Genes involved in interleukin-1 receptor type II (IL1R2) activities are associated with asthma related phenotypes

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We previously demonstrated that IL1R2 (Interleukin-1-receptor-type-II) is overexpressed in bronchial biopsies of allergic asthmatic individuals and we also associated it with atopy (n>5500). This study aims to test for the effect of SNPs and interactions between 182 SNPs belonging to nine genes involved in IL1R2 activities on asthma related phenotypes in the Saguennay-Lac-St-Jean familial asthma collection (SLSJ) and in French families of the Epidemiological study on the Genetics and Environment of Asthma (EGEA). Single SNP analysis was performed using Family-Based Association Tests software (FBAT). In order to correct for multiple tests, we used a critical P-value threshold equal to 2x10⁻⁴ that took into account the number of independent SNPs and independent phenotypes. Interactions between SNPs were tested using Unphased software. SLSJ and EGEA results were combined through meta-analysis using the Stouffer’s Z-score method. No SNP reached the critical threshold for significance but suggestive association were observed. The rs3732131 SNP in IL1R1 was associated with asthma (p=0.0004), atopy (p=0.0005) and allergic asthma (p=0.002). We also found associations between three SNPs in ERAP1 and allergic asthma (0.0006 ≤ p ≥ 0.001). Regarding SNPxSNP interactions, four interactions were found in SLSJ at p<1.0X10⁻⁴ and one of those was replicated in EGEA for atopy (p=0.002, combined p=3.62X10⁻⁷) between rs2241343 of IL1RAP and rs10208708 of IL1R1). The observed SNP-associations in the combined SLSJ and EGEA samples and the SNPxSNP interaction suggest that genes involved in the IL1R2 activities play a role in asthma and, especially in its allergic component.