**Introduction: Inhaled corticosteroids (ICS) are the most effective medication for control of asthma symptoms. However, a proportion of patients do not respond to this medication and suffer exacerbations, due to a combination of environmental and genetic factors. We performed a meta- genome-wide association study (GWAS) to identify genes associated with ICS response in European children.**

**Methods: A GWAS meta-analysis of asthma exacerbations was performed across eight European studies from the Pharmacogenomics in Childhood Asthma (PiCA) consortium including 2,704 asthmatic children and young adults treated with ICS. Imputation of genetic variants was carried out using the Haplotype Reference Consortium as reference panel and association testing was performed by means of logistic regression models. A total of 8.1 million genetic variants with minor allele frequency ≥1% were meta-analyzed.**

**Results: Nineteen polymorphisms were suggestively associated with asthma exacerbations despite use of ICS (p≤5x10-6). These variants were located at 10 segregating sites (minimum p=6.7x10-7). Novel associations were revealed in biologically plausible genes involved in drug metabolism (AOX1) and previously associated with lung function measurements (WNT5A and CNTNAP5). Moreover, variants located at CNTNAP5 were also nominally associated with a change in FEV1 after ICS treatment in SLOVENIA (minimum p=0.025).**

**Conclusions: We revealed genes suggestively associated with asthma exacerbations in children and young adults despite the use of ICS. Replication will be performed in further independent studies.**