**Genome-wide association study of asthma exacerbations in European children treated with inhaled corticosteroids**

**Introduction:** Inhaled corticosteroids (ICS) are the most common asthma controller medication. However, a high proportion of patients does not respond to this medication and suffer exacerbations. We performed a genome-wide association study (GWAS) to identify genes associated with asthma exacerbations in European children taking ICS.

**Methods:** Within the PiCA consortium, we performed a GWAS meta-analysis of asthma exacerbations across three European cohorts (PACMAN, PASS, and followMAGICS) including 1,204 asthmatic children treated with ICS. Imputation of genetic variants was performed using the Haplotype Reference Consortium as reference panel by means of the Michigan Imputation Server. Association testing of 7.5 million genetic variants with minor allele frequency ≥1% was performed using logistic regression models and results were meta-analyzed.

**Results:** A total of 74 variants were suggestively associated with asthma exacerbations despite the use of ICS (p≤5x10-6). The most significant variants were located in 9 different loci (minimum p-value=2.3x10-7), including one gene previously identified as associated with ICS response in Asian populations (ALLC). Additionally, novel associations were revealed in biologically plausible genes with drug metabolism functions and in genes belonging to the Wnt/β-catenin signaling pathway.

**Conclusions:** We identified several novel genes suggestively associated with asthma exacerbations despite the use of ICS. Validation will be performed in further independent studies.