columbia V6H 3V4, Canada; †Centre for Microbial Diseases and Immunity Research, University of British Columbia, Vancouver, British Columbia V6T 1Z4, Canada; ‡James Hogg Research Centre, Providence Heart and Lung Institute, St. Paul’s Hospital, University of British Columbia, Vancouver, British Columbia V6Z 1Y6, Canada; §Children’s Hospital of Eastern Ontario, University of Ottawa, Ottawa, Ontario K1H 8L1, Canada; ¶Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, Ontario M5S 1A8, Canada; ||Department of Pediatrics and Child Health, Faculty of Medicine, University of Manitoba, Winnipeg, Manitoba R3A 1S1, Canada; †Department of Pediatrics, University of British Columbia, Vancouver, British Columbia V6Z 1M9, Canada

1S.A. and A.F.H. contributed equally to this work.

Received for publication April 5, 2012. Accepted for publication February 12, 2013.

This work was supported by operating grants from the AllerGen Networks of Excellence, the British Columbia Lung Association, and the Canadian Institutes of Health Research Team in Mutagenesis and Infectious Diseases. S.E.T. holds the Aubrey J. Tingle Professorship in Pediatric Immunology. S.E.T. and P.M.L. were supported by Clinical Research Scholar Awards from the Michael Smith Foundation for Health Research. D.D. is the recipient of a Michael Smith Foundation for Health Research Career Scholar Award and holds a Tier II Canadian Research Chair appointment. R.E.W.H. was supported by the Grand Challenges in Global Health Research program through the Foundation of the National Institutes of Health and Canadian Institutes for Health Research and is the holder of a Canada Research Chair. T.R.K. is supported in part by a Career Award in the Biomedical Sciences from the Burroughs Wellcome Fund and by a Canadian Institutes of Health Research Training Grant in the Canadian Child Health Clinician Scientist Program. The work contributed by T.R.K. was supported in part by National Institute of Allergy and Infectious Diseases, National Institutes of Health Grant R01 AI50023.

Address correspondence and reprint requests to Dr. Stuart E. Turvey or Dr. Pascal M. Lavoie, Division of Infectious and Immunological Diseases, British Columbia Children’s Hospital and Child & Family Research Institute, 950 West 28 Avenue, Vancouver, BC V5Z 4H4, Canada (S.E.T.) or Division of Neonatology, Department of Pediatrics, University of British Columbia and Child & Family Research Institute, 950 West 28 Avenue, Vancouver, BC V5Z 4H4, Canada (P.M.L.). E-mail addresses: turvey@cw.bc.ca (S.E.T.) or plavoie@cw.bc.ca (P.M.L.)

The online version of this article contains supplemental material.

Abbreviations used in this article: AHR, airway hyperresponsiveness; BPD, bronchopulmonary dysplasia; CI, confidence interval; C&W, Children’s and Women’s Health Centre of British Columbia; LD, linkage disequilibrium; NCBI, National Center for Biotechnology Information; PIV, parainfluenza virus; RSV, respiratory syncytial virus; SNP, single nucleotide polymorphism.

Copyright © 2013 by The American Association of Immunologists, Inc. 0022-1767/13/$16.00
(2). We sought to address this knowledge gap by examining the role of a critical negative regulator of the innate immune system in some of the most prevalent pediatric infectious and inflammatory lung diseases.

NF-kB is a family of protein transcription factors that can orchestrate many inflammatory processes. IkBα, encoded by NFKBIA, is an important inhibitor of NF-kB activity (3). In the resting state, IkBα sequesters NF-kB in the cytoplasm. In response to specific stimuli, IkBα is ubiquitinated and degraded, allowing NF-kB to migrate to the nucleus where it can bind to response elements on proinflammatory genes and initiate their transcription. In vivo observations confirm the critical immunomodulatory role of IkBα in both mice (4) and humans (5).

In light of the vital role played by IkBα in regulating inflammation, proliferation, and apoptosis, it is not surprising that genetic variation in the promoter region of NFKBIA has been linked to alterations in susceptibility to infectious and inflammatory diseases, as well as a variety of cancers (6) (Table I). We hypothesized that these promoter variants in NFKBIA would have functional consequences, altering the “tuning” of immune responsiveness.

The objective of this study was to determine the functional impact of specific variants in the promoter of NFKBIA that appear to influence susceptibility to infectious and inflammatory diseases. To ensure clinical relevance, we built on our in vitro–derived mechanistic insights by examining how functional variants in NFKBIA alter in vivo susceptibility to childhood diseases with an inflammatory component in their pathogenesis: asthma, respiratory syncytial virus (RSV), bronchiolitis, and BPD. Although each of these clinical phenotypes has its own complex etiology, a central contribution of the innate immune system and NF-kB signaling is common to all (7–13). Greater understanding of the genetic control of the NF-kB pathway is particularly important given the growing interest in the identification of biomarkers that predict the risk for disease and the development of novel therapies that modulate NF-kB activity (14).

Materials and Methods

Analysis of NFKBIA promoter structure and population variation

Genetic variation and linkage disequilibrium (LD) patterns were examined using data from the HapMap consortium (http://www.hapmap.org) and Programs for Genomic Applications (http://www.ncbi.nlm.nih.gov/sites/resources/geneticsgenomics/programs/pga.html). The Gene Regulation (http://www.gene-regulation.com/index2) and TFSEARCH (http://www.cbrc.jp/research/db/TFSEARCH.html) bioinformatic tools were used to analyze the NFKBIA promoter for putative transcription factor binding sites.

NFKBIA promoter functional assay

Primers were designed to amplify a 1068-bp region, 13 bp upstream of the NFKBIA transcriptional start site, for cloning into a firefly luciferase reporter vector (Table II). The fragment was amplified with high-fidelity Phusion DNA polymerase (New England Biolabs), inserted into a pCRII-Blunt-TOPO vector (Life Technologies), and cloned into a pGL4.14 promoter-less luciferase-expressing vector (Promega). The pGL4.14-NFKBIA promoter constructs were sequenced to confirm genotype and orientation. CHO-K1 cells were grown in F-12K medium (HyClone) and cotransfected with the promoter constructs were sequenced to confirm genotype and orientation.

Technologies). A custom assay was designed for SNP rs1050851 (Table II).

SNPs were deemed acceptable for analysis if they had call rates > 95%, frequencies did not deviate from Hardy–Weinberg equilibrium (p value > 0.05), and no Mendelian errors were observed in the available complete trios. Genotype call rates were: RSV cohort (rs2233406 = 98%, rs2233409 = 97%), BPD cohort (rs2233406 = 99%; rs2233409 = 99%), and asthma cohort (rs2233406 = 92.7%, rs2233409 = 96.6%). Consequently, rs2233406 was not included in analysis of the asthma cohort.

Allele-specific gene expression

Blood samples were obtained with approval of the University of British Columbia Clinical Research Ethics Board (C08-0534). PBMCs were isolated by density-gradient centrifugation as previously described (15), suspended in RPMI 1640 medium containing 10% FCS (HyClone), and seeded into a 24-well plate (BD Biosciences) before stimulation with LPS (100 ng/ml; Escherichia coli 0111:B4; InvivoGen) or live Streptococcus pneumoniae (serotype 14). The cells were incubated at 37°C in a 5% CO2 atmosphere for 3 h poststimulus before harvesting mRNA with an additional DNAse treatment. Reverse transcription was achieved using the SuperScriptVILO cDNA synthesis kit (Life Technologies).

Modifying the technique described by Zhu et al. (16), we quantified allele-specific gene expression by measuring the expression of alleles of synonymous coding SNP rs1050851. This SNP is in LD (r² > 0.82) with the promoter SNPs (rs3138053, rs2233406, and rs2233409), acting as a “tag” for differentiating between the major (ACC) and minor (GGT) allele transriptions of NFKBIA (Fig. 1). When one rs1050851 allele was overexpressed relative to the other, the probe’s fluorescence signal crossed the predetermined threshold earlier, generating a ΔΔct value. Because PCR efficiency for the two alleles differs slightly, a correction was made by subtracting the ΔΔct derived from heterozygous control genomic DNA (1:1 allele ratio) from the observed ΔΔct derived from the cDNA sample. This corrected measure, designated ΔΔct+, enabled calculation of an accurate allele-expression ratio.

NFKBIA gene and IkBα protein expression

Primers were designed (Table II), and expression of NFKBIA was calculated relative to ACTB by SYBR GreenER chemistry (Life Technologies). A 7300 Real Time PCR System (Applied Biosystems) was used under standard cycling conditions, and relative expression was calculated by the 2–ΔΔct Livak method (17). All quantitative PCR experiments were performed in triplicate. Statistical analysis was performed using the nonparametric Mann–Whitney test. To evaluate IkBα expression, PBMCs were stimulated with LPS (100 ng/ml; E. coli 0111:B4; InvivoGen) over 24 h, and lysates were analyzed by standard Western blotting protocols and probed for IkBα and β-actin (#9246, 4967; Cell Signaling). Band densitometry was calculated with an Odyssey Infrared Imaging System (LI-COR).

Quantifying innate immune responsiveness

Innate immune responsiveness was quantified using published techniques (18–20). Umbilical cord blood was obtained from healthy, full-term infants delivered by elective Caesarian section before the onset of labor. Neonatal cord blood mononuclear cells, isolated by density-gradient centrifugation, were stimulated at 37°C with a panel of TLR ligands at optimized concentrations: E. coli 0111:B4 LPS (TLR4), 3M-003 (an imidazoquinoline; TLR7/8), PAM3CSK4 (TLR2/1), 3M-002 (TLR8), and CpG type A (TLR9). Supernatants were analyzed for cytokine secretion by ELISA after 18 h of stimulation. Statistical comparisons were made using two-way ANOVA with the Bonferroni posttest.

Gene-expression microarray data processing and network analysis

Public microarray datasets were obtained from National Center for Biotechnology Information (NCBI) Gene Expression Omnibus (www.ncbi.nlm.nih.gov/geo) using GEOquery (21), and transcriptional data subsets of interest were identified (Supplemental Table I). The NFKBIA promoter haplotype of these datasets was not known. Associated calculations were performed using the Bioconductor project in the R statistical language, with microarray values normalized using quantile normalization (22). Differential expression of gene probes was calculated using the limma package with empirical Bayes methods (23), and adjusted p values were calculated using the Benjamini–Hochberg method (24). Differential gene expression between affected and control treatment groups was defined as gene fold changes ≥1.5 or ≤−1.5, with an associated adjusted p value ≤0.05. Network analysis was carried out using a previously published approach (25), using InateDB (26). For each dataset, two networks were generated containing interactions between protein products of differentially expressed genes and interactions between the genes and their tran-
The potential functional impact of expressed as a percentile. To assess bioinformatic tools to identify putative transcription factor binding sites. Results were downloaded from the genome variation server and uploaded into Haploview 3.1. Pairwise LD was calculated using the software plugin Cerebral (29) to appreciate network directionality within the cell. Hub degree (the number of protein-level interactions with other members of the network) was determined for each gene “node” in the network using the software plugin cytoHubba for Cytoscape (30).

Network graphs were visualized using the software plugin Cerebral (29) to work using the jActiveModule plugin for Cytoscape, with significance significant subnetworks were identified within the larger interaction network using Cytoscape (2.8.0 for Windows) (27). Statistically significant subnetworks were identified within the larger interaction network using Cytoscape (2.8.0 for Windows) (27).

Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors. Network analysis was carried out by merging these two networks with a first-order interaction network for transcription factors.
control values were randomly shuffled 10,000 times, establishing an empirical p value.  

**Results**  

**NFKBIA promoter structure and population variation**  

Genetic variation in NFKBIA has been examined in a variety of human diseases (Table I). What is most striking from these data is that three promoter variants (rs3138053, rs2233406, and rs2233409) have been repeatedly associated with many human diseases. Intriguingly, the same genetic variants that associate with protection from infectious disease are associated with increased risk for inflammatory conditions. Nevertheless, the functional impact of these variants has not been studied at a mechanistic level.

The promoter structure of NFKBIA and the LD pattern in the region were examined. Two promoter variants (rs2233406 and rs3138053) are in LD ($r^2 = +1$), and analysis of the European population revealed a four-variant haplotype consisting of rs2233409 in strong LD ($r^2 = +0.82$) with rs3138053 and rs2233406, as well as a fourth variant rs11569591 (an 8-bp insertion/deletion structural variant) that displayed LD ($r^2 = +1$) with rs2233406 and rs3138053 (Fig. 1). To model the potential functional impact of NFKBIA promoter variants, we identified putative transcription factor binding sites. Most notably, rs3138053 lies within a binding site for RORα1/2, and rs2233409 lies in the putative binding site of Oct-1. The polymorphisms of interest are also contained within putative binding sites for C/EBPα, SP1, and Egr-1 (Fig. 1). We hypothesized that the NFKBIA haplotype comprising the GTT minor promoter variants (in rs3138053, rs2233406, and rs2233409) would be associated with reductions in both allele-specific and total NFKBIA gene expression and decreased IkBa protein expression, resulting in altered innate immune function.

**Modeling the functional impact of NFKBIA promoter variation**  

The region from −13 to −1081 bp from the transcriptional start site of NFKBIA was cloned into a promoter-less luciferase vector and expressed in CHO-K1 cells. This approach allowed us to directly compare the activity of the NFKBIA promoter containing the ACC common promoter variants (ACC-luc) with an otherwise identical construct containing the GTT minor promoter variants (GTT-luc). ACC-luc–transfected cells expressed double the amount of luciferase compared with the GTT-luc–transfected cells (Fig. 2).

**NFKBIA promoter variants are associated with significant alterations in allele-specific gene expression, total gene expression, and IkBa protein expression**  

To validate our in vitro findings suggesting that the GTT promoter was less active than the ACC variant, we obtained fresh blood samples from healthy humans with different NFKBIA promoter haplotypes. Differential expression of NFKBIA alleles was quantified by an allele-specific expression assay. A synonymous SNP in the transcript (rs1050851) (Table II) was used as a marker to

### Table II. PCR primer and probe sequences

<table>
<thead>
<tr>
<th>Gene</th>
<th>NCBI Accession</th>
<th>Forward (5’→3’)</th>
<th>Reverse (5’→3’)</th>
<th>Region</th>
<th>Product (bp)</th>
<th>Temp (˚C)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Primer sequences for promoter cloning</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NFKBIA</td>
<td>NG_007571.1</td>
<td>GGGCGGCCAGATGGGACTA</td>
<td>CCGCGGCCCTATAAACGCT</td>
<td>g.3905-4972</td>
<td>1068</td>
<td>60</td>
</tr>
<tr>
<td>Primer sequences for gene expression</td>
<td>ACTB</td>
<td>NM_001101.3</td>
<td>GTGCCGTATACCACCTTCCTT</td>
<td>ACCTCACCCGTTCAAGTTT</td>
<td>c.*16-162</td>
<td>147</td>
</tr>
<tr>
<td></td>
<td>NFKBIA</td>
<td>NM_020529</td>
<td>TCAACAGGTTAATCCACTGCAGGT</td>
<td>TCCCTCTGAAACCCGTTGAAACTCT</td>
<td>c.728-902</td>
<td>175</td>
</tr>
<tr>
<td>Primer and probe sequences for custom SNP assay</td>
<td>NFKBIA rs1050851</td>
<td>Primers</td>
<td>AAGTGATCCGCCAGGTGAAG</td>
<td>GCTGCAAGTTTGCTTGGAGT</td>
<td>c.275-334</td>
<td>60</td>
</tr>
</tbody>
</table>

**Probes**  

Probes: ACCGTCGCTCTCCA; ACCGTCGCTCTCCA

Temp, Temperature.
distinguish between the transcripts derived from each allele. To establish the accuracy of the system, various ratios of \textit{NFKBIA} rs1050851 C and T alleles were prepared by mixing genomic DNAs homozygous for each SNP. Allele ratios were calculated from the \( \Delta Ct \) values. There was a strong correlation \((r^2 > +0.96)\) between known and measured allele ratios, confirming the sensitivity of this experimental strategy (Fig. 3A).

The allele ratios of transcripts driven by the promoter haplotypes were quantified in PBMCs from ACC/GTT heterozygotes at baseline and after stimulation with both LPS and live \textit{S. pneumoniae} (serotype 14). These stimuli were selected because genetic variation in the promoter of \textit{NFKBIA} has been associated with altered susceptibility to both invasive pneumococcal infection (37) and Gram-negative organisms (38). In all conditions we detected significant allelic imbalance: specifically, the heterozygote allele ratio in RNA (cDNA) differed from the corresponding 1:1 ratio in genomic DNA (Fig. 3B). Mimicking our observation using the luciferase reporter system, in all conditions the transcript associated with the ACC haplotype was expressed at \(\sim 25\%\) higher levels than the transcript associated with the GTT haplotype.

We determined that changes in relative allelic transcript abundance led to overall changes in \textit{NFKBIA} mRNA levels. Individuals homozygous for the ACC haplotype had a 1.5-fold greater ex-

![FIGURE 3. \textit{NFKBIA} promoter variants are associated with significant alterations in allele-specific gene expression, total gene expression, and \(\text{Ib} \text{Ba}\) protein expression. (A) Allele-specific PCR was used to quantify the differential expression of \textit{NFKBIA} alleles. Allelic imbalance was modeled by mixing different ratios of genomic DNA homozygous for the C or T alleles of rs1050851. There was a strong correlation \((r^2 = +0.96)\) between the measured (as determined by \( \Delta Ct \)) and known allele ratios, allowing us to use this assay to quantify allele ratios in experimental samples. (B) Allele-specific transcript levels in primary cells from white subjects \((n = 12)\) who were confirmed to be heterozygous for both the promoter variants (ACC/GTT) and the “tag” SNP within the coding region (rs1050851, C/T). Allele ratios were quantified in PBMCs at baseline and after 3 h of stimulation with both live \textit{S. pneumoniae} (serotype 14) and LPS. Values represent means with 95% CI. (C and D) PBMCs of individuals homozygous (ACC/ACC) or heterozygous (ACC/GTT) for the \textit{NFKBIA} promoter SNPs were stimulated with 100 ng/ml of LPS and \textit{S. pneumoniae} (serotype 14) for 3 h. Relative \textit{NFKBIA} expression \((2^{\Delta \text{DCt}}\text{method})\) was measured in PBMC cDNA by quantitative PCR. Values represent mean ± SEM of homozygotes \((n = 11)\) and heterozygotes \((n = 13)\). Statistical analysis was performed using the nonparametric Mann–Whitney test. (E) \text{IbBa} protein expression was determined by Western blot in PBMCs stimulated with LPS. Values represent mean fold change (ACC/ACC versus ACC/GTT) with 95% CIs \((n = 4)\).]
pression of NFKBIA compared with individuals who were heterozygous for the promoter variants following stimulation with S. pneumoniae (p = 0.024) and a 1.4-fold greater expression following stimulation with LPS (p = 0.032) (Fig. 3C, 3D).

Finally, we confirmed these differences at the protein level. IκBα protein expression at baseline and following LPS stimulation was significantly higher in individuals homozygous for the ACC haplotype of NFKBIA compared with individuals who were heterozygous for the promoter variants (p < 0.05, Fig. 3E). Because individuals homozygous for the GTT haplotype represent only 3% of the population, we were unable to analyze this rare population.

IκBα-dependent innate immune responses vary significantly among individuals with different NFKBIA promoter variants

Having demonstrated that the haplotype comprising the GTT minor promoter variants was associated with reductions in NFKBIA gene expression and IκBα protein expression, we continued to examine the functional impact of NFKBIA promoter variants on innate immune responsiveness. Cord blood mononuclear cells from ACC/GTT heterozygous neonates produced significantly more TNF-α than homozygous neonates following activation of TLRs (Fig. 4A–D). To determine whether the heightened TLR responsiveness associated with the NFKBIA GTT haplotype was specific to IκBα-dependent signaling pathways, rather than a more global process affecting inflammatory responses, we also measured IFN-α production following stimulation of mononuclear cells from the same individuals with CpG type A (a TLR9 agonist). TLR9 uses an IκBα-independent pathway to produce IFN-α (39, 40), and the response to CpG type A was not influenced by the NFKBIA promoter haplotype (Fig. 4E).

FIGURE 4. IκBα-dependent innate immune responses are significantly modulated by NFKBIA promoter variants. (A–D) Production of TNF-α by mononuclear cells stimulated with IκBα-dependent TLR ligands. (E) Production of IFN-α by the same mononuclear cells stimulated with CpG type A triggering IκBα-independent TLR9 pathways. Values represent mean ± SEM of heterozygotes (n = 5–7) and homozygotes (n = 5–10). *p < 0.05, **p < 0.01, ***p < 0.001, two-way ANOVA with the Bonferroni posttest.

Systems biology validation of NFKBIA as a candidate gene in asthma, RSV infection, and BPD

To validate NFKBIA as a candidate gene in the pathogenesis of asthma, RSV bronchiolitis, and BPD, we used an in silico systems biology approach to map the major innate immune regulatory networks active in each condition using public microarray datasets for patients infected with RSV [GSE17156 (41)], patients with asthma [GSE15823 (42)], and at-risk premature infants who developed BPD [GSE8586 (43)] (Supplemental Table I). Network analysis of the cellular transcriptional responses revealed statistically significant subnetworks containing NFKBIA as a node (Fig. 5, Supplemental Figs. 1–3). NFKBIA was situated as a prominent mid-to-large–sized hub within each of the three networks (Fig. 5), establishing NFKBIA as a biologically plausible candidate gene that may be associated with different outcomes in RSV infection, asthma, and BPD.

Functional NFKBIA promoter variants are associated with differences in susceptibility to AHR, RSV bronchiolitis, and BPD

Informed by the pattern of LD (Fig. 1), we conducted case-control analysis to determine whether rs2233409 and rs2233406, the two functionally active genotypes that are not in complete LD, are differentially represented among subjects at risk for each childhood lung disease. The minor rs2233406 allele was associated with an increased risk for severe RSV bronchiolitis requiring hospitalization (OR = 1.83; 95% confidence interval [CI] = 1.20–2.80, p = 0.005) (Tables III, IV). In analyzing the asthma cohort, we focused on quantification of AHR by methacholine challenge, because this test is reliable, not influenced by variations in symptom perception or diagnostic trends, and closely related to the underlying pathophysiology of asthma. There was no significant
association when AHR was considered in isolation (rs2233409: OR = 1.49, 95% CI = 0.95–2.34, \( p = 0.081 \)). However, when early childhood viral exposures were included in the analysis, significant associations were revealed. Specifically, the minor allele at position rs2233409 was associated with AHR in children with PCR-documented RSV infection (OR = 2.55, 95% CI = 1.26–5.17, \( p = 0.009 \)) or PIV infection (OR = 2.24, 95% CI = 1.12–4.48, \( p = 0.023 \)) in the first 12 mo of life. Additionally, for RSV infection, there was evidence for interaction between rs2233409 and RSV increasing the risk for AHR (\( p = 0.037 \)). There were no significant observations for picornaviruses (Table V). Genotyping of rs2233406 failed rigorous quality control and was not analyzed in the asthma cohort. Finally, the minor alleles at positions rs2233406 and rs2233409 were significantly associated with BPD severity but not prematurity (\( p = 0.174 \)) in preterm infants (Table VI). Together, these data provide compelling evidence for a functional impact of \( \text{NFKBIA} \) promoter variants in influencing the outcome of infectious and inflammatory lung diseases in children.

**Discussion**

In this study we report three major novel findings: common genetic variants in the promoter of \( \text{NFKBIA} \) (rs3138053, rs2233406, and rs2233409) influence \( \text{NFKBIA} \) promoter function, gene and \( \text{IkB} \alpha \) protein expression, and TLR-mediated inflammatory responses; \( \text{NFKBIA}\text{IkB} \alpha \) is a central hub in networked cellular transcriptional responses in RSV infection, asthma, and BPD; and immunologically relevant genetic variation in the promoter of \( \text{NFKBIA} \) is associated with differential susceptibility to severe RSV bronchiolitis, AHR, and severe BPD. We consider these associations particularly compelling given our functional immunological data combined with literature evidence from in vitro animal and human primary immunodeficiency studies that all support a vital role for \( \text{IkB} \alpha \) in regulating inflammatory responses (4, 5).

The multiple published associations linking promoter variants in \( \text{NFKBIA} \) to alterations in susceptibility to malignancy and infectious and inflammatory diseases (Table I) were the motivation for investigating the functional immunological impact of these polymorphisms. Considering both previously published associations and the pattern of LD within the genetic region (Fig. 1), we focused our experimental attention on three \( \text{NFKBIA} \) promoter polymorphisms that were in strong LD (\( r^2 > 0.80 \)): rs3138053, rs2233406, and rs2233409. We confirmed experimentally that these variants are indeed associated with alterations in promoter-driven protein expression, allele-specific and total \( \text{NFKBIA} \) gene expression, and \( \text{IkB} \alpha \) protein expression (Figs. 2, 3).

![Network analysis reveals that \( \text{NFKBIA} \) is a key component of cellular transcriptional signatures during RSV infection (A), BPD (B), and asthma (C). Networks generated for RSV infection, BPD, or asthma were analyzed using jActive to determine the most statistically significant subnetworks within the broader networks. The highlighted regions demonstrate that \( \text{NFKBIA} \) is a statistically significant hub for each of the three disease datasets (shown in full detail as Supplemental Figs. 1–3), as determined by its interconnectivity within the subnetwork. Data used to generate these networks were available to the public (described in Supplemental Table I) and obtained through NCBI Gene Expression Omnibus.](http://www.jimmunol.org/)

**Figure 5.**

**Table III. Demographic data for RSV-association study**

<table>
<thead>
<tr>
<th>Female Gender Frequency</th>
<th>Median Age</th>
</tr>
</thead>
<tbody>
<tr>
<td>Population control</td>
<td>0.51</td>
</tr>
<tr>
<td>Severe RSV</td>
<td>0.42</td>
</tr>
</tbody>
</table>

rs2233409) influence \( \text{NFKBIA} \) promoter function, gene and \( \text{IkB} \alpha \) protein expression, and TLR-mediated inflammatory responses; \( \text{NFKBIA}\text{IkB} \alpha \) is a central hub in networked cellular transcriptional responses in RSV infection, asthma, and BPD; and immunologically relevant genetic variation in the promoter of \( \text{NFKBIA} \) is associated with differential susceptibility to severe RSV bronchiolitis, AHR, and severe BPD. We consider these associations particularly compelling given our functional immunological data combined with literature evidence from in vitro animal and human primary immunodeficiency studies that all support a vital role for \( \text{IkB} \alpha \) in regulating inflammatory responses (4, 5).

The multiple published associations linking promoter variants in \( \text{NFKBIA} \) to alterations in susceptibility to malignancy and infectious and inflammatory diseases (Table I) were the motivation for investigating the functional immunological impact of these polymorphisms. Considering both previously published associations and the pattern of LD within the genetic region (Fig. 1), we focused our experimental attention on three \( \text{NFKBIA} \) promoter polymorphisms that were in strong LD (\( r^2 > 0.80 \)): rs3138053, rs2233406, and rs2233409. We confirmed experimentally that these variants are indeed associated with alterations in promoter-driven protein expression, allele-specific and total \( \text{NFKBIA} \) gene expression, and \( \text{IkB} \alpha \) protein expression (Figs. 2, 3).

To assess the functional immunological impact of the \( \text{NFKBIA} \) promoter polymorphisms, we quantified TLR-mediated innate immune responsiveness (Fig. 4). By carefully selecting TLR ligands and cytokine read-outs, we were able to analyze the impact of \( \text{NFKBIA} \) promoter polymorphisms on both \( \text{IkB} \alpha \)-dependent and -independent TLR signaling in the same responder cell population. Consistent with the current understanding of TLR signaling cascades, the functional \( \text{NFKBIA} \) promoter polymorphisms were associated with differences in TLR-triggered
The common promoter variants (i.e., ACC/ACC) expressed monocytes of individuals homozygous for the haplotype comprising these allele-specific differences in mRNA expression, the stimulated with the minor promoter haplotype (GTT) (Figs. 2, 3). Because of major negative regulator of NF-κB who were heterozygous for the promoter variants (ACC/GTT) (Fig. 4).

By investigating the impact of NFKBIA promoter polymorphisms at multiple molecular levels, we are in a position to develop a biologically coherent model of how NFKBIA promoter polymorphisms may influence innate immune responsiveness. At the level of promoter function and gene transcription, the transcript driven by the common promoter haplotype (ACC) was expressed at ~25% higher levels than the transcript associated with the minor promoter haplotype (GTT) (Figs. 2, 3). Because of these allele-specific differences in mRNA expression, the stimulated monocytes of individuals homozygous for the haplotype comprising the common promoter variants (i.e., ACC/ACC) expressed NFKBIA mRNA and IκB protein at ~1.5-fold higher levels than individuals who were heterozygous for the promoter variants (ACC/GTT) (Fig. 3). Because they expressed higher levels of the gene encoding the major negative regulator of NF-κB, the proinflammatory responses of monocytes from individuals homozygous for the common NFKBIA promoter haplotype (i.e., ACC/ACC) were decreased compared with cells from those with the GTT haplotype comprising the minor promoter variants (i.e., ACC/GTT) (Fig. 4).

The expression level of most genes is regulated by transcription factors that bind to DNA regulatory sequences situated upstream of the site at which transcription is initiated. Polymorphisms located in promoter regions usually affect gene transcription by modifying the coordinated action of multiple regulatory proteins through complex protein–DNA and protein–protein interactions, thus influencing the kinetics and/or specificity of the transcription process. This explanation is consistent with the decrease in NFKBIA transcription that we observed to be associated with the minor promoter variants.

Increasing evidence supports the concept that a balanced NF-κB–driven inflammatory response determines the outcome following infection. Greatly diminished NF-κB responsiveness, as occurs in rare human primary immunodeficiencies caused by genetic mutations affecting NF-κB activation, results in recurrent, severe infections. At the other end of the spectrum, excessive inflammation can also be very harmful, with clinical data suggesting a pathologic role for NF-κB in sepsis and multiple-organ failure (46, 47). Similarly, our data indicate that NFKBIA promoter variants associated with increased TLR-mediated inflammatory responses are associated with severe RSV bronchiolitis and AHR in children with positive nasal swabs for RSV or PIV in the first year of life (Table V).

Innate immune hyperresponsiveness to RSV appears to play an important role in the pathogenesis of severe bronchiolitis (48). Our observations linking hyperinflammatory NFKBIA polymorphisms and severe RSV bronchiolitis are consistent with the published association between increased susceptibility to RSV-induced bronchiolitis and genetic variants mediating increased IL-8 transcription (49). In addition to causing acute bronchiolitis, RSV has strong epidemiological links to asthma and AHR. Children who experience severe RSV-induced bronchiolitis are at increased risk for the development of recurrent wheeze and asthma in later childhood (50). However, this association is bidirectional, because an asthmatic disposition and early wheezing also increase the risk for severe lower respiratory tract infections and RSV hospitalization (51). The bidirectional nature of this association indicates that severe RSV bronchiolitis and asthma may share a common genetic predisposition and/or environmental exposure. Our data suggest that genetic variants in the NFKBIA promoter associated with enhanced innate immune responsiveness may be one common genetic component that increases the risk for both severe RSV infection and AHR.

BPD is a serious chronic inflammatory lung disease frequently observed in premature infants (52). Children suffering from BPD have a dramatically increased risk for severe RSV infection, because up to 50% of preterm infants with BPD require hospitalization due to RSV in the first year of life (53, 54). Recently, our group (36) and other investigators (55) confirmed the strong contribution of complex polygenic influence on BPD susceptibility. In the current study, we found that functional genetic variation in the promoter of NFKBIA is associated with differential susceptibility to severe BPD but not premature birth (Table VI). However, the NFKBIA promoter variants that we investigated did not appear to contribute to the increased risk for severe RSV in-

<p>| Table V. Functional NFKBIA promoter polymorphisms are associated with AHR |
|---------------------------------------------------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------||</p>
<table>
<thead>
<tr>
<th>SNP</th>
<th>Major</th>
<th>Minor</th>
<th>MAF</th>
<th>Virus</th>
<th>Main Effect of SNP</th>
<th>Main Effect of Virus</th>
<th>Interaction</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs2233409</td>
<td>C</td>
<td>T</td>
<td>0.209</td>
<td>RSV</td>
<td>0.009</td>
<td>0.14 (0.60–2.17)</td>
<td>0.037</td>
</tr>
<tr>
<td>rs2233409</td>
<td>PIV</td>
<td>2.24</td>
<td>(1.12–4.48)</td>
<td>0.023</td>
<td>0.138</td>
<td>(0.71–2.68)</td>
<td>0.47 (0.19–1.17)</td>
</tr>
<tr>
<td></td>
<td>PIV</td>
<td>1.62</td>
<td>(0.73–3.58)</td>
<td>0.235</td>
<td>1.08</td>
<td>(0.55–2.12)</td>
<td>0.88 (0.33–2.31)</td>
</tr>
</tbody>
</table>

Text in bold is statistically significant.

MAF, minor allele frequency; PP, permutation p value.
fever experienced by premature infants with BPD, because the common allele at rs2233406 (i.e., C) was associated with an increased risk for severe BPD but was protective in the RSV cohort. Infectious diseases are arguably one of the most influential selective pressures on the course of human evolution and have given rise to strong selective pressure for polymorphisms that decrease susceptibility to pathogens, regardless of their impact on the overall fitness of the host. For example, a polymorphism in the promoter of TNF confers both resistance to infection with tuberculosis and susceptibility to systemic lupus erythematosus, rheumatoid arthritis, and primary Sjögren’s syndrome (56). Consistent with this paradigm, the NFKBIA promoter SNPs that we demonstrate to be associated with inflammatory lung diseases in children were reported to decrease susceptibility to pathogens (Table I), including S. pneumoniae (37), a leading infectious cause of death worldwide. Despite their potentially advantageous nature in the context of infection, SNPs that increase innate immune responsiveness may ultimately increase population level prevalence of other diseases with an inflammatory component, adding support to the concept of innate immunity as a double-edged sword.

Our functional immunological data and system biology analyses highlight the importance of NFKBIA in relevant signaling pathways and provide a biologically coherent model of how NFKBIA promoter polymorphisms may impact innate immune signaling in these childhood lung diseases. It is important to recognize that the genetic variants we are investigating are SNPs that are common in healthy populations, and they are not disabling mutations. Although the functional immunological changes we report are small in magnitude when compared with the changes found in humans with disabling genetic mutations, they are likely to be biologically relevant. Our data demonstrate that genetic variants in the promoter of NFKBIA influence NFKBIA gene expression, IkB protein expression, and TLR-mediated inflammatory responses. When these functional immunological data are considered in the context of the multiple genetic association studies linking NFKBIA promoter polymorphisms with human disease (Tables I, III–VI), the weight of evidence indicates a biologically significant impact of these common NFKBIA promoter polymorphisms. However, our results must be interpreted with some caution given that the associations between the NFKBIA polymorphisms and the clinical phenotypes were of a modest magnitude. Ultimately, the genetic validity of these associations will only be firmly established through future replication studies in additional human cohorts.

In conclusion, we elucidated the functional immunological impact of common genetic variants in the promoter of NFKBIA that have been repeatedly associated with differences in susceptibility to cancer and infectious and inflammatory diseases. We built on these mechanistic in vitro insights to generate novel in vivo data showing that these functional variants in NFKBIA alter susceptibility to childhood AHR, RSV bronchiolitis, and BPD. These results provide new insights into the pathogenesis of childhood infectious and inflammatory lung diseases; strengthen our collective understanding of the importance of inhibitors of innate immunity, such as NFKBIA; and begin to unravel common aspects in the genetic predisposition to BPD, severe RSV bronchiolitis, and childhood asthma.

Acknowledgments
We thank all subjects and their families who volunteered to participate in the patient cohorts.

Disclosures
The authors have no financial conflicts of interest.

References


ONLINE SUPPLEMENTAL MATERIAL

Functional genetic variation in *NFKBIA* and susceptibility to childhood asthma, bronchiolitis and bronchopulmonary dysplasia


*Department of Pediatrics, BC Children’s Hospital and Child & Family Research Institute, University of British Columbia, Vancouver, BC, Canada.
†Centre for Microbial Diseases & Immunity Research, University of British Columbia, Vancouver BC, Canada
‡James Hogg Research Centre, Providence Heart + Lung Institute, St. Paul's Hospital, The University of British Columbia, Vancouver, BC, Canada
§Children’s Hospital of Eastern Ontario, University of Ottawa, Ontario, Canada
¶Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, Canada
||Department of Pediatrics and Child Health, Faculty of Medicine, University of Manitoba, Winnipeg, MB, Canada
#Occupational and Environmental Lung Disease Unit, Respiratory Division, Department of Medicine, University of British Columbia, Vancouver, BC, Canada.

Running title: Functional genetic variation in *NFKBIA* and susceptibility to disease.

‡‡ Aaron Hirschfeld and Salman Ali made an equal contribution.
FIGURE LEGEND

Supplementary Figure S1: Network analysis visualization of PBMC transcriptional responses to infection with RSV.

Network analysis carried out on genes differentially expressed in PBMC during in vivo experimental infection of volunteers with RSV. This statistically significant subnetwork contains 89 gene nodes and 104 unique protein level interactions, with NFKBIA positioned as mid-sized hub with 6 unique interactions. Color of nodes is proportional to their relative fold-change in infected versus control groups, while the size of the node reflects its interconnectivity (hub degree) within the network. Data set derived from GEO accession GSE17156.

Supplementary Figure S2: Systems biology visualization of immune pathways activated in BPD.

Network analysis of genes differentially expressed in cord blood of preterm neonates who developed BPD. This statistically significant subnetwork contains 87 gene nodes and 130 unique protein level interactions, with a downregulated NFKBIA positioned as mid-sized hub with 7 unique interactions. Color of nodes is proportional to their relative fold-change in biopsies from healthy patients, while the size of the node reflects its interconnectivity (hub degree) within the network. Data set derived from GEO accession 17916252.

Supplementary Figure S3: Network analysis visualization of transcriptional responses unique to the airways of asthmatic patients.

Network analysis of genes differentially expressed in lung biopsies of asthmatic patients. This statistically significant subnetwork contains 89 gene nodes and 146 unique protein level interactions, with NFKBIA positioned as large hub with 11 unique interactions. Color of nodes is proportional to their relative fold-change in biopsies from healthy patients, while the size of the node reflects its interconnectivity (hub degree) within the network. Data set derived from GEO accession 15038835.
**Supplementary Table S1:** Microarray datasets identified as containing suitable data subsets for network analysis of transcriptional responses and processed using MetaGEX.

<table>
<thead>
<tr>
<th>GEO accession</th>
<th>Associated publications [PMID]</th>
<th>Experimental description</th>
<th>Data subset used in analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td>GSE17156</td>
<td>19664979</td>
<td>Gene expression profiling of PBMCs from healthy volunteers (n = 60) at baseline, and again after intranasal challenge with human rhinovirus, respiratory syncytial virus (RSV), or influenza A. Blood was collected every 6-8 hours, and only the post-infection sample correlating with each patient’s peak symptoms was analyzed.</td>
<td>Healthy volunteers challenged with intranasal RSV (n = 20), with comparisons between patient-matched pre- and post-infection data.</td>
</tr>
<tr>
<td>GSE8586</td>
<td>17916252</td>
<td>Umbilical cord blood was collected at birth from premature neonates (24-27 weeks gestational age, n = 54). Whole blood was sent for transcriptional profiling and neonates were followed until 36 weeks postmenstrual age.</td>
<td>From the patient sample (n=54), comparisons were carried out between those who developed BPD (n=20) and those who did not (n=34).</td>
</tr>
<tr>
<td>GSE15823</td>
<td>15038835</td>
<td>Comparison of transcriptional signatures from bronchial biopsies obtained from healthy adult subjects (n=4) or patients with allergic asthma, before (n=4) and after (n=4) initiation of inhaled corticosteroid therapy. Biopsies (7-11 per subject) were obtained from segmental bronchial carinae and lobar carinae throughout the lower, middle, and upper lung lobes, pooled, and analyzed.</td>
<td>Healthy adult subjects (n=4) compared to subjects with allergic asthma (n=4) before initiation of inhaled corticosteroid therapy.</td>
</tr>
</tbody>
</table>