**Introduction:** Inhaled corticosteroids (ICS) are the most widely prescribed and effective medication to control asthma symptoms. However, this treatment is insufficient to avoid severe exacerbations in many patients, particularly in African Americans. A few genome-wide association studies (GWAS) of ICS have been performed, but none of them in African-admixed populations. Here, we aimed to identify loci associated with asthma exacerbations in children taking ICS.

**Methods:** Within the PiCA consortium, a meta-analysis of two GWAS of asthma exacerbations was performed in 1,401 African-admixed children from the GALA II and SAGE II studies. 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 8.6 million genetic variants with minor allele frequency ≥1% were meta-analyzed. Variants with p≤5x10-6 were followed up for replication in 1,204 European asthmatic patients from three different studies (PACMAN, follow MAGICS, and PASS).

**Results:** A total of 27 polymorphisms were suggestively associated with asthma exacerbations (p≤5x10-6) in African-admixed populations and 3 of them showed evidence of replication in European individuals (p≤5.4x10-3). These were located in the intergenic region of the APOBEC3B and APOBEC3C genes, which have been linked with viral infections.

**Conclusions:** This study revealed the association of a novel locus with asthma exacerbations in children despite the use of ICS.