Minireview

Role and Regulation of Hepatobiliary ATP-Binding Cassette Transports during Chemical-Induced Liver Injury

Carolina I. Ghanem and Jose E. Manautou

Instituto de Investigaciones Farmacológicas (ININFA-UBA-CONICET) (C.I.G.) and Cátedra de Fisiopatología (C.I.G.), Facultad de Farmacia y Bioquímica, Universidad de Buenos Aires, Argentina; and Department of Pharmaceutical Sciences, University of Connecticut, Storrs, Connecticut (J.E.M.)

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ABSTRACT

Severity of drug-induced liver injury (DILI) ranges from mild, asymptomatic, and transient elevations in liver function tests to irreversible liver damage, often needing transplantation. Traditionally, DILI is classified mechanistically as high-frequency intrinsic DILI, commonly dose dependent or DILI that rarely occurs and is idiosyncratic in nature. This latter form is not dose dependent and has a pattern of histopathological manifestation that is not always uniform. Currently, a third type of DILI called indirect hepatotoxicity has been described that is associated with the pharmacological action of the drug. Historically, DILI was primarily linked to drug metabolism events; however, the impact of transporter-mediated rates of drug uptake and excretion has gained greater prominence in DILI research. This review provides a comprehensive view of the major findings from studies examining the contribution of hepatic ATP-binding cassette transporters as key contributors to DILI and how changes in their expression and function influence the development, severity, and overall toxicity outcome.

SIGNIFICANCE STATEMENT

Drug-induced liver injury (DILI) continues to be a focal point in drug development research. ATP-binding cassette (ABC) transporters have emerged as important determinants of drug detoxification, disposition, and safety. This review article provides a comprehensive analysis of the literature addressing: (a) the role of hepatic ABC transporters in DILI, (b) the influence of genetic mutations in ABC transporters on DILI, and (c) new areas of research emphasis, such as the influence of the gut microbiota and epigenetic regulation, on ABC transporters.

Introduction

Drug-induced liver injury (DILI) can be the outcome of use and/or misuse of prescription and nonprescription drugs, herbal products, and dietary supplements. Gradation of liver injury ranges from mild, asymptomatic elevations in liver function tests to complete acute liver failure (ALF). A large number of drugs have been implicated as potential causes of DILI. The Food and Drug Administration Liver Toxicity Knowledge Base lists over 1000 drugs divided into various categories based on their DILI-causing potential (Chen et al., 2011).

DILI can be historically classified by the presumed mechanism of toxicant action as intrinsic or idiosyncratic. The former, also called predictable, has a high frequency of occurrence and is dose-dependent. It usually occurs shortly after exposure to high therapeutic, supratherapeutic, or toxic doses. This toxicity can also be reproduced in various species of laboratory animals. Acetaminophen (APAP) is the prototype drug for this type of DILI, and misuse of APAP is responsible for approximately 50% of all cases of ALF in the United States (Ostapowicz et al., 2002; Lee, 2003; Larson et al., 2005; Lee, 2017). There is also a considerable number of other drugs that can cause intrinsic hepatic necrosis (i.e., niacin, aspirin, cocaine, amiodarone, methotrexate, cancer chemotherapy drugs).

The second class of DILI is idiosyncratic (IDILI) in nature or unpredictable and of rare occurrence. IDILI is often referred to as dose-independent, which is misleading because an adverse outcome cannot be entirely disassociated from dose. Classic drugs associated with IDILI include antibiotics such as amoxicillin–clavulanic, nitrofurantoin, minocycline, cephalosporins, fluoroquinolones, and isoniazid. In many developing countries, tuberculosis medications are the leading cause of IDILI (Ramachandran et al., 2013). This form of DILI seems to be the outcome of an interplay between drug exposure and environment...
and/or host factors, such as adaptive immunity to damage-associated molecular pattern molecules (reviewed in Tujios and Fontana, 2011). IDILI usually occurs at a very low frequency, with drug treatment lasting several months to even years before toxicity manifests. These features make IDILI often difficult to identify, and its occurrence is often underestimated (Shapiro and Lewis, 2007). IDILI accounts for roughly 13% to 17% of all cases of ALF in the United States and Sweden (Ostapowicz et al., 2002; Wei et al., 2007).

A third type of DILI called indirect hepatotoxicity has been described. This classification includes pharmaceuticals that can induce liver injury because of the drug’s own pharmacological action, rather than through inherent hepatotoxic potential or immunogenicity. Examples of drugs associated with indirect DILI are certain antineoplastic agents, glucocorticoids, monoclonal antibodies, and tumor necrosis factor α, as well as inhibitors of checkpoint proteins and protein kinases (Hoofnagle and Björnsson, 2019). This third form is of much greater frequency than the idiosyncratic form and can have a distinct clinical manifestation. As yet, indirect hepatotoxicity is not a widely accepted classification distinct from intrinsic and idiosyncratic.

An important point to consider when defining mechanisms of DILI is that the concentration of a drug (or its metabolite) in hepatocytes is not only dependent upon drug metabolism but also interindividual variability in the rates of drug uptake and excretion. These transport processes significantly influence drug cellular concentration, tissue dosimetry, and ultimate DILI outcome. Given the interconnectivity of drug metabolizing enzymes and transporters, each drug can have distinct combinations of biotransformation and disposition pathway(s) that define the drug’s pharmacokinetic and pharmacodynamic behavior as well as safety. Particularly in liver, there are two superfamilies of transporters, the solute carrier transporters and the ATP-binding cassette (ABC) transporters. The first one includes organic anion transporting polypeptides, organic anion transporters, organic cation transporters, and the sodium/tartrate-cotransporting polypeptide. These drug transporters are principally located in the plasma membrane of hepatocytes, mediating drug influx from sinusoidal blood into the cell. By contrast, the superfamily of ABC transporters is involved in drug efflux from sinusoidal blood into the bile. When the transporter is localized to the canalicular membrane, or into sinusoidal blood for transporters localized basolaterally. Intrinsic variability across individuals in the expression and function of drug transporters due to genetic polymorphisms and variable responses to environmental stressors and drugs is a well-recognized key contributor to the development, severity, and overall DILI outcome. This review focuses and summarizes the major findings from studies examining the role hepatic ABC transporters in the development or prevention of DILI.

**Brief Historical Perspective**

Studies on the mechanisms of DILI were initially centered on the role of phase I and II drug metabolism enzymes in the generation and net availability of cytotoxic reactive intermediates, as well as the ability of such reactive intermediates to covalently bind to cellular macromolecules, including proteins. Protein adduction by reactive intermediates may lead to loss of function, abnormal localization, or formation of immunogenic haptons. The potential consequences of such protein modifications are production of oxidative stress, mitochondrial dysfunction, and the triggering of an immune response against the liver (for a complete review, see Andrade et al., 2019).

The discovery of drug transporters and the increasing understanding of their role in cancer multidrug resistance in the 1980s and 1990s (Doming and Petzinger, 2014) opened the door for the study of their normal physiologic functions and pathophysiologic consequences of altered expression, including DILI. The largest group of protein transport systems is the ABC class transporters. This transporter family is composed of 49 genes and 20 pseudogenes, divided into eight subfamilies, named from ABCA to ABCG. In the liver, all ABC proteins are efflux transporters with the capacity to transport a vast array of substances (for a complete review, see Kroll et al., 2021). Multidrug resistance-associated proteins (MRP) are members of the ABCC subfamily. Among them, MRP2 (ABCC2) is the only one located on the canalicular membrane of hepatocytes, while the remainder are located in the basolateral domain, with the most important and studied being MRP1 (ABCC1), MRP3 (ABCC3), and MRP4 (ABCC4). The only ABCA transporter localized to basolateral membranes of hepatocytes is ABCA1, which is involved in cholesterol efflux. The remainder of the ABC transporters present in the liver are located in the canalicular membrane, namely, the bile acid export pump (BSEP; ABCB11), multidrug resistant gene 3 (MDR3; ABCB4), MDR1 or P-glycoprotein (PGP; ABCB1), breast cancer resistance protein (BCRP; ABCG2), and ABCG5.

**Key Recent Advances**

In this review, key recent advances in the current understanding of the role of ABC transporters in drug liver damage are divided into intrinsic and idiosyncratic DILI.

**Role of ABC Transporters in Intrinsic DILI**

Intrinsic DILI is associated with ingestion of supratherapeutic or toxic doses of a compound. APAP is highlighted in this review as prototype compound, since it is extensively used in elucidating the role of ABC transporters in DILI.

**The Role of ABC Transporters in APAP Metabolism.** Ingestion of high doses of APAP saturates its normal detoxification routes of metabolism, sulfate, and glucuronide conjugation (Fig. 1) APAP undergoes bioactivation by cytochrome P450 enzymes to produce N-acetyl-p-benzo-quinoneimine (NAPQI). The conjugation of this reactive metabolite with glutathione (GSH) neutralizes its reactivity and produces nontoxic conjugates that are readily eliminated via bile and urine. However, upon depletion of the GSH intracellular pool, excess NAPQI is free to react with negatively charged macromolecules. This produces APAP–protein covalent adducts, mitochondrial dysfunction, and oxidative stress, which finally results in hepatocellular damage (for a review, see Ramachandran and Jaeschke, 2018).

The ABC transporters known to mediate APAP metabolites transport and directionality are shown in Fig. 1. APAP-glucuronide (APAP-Glu) is a known substrate for sinusoidal Mrp3 (Slitt et al., 2003; Manautou et al., 2005) and canalicular Mrp2 (Xiong et al., 2000; Chen et al., 2003; Silva et al., 2005). APAP-sulfate (APAP-Sulf) is primarily excreted into plasma, principally by Mrp4 and to a lesser extent by Mrp3 (Zamek-Gliszczynski, N ezasa, Tian, Bridges et al., 2006), while BCRP principally transports this metabolite into bile with some contribution by Mrp2 (Zamek-Gliszczynski et al., 2005; Zamek-Gliszczynski, N ezasa, Tian, Kalvass et al., 2006; Lee et al., 2009). Similarly, APAP-gluthione is transported into bile by Mrp2 and into plasma by Mrp1 and Mrp4 (Chen et al., 2003). The latter is known to also transport APAP-cysteine (Koenderink et al., 2020). The basal hepatic expression of MRP1 is very low, while MRP3 and MRP4 are expressed in liver, with interindividual variability in their expression and function (Borst and Elferink, 2002).

**The Role of ABC Transporters in Modulation of APAP Toxicity and Autoprotection.** The functional consequences of altered ABC transporters expression in DILI have been the subject of multiple investigations. Significant increments in the expression of the sinusoidal ABC transporters MRP1 and MRP4 at the mRNA level, with induction
of Mrp4 mRNA expression and protein levels by APAP in both mice and humans (Aleksunes et al., 2006; Campion et al., 2008). Increments in Mrp3 and Mrp4 expression colocalize within regions of the hepatic lobule where cell proliferation is occurring in response to APAP toxicity, principally in hepatocytes surrounding the central vein (Aleksunes et al., 2006). The mechanism of the induction of both transporters is not totally understood, but there is evidence that induction is dependent on the paracrine actions of cytokines, such as tumor necrosis factor α and interleukin-1β (IL-1β), since depletion of Kupffer cells by liposomal clodronate treatment abolishes Mrp4 induction and sensitizes mice to APAP hepatotoxicity (Campion et al., 2008). APAP-mediated induction of Mrp3 and Mrp4 also involves activation of nuclear factor E2-related factor 2 (Nrf2), since mice with genetic ablation of Nrf2 do not show induction of Mrp3 and Mrp4 in response to APAP (Aleksunes, Slitt et al., 2008).

Mrp3 plays also plays a role in the hepatobiliary disposition of APAP and susceptibility to hepatotoxicity. Since Mrp3 preferentially transports glucuronide conjugates, it is not surprising that the intrahepatic accumulation of APAP-Glu is 20-fold higher in Mrp3 null mice, with a concomitant reduction in plasma APAP-Glu and greater biliary excretion (Manautou et al., 2005). Furthermore, Mrp3 null mice are more resistant to APAP-induced hepatotoxicity and experience a faster replenishment of hepatic GSH than wild-type mice. Thus, the basolateral excretion of APAP-Glu in mice is nearly completely dependent on Mrp3 activity, and altered disposition of APAP in the Mrp3 null mice is associated with lower hepatotoxicity.

There are species differences in basal expression of transporters and differential susceptibility to APAP dosing (Wang et al., 2015). For example, the expression of Mrp3 is very low in normal rats (Hirohashi et al., 1998) and much higher in mice (Zelcer et al., 2005). By contrast, Mrp4 is very lowly expressed in liver of mice (Aleksunes et al., 2005), rats (Chen and Klaassen, 2004), and humans (Barnes et al., 2007). In the normal human liver, high MRP3 mRNA expression has been reported. However, modest amounts of MRP3 protein are observed (König et al., 1999; Kool et al., 1999), with a high degree of variability among individuals (up to 80-fold) (Lang et al., 2004). This difference may be due to a single nucleotide polymorphism, 2211C>T, in the promoter region of MRP3, which lowers the binding affinity of nuclear transcription factors.

Induction of hepatic expression of Mrp3 (rats) and Mrp4 (mice) is associated with an increased resistance to subsequent toxic APAP treatment or re-exposure. This phenomenon is known as APAP autoprotection. It is observed with APAP (Aleksunes, Campion et al., 2008; Ghanem et al., 2009) as well as other drugs or nondrug xenobiotics that produce hepatotoxicity. In humans, evidence indicates that long-term abuse of opioid/APAP combination products or consumption of 3 times or more the daily recommended dose of APAP does not necessarily result in APAP hepatotoxicity, which is indicative of adaptation and development of tolerance (Tredger et al., 1995; Shayiq et al., 1999; Forootan et al., 2017). Interestingly, similar changes in hepatic expression of ABC transporters to those reported in mice and rats have also been reported in humans with toxic APAP exposure.

Although the precise mechanism of this adaptation remains unknown, the shift in APAP-Glu excretion from bile into urine following APAP pretreatment in rats (Ghanem et al., 2005) could be a contributing factor to the development of resistance to APAP DILI. This shift in the disposition pathway of APAP-Glu decreases its biliary excretion and therefore the amount of this conjugate that appears in intestinal tissue, where it is normally cleaved by bacterial glucuronidases, releasing free APAP that then undergoes intestinal reabsorption. The ultimate consequences are decreased enterohepatic circulation, less APAP hepatic exposure, and lower likelihood of hepatotoxicity (Watari et al., 1983; Ghanem
et al., 2009). It is worth noting that this observation obtained from rat studies is also reported in humans. Tredger et al. (1995) reports that the development of tolerance to APAP hepatotoxicity is associated with an increment in APAP-Glu and APAP-Sulf concentrations in serum and urine of patients, when compared with normal volunteers. Allegaert et al. (2005) reports an increase in urine APAP-Glu/APAP-Sulf ratio in newborns chronically treated with APAP.

The introduction of colchicine, an antimitotic agent, to the APAP autotoprotection treatment regimen of mice not only blocked APAP-induced compensatory hepatocellular proliferation, but it also prevented the induction of Mrp4 and restored the normal susceptibility of mice to APAP hepatotoxicity (abolishment of autotoprotection). These findings greatly reinforced the association between Mrp4 induction, compensatory hepatocellular proliferation, and susceptibility to APAP-induced hepatic damage (Alexksunes, Campion et al., 2008).

The basis of the hepatoprotective role of MRP3 induction by itself or in combination with Mrp4 induction by APAP treatment is currently not known. It is known that induction of these two transporters leads to more efficient disposition of APAP metabolites, which should prevent inhibition of drug metabolizing enzymes (e.g., phase II enzymes) by their metabolic/detoxification products. Induction of these transporters can also dampen cellular injury by increasing efflux efficiency of endogenous molecules that are potential mediators of cytotoxic responses (Borst et al., 2007), such as bile salts (Bohan et al., 2003), acyl glucuronides (Iwamura et al., 2017), bilirubin, and other signaling molecules from hepatocytes into the bloodstream for subsequent renal excretion. These transporters also export multiple other endogenous molecules, such as folic acid (Zeng et al., 2001; Kitamura et al., 2010) and leukotriene C4 (Zeng et al., 2000) for Mrp3 and cAMP (Chen et al., 2001), cyclic guanosine monophosphate (van Aubel et al., 2002), prostaglandin E2 and F2α (Reid et al., 2003), thromboxane B2, and prostaglandin F2α (Rius et al., 2005) for Mrp4. Therefore, their overexpression can also contribute to modulating signaling events occurring in adjacent hepatocytes and/or nonparenchymal cells that modify the hepatic microcirculation (Vollmar and Menger, 2009) and aid in recovery from injury (Alvarez and Lorenzetti, 2021).

Drugs and Pathologic Conditions That Modify the Expression of ABC Transporters and Their Impact on APAP Hepatotoxicity. Modulation of Mrp3 and Mrp4 gene expression in the liver results from several compounds, such as ciprofloxacin, clotrimazole, clofibrate, or various pathologic conditions, such as primary biliary cholangitis, hepatitis, and cholestasis (for a review, see (Ghanem and Manautou, 2019). Pretreatment with tanshinone IIA, an active component in the dried root of Salvia miltiorrhiza commonly used in traditional Chinese medicine, protects mice against APAP hepatotoxicity in a Mrp4- and Mrp2-dependent manner (Zhang et al., 2020). This study also shows that induction of these two transporters is mediated by activation of Nrf2, a transcriptional regulator that binds to antioxidant responsive elements on the Mrp4 and Mrp2 gene promoters. Increased Mrp3 and Mrp4 expression is seen in animals models with hereditary deficiency in Mrp2, such as transport-deficient rats (Chen et al., 2005), or with experimental obstructive cholestasis (Hirohashi et al., 1998; Konig et al., 1999; Soroka et al., 2001; Keppeler, 2011a). Induction is also seen in some forms of human cholestatic disease (Shoda et al., 2001). The severity of APAP toxicity is lower in the Mrp2-deficient, transport-deficient rats in comparison with wild-type rats (Silva et al., 2005) or after an obstructive cholestasis of 7 days in rats with bile duct ligation (Acevedo et al., 1995). Similarly, cholestasis induced by model organic anions, such as indocyanine green, protects from APAP hepatotoxicity in mice (Silva et al., 2006).

Role of ABC Transporters in IDILI
Cholestatic and mixed forms of hepatitis are the most frequent presentations of IDILI. The presence of jaundice, pruritus, and elevated levels of serum alkaline phosphatase (AP) are the main characteristics of drug-induced cholestasis (DIC) (Stapelbroek et al., 2010).

ABC Transporters Involved in Bile Formation. Bile formation is basically a mechano-osmotic process resulting from a concentrative process that brings primarily bile salts, GSH, and bicarbonate, among other substances, into the bile canaliculus. The canalicular translocation of these solutes is then followed by osmotic water diffusion primarily through aquaporin channels. It is known that ABC transporters play a crucial role in this highly concentrative process for these solute components of bile. Figure 2 summarizes the more important steps in bile formation and enterohepatic circulation. In addition, peristaltic gut contractions and paracellular fluid movement are also important for bile formation (for a review, see Boyer and Soroka, 2021). As the name implies, bile salt export pump (BSEP, ABCB11) is responsible for bile salt efflux at the canalicular level (Stieger et al., 1992; Gerloff et al., 1998) and is the rate-limiting factor for bile salt-dependent flow (see Fig. 2). Also, at the canalicular pole, Mrp2 is responsible for the efflux of a wide array of substances, such as GSH and GSH conjugates of bile salts, glucuronidated bile salts, and conjugated bilirubin (Chen et al., 2003). Mrp2 is the main transporter responsible for

![Fig. 2. ABC transporters involved in most frequent idiosyncratic form of DILI: drug-induced cholestasis. This figure shows the principal transporters involved in primary bile production by hepatocytes and the secondary modifications produced by cholangiocytes before mature bile arrives in the small intestine. Through the process of enterohepatic circulation, BS arrives in the liver via blood, entering hepatocytes via sodium/taurocholate cotransporting polypeptide and various organic anion transporting polypeptides, where they can be conjugated with glucuronide or GSH. At the apical side of hepatocytes, BSEP is the main transporter responsible for BS efflux (magenta dotted line) and the rate-limiting factor for bile salt independent flow generation. MRP2 is responsible for the canalicular efflux of GSH, GS-B, and GS-X, as well as BS-Glu and X-Glu (e.g., bilirubin), with GSH being the main contributor to the establishment of the bile salt independent flow (brown dotted line). The osmotic concentration generated by these transport processes is then followed by passive inflow of water, principally through to aquaporin channels. This primary secretion then is modified in bile ducts by cholangiocytes. These biliary epithelial cells also contribute to the establishment of the bile salt independent flow through bicarbonate excretion via the chloride-bicarbonate anion exchanger and cystic fibrosis transmembrane conductance regulator. Bile acids self-aggregate into micelles, a process aided by phosphatidylcholine efflux into the bile canaliculus by MDR3 (violet dotted line) and cholesterol efflux by ABCC11/ABCG5 heterodimer (brown dotted line). BCRP collaborates with taurocholate-sulfate and probably other BS (green dotted line). DIC is often the result of intrahepatic BS accumulation (orange arrows) produced by decreased activity of primarily BSEP and MRP2. Additionally, MRP3 and MRP4 mediates to basolateral efflux of BS (yellow and red dotted lines), so a decrease in MRP3 expression can also contribute to BS intrahepatic accumulation. Bil, bilirubin; CFT, cystic fibrosis transmembrane conductance regulator; TLC, taurocholate; X, xenobiotic.](image-url)
establishing the bile salt-independent component of bile flow. MDR3 is a flipase, which exports phosphatidylcholine by its translocation from the inner to the outer membrane of the hepatocyte (Oude Elferink and Pau-lusma, 2007). In vitro studies have demonstrated that Bcrp is able to transport tauroliothiocholate sulfate (Suzuki et al., 2003); therefore, it might also contribute to the excretion of bile salts in vivo. After self-association due to their amphipathic properties, bile acids form micelles (Hofmann and Hagay, 2014) that are then charged with cholesterol and effluxed out of hepatocytes into bile via the ABCG8/ABCG5 heterodimer protein complex (Wittenburg and Carey, 2002). This primary secretion undergoes modifications in bile ducts by cholangiocytes. Micellar bile acids secretion is variable, and depending on the species, it can account for up to 40% of the total volume of daily bile output. The osmotic driving force provided by cholangiocytes is primarily generated by bicarbonate excretion via the chloride-bicarbonate anion exchanger, with chloride excreted by the cystic fibrosis transmembrane conductance regulator (ABCC7). However, regulation of the activity of these two apical proteins is very complex, involving not only intracellular levels of cAMP and calcium, but also luminal ATP that interacts with P2Y receptors to stimulate intracellular Ca2⁺ release (for a review, see Rodrigues et al., 2018). The exact contribution of MDR1 to bile formation has not been established yet, but it is well known that this is the main transporter of cationic drugs, and its contribution to the canalicular excretion of drugs and other xenobiotics into bile is well established (Pauli-Magnus and Meier, 2006).

DIC can be the result of the presence and/or generation of a toxic metabolite within the biliary system or from xenobiotic-mediated modulation in expression and/or inhibition of ABC transporters function. As a consequence, the intracanalicular accumulation of bile acids can produce hepatocellular injury due to their detergent properties that disrupt cell membranes (Hofmann and Hagay, 2014) and promotes generation of reactive oxygen species and mitochondrial damage (Krähenbühl et al., 1994). Furthermore, hydrophobic bile acids can also induce apoptosis by two different mechanisms. The first one is induction of the death signaling complex, which starts with the recruitment of Fas-associated death domain adaptor protein. The second one involves downregulation of the antiapoptotic Fas-associated death domain-like IL-1β-converting enzyme inhibitory protein, thus promoting caspase activation and apoptosis (for a review, see Engin, 2021). In summary, accumulation of bile acids contributes to hepatocyte necrosis and apoptosis, which can result in pathological tissue injury (Tujios and Fontana, 2011).

The functional activity of ABC transporters is dependent upon various factors, such as gene polymorphisms, transcriptional and post-translational modifications (e.g., glycosylation), allosteric modulators, membrane localization status, and changes in the transmembrane environment through alterations in lipid composition (Garzel et al., 2019).

Although an in-depth discussion of hepatic genetic diseases, such as progressive familial intrahepatic cholestasis, is beyond the scope of this article, it is important to mention that there is a heterogeneous group of autosomal recessive disorders related to gene mutations that affect bile production and bile acids secretion. Most of these mutations are on ABC transporters genes, and the phenotypic manifestations of these diseases are generally consistent with the function of these transporters (for a review, see Felzen and Verkade, 2021). These diseases are typically detected in early childhood, often followed by a severe course that can ultimately result in the need for liver transplantation either before or during adulthood. For some drug transporters, knockout mouse models develop a phenotype that is evidently independent of animal manipulation and/or treatment, while other transporters knockout animal models lack a phenotype unless challenged (Keppeler, 2011b).

**ABC Transporters Associated with DIC: Effect of Gene Mutations.** The precise nature of the association between certain polymorphic forms of ABC transporters and DILI remains controversial, and more research is needed to bring clarity to this issue. It is well known that polymorphic forms of drug metabolic enzymes and certain human leukocyte antigen haplotypes are well associated with increments in susceptibility to DILI. However, genome-wide association studies have failed to identify similar associations between DILI and polymorphic forms of ABC transporters (Urban et al., 2012), at least on an individual basis. Despite the lack of a definite association between monogenetic variations in ABC transporters and DILI from genome-wide association studies, there are particular transporters polymorphisms that are more prevalent for certain drugs with a history of producing DILI (Daly, 2017). This is summarized in Table 1.

There are four highly conserved nonsynonymous mutations in genes of the ABC family of transporters, two in MDR3 and two in BSEP (Lang et al., 2007). In MDR3, there is a 1764L polymorphism in the transmembrane domain and a L1082Q located close to the ATP-binding domain, both of them in evolutionarily conserved codons. The presence of these two heterozygous nonsynonymous mutations have been associated with the development of DILI in patients treated with risperidone and amoxicillin/clavulanic, respectively (Lang et al., 2007). This study also shows the presence of a common BSEP polymorphism in exon 13 (1331T>C-V444A) previously described in intrahepatic cholestasis of pregnancy (Keitel et al., 2006) and a newly reported one, D676Y. This latter polymorphic form of BSEP is more frequent in patients with DIC induced by fluvasitatin. However, there are no differences in taurocholate transport when analyzed in vitro using an expression system for D676Y. In contrast, the V444A single nucleotide polymorphism, which is also more frequent in patients with DIC than in healthy controls or in patients with drug-induced disease, does exhibit lower transport activity when a construct of this polymorphic form of BSEP is expressed in vitro (Meier et al., 2006). Quantitative structure-activity relationship analysis shows that carriers of this mutation have an increased risk of developing hepatocellular DILI if treated with drugs containing a carbocyclic system with aromatic rings, such as some nonsteroidal anti-inflammatory drugs (Ulzzarrun et al., 2013). It is important to note that this same mutation is associated with intrahepatic cholestasis of pregnancy (Pauli-Magnus et al., 2004).

The ABCB2 24C>T polymorphism (rs717620 T) is associated with increased risk of hyperbilirubinemia and mortality in a population of Japanese patients with DILI (Huang et al., 2021). This mutation is also more frequent in patients of European ethnic origin hospitalized due to diclofenac-induced DILI (Daly et al., 2007). A second well-characterized polymorphism for MRP2, c –1774delG, shows a strong association with cholestatic or mixed-type hepatitis in the Korean population due to a decrease in MRP2 promoter activity and inducibility, principally by bile acids (Choi et al., 2007).

Mutations in BCRP are reported to alter transport activity and are also associated with DILI. The homozygous presence of the genetic polymorphism 421C>A (Q141K, rs2231142) in BCRP is associated with liver injury induced by the tyrosine kinase inhibitor sunitinib (Miura et al., 2014). This drug is a known substrate of BCRP, and the presence of this variant reduces its transport, leading to intracellular accumulation and drug toxicity. This polymorphism is approximately 3-fold higher in Asians than in Caucasians, and it is also associated with other adverse events, including thrombocytopenia (Low et al., 2016). Additionally, in vitro results from cells expressing the Q141K polymorphism showed decreased transport of mitoxantrone, a prototypic substrate for BCRP efflux (Morisaki et al., 2005). Finally, the MDR1 polymorphism 3435C>T has been associated with nevirapine-induced DILI in African (Haas et al., 2006) and US patients (Ritchie et al., 2006). Although the mechanistic role of this MDR1 mutation in DILI remains unknown, the presence of this variant alters PGP substrate
<table>
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<th>ABC</th>
<th>Physiologic substrates</th>
<th>Drugs Associated with DILI (Wild Transporter or in the Presence of Polymorphism/s)</th>
<th>Determined polymorphism</th>
<th>Reference(s)</th>
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<tr>
<td>BCRP (ABCG2)</td>
<td>Sulf-conjugates Anionic drug</td>
<td>Sunitinib (TKI)</td>
<td>421C&gt;A Q141K; (rs2231142) Cholestatic (Reduction in transport activity)</td>
<td>(Miura et al., 2014)</td>
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<td>BSEP (ABCB11)</td>
<td>BS (taurocholate and other cholate conjugates)</td>
<td>Bosentan; erythromycin; troglitazone; cyclosporine A; nefazodone; simvastatin; estolate; glibenclamide; sulindac; ethinylestradiol-17-glucuronide (trans inhibition)</td>
<td>No association with wild-type transporter</td>
<td>(Stieger et al., 2000; Fattinger et al., 2001; Meier et al., 2006; Lang et al., 2007; Ulzurrun et al., 2013)</td>
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<td>MDR3 (ABCB4)</td>
<td>Phosphatidylcholine</td>
<td>Oral contraceptives antifungal azoles (itraconazole)</td>
<td>No association with wild transporter</td>
<td>(Lang et al., 2007; Davit-Spraul et al., 2010; Yoshikado et al., 2011; Mahdi et al., 2016)</td>
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<tr>
<td>MRP2 (ABCC2)</td>
<td>Bilirubin-Glu</td>
<td>Ceftriaxone; diclofenac; synthetic estrogen</td>
<td>No association with wild transporter</td>
<td>(Choi et al., 2007; Daly et al., 2007; Braga et al., 2016; Huang et al., 2021)</td>
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<tr>
<td>PGP (ABCB1)</td>
<td>Organic Cation Drugs (+)</td>
<td>Cyclosporine A; verapamil; erythromycin chlorpromazine; ivermectin Nevirapine</td>
<td>No association with wild-type transporter</td>
<td>(Haas et al., 2006; Ritchie et al., 2006)</td>
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</table>
A factor contributing to the development of DIC is the level of expression of drug transporters. In one study, 8 out of 12 patients with DIC showed decreased expression of BSEP, MRPs, and MRP2 (Zollner et al., 2014). As with many other genes, ABC transporters expression is tightly regulated by transcriptional (for a review, see Rigalli et al., 2019) and post-transcriptional mechanisms (for a review, see Czuba et al., 2018). Nuclear receptors are the principal modulators of transcriptional expression of ABC transporters (for a review, see Rigalli et al., 2019). Among them, and tightly correlated with drug-induced cholestasis, is the farnesoid X receptor (FXR, NR1H4). This transcription factor is the main regulator of BSEP expression and function (Pluss et al., 2002). FXR also regulates MDR3 (Huang et al., 2003), MRP2 (Pluss et al., 2002), and PGP (Jiang et al., 2013). When bile acids, such as chenodeoxycholic acid, deoxycholic acid, and cholic acid, bind to FXR, this interaction promotes FXR heterodimerization with the retinoid X receptor (Yu et al., 2002). This signaling-competent heterodimer binds to the

**ABC Transporters Associated with DIC: Effect of Other Factors.** In addition to drugs, changes in membrane microenvironment can modulate the activity of ABC transporters. For example, Bsep and Mrp2 are located in separate membrane microdomains and are both co-localized with ATP8B1 (Ismir et al., 2009). ATP8B1, a member of the P4 subfamily of the P-type ATPase superfamily, is a phosphatidylinerse translocase that flips phospholipids from the outer to the inner leaflet of the plasma membrane (Ujhazy et al., 2001). ATP8B1 has a protective function by making the outer leaflet more resistant to the detergent action of bile salts in the canalicular lumen due to its richness in phosphatidyglcerol, sphenomyelin, and cholesterol (Amigo et al., 1999). Decreased ATP8B1 activity is associated with a decrease in the activity of both Bsep and Mrp2 resulting from asymmetry in membrane microdomains characterized by an increment in phosphatidylinerse outer membrane content, with these events leading to cholestasis (Paulusma et al., 2009).
FXR response elements in the promoter region of target genes, inducing the expression of the aforementioned ABC transporters.

Interestingly, post-transcriptional modifications of FXR occurs under cholestatic conditions with an increased acetylation of lysine 217, which decreases its DNA binding and transactivation activity (Kemper et al., 2009; Kulkarni et al., 2016). FXR itself and its surrounding histones, when bound to DNA, can be deacetylated by sirtuin 1 (SIRT1), a class III nicotinamide adenine dinucleotide–dependent histone deacetylase; therefore, SIRT1 inactivation decreases DNA–FXR binding. SIRT1 lacks a DNA-binding domain, so it needs to be transactivated by FXR for recruitment into its own target genes promoters (Yang et al., 2017). Activation of the SIRT1/FXR pathway by small molecules produces FXR deacetylation, which helps reverse DFC (Qu et al., 2018; Zhao et al., 2019). However, continuous activation or overexpression results in ubiquitination and proteasomal degradation of FXR, which can revert back the cholestatic condition (Blobker et al., 2019).

Additional transcription factors can play a role in the regulation of hepatobiliary drug transporters. Hepatocyte-specific liver receptor homolog-1 (NR5A2) (Zwicker and Agellon, 2013) and the oxidative stress sensor Nrf2 regulate BSEP expression (Weerachayaphorn et al., 2009). Nrf2 is also involved in the induction of hepatic metabolic enzymes mediating phase I and II reactions in a coordinated fashion with the regulation of other ABC transporters, such as MRP3 and MRP4 (Taoka et al., 2016). Pregnane X receptor (PXR) is another ligand-dependent nuclear receptor that controls the inducible expression of drug metabolizing enzymes and drug transporters (Aleksunes and Klaffen, 2012). Transcriptional regulation of BSEP by PXR is particularly well-characterized. The recruitment of other components to the PXR/retinoid X receptor heterodimer to PXR responsive element complexes enhances BSEP expression. One of them is the coactivator-2-containing complex (ASCOM), which normally interacts with FXR as the activating signal but is disrupted during cholestasis, decreasing BSEP expression (Ananthanarayanan et al., 2011). Other known PXR coregulators are coactivator-associated arginine methyltransferase 1 (Ananthanarayanan et al., 2004) and steroid receptor coactivator 2 (Chopra et al., 2011; for a review, see Sobail and Dönmez-Cakil, 2021).

Post-transcriptional targeting of Bsep, Mdr2 (the rat homolog of human MDR3), and Mrp2 to the canalicular membrane of hepatocytes is necessary to sustain bile formation functionality and biliary elimination of xenobiotics and endogenous compounds. (for a review, see Romas et al., 2008). Several ABC transporters, but more prominently Bsep, are constantly recycled between apical membranes and intracellular subapical endosomal compartments (Wakabayashi et al., 2004). When this recycling balance is disrupted by a shift toward greater endocytic internalization, reduced bile acid extraction from hepatocytes occurs, which can result in cholestasis (Crocenzi et al., 2012). In a model of intrahepatic cholestasis of pregnancy produced by estradiol-17β-D-glucuronide (Crocenzi et al., 2003) and in cholestasis produced by cyclosporin A (Román et al., 2003), an enhanced retrieval of Bsep into the subapical endosomal compartment has been demonstrated. This transporter recycling is a clathrin-dependent endocytosis process (for a review, see Miszcuk et al., 2018). Basically, this Ca2+-dependent internalization process during cholestasis induced by estradiol-17β-D-glucuronide is mediated by signaling events involving protein kinase C–p38 and phosphoinositide 3-kinase–extracellular signal-regulated kinase 1/2 (Crocenzi et al., 2008; Boaglio et al., 2010). Bsep internalization is decreased when its association with α- and μ2-adaptin (subunits of the AP2 adaptor complex) (Hayashi et al., 2012), and hematopoietic cell–specific Lyn substrate 1–associated protein X1 (HAX1) is disrupted (Ortiz et al., 2004). The same authors also demonstrated that HAX1 co-localizes with BSEP, MDR1, and MDR2 in the canalicular membrane. RNA interference that silences HAX1 leads to increases in BSEP protein levels in the apical membrane domain of Madin–Darby canine kidney cells in culture.

While individual factors can mechanistically modulate the expression and activity of ABC transporters, it is quite common for more than one mechanism to converge in the pathophysiology of DILI. The immunosuppressant drug cyclosporin A illustrates this concept (Tazuma, 2006). This drug, initially described as a competitive inhibitor of BSEP (Stone et al., 1987; Böhme et al., 1993), also decreases the targeting of Bsep to the canalicular membrane of hepatocytes (Román et al., 1990). Cyclosporin A also decreases Bsep activity by altering its microenvironment through a reduction in canalicular membrane fluidity (Yasumiba et al., 2001). The transport inhibitory function of cyclosporin A is not limited to Bsep; it also affects Mrps transporters and Pgp (Böhme et al., 1993). The coadministration of cyclosporin A and verapamil, another well-known inhibitor of Pgp, worsens the cholestasis produced by cyclosporin A alone in a rat model (Delle Monache et al., 1999). This interaction has also been demonstrated in humans (Padda et al., 2011).

Drugs that produce mitochondrial dysfunction and/or loss of mitochondrial integrity carry a risk of DILI (Dykens and Will, 2007; Labbe et al., 2008). This risk can be greater when the drug simultaneously interferes with ABC transporters function or by combining drugs that inhibit mitochondrial and transporter function separately. In this latter instance, the combined effect of a transporter inhibitor and a mitochondrial toxicant could lead to more severe forms of DILI (Poreduo et al., 2012). Illustrative of this, a high-throughput in vitro screening that used isolated mouse liver mitochondria was carried out with 124 chemicals (primarily drugs) to determine whether DILI can be predicted by the ability of these chemicals to impair mitochondrial function. Eighty-seven of the 124 chemicals had previously documented clinically relevant DILI, while the remaining 37 did not. Valproic acid, aspirin, tamoxifen, diclofenac, and tacrine are among the list of DILI compounds tested. This screening conclusively established a strong relationship between mitochondrial dysfunction (or toxicity) and DILI and had a high predictive value. Mitochondria targeting might explain the synergistic worsening of DILI when drugs that inhibit ABC transporter function are combined with drugs that interfere with mitochondrial function or drugs with both effects (Aleo et al., 2014). Another link between mitochondrial dysfunction and transporter activity is limitation in intracellular ATP availability, essential for driving ABC transporter function.

Current Challenges and Knowledge Gaps

Nowadays, polypharmacy is a very frequent practice that is primarily seen in elderly patients and can carry an increased risk of DILI (Chen et al., 2015). The current liver parameters recommendations, alanine aminotransferase, and AP values, generated by an international DILI Expert Working Group, allow for diagnosis and partial characterization of the DILI etiology (Aithal et al., 2011). However, these diagnostic endpoints cannot accurately predict the clinical course and ultimate DILI outcome, nor can they help identify the causative agent or the precise mechanism involved when more than one medication is used by the patient.

The current animal models available for studying intrinsic DILI are reproducible and mechanistically relevant to the human situation. The prototypical example is APAP, a classic hepatotoxicant studied for five decades. In contrast, for IDILI, there are relatively few animal models for its study, since its manifestation is dependent on the interaction of drug–host-environment (reviewed in Corsini et al., 2012). Despite the assumptions of similar modes of action/activation of the drug, there are limitations in traditional animal studies. A principal one is due to species differences resulting from the different genetic backgrounds that can influence drug–host interactions. A second limitation of animal
studies for IDILI is that only a limited number of drugs mimic the degree of injury produced in humans, and toxicity is observed in a small number of the animals treated. Lastly, animal studies often require prolonged drug exposure periods, increasing the study costs.

New biomarkers of DILI, such as high mobility group box protein 1, K18, and microRNA-122, are being studied in terms of increasing sensitivity, specificity, severity, and DILI predictability. The era of integrative “omics” approaches and their application in investigative toxicology is expected not only to advance understanding of mechanisms of DILI but also to accurately identify drugs responsible for producing liver adverse events in humans (for a review see, Kullak-Ublick et al., 2017). Progress is further enhanced by the development of novel in vitro assays.

In the last decade, a biologic test called MetaHeps was recently introduced into the market. The assay is based on the use of monocyte-derived hepatocyte-like (MH) cells from the patient’s own peripheral mononuclears that are then cultured under a patented protocol (Benesic et al., 2012). A panel of drugs is then assayed for in vitro toxicity by lactate dehydrogenase release. MH cells have the same characteristics as primary human hepatocytes derived from the same donor, including drug-metabolizing enzymes capacity and ABC transporters function (Benesic et al., 2016). The MH cells assay was useful in identifying the culprit drug causing idiosyncratic DILI in a prospective study in patients consuming more than one medication (Benesic et al., 2016). Similarly, another prospective study demonstrated the value of this assay for studying hepatotoxicity of herbal and dietary supplements (Weber et al., 2021). This assay is useful to examine potential drug–drug interactions at the onset of DILI (Benesic et al., 2019). Adoption of the MH cell assay could be a tool to better define the origins of DILI reactions, particularly in patients on polypharmacy. Once the drug(s) responsible for DILI are identified, a systematic study of the drug metabolizing and transporters capacity can be performed on the same patient using the same MH cell tool. This investigative work could generate a much more robust comprehension of the interaction between drug therapy and host characteristics in a patient-by-patient manner.

Considering the current gaps in understanding of drug–host interactions, it is quite challenging to establish a comprehensive interplay between drug metabolism and transport networks activated and/or inhibited by drugs and its relationship to DILI. Future studies should be aimed at identifying factors that can modify risk, and research into the interactions of host–drugs is needed to deepen our knowledge of these interactions, allowing us to move toward a safer and more personalized medicine approach to treatment.

**Perspective on Future Directions**

The gastrointestinal (GI) microbiota and epigenetic regulation of drug-metabolizing enzymes and transporters are two research areas of emerging importance that can advance understanding of the pathogenesis of DILI and interindividual variability in DILI frequency and severity. The GI microbiota has the capacity of digesting food nutrients, producing endogenous metabolites, and biotransforming xenobiotics. The metabolic activity of intestinal microbes can produce dual and opposing effects, sometimes contributing to the maintenance of health, while in other instances promoting hepatopathological conditions, such as fatty liver disease (Dietert and Dietert, 2015; Sharpton et al., 2019).

Illustrative of the importance of the gut–liver axis in liver disease is lithocholic acid, a secondary bile acid generated by the gut microbiota and a PXR antagonist that decreases BSEP expression and could produce cholestasis if abundantly generated (Yu et al., 2002). Glucuronidases in the intestinal microbiota cleave APAP-Glu or tacrine–glucuronide conjugates, releasing the parent compound that can then be reabsorbed and transported to the liver via enterohepatic circulation, re-exposing the liver again to the drug and increasing its potential for producing toxicity (Ghanem et al., 2009; Yip et al., 2018). Another area that deserves attention for its potential contribution to interindividual variability in DILI frequency and magnitude is circadian variations in the function of the GI microbiota (Gong et al., 2018).

The mechanistic link between the gut microbiota to the pathophysiology of DILI remains largely unknown and should receive greater attention. There is relatively recent new evidence indicating that the gut microbiota modulates several clusters of hepatic genes involved in xenobiotic metabolism through modulation of PXR binding to DNA (Selwyn et al., 2016). Selwyn et al. (2016) demonstrated that germ-free mice have a different pattern of Cyp450 gene expression. These mice showed a marked downregulation in the expression of Cyp3a gene isoforms, occurring concomitantly with an upregulation of Cyp4a isoforms. These changes correlated well with alterations in both PXR and peroxisome proliferator-activated receptor α DNA binding. Additionally, analysis of cholestasis induced by 5-day bile duct ligation using conventional and germ-free mice showed that in mice devoid of gut microbiota, hepatic bile infarcts are more pronounced, and there is greater susceptibility to hepatic inflammation. These findings are associated with microbiota-dependent alterations in the expression of genes involved in metabolism of fatty acids and amino acids and also due to increased gene expression of IL-1β and activation of the extracellular signal-regulated kinase/mitogen-activated protein kinase pathway. By contrast, the presence of gut bacteria enhances ductular reactions, cell proliferation, deposition of collagen 1, and cell autophagy (Juuola et al., 2021). Despite the dramatic surge in microbiome research in the last decade, much more needs to be known about the relationship between the gut microbiome and health and disease, including how changes in its composition and function influence liver diseases, including DILI (Forootan et al., 2017; Chan and Benet, 2018; Li et al., 2021).

Finally, epigenetic regulation of drug metabolizing enzymes (Jin et al., 2016) and transporters (Zappe and Cichna-Mark, 2020), such as DNA methylation, histone modification, and noncoding RNAs, has gained considerable attention recently. However, there are no systematic studies that associate epigenetic modifications with DILI susceptibility. There is evidence, however, that epigenetic mechanisms are involved in the pathogenesis of primary biliary cholangitis (Li et al., 2020) and intrahepatic cholestasis of pregnancy (Xiao et al., 2021). The H3K4me3 epigenetic mark is downregulated during cholestasis, decreasing the recruitment of the ASCOM complex to FXR binding elements in the BSEP and MRP2 gene promoters (Ananthanarayanan et al., 2011). It has been demonstrated that perturbations in the intrauterine environment during intrahepatic cholestasis of pregnancy produce an epigenetic imprinting during postnatal life that predisposes offspring to metabolic diseases in adulthood (Borges Manna et al., 2020).

This review highlights many recent advances in the study of drug transporters and DILI, yet more attention needs to be dedicated to addressing the knowledge in drug–host interactions, the role of GI microbiota, and the epigenetic regulation in the expression and activity of ABC transporters and their individual and combined contributions to DILIs.

**Conclusion**

Collectively, this review summarizes substantive evidence indicating that drug transporters, particularly ABC transporters, play a pivotal role in the development of DILI. The following statements capture the major points addressed in this review:

- ABC transporters are involved in the hepatobiliary disposition and hepatotoxicity of APAP, the most frequent drug causing intrinsic DILI.
The pharmacokinetics and pharmacodynamics of multiple other drugs that are strongly associated with DIC and various forms of IDILI have well-documented interplays with drug transporters. There are different polymorphisms in hepatobiliary transporters identified, principally associated with BSEP, that modify protein expression and/or activity for this main efflux pump for bile acids. These polymorphisms are associated with DILI-causing drugs.

Post-transcriptional modulation of transporters expression and/or function are considered to be causative of several types of DILI. The continuous development and increase in sophistication of multilaminar platforms provide unique opportunities to deepen the mechanistic understanding of the role of ABC transporters in the various types of DILI.

Greater knowledge is emerging from the fields of the gut microbiome and epigenetics. Although the GI microbiota status and composition is known to influence drug biotransformation, significantly less is known about its impact on drug transporters expression and function. Similarly, an increased understanding on the epigenetics of drug transporters can be instrumental in better defining mechanisms of DILI.

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Wrote or contributed to the writing of the manuscript: Ghanem, Manautou.

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Address correspondence to: Dr. José E. Manautou, Department of Pharmaceutical Sciences, University of Connecticut, 69 North Eagleville Road, Storrs, CT 06269-3092. E-mail: jose.manautou@uconn.edu