Introduction

We have performed a meta-analysis of genome wide association data for self-reported allergy across participants in the 23andMe Personal Genomics Service, and members from the Avon Longitudinal Study of Parents and Children (ALSPAC). We examined four phenotypes (pollen allergy, dust mite allergy, cat allergy, and any allergy), each representing a total of more than 20,000 cases. In total, we identified 8 independent loci with P<5.0E-08 for one or more allergens. All these associations are in or near genes that have previously been implicated as having roles in immune function, with previously reported associations with phenotypes such as asthma, atopic dermatitis, and atopic disease. We also replicate many known associations with asthma, with effect sizes consistent with those of original reports. Our results support the existence of a shared genetic etiology for these conditions, as well as suggesting distinct patterns of association phenotypes. Our findings also demonstrate that self-report is an effective method for collecting phenotypic information for genetic analysis of allergy and related phenotypes.

Methods

Self-reported allergy and asthma phenotypes were assessed in the 23andMe participant cohort (Erickson et al., 2010) and the ALSPAC mothers (Golding et al., 2010) using web-based and paper surveys, respectively. For 23andMe, allergies were assessed mainly through an "Allergies and Asthma" survey. For genome wide analyses, we focused on four binary allergy phenotypes with close agreement between the 23andMe and ALSPAC surveys: cat, dust mite, pollen, and any allergy. Pollen allergy was considered the union of grass, tree, and weed allergies in the 23andMe survey. We also assessed asthma (5,984 cases, 25,771 controls), using the 23andMe general health survey. All participants provided informed consent for use of their data for research.

23andMe participants were genotyped on custom versions of either the Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the 23andMe participants were genotyped on custom versions of either the Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the 23andMe participants were genotyped on custom versions of either the Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the 23andMe participants were genotyped on custom versions of either the Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the 23andMe participants were genotyped on custom versions of either the Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplotypes, using Beagle for Illumina HumanHap550 or the OmniExpress, then imputed against the August 2010 release of 1000 Genomes haplo...