

Genome-wide genotyping of 55 Indian anti-TB DILI cases & 1199 Indian controls

Genome-wide genotyping on 70 European anti-TB DILI cases & 10397 population controls

After imputation of additional SNPs, assess association of individual SNPs with DILI by logistic regression, using additive model and adjusting for population structure. Perform separately in both cohorts followed by meta analysis.

Impute HLA genotypes from genome-wide genotyping data for cases and controls. 217 alleles were imputed in Europeans and 192 in Indians. Assess association of individual alleles with DILI. Set p for significance at less than  $2.5 \times 10^{-4}$ . Perform separately in both cohorts followed by meta analysis.

Extract NAT2 genotypes from imputed GWAS data. Assess association of individual SNPs and acetylator genotypes with DILI in cases and controls. Perform separately in both cohorts followed by meta analysis.

Extract individual SNPs in additional candidate genes from imputed GWAS data. Assess association of SNPs individually with DILI in cases and controls. Set significance of  $p < 0.003$  for 16 multiple comparisons. Perform separately in both cohorts.