

Sulfasalazine-Induced Agranulocytosis Is Associated With the Human Leukocyte Antigen Locus

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Agranulocytosis is a serious, although rare, adverse reaction to sulfasalazine, which is used to treat inflammatory joint and bowel disease. We performed a genome-wide association study comprising 9,380,034 polymorphisms and 180 HLA alleles in 36 cases of sulfasalazine-induced agranulocytosis and 5,170 population controls. Sulfasalazine-induced agranulocytosis was significantly associated with the HLA region on chromosome 6. The top hit (rs9266634) was located close to *HLA-B*, odds ratio (OR) 5.36 (95% confidence interval (CI) (2.97, 9.69) $P = 2.55 \times 10^{-8}$). We HLA-sequenced a second cohort consisting of 40 cases and 142 treated controls, and confirmed significant associations with *HLA-B*08:01*, OR = 2.25 (95% CI (1.02, 4.97) $P = 0.0439$), in particular the *HLA-B*08:01* haplotype *HLA-DQB1*02:01-DRB1*03:01-B*08:01-C*07:01*, OR = 3.79 (95% CI (1.63, 8.80) $P = 0.0019$), and with *HLA-A*31:01*, OR = 4.81 (95% CI (1.52, 15.26) $P = 0.0077$). The number needed to test for *HLA-B*08:01* and *HLA-A*31:01* to avoid one case was estimated to be 1,500. We suggest that intensified monitoring or alternative treatment should be considered for known carriers of *HLA-B*08:01* or *HLA-A*31:01*.

Study Highlights

WHAT IS THE CURRENT KNOWLEDGE ON THE TOPIC?

☑ Agranulocytosis is a serious, although rare, adverse reaction to sulfasalazine—a drug used to treat inflammatory joint and bowel disease. The risk is most pronounced during the first 3 months of treatment, and agranulocytosis should be suspected in patients with unexplained fever or nonspecific illness during this period. There are no good predictors for sulfasalazine-induced agranulocytosis.

WHAT QUESTION DID THIS STUDY ADDRESS?

☑ The aim was to identify genetic variants predisposing to sulfasalazine-induced agranulocytosis in a European population.

WHAT DOES THIS STUDY ADD TO OUR KNOWLEDGE?

☑ We performed a genome-wide association study (GWAS) and identified genetic variants in the HLA region that increased the risk of sulfasalazine-induced agranulocytosis significantly.

HOW THIS MIGHT CHANGE CLINICAL PHARMACOLOGY OR TRANSLATIONAL SCIENCE?

☑ We suggest that known carriers of *HLA-B*08:01* or *HLA-A*31:01* should be placed under intensified monitoring when starting sulfasalazine or be offered an alternative drug.

Agranulocytosis is a blood dyscrasia characterized by an absolute neutrophil count below $0.5 \times 10^9/L$ ($500/\mu L$).¹ The vast majority of cases are drug-related, either through direct dose-dependent cytotoxicity or idiosyncratic reactions to at least 125

nonchemotherapy drugs.^{2–4} Idiosyncratic agranulocytosis leads to a rapid decline in neutrophils that causes a high risk of overwhelming infection, with an average mortality rate of about 5%.^{5–7} The onset of drug-induced idiosyncratic agranulocytosis is

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usually within months of starting therapy, and the reaction is generally believed to be immune-mediated.⁴ In the few instances where genetic studies have been performed, associations with human leukocyte antigen (HLA) genes or other genes associated with the immune response have been found.⁴ This provides further evidence for an immune-mediated mechanism for drug-induced idiosyncratic agranulocytosis.

Sulfasalazine (Salazopyrin, Pfizer, Groton, CT), a drug developed in the 1930s for the treatment of inflammatory joint and bowel disease, was reported to cause fatal idiosyncratic agranulocytosis already in 1942.⁸ In nonfatal cases, patients usually recover within weeks of drug withdrawal.⁷ The incidence was estimated to be 1 in 2,400 patients during the first month of treatment, 1 in 700 during the second and third months (0.14%), and 1 in 11,200 after more than 3 months of treatment in a Swedish population.⁹ In the same population, the background incidence of agranulocytosis was approximately 1 in 150,000 inhabitants.⁹

Sulfasalazine-induced agranulocytosis is believed to be a host immune response to a reactive metabolite of sulfasalazine.⁴ Sulfasalazine is first split into 5-amino salicylic acid and sulfapyridine by intestinal bacteria.¹⁰ Sulfapyridine is in contrast to 5-amino salicylic acid rapidly absorbed into the bloodstream. It is further metabolized in the liver into N-acetyl-sulfapyridine by the enzyme N-acetyltransferase 2 (NAT2).^{11,12} N-acetyl-sulfapyridine is primarily bioactivated by the enzyme CYP2C9 into a cytotoxic hydroxylamine that is subsequently excreted as a glucuronic acid conjugate.¹³ Inherited variants of the drug-metabolizing enzymes NAT2 or CYP2C9 could in theory shunt the metabolism towards more toxic metabolites.¹⁴ It has been speculated that slow NAT2 acetylators treated with sulfonamides may be predisposed to idiosyncratic toxicity, such as severe skin reactions and systemic lupus erythematosus.^{15–18} In a previous study, we investigated whether coding variants in the NAT2 gene influenced the risk of sulfasalazine-induced agranulocytosis.¹⁹ A higher proportion of slow acetylators was seen among 39 cases of sulfasalazine-induced agranulocytosis (69%) compared with 75 sulfasalazine-tolerant patients (45%). However, no difference in slow acetylator frequency was seen between the 39 cases and 448 population-based control subjects. We further genotyped these cases and treated controls for CYP2C9*2 and *3, but no association between agranulocytosis and genotype was seen (unpublished results). A subsequent study investigated the possible association between sulfasalazine-induced agranulocytosis and mutations in the human neutrophil elastase gene (ELANE) that causes severe congenital neutropenia (SCN).²⁰ None of the mutations previously reported to cause SCN were found in 36 patients with agranulocytosis induced by sulfasalazine. No other studies on candidate genes for sulfasalazine-induced agranulocytosis have to our knowledge been published. The European Drug-induced Agranulocytosis Consortium (EuDAC, see Acknowledgments) was initiated with the aim to perform a genome-wide association study (GWAS) to identify novel genetic variants predisposing to agranulocytosis. We here present the results on sulfasalazine-induced agranulocytosis.

RESULTS

Characteristics of 36 cases of agranulocytosis induced by sulfasalazine and 5,170 population controls collected in Sweden, Germany, France, and Spain are shown in **Supplementary Table S1**. Comparisons of demographic and clinical factors between the 30 cases recruited in Sweden and their 183 matched controls are shown in **Table 1**.

Genome-wide association analyses

Sulfasalazine-induced agranulocytosis was associated with the major histocompatibility complex (MHC) region (HLA region) on chromosome 6 on a genome-wide level after adjusting according to sex and genetic principal components 1–4, $P < 5 \times 10^{-8}$ (**Figure 1**, **Supplementary Figure S1**). The single nucleotide polymorphism (SNP) with the best evidence for association was rs9266634, which is located in an intergenic region 22,000 bases from *HLA-B*, odds ratio (OR) 5.36 (95% confidence interval (CI) 2.97, 9.69) $P = 2.55 \times 10^{-8}$, (**Table 2**, **Supplementary Table S2**, **Supplementary Figure S1**). There was also a significant association with the intergenic insertion rs202233001 positioned in a repeat region close to the paired box 1 gene (*PAX1*) on chromosome 20, OR = 6.76 (95% CI 3.41, 13.38), $P = 4.19 \times 10^{-8}$. When the data were adjusted for the top hit rs9266634, the chromosome 20 SNP rs202233001 was no longer significantly associated.

Follow-up analyses were performed adjusting for each top hit in a sequential manner (**Table 2**). After adjusting for rs9266634 on chromosome 6, rs111876221 on chromosome 5 reached genome-wide significance. This SNP is located in intron 1 of the serine incorporator 5 gene (*SERINC5*). After adjusting for the two independently associated rs9266634 and rs111876221, the SNP rs113887891 on chromosome 1 was significant on a genome-wide level. This intron variant is in a repeat region in the gene for the nonprotein-coding transcript *LINC01762*. After adjusting also for rs113887891, the SNP rs12082628 on chromosome 1 was significant on a genome-wide level. This variant is in a repeat region in an intron of the cholinergic receptor, muscarinic 3 gene (*CHRM3*). All associated variants outside the HLA-region were infrequent, and none of them had strong evidence of being functional in primary B cells from peripheral blood.²¹ After adjusting for rs9266634, rs111876221, rs113887891, and rs12082628, no genome-wide significant association remained.

Analysis of classical HLA alleles at second field resolution

The HLA alleles *HLA-C*14:02* and *HLA-B*08:01* were associated with sulfasalazine-induced agranulocytosis on an HLA-wide level ($P < 2.8 \times 10^{-4}$), OR = 7.72 (95% CI (2.90, 20.58) $P = 4.36 \times 10^{-5}$) and 2.92 (95% CI (1.71, 4.98) $P = 8.37 \times 10^{-5}$), respectively (**Table 2**, **Supplementary Table S3**). The top genome-wide SNP rs9266634 was in linkage disequilibrium (LD) with both *HLA-C*14:02* ($D' = 0.87$, $r^2 = 0.01$, $P < 2.22 \times 10^{-16}$) and *HLA-B*08:01* ($D' = 0.99$, $r^2 = 0.16$, $P < 2.22 \times 10^{-16}$). A multiple analysis, including all associated HLA alleles and the top SNP, shows that rs9266634 had a small independent effect (**Supplementary Figure S2**). Top HLA types obtained by sequential adjustment for each significantly associated type are

Table 1 Characteristics of cases and matched controls recruited in Sweden for the discovery cohort

	Cases (n = 30)	Matched controls (n = 183)	P
Gender, male [%]	14 [46.7]	80 [43.7]	0.92
Age, years	at agranulocytosis [%]	at diagnosis [%]	
<25	1 [3.3]	6 [3.3]	0.49
25-29	2 [6.7]	10 [5.5]	
30-34	2 [6.7]	4 [2.2]	
35-39	2 [6.7]	7 [3.8]	
40-44	1 [3.3]	12 [6.6]	
45-49	1 [3.3]	15 [8.2]	
50-54	5 [16.7]	14 [7.7]	
55-59	7 [23.3]	43 [23.5]	
60-64	5 [16.7]	25 [13.7]	
65-69	2 [6.7]	27 [14.8]	
70-74	0	14 [7.7]	
>74	2 [6.7]	6 [3.3]	
Diagnosis ^a	[% of cases]	[% of controls]	
Rheumatoid arthritis	14 [46.7]	75 [41.0]	0.56
Crohn's disease	3 [10.0]	41 [22.4]	0.15
Ulcerative colitis	3 [10.0]	48 [26.2]	0.06
Psoriasis arthritis	5 [16.7]	13 [7.1]	0.15
Ankylosing spondylitis	1 [3.3]	5 [2.7]	1.00
Arthritis unspecified	5 [16.7]	8 [4.4]	0.02
Sjögren's syndrome	1 [3.3]	12 [6.6]	0.70
Total number of diagnosis	32	202	

Cases included one of Swedish–Italian, one of Swedish–Finnish, and one of Finnish origin. Matched controls all had a diagnosis that is an indication for sulfasalazine treatment.

^aTwo cases had two diagnosis: rheumatoid arthritis and psoriasis arthritis, and Crohn's disease and unspecified arthritis. Among the controls, 17 had two diagnosis and one had three diagnosis. Tests used: χ^2 test for comparisons of age, otherwise Fisher's exact test.

shown in **Table 2**. The association with *HLA-B*08:01* was strengthened after adjusting for *HLA-C*14:02*, OR = 3.24 (95% CI (1.988–5.57) $P = 2.26 \times 10^{-5}$). *HLA-A*31:01* consistently had odds ratios around 4, but P -values were above the defined HLA-wide significance level.

We corrected for possible confounding by indication and population stratification by considering the Swedish cohort separately (**Table 1**). The odds ratio for *HLA-C*14:02* was 11.08 (95% CI (4.10, 29.89) $P = 2.05 \times 10^{-6}$) when Swedish cases and population controls were compared, and 10.30 (95% CI (2.44, 43.52) $P = 1.51 \times 10^{-3}$) when Swedish cases were compared with controls matched for diagnosis of inflammatory disease (**Figure 2**). The odds ratio for *HLA-B*08:01* was 3.15 (95% CI (1.78, 5.57) $P = 7.83 \times 10^{-5}$) compared with population controls, and 5.43 (95% CI (2.40, 12.27) $P = 4.82 \times 10^{-5}$) compared with matched controls. The corresponding odds ratios for *HLA-A*31:01* were 3.70 (95% CI (1.54, 8.90) $P = 3.39 \times$

10^{-3}), and 4.97 (95% CI (1.54, 16.01) $P = 7.25 \times 10^{-3}$) (**Figure 2**).

Replication of SNPs and HLA alleles

An independent cohort recruited in Sweden was used for replication of the association with HLA (**Table 3**). We sequenced *HLA-A*, *HLA-B*, *HLA-C*, *HLA-DRB1*, *HLA-DQB1*, and *HLA-DPB1* in 40 cases of sulfasalazine-induced agranulocytosis and 142 controls treated with sulfasalazine for at least 90 days. Due to correction for multiple testing of the five top HLA types shown in **Table 2**, the cutoff for significance was $P < 0.01$. *HLA-B*08:01* was nominally associated with agranulocytosis, OR = 2.25 (95% CI (1.02, 4.97) $P = 0.0439$, C-statistic = 0.57) (**Table 4**). Thirteen cases (32.5%) were heterozygous for *HLA-B*08:01*, as compared to 25 controls (17.6%), and none were homozygous. We hypothesized that these patients carried the most frequent *HLA-B*08:01* haplotype, *HLA-DQB1*02:01-*

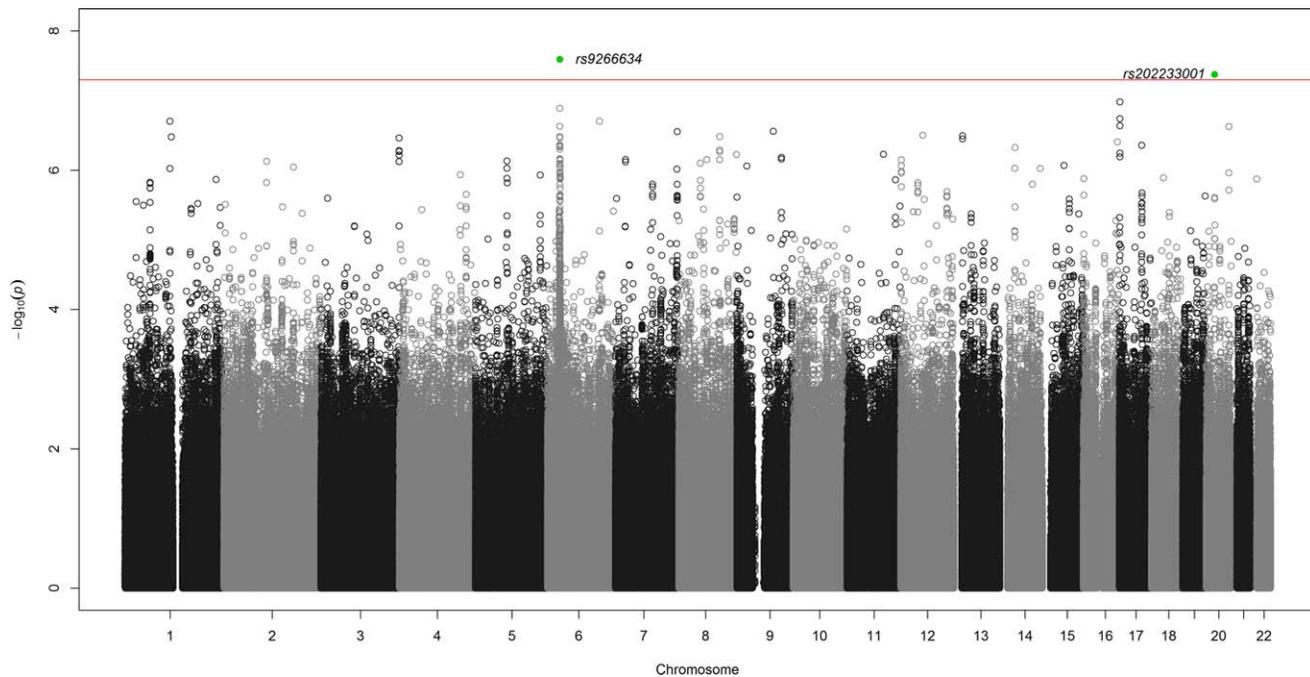


Figure 1 Manhattan plot of the genome-wide association analysis. Analysis of 36 cases induced by sulfasalazine vs. all controls with 9,380,034 SNPs after imputation, adjusted by sex and genetic principal components 1–4. The red line shows the threshold for genome-wide significance of 5×10^{-8} . The top SNP was rs9266634 marked in green is located in an intergenic region close to *HLA-B* on chromosome 6. There was also a significant association with an intergenic insertion/deletion on chromosome 20, rs202233001, marked in green. The closest protein coding gene to this variant is the transcription factor gene Paired Box 1 (*PAX1*). After adjustment for rs9266634, the intronic SNP rs111876221 in the gene serine incorporator 5 (*SERINC5*) on chromosome 5, reached genome-wide significance. After adjustment for both rs9266634 and rs111876221, rs113887891 in a nonprotein coding RNA gene (*LINC01762*) on chromosome 1 was significant on a genome-wide level. After adjusting also for this SNP, the intron variant rs12082628 in the gene cholinergic receptor, muscarinic 3 (*CHRM3*) on chromosome 1 gave a significant result. SNP = single nucleotide polymorphism, HLA = human leukocyte antigen, RNA = ribonucleic acid.

*DRB1*03:01-B*08:01-C*07:01*, which is present in 7.4% of Europeans.²² Notably, all 13 cases with *HLA-B*08:01* carried *HLA-C*07:01*, *DQB1*02:01*, and *DRB1*03:01*, and thus probably had the common haplotype. In comparison, only 16 of 25 sulfasalazine-treated controls with *HLA-B*08:01* carried this combination of HLA alleles. The odds ratio for carrying *HLA-DQB1*02:01-DRB1*03:01-B*08:01-C*07:01* was 3.79 (95% CI (1.63, 8.80) $P = 0.0019$, C-statistic = 0.61), which was statistically significant (Table 4). Furthermore, the association with *HLA-A*31:01* was statistically significant, OR = 4.81 (95% CI (1.52, 15.26) $P = 0.0077$, C-statistic = 0.57) (Table 4). The allele frequency of *HLA-A*31:01* was high among cases (9%) compared with the expected frequency 2.7% in Europeans.²² *HLA-C*14:02* was only present in one control, and therefore too rare to be assessed.

Predictive ability and clinical implications

The specificity to predict risk of agranulocytosis increased from 82.4% to 88.7% when using *HLA-DQB1*02:01-DRB1*03:01-B*08:01-C*07:01* instead of *HLA-B*08:01*. This indicates that fewer patients would be falsely predicted as being at risk when using the full haplotype. The sensitivity was 32.5% with either *HLA-B*08:01* or the full haplotype, but when combining *HLA-B*08:01* with *HLA-A*31:01*, the sensitivity increased to 47.5%. With a sensitivity of 47.5% and an incidence of 0.0014 (1 in 700

patients receiving treatment),⁹ we could theoretically reduce the incidence of agranulocytosis to 0.000735 (0.0014–0.475*0.0014) by screening for *HLA-B*08:01* and *HLA-A*31:01*. The number needed to genotype (NNG) for *HLA-B*08:01* and *HLA-A*31:01* to avoid one case was estimated to be about 1,500, which is the reciprocal of the absolute risk reduction, $1/(0.0014*0.475)$.

DISCUSSION

The sulphonamide sulfasalazine is known to carry a high risk of agranulocytosis,⁸ and the relative risk is estimated to be almost 10 times higher than for the sulphonamide sulfamethoxazole.²³ The characteristics of our cases (53% women, median age 55–59 years, median treatment time to onset 50 days) were similar to those found in a previous study on the epidemiology of sulfasalazine-induced agranulocytosis in Sweden.⁹ In the present study, sulfasalazine-induced agranulocytosis was mainly associated with the MHC region on chromosome 6 that encodes HLA genes. Agranulocytosis induced by other drugs has previously been associated with HLA.^{4,24–26} We found an association between sulfasalazine-induced agranulocytosis and *HLA-B*08:01* that was replicated with similar ORs (2.92 vs. 2.25). All HLA sequenced cases carrying *HLA-B*08:01* also carried *DQB1*02:01*, *DRB1*03:01*, and *HLA-C*07:01*, and the full haplotype conferred a higher OR (3.79). This indicates that the *HLA-*

Table 2 Top genome-wide associations and HLA associations with agranulocytosis induced by sulfasalazine in the discovery cohort

Associations	CHR	SNP	BP	Alleles (major/minor)	N	MAF case	MAF control	OR [95% CI]	P	Nearby gene
a. Genome-wide										
Adjusted by sex and genetic PC 1-4	6	rs9266634	31346978	A/T	5,183	0.81	0.44	5.37 [2.97, 9.69]	2.55×10^{-8}	HLA-B
Adjusted by sex, genetic PC 1-4 and rs9266634	20	rs202233001	21735353	C/CACA	5,081	0.14	0.03	6.76 [3.41, 13.38]	4.19×10^{-8}	PAX1
Adjusted by sex, genetic PC 1-4, rs9266634 and rs111876221	5	rs111876221	79535200	A/G	5,152	0.10	0.02	12.65 [5.15, 31.1]	3.22×10^{-8}	SERINC5
Adjusted by sex, genetic PC 1-4, rs9266634 and rs111876221	1	rs113887891	117006870	G/T	5,041	0.13	0.02	9.52 [4.24, 21.37]	4.78×10^{-8}	LINC01762
Adjusted by sex, genetic PC 1-4, rs9266634, rs111876221 and rs113887891	1	rs12082628	239797706	A/G	4,872	0.09	0.01	14.99 [5.75, 39.04]	3.00×10^{-8}	CHRM3
b. HLA										
Adjusted by sex and PC 1-4	6	HLA-C*14:02	31346171	A/P	5,206	0.07	0.01	7.72 [2.90, 20.58]	4.36×10^{-5}	
Adjusted by sex, PC 1-4 and HLA-C*14:02	6	HLA-B*08:01	31431272	A/P	5,206	0.26	0.11	2.92 [1.71, 4.99]	8.37×10^{-5}	
Adjusted by sex, PC 1-4 and HLA-C*14:02	6	HLA-C*02:06	31346171	A/P	5,206	0.01	0.00	92.68 [8.02, 1071]	2.86×10^{-4}	
Adjusted by sex, PC 1-4 and HLA-C*14:02	6	HLA-B*08:01	31431272	A/P	5,206	0.26	0.11	3.24 [1.88-5.57]	2.26×10^{-5}	
Adjusted by sex, PC 1-4, HLA-C*14:02 and B*08:01	6	HLA-C*07:01	31346171	A/P	5,206	0.29	0.14	2.72 [1.62, 4.57]	1.49×10^{-4}	
Adjusted by sex, PC 1-4, HLA-C*14:02 and B*08:01	6	HLA-A*31:01	30019970	A/P	5,206	0.10	0.03	3.72 [1.63, 8.47]	1.74×10^{-3}	
Adjusted by sex, PC 1-4, HLA-C*14:02 and B*08:01	6	HLA-C*02:02	31346171	A/P	5,206	0.15	0.06	3.52 [1.81, 6.84]	2.09×10^{-4}	
Adjusted by sex, PC 1-4, HLA-C*14:02 and B*08:01	6	HLA-A*31:01	30019970	A/P	5,206	0.10	0.03	4.24 [1.83, 9.82]	7.57×10^{-4}	
Adjusted by sex, PC 1-4, HLA-C*14:02 and B*08:01	6	HLA-C*07:02	31346171	A/P	5,206	0.25	0.15	2.67 [1.50, 4.77]	8.51×10^{-4}	
Adjusted by sex, PC 1-4, HLA-C*14:02, B*08:01 and C*02:02	6	HLA-B*07:02	31431272	A/P	5,206	0.24	0.15	3.57 [1.90, 6.72]	7.74×10^{-5}	
Adjusted by sex, PC 1-4, HLA-C*14:02, B*08:01 and C*02:02	6	HLA-C*07:02	31346171	A/P	5,206	0.25	0.15	3.16 [1.74, 5.75]	1.67×10^{-4}	
Adjusted by sex, PC 1-4, HLA-C*14:02, B*08:01, C*02:02 and B*07:02	6	HLA-A*31:01	30019970	A/P	5,206	0.10	0.03	3.87 [1.64, 9.12]	1.99×10^{-3}	
Adjusted by sex, PC 1-4, HLA-C*14:02, B*08:01, C*02:02 and B*07:02	6	HLA-A*31:01	30019970	A/P	5,206	0.10	0.03	4.42 [1.83, 10.68]	9.48×10^{-4}	
Adjusted by sex, PC 1-4, HLA-C*14:02, B*08:01, C*02:02 and B*07:02	6	HLA-B*51:01	31431272	A/P	5,206	0.14	0.05	3.18 [1.25, 8.11]	1.55×10^{-2}	
Adjusted by sex, PC 1-4, HLA-C*14:02, B*08:01, C*02:02 and B*07:02	6	HLA-B*55:01	31431272	A/P	5,206	0.03	0.01	5.48 [1.23, 24.31]	2.53×10^{-2}	

a. Top GWAS results based on 9,380,034 SNPs after imputation in 36 patients with sulfasalazine-induced agranulocytosis vs. all 5,170 controls. All results were adjusted for sex and four genetic principal components (PC). No genome-wide significant signals were left after adjusting for four SNP variants. b. Odds ratios for the top HLA alleles for patients with sulfasalazine-induced agranulocytosis. The effect was modeled per increase of one present HLA allele. Chromosomal location is according to the Genome Reference Consortium human assembly GRCh37. Complete lists of associated SNPs and HLA types are available in the appendix.

GWAS = genome-wide association study, CHR = chromosome, PC = genetic principal components, SNP = single nucleotide polymorphism, BP = base pair, N = number, MAF = minor allele frequency, OR [95% CI] = odds ratio with 95% confidence interval. When referring to HLA allele: A = absent, P = present.

*DQB1*02:01-DRB1*03:01-B*08:01-C*07:01* haplotype could be a better predictor of agranulocytosis than *HLA-B*08:01*. However, the sensitivity did not change when adding the full haplotype, while it was higher when combining *HLA-B*08:01* with *HLA-A*31:01*.

Notably, *HLA-B*08:01* and *HLA-A*31:01* have both been shown to increase the risk of carbamazepine hypersensitivity.^{27,28} In a European study on carbamazepine, individuals homozygous for *HLA-B*08:01* were more likely to suffer severe hypersensitivity than those carrying at least one copy of the common *HLA-B*07:02* allele.^{22,27} Several studies have shown that *HLA-A*31:01* increases the risk of carbamazepine hypersensitivity.²⁸

There is no apparent chemical structural similarity between sulfasalazine and carbamazepine. We did not replicate our association with the rare *HLA-C*14:02* allele in the HLA sequenced cohort. *HLA-C*14:02* has an expected allele frequency of only 1.3% in Europeans, but is more common in Asia, with allele frequencies up to 8.2%.²² *HLA-C*14:02* has previously been associated with serious skin reactions due to phenytoin in patients of Thai ancestry.²⁹

There are three main proposed hypotheses through which HLA can interact with a drug to trigger an inappropriate immune response.²⁸ According to the first model, the drug binds covalently to a peptide fragment that is presented on the MHC

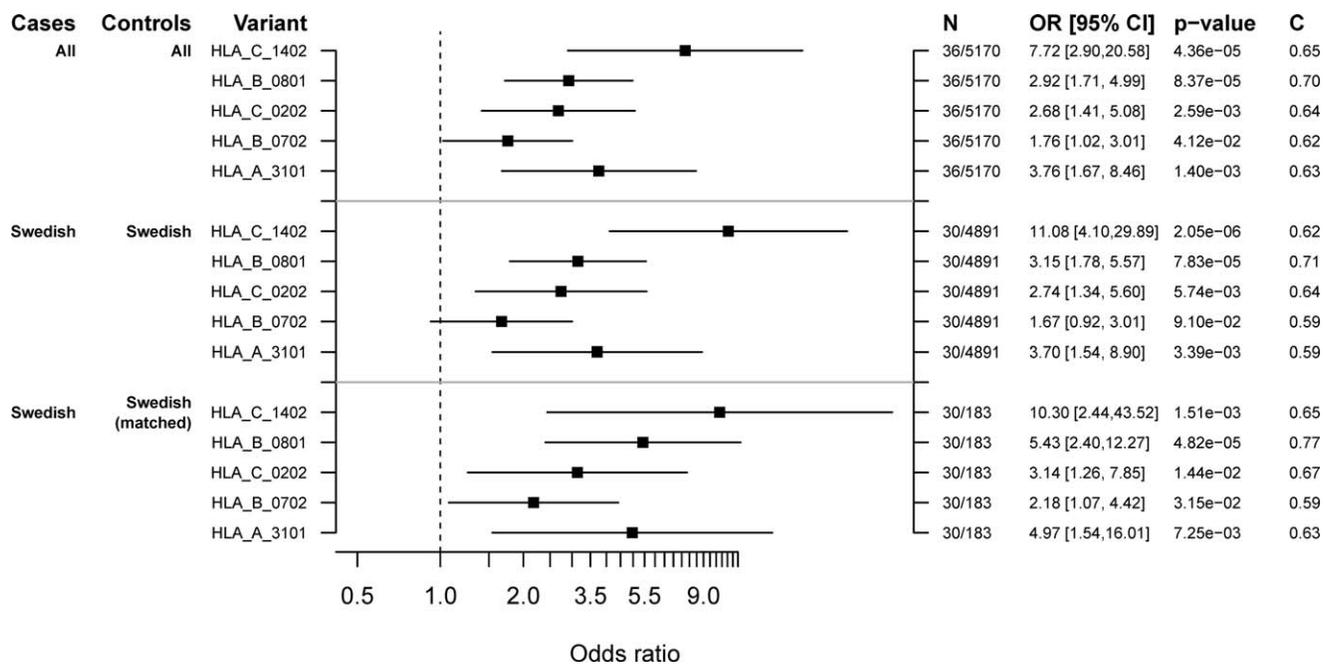


Figure 2 Forest plot of associations with HLA in the discovery cohort. Estimated odds ratio (OR) with 95% confidence intervals (CI), *P*-value and *C*-statistic for the independently associated HLA types *HLA-C*14:02*, *HLA-B*08:01*, *HLA-C*02:02*, *HLA-B*07:02*, and *HLA-A*31:01* in 1) all discovery cases and controls, 2) Swedish discovery cases and controls, and 3) Swedish discovery cases with matched controls. Matched controls were individuals who had been treated with sulfasalazine and/or had been diagnosed with inflammatory joint or bowel disease. The effect is adjusted for sex and genetic principal components 1–4. HLA = human leukocyte antigen.

molecule, while the second model proposes that the drug binds directly to the T-cell receptor or MHC molecule. In the third model, the drug binds noncovalently to the antigen-binding cleft of the HLA protein, which alters the repertoire of peptides it can bind.²⁸ This last model has been demonstrated for abacavir, a drug strongly associated with acute hypersensitivity syndrome among carriers of the *HLA-B*57:01* allele.³⁰ It is not known whether any of the proposed mechanisms explain agranulocytosis induced by sulfasalazine. There is evidence that another sulphonamide, sulfamethoxazole, triggers an immune response by binding both covalently to proteins including MHC, and noncovalently to MHC/peptide complexes.³¹

Although we found associations between sulfasalazine-induced agranulocytosis and classical *HLA* alleles, we cannot exclude influence from nearby noncoding regulatory variants. In the HLA-region, it is generally difficult to identify an actual causative variant due to a high degree of gene density and polymorphism, and extended linkage disequilibrium.^{32,33} Apart from our top hit close to *HLA-B*, a genome-wide significant association was observed in an intergenic region on chromosome 20 close to *PAX1*, a member of the paired box family of transcription factors. This infrequent variant is located in a repeat region and has no evidence of being functional in primary B cells from peripheral blood.²¹ After correcting for the top HLA hit, we found an association with a rare intronic variant in *SERINC5*, which encodes a protein that restricts human immunodeficiency virus (HIV) infectivity.³⁴ Based on imputed data from the Roadmap Epigenome project, the *SERINC5* SNP is located in a weak enhancer region in primary B cells from peripheral blood characterized by

histone 3 being monomethylated at lysine 4 (H3K4me1) and acetylated at lysine 27 (H3K27ac).²¹ Lastly, after sequentially adjusting for the other top hits, two infrequent SNPs on chromosome 1 were independently associated on a genome-wide level. However, these associations were likely to be spurious since both SNPs are in repeat regions and have no evidence of being regulatory variants in B-cells.²¹

There are several limitations of this study. First, sulfasalazine-induced agranulocytosis is a rare event, and it is difficult to identify a large enough number of cases. For the present study, cases were collected over a period of 20 years, which resulted in a total of 76 cases. Second, HLA sequencing could not be performed in the discovery phase since we did not have access to DNA from the controls. In the replication phase all cases and controls were HLA-sequenced, thus making the results more reliable. Third, several polymorphisms in the HLA loci are known to confer genetic susceptibility to inflammatory arthritis or bowel disease.³² Due to the small sample size we did not stratify by disease; however, the distribution of diseases was similar among cases and matched controls. We therefore believe that there was no confounding by indication. Fourth, the most frequent disease in our cohort, rheumatoid arthritis, is strongly associated with a subgroup of *HLA-DRB1*04* alleles, and to a lesser extent seronegative rheumatoid arthritis is associated with *HLA-B*08*.³⁵ We did not discriminate between seropositive and seronegative rheumatoid arthritis, and could not test whether serotype influenced the detected association with *HLA-B*08:01*. Fifth, the number needed to screen (NNG) for *HLA-B*08:01* and *HLA-A*31:01* to avoid one case was high, 1,500. *HLA-A*31:01* also increases

Table 3 Characteristics of the patients in the replication cohort collected in Sweden

	Cases (<i>n</i> = 40)	Controls treated ≥ 90 days (<i>n</i> = 142)	<i>P</i>
Gender, male [%]	18 [45.0]	64 [45.1]	1.00
Age, years	at agranulocytosis [%]	at enrolment [%]	
<25	4 [10.3]	8 [5.6]	0.21
25-29	0	7 [4.9]	
30-34	1 [2.6]	14 [9.9]	
35-39	2 [5.1]	11 [7.7]	
40-44	2 [5.1]	14 [9.9]	
45-49	6 [15.4]	16 [11.3]	
50-54	4 [10.3]	20 [14.1]	
55-59	2 [5.1]	14 [9.9]	
60-64	4 [10.3]	11 [7.7]	
65-69	5 [12.8]	7 [4.9]	
70-74	6 [15.4]	8 [5.6]	
>74	3 [7.7]	12 [8.5]	
Diagnosis ^a	[% of cases]	[% of controls]	
Rheumatoid arthritis	20 [50.0]	71 [50.0]	1.00
Crohn's disease	1 [2.5]	3 [2.1]	1.00
Colitis, ulcerative or unspecified	10 [25.0]	5 [3.5]	1.25 × 10 ⁻⁴
Psoriasis arthritis	2 [5.0]	18 [12.7]	0.25
Ankylosing spondylitis	0	24 [16.9]	0.07
Arthritis unspecified	6 [15.0]	22 [15.5]	1.00
Plantar fasciitis	1 [2.5]	0	0.22
Total number of diagnosis	40	143	
Mean time to onset in days [range]	43 [16-90]	—	
Mean lowest neutrophil count x10 ⁹ cells/l [range]	0.03 [0-0.5]	—	
Mean daily dose in mg ^b [range]	2062 [500-4000]	1963 [500-3000]	0.40
Cases with co-suspected drugs [%]	0	—	

Controls were patients treated with sulfasalazine for at least 90 days without reacting with agranulocytosis.

^aOne control had two diagnosis: ulcerative colitis and arthritis. ^bDose missing for four controls. Tests used: chi² test for comparisons of age, *t*-test for mean daily dose, otherwise Fisher's exact test.

Table 4 Replication of HLA types associated with sulfasalazine-induced agranulocytosis

HLA allele	<i>N</i>	<i>N</i> Case	<i>N</i> Control	MAF Case	MAF Control	OR	95% CI	C Stat	<i>P</i>
C*14:02	182	40	142	0.00	0.00	N/A			
B*08:01	182	40	142	0.16	0.09	2.25	[1.02, 4.97]	0.574	0.0439
Full haplotype	182	40	142	0.16	0.06	3.79	[1.63, 8.80]	0.606	0.0019
C*02:02	182	40	142	0.09	0.09	0.99	[0.39, 2.50]	0.501	0.9876
B*07:02	182	40	142	0.19	0.12	1.67	[0.84, 3.28]	0.571	0.1406
A*31:01	182	40	142	0.09	0.02	4.81	[1.52, 15.26]	0.566	0.0077

The HLA types were selected by sequential adjustment for each significant association in the discovery cohort. Associated HLA types were compared between replication cases and controls treated 90 days or more using logistic regression. The effect was modeled per increase of one present HLA type. The full haplotype is HLA-DQB1*02:01-DRB1*03:01-B*08:01-C*07:01.

N = number, OR = odds ratio, 95% CI = 95% confidence interval, C Stat = C statistic, N/A = not available.

the risk of carbamazepine-induced hypersensitivity or skin reaction.²⁸ Since *HLA-A*31:01* is prevalent throughout the world, and the reactions are common, only 15–43 patients starting carbamazepine need to be screened for *HLA-A*31:01* to avoid one case. There are other examples where preemptive genotyping is recommended despite a high NNG, although this is unusual.^{28,36} *HLA-B*15:02* is a strong predictor of the serious skin reactions Stevens–Johnson’s syndrome and toxic epidermal necrolysis in East Asia, where this HLA type is prevalent.²⁸ Before starting carbamazepine, patients originating from East Asia should be tested for *HLA-B*15:02*. Even in Asia, 10,000–24,665 patients need to be screened to avoid one case, due to the rarity of these serious skin reactions.

Strengths of this study are that it has a fairly large and homogeneous discovery cohort, and that the finding was replicated in a second cohort. In general, pharmacogenomic associations are robust and more likely to be translated into clinical practice than genetic associations with complex traits.³⁷ There are several reasons. First, genetic variants associated with drug-related phenotypes usually have larger effect sizes than those associated with complex disease risk. Second, pharmacogenomic variants tend to have higher allele frequencies than variants associated with complex traits. This is possibly due to the fact that complex traits have been subject to negative selection over the course of human evolution, while pharmacogenomic variants only are deleterious in the presence of a certain drug, and drug treatment is a relatively new intervention. Third, pharmacogenomic variants are more likely to be actionable, since it is easier to select an alternative drug than to modify risk factors for complex disease, such as lifestyle. Fourth, it has been predicted that before long patients will have their pharmacogenome readily available in their medical records, thus removing the necessity to order the test.³⁸

In conclusion, we have confirmed that sulfasalazine-induced agranulocytosis is associated with *HLA-B*08:01* and *HLA-A*31:01* in Europeans. The association was stronger for the *HLA-DQB1*02:01-DRB1*03:01-B*08:01-C*07:01* haplotype than for *HLA-B*08:01* alone, but the NNG did not change when using the full haplotype. Whether to use genetics in translational medicine to adapt drug treatment depends on the severity of the expected adverse drug reaction (ADR) and the existence of other treatment options.³⁶ We believe that the drug sulfasalazine fulfils these criteria, although the high NNG makes testing challenging. The solution could be to include *HLA-B*08:01* and *HLA-A*31:01* into preemptive screening programs, where multiple tests are performed at a low cost. Known carriers of *HLA-B*08:01* or *HLA-A*31:01* starting sulfasalazine could then be placed under intensified monitoring or be offered an alternative drug. This individualization would be a further step towards personalized treatment of inflammatory disease.

METHODS

Ethical statement

The study was approved by the local Ethics Committees (2008/213 and 2010/231, Uppsala, Sweden; Dec. 22, 2014, Málaga, Spain; RTF011, Barcelona, Spain; Charité-Universitätsmedizin Berlin, Germany; CPP Sud-Ouest et Outre-Mer I No. 1-09-24, Toulouse, France; and for

recruitment of Swedish controls Stockholm Dnr 2007-644-31 and 2011/463-32). Research was carried out in accordance with the latest update of the Declaration of Helsinki. Written informed consent was obtained from all participants. The study protocol has been indexed in the European Network of Centres for Pharmacoeconomics and Pharmacovigilance (ENCePP) register at www.encepp.eu (“The EuDAC Study”). Part of the replication cohort that had previously been collected for genetic studies of sulfasalazine-induced adverse reactions was approved by the Ethics Committee of the Medical Faculty, Uppsala University, Sweden (95-200 and 97-312).

Sample description

EuDAC consists of a network of investigators in Sweden, Spain, France, and Germany. The basis for case recruitment in Sweden (www.swedegene.se) and France was through nationwide spontaneous ADR reports sent from healthcare professionals to the respective national drug regulatory authority. In Spain, cases were recruited both from spontaneous ADR reports and through active surveillance at 17 hospitals in Barcelona. German cases were recruited through active surveillance at 50 hospitals in Berlin, as described.²

Each included subject was at least 18 years of age and able to give informed consent. We defined cases as patients who had developed an absolute neutrophil count of $0.5 \times 10^9/L$ or less ($\leq 500/\mu L$) during drug therapy or within 7 days of stopping medication. Each case was required to exhibit complete recovery after cessation of the drug with an absolute neutrophil count $>1.0 \times 10^9/L$ ($>1000/\mu L$) or a compatible bone marrow aspirate or biopsy. Additional inclusion and exclusion criteria have been described previously.³⁹ We collected clinical data (demographics, medical history, drug treatment history, laboratory data, and ancestry) through interviews using a standardized questionnaire, and by obtaining and reviewing medical records. At each center, cases were evaluated by at least one senior investigator, and a final adjudication of the complete dataset was performed by a specialist in hematology. Causality assessment was according to the WHO standard algorithm.⁴⁰

Overall, 243 cases were collected for the study. Seven Swedish cases and two Spanish cases were excluded after adjudication due to either exposure to chemotherapy, negative rechallenge, unknown white blood cell count, diagnosis of chronic lymphatic leukemia, or missing clinical data. No German or French case was excluded. Out of the 234 cases of drug-induced agranulocytosis fulfilling all requirements, 36 were associated with sulfasalazine, which is the focus of this study. These cases originated from Sweden ($n = 30$), Germany ($n = 3$), and France ($n = 3$), while Spain had no case induced by sulfasalazine (**Supplementary Table S1**).

Consenting population controls were available from Sweden, Spain, and Germany. In total, 5,170 controls were utilized: 4,891 unrelated individuals from the Swedish Twin Registry,⁴¹ 183 Spanish, and 96 German individuals.² Of the 183 Spanish controls, 147 had been recruited in a previous study of upper gastrointestinal bleeding,⁴² while the remaining 36 were healthy control subjects. Controls with a known history of agranulocytosis or neutropenia from any cause were excluded. Matching of controls from the Swedish Twin Registry was performed by linking with individual data from the Swedish National Patient Register, and the Swedish Prescribed Drug Register. Matched controls were those with a hospital diagnosis that is an indication for sulfasalazine treatment (data available from 1964). Diseases included were Crohn’s disease, ulcerative colitis, rheumatoid arthritis, ankylosing spondylitis, psoriasis arthritis, unspecified arthritis, and Sjögren’s syndrome. Some of these controls had also collected prescriptions of sulfasalazine (data available from July 2005). Patient characteristics were compared between discovery cases and controls using Fisher’s exact and χ^2 tests (**Table 1**).

For the replication, we used 40 cases of sulfasalazine-induced agranulocytosis and 142 controls who had been treated with sulfasalazine for a minimum of 3 months (90 days) without developing agranulocytosis (**Table 3**). Twenty-nine of the cases and all the controls had been collected previously in Sweden for genetic studies of sulfasalazine-induced adverse reactions.^{19,20} In addition, 11 new cases of sulfasalazine-induced

agranulocytosis collected in Sweden were included in the replication. All patients and controls had been treated with sulfasalazine for inflammatory joint disease, inflammatory bowel disease, or Sjögren's syndrome. Patient characteristics were compared between replication cases and controls using Fisher's exact, χ^2 and t -tests.

Power calculation

Given a genome-wide significance level of 5×10^{-8} , an ADR incidence of 0.14% (9), and using an additive genetic model, our sample size was powered to detect common genetic variants with effect sizes of clinical utility.⁴³ For example, with 36 cases and 5,000 controls, we had 80% power to detect an OR of 4 for variants with a minor allele frequency (MAF) of 40%, and 80% power to detect OR slightly above 5 for variants with an MAF of 20% (Supplementary Figure S3).

Genome-wide array data and analyses

DNA was extracted from peripheral venous blood. Thirty-three cases recruited in Sweden and France, and 147 Spanish controls were genotyped with the Illumina HumanOmni 2.5M chip (Illumina, San Diego, CA; Figure 3). The remaining 36 Spanish controls had been genotyped with the Illumina HumanOmni1-Quad 1M chip. Three cases and 96 controls from Germany were genotyped with the Illumina HumanOmniExpress 700K array, as were 4,891 controls from the Swedish Twin Registry. Genotype calls were generated using the Genome Studio software from Illumina and the Genome Reference Consortium human assembly GRCh37.

GWAS quality control (QC) and data management was performed using PLINK v. 1.9. The resulting merged data included 596,010 SNPs. Imputation of genotypes was performed using PhaseIT⁴⁴ and Impute v. 2⁴⁵ with the 1000 Genomes Project reference set (phase III, v. October 2014). The total number of SNPs after imputation was 9,380,034. All cases and controls were within the European cluster according to genetic principal component analysis (PCA) (Supplementary Figures S4, S5). Due to cases and controls being from different countries of Europe, sensitivity analyses were performed by reanalyzing each top finding in the largest group of cases and controls, which was from Sweden. See Supplementary Methods for additional details on QC, PCA, and imputation.

All genome-wide analyses were adjusted for sex and the first four principal components. SNP effects were modeled only as additive. The conventional genome-wide significance threshold $P < 5 \times 10^{-8}$ was used to correct for multiple testing.⁴⁶ Results are presented as Manhattan plots. When genome-wide significant signals were found, analyses were performed sequentially by adjusting for each genome-wide significant signal until none were left. Logistic regression was used to estimate univariate and multiple models. Genome-wide statistical analyses were performed using PLINK v. 1.9^{47,48} and individual SNPs were analyzed statistically, including LD calculation, using R 3.3.1 and the R packages rms and genetics (R Foundation for Statistical Computing, Vienna, Austria). The Q-Q plot is shown in Supplementary Figure S6.

HLA allele imputation and analysis of the discovery cohort

Imputation to first and second field resolution of 180 classical HLA alleles, amino acid residues, and individual SNPs was performed on the nonimputed merged and quality-controlled genome-wide data using the software SNP2HLA with a reference panel of 5,225 individuals.⁴⁹ Logistic regression was used to test the association between HLA types and agranulocytosis. The HLA-wide significance level was set to $0.05/180 = 2.8 \times 10^{-4}$. When HLA-wide significant signals were found, analyses were performed sequentially by adjusting for each HLA-wide significant signal until none remained. To avoid confounding by indication, top HLA signals were tested using a cohort of cases and controls matched for sulfasalazine treatment and/or inflammatory joint or bowel disease that was available from Sweden.

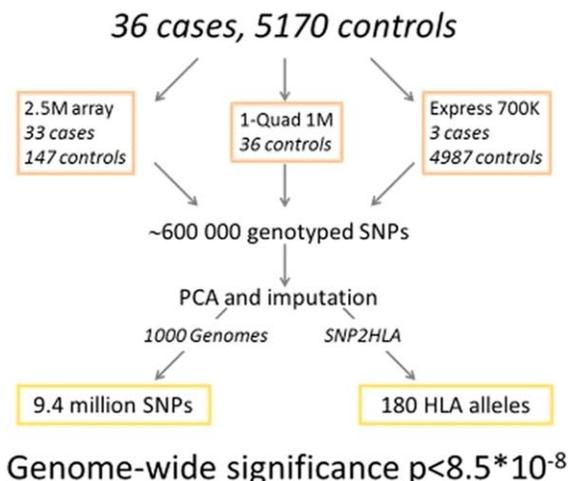


Figure 3 Study design. Design of the EuDAC study on sulfasalazine-induced agranulocytosis.

HLA sequencing of the replication cohort

For the replication cohort, HLA sequencing of HLA A, B, C, DP, DQ, and DR was performed on MiSeq (Illumina) as previously described by Cereb *et al.*⁵⁰ The top HLA types were obtained by sequential adjustment for each significant HLA type in the discovery cohort. These five HLA types were tested for statistical associations, thus correction for five multiple tests was performed ($P < 0.01$).

Analysis of predictive ability

The predictive ability of logistic regression models for selected HLA analyses was expressed as the C-statistic (equivalent to the area under the receiver operating characteristic curve), which is a measure of the ability of the model to discriminate between cases and controls. A C-statistic of 0.5 indicates predictive ability similar to chance (a 50:50 likelihood of predicting the outcome), while 1 indicates perfect discrimination. The number needed to genotype (NNG) to avoid one case was estimated from the reciprocal of the predicted absolute risk reduction, where the absolute risk reduction is calculated as the prevalence (adverse drug reaction in the population) \times the sensitivity of the diagnostic test.

SUPPLEMENTARY MATERIAL is linked to the online version of the article at <http://www.cpt-journal.com>

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CONFLICT OF INTEREST

The authors declare no conflicts of interest.

AUTHOR CONTRIBUTIONS

M.W., N.E., R.K., L.I., M.I.L., M.M., P.K.E.M., M.B., and P.H. wrote the article; M.W., N.E., R.K., E.B-G., L.I., A.C., M.I.L., M.M., Q-Y.Y., and P.H. designed the research; M.W., N.E., R.K., E.B-G., L.I., A.C., M.I.L., E.S.P., M.M., J.M., T.A., H.K., Q-Y.Y., P.K.E.M., M.B., and P.H. performed the research; M.W., N.E., M.B., and P.H. analyzed the data.

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