**Introduction**

Adverse drug reactions (ADRs) cause harm. Pharmacogenomic studies can be used to identify individuals at increased risk of specific ADRs. Multiple pharmacogenomic association studies in asthma have been undertaken.

**Aim**

To undertake a systematic review of pharmacogenomic studies of ADRs related to medications used to treat asthma in adults and children and establish future research priorities.

**Methods**

Medline, Embase, and Cinahl databases were searched until January 2018 for eligible studies. Studies were eligible if genetic polymorphisms were compared with suspected ADR(s) in a patient with asthma as either a primary or secondary outcome. A survey of members of the Pharmacogenomics in Childhood Asthma (PiCA) consortia was conducted.

**Results**

Five studies met the inclusion criteria. Three studies examined corticosteroids (one included inhaled, all included oral), one examined inhaled short acting beta-2 agonists (SABA), and one long acting beta-2 agonists (LABA). The SABA and LABA studies used a candidate gene approach, while the corticosteroid studies were genome wide association studies. The ADRs and polymorphisms identified were change in lung function tests (rs1042713), adrenal suppression (rs591118), and decreased bone mineral density (rs6461639) and bone mineral accretion (rs9896933, rs2074439). Internal replication was undertaken in two studies, but none have been externally replicated to date. Priorities from PiCA consortia members (15 institutes in eight countries) for future pharmacogenomic ADR studies in asthma were tachycardia (SABA/LABA), adrenal suppression/crisis and growth suppression (corticosteroids), sleep/behaviour disturbances (leukotriene receptor antagonists), and nausea and vomiting (theophylline).

**Conclusion**

Future pharmacogenomic studies in asthma should collect relevant ADR data as well as markers of efficacy. Drug specific ADR priorities have been established.