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Title: IgE levels in asthmatics and non-asthmatics are affected by different SNPs in FCER1A

Body: Background: Recently, three genome wide association studies (GWAS) demonstrated FCER1A, the gene encoding the α-subunit of the high-affinity IgE receptor, to be a major susceptibility locus for total serum IgE. The top association signal differed between the two studies from the general population and one study based on an asthma case-control design. Objective: To investigate if different FCER1A single-nucleotide polymorphisms (SNPs) are associated with total serum IgE in the general population and asthmatics. Methods: Nineteen SNPs were studied in FCER1A based on a detailed literature search and a tagging approach. SNPs were genotyped by the Illumina HumanHap300Chip (6) or MALDI-TOF-MS (13) in
at least 1303 children (651 asthmatics) derived from the German ISAAC- and MAGIC studies. Results: Similarly to two population-based GWAS the peak association with total serum IgE was observed for SNPs rs2427837, rs2251746 and rs2511211 (mean $r^2 > 0.8$), with the lowest p-value of $4.37 \times 10^{-6}$. The same 3 SNPs showed the strongest association in non-asthmatics (lowest p=0.0003). While these SNPs were also associated with total serum IgE in asthmatics (lowest p=0.003), additional SNPs (rs3845625, rs7522607 and rs2427829) demonstrated associations with total serum IgE in asthmatics only (lowest p=0.01). SNPs rs2427837, rs2511211, rs3845625 and rs2427829 were also associated with atopic asthma (lowest p=0.02). Conclusions: These data suggest that SNPs in FCER1A specifically influence IgE levels in asthmatics on top of genetic determinants of “basal” IgE levels also present in FCER1A as previously identified by GWAS. Thus, FCER1A variants and IgE-related mechanisms could be involved in specific asthma phenotypes. These authors contributed equally.