Genetic Polymorphisms and Toxicities of First-Line Antituberculosis Drugs: Systematic Review of the Literature

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Abstract

Introduction: Polymorphisms are the main genetic factors associated with toxicities of antituberculosis drugs. This literature review summarizes the polymorphisms of the genes that code for the enzymes of the metabolism of antituberculosis drugs and their transmembrane transporters. Some mechanisms of drug-associated toxicities and strategies for their management have also been described in this review. Methods: The bibliographic searches were exclusively carried out in PubMed, over a period of ten years (2010-2020). The search terms were the words "toxicity + antituberculosis drug + one or two word(s) among the following: polymorphism, genetics, mutation, SNP, HLA or haplotype". Publications in English or French, relating to the various toxicities associated with first-line anti-tuberculosis drugs (Rifampicin, Isoniazid, Ethambutol and Pyrazinamide) administered to patients with pulmonary tuberculosis, extrapulmonary tuberculosis or co-infected with TB/HIV were included in this review. Duplicates, in vitro, in silico or drug-induced toxicity studies other than antituberculosis drugs and genetic mutations of Mycobacteria strains were not included. Results: The studies selected and included were case reports, cohort studies, original studies, systematic reviews and meta-analyses on human subjects of different ethnic origins. Hepatotoxicity is the most common toxicity associated with NAT2, CYP2E1, GSTM1 and GSTT1 polymorphisms in patients on antituberculosis drugs. Other forms of toxicity, less frequent, occurring in certain patients under concomitant treatment with nonsteroidal anti-inflammatory drugs (NSAIDs), antiretrovirals (ARVs), antibiotics or antiepileptics have also been identified. Conclusion: The genetic polymorphisms associated with the toxicities of antituberculosis drugs concern both the main enzymes of the metabolic pathways (NAT2, CYP2E1, GST) and the transmembrane transporters (SLCO1B1 and ABCB1). Other genetic
polymorphisms (**TXNRD1**, **SOD2**, **TYMP**) have been suspected but their mechanisms are not yet well understood.

**Keywords**
Polymorphism, Genetics, SNP, Toxicity, Rifampicin, Isoniazid

### 1. Introduction

Tuberculosis (TB), a disease caused by Mycobacterium tuberculosis, is the second leading cause of death by infectious disease in adults after HIV/AIDS [1]. According to the current recommendations of the World Health Organization (WHO), the first-line treatment of drug-susceptible TB is a combination chemotherapy of four anti-TB drugs (Rifampicin, Isoniazid, Ethambutol and Pyrazinamide) [1]. Despite its effectiveness, this polychemotherapy has adverse effects that are sometimes serious, mainly occurring during the first trimester of treatment. These side effects can also have a major impact on the outcome of patients’ TB treatment [2].

Multidrug therapy for tuberculosis would increase the risk of serious adverse reactions such as hepatotoxicity, gastrointestinal disorders, allergic reactions, arthralgia, neurological disorders and other symptoms [3]. Drug-induced hepatic lesions are the most frequent and most severe encountered during the first trimester of tuberculosis treatment [3]. Among these hepatic lesions, hepatotoxicity could lead to early discontinuation of treatment, thus compromising the effectiveness of tuberculosis control [3]. About 60% of patients on anti-tuberculosis have adverse reactions, one third of which are related to immune sensitization [2]. These cause pressure on health care providers due to their high morbidity, mortality, and increased treatment costs [4].

Depending on the treatment regimen and patient characteristics, the incidence of hepatotoxicity is 2% - 28% [4]. It is manifested by clinical signs (jaundice, gastralgia, nausea, vomiting) associated or not with biological signs (elevation of transaminases > 2 the upper limit of normal values (ULN), elevation of total bilirubin, Gamma-GT and alkaline phosphatase) [5]. Clinical characteristics (HIV status, gender, extrapulmonary tuberculosis), genetic polymorphisms, co-infections with hepatitis B and C viruses as well as certain concomitant treatments constitute high risk factors for liver toxicity during anti-tuberculosis treatment [5] [6] [7].

Isoniazid is the most hepatotoxic major anti-tuberculosis drug but also the most widely used as monotherapy for anti-tuberculosis chemoprophylaxis in non-active tuberculosis patients or in combination with Rifampicin, Pyrazinamide and Ethambutol for the treatment of drug-sensitive tuberculosis. It is mainly responsible for hepatotoxicity associated with polymorphisms of the genes that code for its metabolizing enzymes and/or its transmembrane trans-
porters [5]. These enzymes are N-acetyltransferase 2 (NAT2), cytochrome P450 2E1 (CYP2E1), Glutathione-S-Transferase Mu 1 (GSTM1) and Theta 1 (GSTT1) [4]. The activation capacities of these enzymes are affected by polymorphisms which can alter the chemical composition of antituberculosis drugs and their metabolites in the liver, subsequently causing adverse hepatic effects [4].

Numerous publications have shown that genetic factors constitute one of the main causes of the variability of responses to antituberculosis treatment. According to the first studies conducted in Africa, these genetic factors are very heterogeneous within the populations studied, justifying the need to conduct new studies to identify these genetic factors, determine their frequency and better understand the mechanisms of their involvement in variations in therapeutic responses. This systematic review made it possible to identify the most frequent genetic factors: genetic polymorphisms, haplotypes, genetic associations and gene-environment interactions.

The objective of this review was to summarize the genetic polymorphisms associated with the different toxicities of first-line antituberculosis drugs. Molecular mechanisms of action and strategies for the management of toxicities will also be presented in this review.

2. Methodology

2.1. Bibliographic Research Strategy

The bibliographic search was carried out in PubMed, over a period of ten years (2010-2020). The terms used were the words “toxicity + antituberculosis drug + one or two word(s) among the following: polymorphism, genetics, mutation, SNP, HLA or haplotype”.

2.2. Inclusion Criteria

The publications included were in English or French, relating to all the toxicities associated with first-line antituberculosis drugs administered to patients with pulmonary tuberculosis, extra-pulmonary tuberculosis or co-infected with TB/HIV. For publications concerning tuberculosis patients who received in addition to first-line anti-tuberculosis drugs, antiretrovirals or other drugs (antibiotics, non-steroidal anti-inflammatory drugs, antiepileptics, etc.), the inclusion depended on the relevance of the evidence of the imputability of toxicity to anti-tuberculosis treatment. For example, occurrence of toxicity after initiation of anti-TB treatment, favorable outcome after discontinuation of anti-TB treatment or after Pyridoxine supplementation, patients with genetic polymorphisms identified in previous studies and associated with toxicity tuberculosis drugs, etc.

2.3. Exclusion Criteria

The publications excluded were duplicates, studies of toxicity in vitro, in silico or induced by drugs other than antituberculosis drugs, genetic mutations of strains of Mycobacteria (Figure 1).
3. Results and Discussion

3.1. Characteristics of Selected Studies

The studies selected were conducted in several countries, included at least one patient (cases reports studies) or several hundred (cases-controls, retrospective, or prospective studies), and the polymorphisms were genotyped by a range of molecular techniques (Table 1).

3.2. Toxicities of Anti-Tuberculosis Drugs

Rifampicin, Isoniazid and Pyrazinamide toxicities occur during the intensive phase of anti-tuberculosis treatment [6] [8]. Isoniazid-associated hepatotoxicity is the most frequent and its mechanisms are fairly well known, having been the subject of numerous studies [9]-[13]. Despite its hepatotoxicity, isoniazid is still widely used because it is inexpensive and has potent anti-mycobacterial activity [14].

The toxicities of Rifampicin and Pyrazinamide are unpredictable and their mechanisms less well understood than those of Isoniazid [4]. Finally, toxicities associated with Ethambutol have been rarely described because evidence of its imputability is non-existent or still insufficient [4].
Table 1. Characteristics of selected studies.

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\(^a\) Non-steroidal anti-inflammatories, \(^b\) Denaturing High Performance Liquid Chromatography (DHPLC).

3.3. Genetic Polymorphisms of Metabolizing Enzymes

3.3.1. CYP2E1 Polymorphisms (Cytochrome P450 2E1)

CYP2E1 is an enzyme involved in phase I of isoniazid metabolism [5]. This enzyme leads to the formation of metabolites among which, the more reactive hydrazine, potentiates the direct toxicity of isoniazid.

CYP2E1 polymorphisms have been associated with hepatotoxicities including isoniazid (INH)-induced hepatitis [5]. The c1/c2 genotype of CYP2E1 polymorphisms (CYP2E1 c1/c2) and those of NAT2 were also associated with the development of severe polyneuropathy (PNP) in a 23-year-old man who received INH-containing therapy [15]. Indeed, during his treatment, laboratory results had shown incipient liver and kidney damage [15]. Later, the genetic analyzes carried out revealed the existence of these two polymorphisms in the patient [15].

CYP2E1 has been associated with isoniazid-induced hepatotoxicity due to its
ability to activate acetylhydrazine, subsequently forming various hepatotoxins [16]. There is evidence associating CYP2E1 levels with interindividual variation [16]. The CYP2E1*5 allelic variant is common in Japanese (Frequency 0.27) but rare in Europeans (Frequency 0.02). Isoniazid’s toxic metabolites can also cause other toxicities such as peripheral neuropathy and maculopapular rash [4].

Isoniazid hepatotoxicity was significantly associated with the CYP2E1 RsaI polymorphism and the 96 bp deletion-insertion single nucleotide polymorphism of the CYP2E1 gene [1]. Patients with a homozygous or heterozygous mutant genotype for the CYP2E1 RsaI polymorphism are less likely to present with hepatotoxicity compared to homozygous wild-type patients [1]. On the other hand, the CYP2E1 DraI and PstI polymorphisms are not significantly associated with isoniazid-induced hepatotoxicity [1].

In the absence of discontinuation of antituberculosis treatment, hepatotoxicity can lead to death in 6% to 12% of cases [1].

According to Wang et al., the CYP2E1 c1/c1 genotype significantly increases the risk of isoniazid-induced hepatotoxicity [1]. Isoniazid reactive metabolites destroy hepatocytes by directly interfering with cellular homeostasis or by triggering immunological reactions [17].

The hepatic enzyme CYP2E1 is thought to be involved in the metabolism of Rifampicin [18]. Indeed, its polymorphisms have been associated with elevated plasma concentrations of Rifampicin in poor CYP2E1 metabolizers [18]. Some TB patients who were extensive metabolisers had higher hepatic cytolysis (ALT, AST) and biliary stasis (Gamma-GT) indices compared to poor metabolisers before and after hospital treatment [18].

CYP2E1 polymorphism is a genetic marker of susceptibility to hepatotoxicity before and during antituberculosis treatment [18]. However, Xiang et al. found no association between hepatotoxicity and CYP2E1 RsaIc1/c1, CYP2E1 RsaIc1/c2, or c2/c2 polymorphisms [3].

The pathogenetic mechanism of antituberculosis drug-induced hepatotoxicity is still unclear. A better understanding of this mechanism would help guide the medical approach for rapid and optimal patient care. The combination of Isoniazid and Pyrazinamide would increase the risks of hepatotoxicity from Isoniazid. It is therefore possible that there is a drug interaction potentiating the hepatotoxicity of isoniazid.

Hepatotoxins (Hydrazine or acetylhydrazine) generated by CYP2E1 or NAT2 are detoxified after conjugation by Glutathione S-Transferases (GSTM1 and GSTT1) in the liver [3]. Acetylhydrazine can also be detoxified after a second acetylation by NAT2 forming diacetylhydrazine, a non-toxic metabolite of isoniazid. Antituberculosis metabolizing enzymes are polymorphic and their distribution varies according to ethnic groups [3].

The heterozygous CYP2E1 c1/c2 genotype would contribute to a high risk of hepatotoxicity [19]. On the other hand, the absence of the “c2” allele in women would be a protective factor against the onset of hepatotoxicity, while in men,
the presence of the “c1/c2” allele would contribute to a high risk of onset. hepatotoxicity [19].

In CYP2E1, two polymorphisms are most commonly studied (RsaI/PstI (rs-2031920/rs3813867) and Dral (rs6413432). A recent meta-analysis revealed that the RsaI/PstI c1/c1 polymorphism confers a higher risk of hepatotoxicity induced by Isoniazid compared to c1/c2 or c2/c2 genotypes, but no increased risk of Dral polymorphism [20]. Isoniazid may also cause peripheral neuropathy in some patients during treatment [21].

CYP2E1 could be a good genetic marker of isoniazid-induced hepatotoxicity but larger studies are needed to validate its relevance as a risk factor [16].

3.3.2. Polymorphisms of NAT2 (N-Acetyltransferase Type 2)
NAT2 is one of the phase II enzymes that plays an essential role in the detoxification and metabolism of several environmental toxins and many drugs including Isoniazid [17] [22] [23]. It is the main cause of toxicity of antituberculous drugs in patients carrying mutations [24]. It is mainly found in the liver and intestine [25].

The NAT2 enzyme is encoded by the highly polymorphic NAT2 gene with 108 haplotypes in the general population [26]. NAT2 polymorphisms are responsible for a tri-modal distribution of isoniazid pharmacokinetics [27]. Thus, a distinction is made between slow, intermediate or normal and fast acetylators [27]. Slow acetylators are at risk of hepatotoxicity while fast acetylators face treatment failure [27]. The seven most common NAT2 polymorphisms are located at its exon 2 [26].

About 35 different NAT2 alleles have been reported in the Indian population [28]. The NAT2*4 allele has historically been referred to as “wild type” because it is most common in certain ethnic groups [28]. The NAT2 polymorphisms allowed to distinguish 3 phenotypes of acetylators: the fast acetylators (Homozygotes having two fast alleles), the intermediate acetylators (Heterozygote having a fast allele and a slow allele) and the slow acetylators (Homozygotes, having two slow alleles) [28]. Of these three acetylator phenotypes, the slow acetylator phenotype is clinically the most important [28]. On the other hand, in TB/HIV co-infected patients, there would be a discrepancy between the genotype and the NAT2 acetylator phenotype [28].

The combination of the slow acetylator profile and the c2 variant of the CYP2E1 gene is responsible for an increase in the hepatotoxicity of antituberculosis drugs [29]. A case of isoniazid-induced polynuropathy has been reported in a 23-year-old patient, carrier of NAT2 and CYP2E1 mutations [15].

Renal failure is also a risk factor for isoniazid-induced hepatotoxicity [14]. In addition, other toxicities linked to the existence of a co-morbidity can also occur during the antituberculous treatment associating isoniazid. Thus, a severe case of encephalopathy was reported in a 71-year-old patient of African origin after being put on anti-tuberculosis treatment [14].

In hemodialysis patients and carriers of the slow isoniazid acetylator pheno-
type, a reduction in the dosage of isoniazid associated with an increase in the
doses supplemented with Vitamin B6 or Pyridoxine (>100 mg/day instead of 10-
25 mg/day) reduce the occurrence of hepatotoxicity, encephalopathy and neu-
rupathy [14].

Isoniazid hepatotoxicity occurs by a molecular mechanism that depends on
the presence of active alleles of the NAT2 gene (NAT2*4 and NAT2*12) [14].

In a study conducted in 2020 by Zahra et al., four new haplotypes NAT2*5TB,
NAT2*5AB, NAT2*5ZA and NAT2*6W corresponding to the slow acetylator
phenotype were identified [25]. The most frequent single nucleotide polymo-
rphisms and haplotypes in the participants of this study were NAT2 803 A > G
(0.510) and NAT2 341T > C (0.427), respectively, then NAT2*6C (25.00%) and
NAT2*5A (22.92%) corresponding to the slow acetylator phenotype [25].

The effectiveness of isoniazid-based chemotherapy depends on the acetylator
status or phenotype and the patient’s medical condition [27]. Yet, a standard
FDA-recommended dose is administered regardless of acetylator phenotype or
immune status resulting in adverse effects occurring in 5% - 33% of patients [27].
Specific dose adjustments according to acetylator phenotype have been suggested
to ensure optimal treatment results [27]. Thus, a reduced dose administered to
slow acetylators significantly reduces exposure to toxic metabolites and therefore
the risk of adverse events, while maintaining sufficient treatment efficacy [27].

In contrast, intermediate and rapid acetylators receive higher doses of isoniazid
on a twice-daily schedule [27].

Slow acetylator phenotype, CYP2E1 c2 or A4 variant genotype, and female
gender are significantly associated with anti-TB drug-induced hepatotoxicity
in some TB patients [29]. Patients with the slow acetylator profile and the c2 va-
riant are more at risk of developing hepatotoxicity [29]. In some patients carry-
ing the GSTT1 and CYP2E1 polymorphisms, there is a synergistic interaction
leading to epistaxis and increasing the risk of hepatotoxicity [29].

The increase in plasma concentrations of isoniazid following accumulation by
slow acetylators exposes them to toxic effects, in particular hepatotoxicity [4]. It
may also benefit the therapeutic efficacy of isoniazid [4]. On the other hand, in
fast acetylators, the plasma concentrations of isoniazid are lower with the con-
sequences of the absence of toxicity, the reduction of the efficacy of the drug, the-
rapeutic failure and the appearance of resistant strains of mycobacteria [4]. Fast
acetylators are homozygotes of the NAT2*4, NAT2*11A, NAT2*12A, NAT2*12B,
NAT2*12C or NAT2*13 alleles. On the other hand, heterozygous subjects or
 carriers of the wild-type allele are respectively intermediate or slow acetylators
[4].

Isoniazid has been associated with a case of severe encephalopathy in a chronic
hemodialysis patient [14]. Investigations revealed that he had a slow acetylator
phenotype and that Pyridoxal phosphate, the active metabolite of Pyridoxine
used for supplementation, would have been removed by dialysis [14]. The risk of
isoniazid toxicity is high in hemodialysis patients with NAT2 polymorphisms
The incidence of hepatotoxicity induced by antituberculosis drugs including isoniazid ranges from 1% to 36%, and mortality in such cases is not uncommon [30]. NAT2 exhibits a hereditarily determined polymorphism [30].

There are approximately 36 NAT2 polymorphisms reported in the literature [17]. Fast acetylators metabolize INH five to six times faster than slow acetylators [17].

The slow C 481 A 590 G 857 haplotype and an intermediate acetylator T 481 A 590 G 857 haplotype have been associated with the development of hepatotoxicity [19].

NAT2 genotypes (NAT2*5/*5, NAT2*5/*6, NAT2*6/*6 and NAT2*6/*14) corresponding to the slow acetylator profile are very frequent in certain countries such as Morocco (78%) [31].

The major NAT2*4 haplotype would protect against hepatotoxicity [32]. The increased susceptibility to Isoniazid (INH)-induced hepatotoxicity due to the presence of NAT2 polymorphism has been demonstrated in the West Indian population [32].

The prevalence of isoniazid-induced hepatotoxicity was higher in men than in women, and there was a weak association with NAT2*5 genotypes [3]. In Uyghur tuberculosis patients in Xinjiang, China, liver damage has been associated with the NAT2*5 genetic variant [3].

Multidrug therapy for tuberculosis increases the risk of serious adverse drug reactions such as hepatotoxicity, gastrointestinal disorders, allergic reactions, arthralgias, neurological disorders and other symptoms [3]. Hepatotoxicity results from the production of toxic metabolites associated with the presence of hepatic enzyme polymorphisms [3].

Several candidate single nucleotide polymorphisms have been identified but their clinical utility in predicting isoniazid-induced hepatotoxicity remains uncertain [20]. The NAT2 polymorphisms rs1041983 and rs1495741 have been associated with isoniazid hepatotoxicity in a Singaporean population and have demonstrated clinical utility in the prediction of INH-induced hepatotoxicity [20].

Isoniazid can cause asymptomatic elevation of liver enzymes in 10% - 20% of patients on treatment, clinically significant hepatitis, or even in less than 1% of cases, acute liver failure [21]. Risk factors associated with Isoniazid hepatotoxicity are age, female gender, black race, alcoholism, liver disease, and concurrent use of other drugs such as Rifampin and Pyrazinamide [21]. The molecular mechanisms of isoniazid hepatotoxicity are not yet well understood, but the accumulation of toxic intermediate metabolites is thought to play an important role [21]. From another point of view, pharmacogenetic studies have so far only focused on the main enzymes (NAT2, CYP2E1 and GST) directly involved in the metabolism of isoniazid [21].

Isoniazid hepatotoxicity usually occurs between 2 weeks and 6 months after
the start of treatment. The late onset of isoniazid hepatotoxicity indicates the existence of an immunological mechanism that may involve the antioxidant and detoxification pathway genes, the human leukocyte antigen (HLA) system and tumor necrosis factor-α (TNF-α) [21].

Of the many NAT2 polymorphisms, seven alleles (rs1801279, rs1041983, rs1801280, rs1799929, rs1799930, rs1208, and rs1799931) define 34 haplotypes, but most studies consider only a subset to determine the acetylator phenotype of patients [21]. A novel NAT2 polymorphism rs1495741 has recently been associated with isoniazid hepatotoxicity, although it may not be a good marker for determining the acetylator phenotype of patients [21].

Reactive metabolites of isoniazid may cause peripheral neuropathy or maculopapular eruptions [4].

NAT2 polymorphisms have also been associated in some studies with bladder cancer, colorectal cancer, rheumatoid arthritis, and diabetes mellitus [25].

In addition to genetic polymorphisms, environmental factors and concomitant drug intake can modulate the activity of antituberculosis metabolizing enzymes [28]. Thus it has been reported that Isoniazid would cause the decrease in the clearance of many drugs such as Phenytoin, Carbamazepine, Diazepam, Vin-cristine, and Acetaminophen. [28]. For example, in patients with tuberculous meningitis or tuberculoma having convulsions, the simultaneous use of Isoniazid and Phenytoin leads to an increase in plasma concentrations of the latter and the appearance of its intoxication [28].

It is important to determine the phenotypic status of patients before starting them on an antituberculcore treatment regimen including isoniazid [26]. NAT2 genotyping could serve as a marker for the identification of patients predisposed to hepatotoxicity of antituberculosis drugs [32].

3.3.3. Polymorphisms of GSTs (Glutathione S-Transferases)

GSTs represent a superfamily of enzymes involved in phase II reactions in the metabolism of many drugs, including antituberculosis drugs [33]. They play a protective role in the processes of biological detoxification of drugs by catalysing the conjugation reactions of Glutathione and toxic intermediate metabolites, subsequently facilitating their elimination and then reducing their hepatotoxicity [33]. They exist in two forms (oxidized and reduced) and are involved in maintaining the redox potential of the cytoplasm of hepatic cells [34].

GSTs hydrolyze acetylhydrazine, the hepatotoxic metabolite of isoniazid [29]. These enzymes detoxify a variety of drugs by conjugation with glutathione. They also play a role in the detoxification of the products of oxidative stress [16].

The GSTM1 and GSTT1 isoforms are absent in several individuals because of the large genetic deletions resulting in null genotypes. Carriers of these null genotypes have no functional enzymatic activity and do not express the proteins [34]. It is possible that the GSTM1 and GSTT1 genotypes influence the risk of isoniazid-induced hepatotoxicity. Several independent studies have found an association between GSTM1 null genotypes and hepatotoxicity [35] [36]. The re-
suits of these studies had demonstrated that the frequencies of GSTM1 null genotypes were higher among the cases of hepatotoxicity in contrast to the controls [35] [36].

GST deficiency is due to mutations in the Glutathione S-Transferase Mu 1 (GSTM1) and Glutathione S-Transferase Theta 1 (GSTT1) null genes [29]. The genetic polymorphisms frequently associated with the toxicity of antituberculosis drugs are those of the genes Glutathione S-Transferase Mu 1 (GSTM1), Glutathione S-Transferase Theta 1 (GSTT1), and Glutathione S-Transferase Pi 1 (GSTPI) [5] [35] [37] [38]. However, deletions of the GSTM1 and GSTT1 genes are not associated with drug toxicity [39]. The high frequencies of deletions of the GSTM1 and GSTT1 genes in human populations would explain the interindividual variability of the metabolism of xenobiotics [5].

Null genotypes of the GSTM1 and GSTT1 genes are risk factors for hepatocellular carcinoma [40]. Indeed, these genes would be involved in the mechanisms of detoxification of environmental carcinogens, environmental toxins and radicals resulting from oxidative stress [40]. GST genes in the occurrence of hepatotoxicity and schizophrenia in patients on antituberculosis drugs has been reported [41]. In the Iranian population, the distributions of genetic polymorphisms of GSTT1 are more significant than those of other GSTs [42]. GSTM1 and GSTT1 gene deletions (42.9% and 12.4% respectively) in Brazilian populations, these are not associated with the toxicity of antituberculosis drugs [5]. However, this mutation has no influence on drug response [5].

There is a synergistic interaction between the GSTT1 and CYP2E1 genes associated with an increased risk of anti-TB drug-induced hepatotoxicity [29]. Isoniazid inhibits CYP2E1 activity less in individuals carrying the CYP2E1 *1A/*1A genotype compared to other genotypes [4]. Therefore, people carrying the CYP2E1 *1A/*1A genotype would have higher CYP2E1 activity, which leads to the formation of a greater amount of hepatotoxins [4]. Rifampicin and Pyrazinamide have also been associated with hepatotoxicity of antituberculosis drugs [4]. However, their mechanisms are still unknown and unpredictable. OATP1B1 transmembrane transporter polymorphisms have been associated with rifampicin toxicity [4]. Several studies have shown that if GST is not expressed, there will be an accumulation of reactive metabolites, which increases their interactions with cellular macromolecules [17].

East Asian patients carrying a GSTM1 null genotype have a higher risk than Caucasians, while Caucasians carrying a homozygous GSTT1 null genotype are at higher risk of hepatotoxicity unlike Asian patients. GST polymorphisms are highly variable depending on the ethnic groups and the age of the patients [33]. The association between GSTM1/GSTT1 null mutations and an increased risk of anti-TB drug hepatotoxicity has been demonstrated in adults. On the other hand, in children, there would be no significant association.

3.3.4. Polymorphisms of UGTs (UDP-Glucuronosyl-Transferases)

UDP-Glucuronosyl-Transferases (UGT) are phase II enzymes in the metabolism
of certain drugs, including isoniazid. They are responsible for the glucuronida-
tion of endobiotics and xenobiotics [43]. These enzymes are often considered
detoxifiers although they also have roles in the formation of reactive interme-
diates such as acylglucuronides, responsible for hepatotoxicities [16].

UGT1A1 polymorphisms lead to detoxification deficit of free bilirubin and
organic anions such as Rifampicin [43]. These genetic mutations are responsible
for a double toxicity on the one hand due to the accumulation of free bilirubin
and on the other hand, by default of elimination of the metabolites of Rifampi-
cin. The heterozygous variants UGT1A1*27 and UGT1A1*28 would be associated
with a high risk of hepatotoxicity in Taiwanese patients [43].

Rifampicin can induce cytochrome P450 3A4 and increase the formation of a
by-product, 6-Alpha-hydroxylated bile acid requiring UGT for glucuronidation
before renal excretion [43].

Subject to confirmation of this association by studies on a larger number of
patients, screening for UGT1A1 polymorphisms before treatment for tubercul o-
sis may reduce the incidence of ATDH and improve compliance with treatment
[43].

3.4. Polymorphisms of Transmembrane Transporters

Transporters are membrane proteins whose main function is to facilitate the
flow of molecules into or out of cells [44]. They are also involved in the bioavail-
ability, therapeutic efficacy and pharmacokinetics of various drugs [44]. There
are many genetic polymorphisms of the two main families of ABC and SLC
transporters.

Polymorphisms and haplotypes of the genes coding for these transporters do
not lead to drug-induced hepatitis in Korean patients on antituberculous drugs
[45].

3.4.1. P-Glycoprotein Polymorphisms

P-glycoprotein is a transmembrane efflux pump whose synthesis is encoded by
the ABCB1 gene, the polymorphisms of which are responsible for resistance to
drugs transported by this protein [46]. Among these drugs, resistance to Rifam-
picin and Ethambutol has not yet been fully elucidated [46]. However, findings
from some studies associate ABCB1 polymorphisms and other risk factors with
Ethambutol resistance [46]. It should be noted that these resistances are not al-
ways of bacterial origin but sometimes linked to the host [46].

3.4.2. MRP2 Polymorphisms

MRP2 or multi-drug resistance protein 2 is a transmembrane protein whose
synthesis is encoded by the ABCC2 gene. This protein transports bilirubin out of
liver cells and into bile.

More than 40 ABCC2 polymorphisms have been associated with Dubin-John-
son syndrome. It is a disease characterized by yellowing of the skin and the whites
of the eyes, which usually appears in adolescence or early adulthood. The major-
ity of mutations are single nucleotide polymorphisms that alter a single amino acid in the primary sequence of the MRP2 protein.

3.4.3. OATP1B1 Polymorphisms
The SLCO1B1 gene (Solute Carrier Organic Anion transporter family member 1B1) codes for the synthesis of a transmembrane protein, the organic anion transporter polypeptide 1B1 (OATP1B1). This protein present in the hepatocyte ensures the transport of endogenous substances (bilirubin, hormones, various toxins, etc.) and xenobiotics (statins, antihypertensives, anticancer drugs, antibiotics, etc.) from the blood to the liver for their elimination. SLCO1B1 polymorphisms have been associated with impaired transport functions of the OATP1B1 protein. This is because the mutated protein produced is less efficient in transporting compounds through the liver, leading to elevated levels of compounds in the body. Certain SLCO1B1 polymorphisms are implicated in Rotor syndrome manifesting as elevated levels of bilirubin in the blood. In some cases, the disease is caused by a deletion that removes parts of the SLCO1B1 gene so that no functional OATP1B1 protein is produced. Genetic polymorphisms of this transporter are associated with rifampicin toxicity [4]. However, the scientific evidence for this association is still insufficient.

3.5. HLA Polymorphisms
They are mainly responsible for the occurrence of allergic reactions and other undesirable effects during anti-tuberculosis treatment. Many HLA alleles have been associated with hepatotoxicity of antituberculosis drugs in tuberculosis patients or patients co-infected with TB/HIV [47]. For example, the HLA-DBQ1*0201 allele is associated with hepatotoxicity of antituberculosis drugs in some Indian patients [16].

The strongest associations were observed with HLA class I and II genes. The mechanism underlying the association of HLA polymorphisms with antituberculosis drug toxicity could involve T cell responses to drug-protein adducts or drug alone, but requires further investigation.

Antituberculosis drug toxicity reactions can be classified into immune-mediated toxicity and non-immune-mediated toxicity [16]. In humans, these two toxicities are encoded by the Major Histocompatibility Complex located on chromosome 6, in a highly polymorphic region of the genome [16]. Immune-mediated liver toxicity reactions may involve the formation of a covalent complex between the drug or its metabolite and cellular proteins. This complex will then be presented to T cells by the particular HLA molecules resulting in an inappropriate local response that can subsequently cause cellular damage [16]. Drugs can also interact directly with HLA molecules and induce a T cell response without initial formation of a covalent complex.

In general, HLA associations are an important component of genetic susceptibility to drug-induced hepatotoxicity. However, it is possible, as in the hepatotoxicity of isoniazid, that the association is weakly significant, as is the case in
Indian patients carrying the HLA-DQB1*0201 allele [16]. It is therefore possible that some additional factors or other genes add to the HLA to contribute to the genetic susceptibility to anti-TB drug hepatotoxicity.

Some TB/HIV co-infected patients carrying the HLA-B*57 alleles (B*57:03 and B*57:02) are likely to develop cholestatic-type hepatotoxicity induced by antituberculosis drugs and ARVs [48].

Antituberculosis drugs can also be responsible for severe adverse cutaneous effects, the prevention and confirmation of which are difficult [49]. HLA-B alleles have been associated with the occurrence of these adverse effects [49].

HLA-B pre-screening can only identify a small minority of subjects at risk of developing severe cutaneous adverse effects. On the other hand, the cells releasing the specific IFN-γ of the antituberculosis drug are detectable in approximately half of the patients. Identifying the anti-tuberculosis drug responsible for the side effects requires the search for new strategies for better prevention [49].

Some severe adverse skin reactions are life-threatening. These include acute generalized pustular exanthematous reactions, drug reactions with eosinophilia and systemic symptoms, Stevens-Johnson syndrome (SJS) and toxic epidermal necrosis (TEN) [49].

Several studies have shown that HLA-B alleles are strongly associated with an elevated risk of drug-induced adverse skin effects [49]. HLA-B screening genotyping may be beneficial in preventing these HLA-B allele cutaneous adverse effects. However, it should be noted that systematic HLA-B pre-screening before the prescription of certain drugs in high-risk populations has not yet been approved by a working group of experts.

The tools currently available for the identification and confirmation of the suspected drug, the skin test and the lymphocyte transformation test (LTT), are only recommended for patients after remission from a drug allergy episode [49]. Use of the enzyme immunoassay ELISpot can be considered as is the case in patients who have presented with a maculopapular exanthema or an anaphylactic reaction due to the use of certain anti-infectives (Amoxicillin, Cephalosporins, etc.) [49]. Indeed, this test, which can be performed during the acute stage of drug allergy, has shown a higher sensitivity than LTT and a positive response even in patients who were taking immunosuppressive drugs [49].

3.6. Haplotypes

A haplotype of NAT2 polymorphisms was identified in a 71-year-old patient, on hemodialysis, of African origin, in whom severe encephalopathy occurred after taking isoniazid [14]. This is the only case reported in one of the articles in this literature review. It is quite possible that other cases have not been published or that they have been reported in a journal not indexed in the PubMed bibliographic database that we used exclusively for this study.

Rifampicin liver toxicity has been associated with the OATP1B1*15 haplotype identified as an important risk factor [1].
3.7. Other Genetic Polymorphisms

Some genetic polymorphisms initially identified in animals have been found in some patients with hepatotoxicity induced by antituberculosis drugs. This is the example of the thioredoxin reductase 1 (TXNRD1) gene identified as a candidate marker of hepatotoxicity [50].

The SOD2 polymorphism (gene encoding the mitochondrial protein MnSOD) is a predictive factor for hepatotoxicity of antituberculous drugs and other therapeutic classes [51]. Indeed, the MnSOD protein generates toxic hydrogen peroxide for liver cells. This polymorphism, also associated with higher MnSOD activity, is a risk factor for cellular and/or cholestatic damage [51]. In cases of hepatic cholestasis, GPX1 polymorphisms are more common with reduced activity levels [51]. In some patients, there are strong associations of SOD2/GPX1 polymorphisms [51].

Polymorphisms in genes encoding inflammatory mediators may contribute to the susceptibility to hepatotoxicity of many drugs, including antituberculosis drugs [51].

Ethambutol has been associated with toxic optic neuropathies that occur in patients with mutations in a fusion gene, OPA1, responsible for the autosomal dominant inheritance of optic atrophy [52]. A case of CMT2A2 (MFN2 Mutation: T669G, F223L) has been reported in a patient who received Ethambutol and subsequently developed accelerated weakness, vocal cord paralysis and optic atrophy [52]. The deterioration in the patient’s condition began one month after the start of treatment and stabilized on discontinuation of treatment followed by improvement in visual fields [52]. This case shows that patients with CMT2A2, and possibly other mitochondrial fusion defects, may be particularly susceptible to ethambutol-induced neurotoxicity [52].

Mutations in the TYMP gene have also been associated with a case of mitochondrial neurogastrointestinal encephalomyopathy (MNGIE), a rare autosomal recessive multisystem disease [53]. A first case of an MNGIE patient diagnosed in Bulgaria carrying a new homozygous TYMP mutation (p.Leu347Pro) has been reported [53]. This patient had presented several months after the start of anti-tuberculosis treatment, gastrointestinal disorders, cachexia, hearing loss, ptosis, ophthalmoparesis, polyneuropathy, cognitive disorders and leukoencephalopathy of the brain [53]. His motor ability had drastically diminished, making him dependent on a wheelchair [53]. This case suggests the existence of mitochondrial toxicity of antituberculosis drugs in some patients carrying TYMP mutations [53].

Drug-induced hepatotoxicity due to some anti-infectives is related to polymorphisms in the human leukocyte antigen (HLA) region [54]. Thus the HLA-DQB1*06:02 polymorphism has been associated with the hepatotoxicity of Amoxicillin-Clavulanic Acid, HLA-B*57:01 with that of Fucloxacillin, etc. [54]. GWAS results offer molecular insights into the central role of the immune system in idiosyncratic drug-induced hepatotoxicity [54]. It is therefore not ex-
cluded that certain HLA polymorphisms are also associated with the various forms of toxicity of antituberculosis drugs.

3.8. Associations of Genetic Polymorphisms

It is not uncommon to encounter in some patients, an association of CYP2E1, NAT2, GST, and SLC01B1 polymorphisms [55]. In these patients, the manifestations of the toxicity of antituberculosis drugs are severe and can lead to death.

Hepatotoxicity is only observed in patients carrying combination polymorphisms including the NAT2 gene [5]. There is no synergistic effect between CYP2E1, GSTM1, and GSTT1 polymorphisms [5]. On the other hand, there is a very significant association between hepatotoxicity, slow phenotype of the NAT2 gene and polymorphism of the CYP2E1 gene.

Isoniazid was associated with severe PNP in a 23-year-old man, with liver and kidney damage [15]. Genetic analyzes revealed the presence of a combination of NAT2 and CYP2E1 c1/c2 polymorphisms in this subject [15]. These two polymorphisms having been associated with a high risk of toxicity would justify the neurological, hepatic and renal toxicities reported in this subject [15]. Individual genotyping, performed before treatment or at least if elevated liver parameters are observed, can reduce the risk of severe cases of PNP by early adjustment of treatment [15].

3.9. Interactions between Genes, Environmental Factors and Toxicity of Antituberculosis Drugs

Several genes associated with the toxicity of antituberculosis drugs may be present in some patients, thus increasing the toxic effects. This is the example of the CYP2E1 and GSTT1 genes which interact by increasing the hepatotoxicity of antituberculosis drugs [29]. Adverse effects of anti-tuberculosis drugs are also linked to the interaction between the NAT2, GSTM1, GSTT1, CYP2E1 genes and environmental factors [56]. There is no association between liver toxicity and GSTM-1/GSTT1 gene interaction [57].

There are synergistic interactions between GSTT1 and CYP2E1 polymorphisms manifested by epistaxis associated with an increased risk of hepatotoxicity. A significant gene-environment interaction is also associated with an increased risk of hepatotoxicity [29].

Slow acetylator profile, CYP2E1 c2 or A4 variant genotype, and female sex are significantly associated with antituberculosis drug-induced hepatotoxicity [29]. Patients carrying the slow acetylator profile and the c2 variant are more at risk of developing hepatotoxicity [29]. In some patients with GSTT1 and CYP2E1 polymorphisms, there is a synergistic interaction leading to epistaxis and increasing the risk of hepatotoxicity [29].

3.10. Management of Adverse Effects

The etiology of severe skin reactions occurring in some patients on anti-tuberculosis treatment can be determined by the patch test [2]. However, systemic
reactions to this test are particularly common in TB/HIV co-infected patients [2]. In vitro tests are still limited to specialized centers, but specific lymphocyte responses to antituberculosis drugs have been identified in patients with skin and/or liver reactions.

Desensitization of patients with severe skin reactions is possible but very risky [2]. The management of these patients remains sub-optimal [2].

Patients with chronic renal failure on hemodialysis with a slow acetylator phenotype are at risk of developing encephalopathy [14]. One of the hypotheses that could explain the occurrence of this encephalopathy would be the elimination of pyridoxine phosphate (active metabolite of pyridoxine) by dialysis and the accumulation of isoniazid and/or its toxic metabolites in the blood of patients [14]. Discontinuation of isoniazid with supplementation with high doses of pyridoxine resulted in a favorable outcome [14]. Caregivers should be aware of the risk of isoniazid toxicity that may occur in hemodialysis patients receiving isoniazid or a tuberculosis treatment regimen containing this isoniazid [14]. Context-appropriate prescribing of either high doses of Pyridoxine or reduced doses of Isoniazid can reduce the risk of life-threatening Isoniazid toxicity in patients on hemodialysis and/or slow acetylators [14].

4. Conclusion

Hepatotoxicity is the most frequent of first-line antituberculosis drugs toxicities. The genetic polymorphisms associated with their toxicities concern the metabolizing enzymes (NAT2, CYP2E1, GST) and membrane transporters (SLCO1B1 and ABCB1). Other genetic polymorphisms have been suspected but their effects depend in some cases on interactions between genes or genes-environment. Genetic polymorphisms could be used to screen high-risk patients and guide the choice of a more effective and safe treatment.

Contribution of the Authors

SS (Bibliographic research, drafting of the manuscript). All authors have read, commented on and approved the final manuscript.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

References


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