including obesity and both asthma and diabetes. The association between type 2 diabetes and asthma is not surprising as a high proportion of youth were overweight or obese (90.6%) and the linkage between asthma and increased BMI is well described in many studies. It is interesting to note that children whose asthma was treated with leukotriene modifiers, alone or in combination with inhaled corticosteroids or rescue inhalers, had the lowest prevalence of poor glycemic control; in fact, 72% had good glycemic control. The authors speculate that this could be because leukotriene synthesis or receptor blockers may help reduce the systemic inflammation present in both obesity and diabetes as well the direct effect on ameliorating airway inflammation.

DNA Hypomethylation at ALOX12 Is Associated With Persistent Wheezing in Childhood
PURPOSE OF THE STUDY. To determine if epigenetic changes play a role in asthma phenotypes.

STUDY POPULATION. There were 2 groups studied, both involved children enrolled from pregnancy cohorts. The first group (Menorca cohort) was 122 children with data available through age 6 years. The second group (Sabadell cohort) was 236 children with available DNA extracted from whole cord blood.

METHODS. Children were assigned wheezing phenotypes at age 4 to 6 years based on validated questionnaires (never, transient, late-onset, or persistent wheezing). Prenatal exposure data were collected through questionnaire and by measuring for presence of a specific pollutant, dichlorodiphenyldichloroethylene, in cord blood.

RESULTS. DNA hypomethylation was associated with increased risk for persistent wheezing in both studies, although only 1 of the 2 was statistically significant (Menorca: odds ratio 1.13, 95% confidence interval 0.99–1.29, P = .077; Sabadell: odds ratio 1.16, 95% confidence interval 1.03–1.37, P = .017). Higher levels of dichlorodiphenyldichloroethylene were associated with hypomethylation of ALOX12 in the Menorca study (P = .033), but not the Sabadell study (P = .377). Level of methylation at ALOX12 was strongly influenced by polymorphisms in the gene.

CONCLUSIONS. DNA hypomethylation at ALOX12 was associated with a higher risk of persistent wheezing. This may be an epigenetic biomarker that predicts increased likelihood of persistent wheezing in childhood.

Identification of IL6R and Chromosome 11q13.5 as Risk Loci for Asthma
PURPOSE OF THE STUDY. To identify novel genetic variations imputing asthma risk.

STUDY POPULATION. Pediatric and adult Australians of European descent consisting of 2669 asthmatic subjects (28% diagnosed by clinical examination, 54% childhood onset, 59% atopic) and 4528 controls (40% with unknown asthma status) produced candidate asthma genetic variations. Meta-analysis of 12 475 physician-diagnosed asthmatic subjects and 19 967 controls provided a prioritization cohort. Four additional individual cohorts totaling 3322 asthmatic subjects and 22 036 controls provided replication.

METHODS. Microarray-derived genotypes of Australian asthmatic subjects and controls underwent a genome-wide association study to produce asthma candidate loci. Meta-analysis using unique adult Australian and previously published GABRIEL genotypes prioritized candidate novel genetic loci. The prioritized, novel genetic loci endured replication analysis via 4 individual cohorts and a combined meta-analysis. A genomic phenotype prediction model for asthma was produced and subsequently tested. Secondary analysis considered asthma and other immune disease associations.

RESULTS. Two novel loci were significantly associated with asthma risk. The interleukin-6 receptor (IL6R) loci on chromosome 1q21.3 associated more significantly (odds ratio [OR] = 1.09, P = .0033) than the indeterminate loci (rs7130588) at chromosome 11q13.5 (OR = 1.07, P = .328) in the replication cohorts. However, when considering all available data, 1q21.3 and 11q13.5 both demonstrated very significant asthma association (OR = 1.09, P = 2.3 × 10⁻⁸ and OR = 1.09, P = 1.8 × 10⁻⁸, respectively). Secondary analyses of 11q13.5 revealed an association with atopy and no asthma risk association.
The Alarmin Interleukin-33 Drives Protective Antiviral CD8^+ T Cell Responses

PURPOSE OF THE STUDY. Pathogen-associated molecular patterns decisively influence antiviral immune responses, whereas there is less known about how endogenous signals of tissue damage (known as alarmins) are involved in antiviral defenses.

METHODS. Mice were infected with lymphocytic choriomeningitis virus (LCMV), a single-stranded RNA virus, and a genome-wide cDNA expression analysis of total spleen tissue was performed and compared with the uninfected mouse. From a large panel of interleukins and inflammatory cytokines, interferon-γ and interleukin (IL)-33 (along with its receptor ST2) were the most highly upregulated. Infection with LCMV, as well as a murine herpesvirus (MHV-68), was performed in wild-type mice, mice deficient in IL-33 (in IL-33^−/−), and mice in which IL-33 effects were blocked with a soluble decoy receptor (III-11-Fc). Proliferative responses of cytotoxic lymphocytes (CTLs) specific for LCMV were measured.

RESULTS. Levels of IL-33 peaked at 3 to 5 days after infection, mirroring levels of LCMV mRNA. After infection with LCMV, proliferative responses of virus-specific CD8^+ T cells were 90% lower in IL-33^−/− mice and in mice with IL-33 decoy receptors, and CTL responses were absent. Productive viral replication was necessary for IL-33–mediated CTL proliferation. Additionally, recombinant IL-33 significantly augmented CTL responses to other viruses (vaccinia-based vectors), and CTLs appeared to respond to IL-33 directly. Last, the authors provided evidence that IL-33 expression was produced by fibroblastic reticular cells, a stromal cell population of the T-cell zone of the spleen and an important target of LCMV infection.

CONCLUSIONS. These findings suggest that the alarmin IL-33 provides a molecular link to understand how viral replication can enhance CTL responses to infection. IL-33 also serves as a signal from nonhematopoietic cells that acts directly on CTLs to augment protective responses.

High Environmental Relative Moldiness Index During Infancy as a Predictor of Asthma at 7 Years of Age

PURPOSE OF THE STUDY. To further assess a cohort of children examining the relationship between mold exposures at 1 and 7 years of age and asthma at age 7 years.

STUDY POPULATION. The sample included 176 children with at least 1 atopic parent followed from birth to age 7 years.

METHODS. Home assessments, inspections, and floor dust sampling were done at age 1 and 7 years. Clinical examinations were performed at 1, 2, 3, 4, and 7 years of age and included history and skin testing to aeroallergens. At 7 years of age, spirometry pre- and postbronchodilator were performed, and, if negative, a methacholine challenge was undertaken. Children were defined as asthmatic if they had asthma symptoms and objective confirmation.
Identification of IL6R and Chromosome 11q13.5 as Risk Loci for Asthma
Timothy David Trojan and J. Andrew Bird

*Pediatrics* 2012;130;S26
DOI: 10.1542/peds.2012-2183PP

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