

## Asthma

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**GENOME-WIDE INTERACTION STUDY ON OCCUPATIONAL HAZARDS AND ASTHMA, THE EUROPEAN COMMUNITY RESPIRATORY HEALTH SURVEY (ECRHS)**

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**Objectives** Very few studies have addressed gene-environment (GxE) interactions in asthma at the genome-wide level and none in the context of occupational hazards. Our objective was to detect GxE interactions for asthma and job exposure in a population-based cohort.

**Methods** Occupational exposures for 2205 adults from the ECRHS were assessed through job histories, an asthma-specific JEM and expert assessment. We performed a genome-wide interaction analysis for asthma as a whole and adult onset asthma by using 582 892 single nucleotide polymorphisms (SNP) and work exposure to high-molecular weight agents (HMW) and latex. Two analytical strategies were used to detect GxE interactions: 1) a global genome-wide analysis and 2) a two-stage approach.

**Results** In the global analysis, a single SNP with marginal genome-wide significance ( $p < 1.E-07$ ) emerged to interact with latex for adult onset asthma. In the two-stage approach, SNPs associated with exposure ( $p < 1.E-05$ ) at the first step were then tested for association with outcomes at the second step. In this approach, two SNPs were detected to interact with HMW and four SNPs with latex for adult onset asthma ( $p < 0.05$ ). These SNPs were not among the top 30 SNPs in the global analysis.

**Conclusions** We found very few clues on GxE interactions. Results depended not only on exposure and outcome definitions, with slightly lower p-values for the more specific definitions (adult onset, latex) but also on the analytical strategy followed. Replication of these findings will be presented using two additional studies (EGEA and Sapaldia).