various autoimmune diseases in family. Testing of other genes is in progress now.

291

ASSOCIATION OF ADAM33 GENE POLYMORPHISM WITH BRONCHIAL ASTHMA

S. Awasthi[1], P. Tripathi[1], N. Husain[1], S. Ganesh[2]

[1]King George's Medical University, Lucknow, [2]IIT, Kanpur, India

Background: Genetic association studies have linked occurrence of asthma with ADAM33 gene polymorphisms in different populations, but none from India. Such studies will improve individualized case management strategies over time.

Objectives:

Primary: To assess association of ADAM33 gene polymorphisms (F+1 G/A, S2 G/C, ST+4 A/C, ST+5 C/T, V4 C/G) with asthma.

Secondary: Among asthmatics, to assess association of hospitalization, family history and severity of asthma and environmental exposure with ADAM33 gene polymorphisms.

Study design: Case-control.

Methods: Diagnosis of asthma was done according to GINA guidelines 2007. Controls were age and sex matched non-relatives of cases without any respiratory disease. Genotyping was done with PCR-RFLP method.

Results: From August 2007 to November 2009, 211 cases (aged 74.4 months ±4.6, with 32.2% females) and 137 controls (aged 73.6 months±42.6, with 29.9% females) were recruited. Distributions of S2, ST+5 and F+1 genotypes were statistically significantly different, while allele frequencies were statistically significantly different for all 5 markers between cases and controls ($p< 0.05$). In ST+5 total hospitalization rate was high among cases with wild & hetero genotype [OR =3.75(95% CI: 1.33-1.63), $p < 0.05$]. Significant association of ST+4 wild and hetero [OR=4.147(95% CI: 1.52-11.33), $p < 0.05$] and ST+5 hetero [OR=2.77(.99-7.95), $p < 0.05$] genotypes was observed with positive family history patients. No association was found of ADAM33 gene polymorphisms genotypes in cases with severity of asthma or environmental exposure to pollutants.

Conclusion: The SNPs (F+1 G/A, S2 G/C, ST+4 A/C, ST+5 C/T, V4 C/G) of the ADAM33 gene are associated with asthma.

292

A GENOME-WIDE ASSOCIATION STUDY OF SPONTANEOUS PRETERM DELIVERY

H. Boyd[1], B. Feenstra[1], F. Geller[1], E. Feingold[2], K. Ryckman[3], J. Shaffer[2], C. Laurie[4], Q. Zhang[4], K. Doheny[5], E. Pugh[5], T. Manolio[6], M. Marazita[2], M. Melbye[1], J. Murray[3], GENEVA Consortium

[1]Epidemiology Research, Statens Serum Institut, Copenhagen, Denmark, [2]Human Genetics, University of Pittsburgh, Pittsburgh, PA, [3]Pediatrics, University of Iowa, Iowa City, IA, [4]Biostatistics, University of Washington, Seattle, WA, [5]Institute of Genetic Medicine, Johns Hopkins University, Baltimore, [6]National Human Genome Research Institute, NIH, Bethesda, MD, USA

Background and aims: Up to 40% of preterm deliveries (PTDs) may have a genetic component. PTD inheritance patterns are consistent with maternal genotype effects, fetal genotype effects via maternally-derived alleles, or both. However, while many candidate genes have been proposed, no common genetic variant has yet been confirmed as contributing to PTD. A genome-wide association study (GWAS) of PTD has never before been undertaken. Consequently, our objective was to examine maternal and fetal genetic contributions to spontaneous PTD in a GWAS.

Methods: We selected 1,000 preterm (gestation < 37 weeks) mother-child pairs and 1,000 term (40-week gestation) pairs, all with spontaneous onset of delivery, from the Danish National Birth Cohort, and genotyped them using the Illumina Human660W-Quad BeadChip. We analyzed the effect of genotype (maternal and fetal separately) on PTD using case-control methods and also by treating gestational length as a quantitative trait. We further examined spontaneous PTD subtypes separately.

Results: While no SNP in either maternal or fetal genotype reached formal GWAS significance ($p < 10^{-7}$) for PTD overall, 7 SNPs had p-values $\leq 10^{-6}$. SNPs mostly strongly associated with PTD were not in or near known candidate genes.

Conclusions: The GWAS approach allowed us to identify new chromosomal regions of potential importance to PTD etiology. Replication of promising SNPs in independent populations is underway to determine if any of our findings represent true positives and thereby potential new insights into the causes of PTD.