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The Role of Canalicular ABC Transporters in Cholestasis

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ABSTRACT

Cholestasis, a hallmark feature of hepatobiliary disease, is characterized by the retention of biliary constituents. Some of these constituents, such as bile acids, inflict damage to hepatocytes and bile duct cells. This damage may lead to inflammation, fibrosis, cirrhosis, and eventually carcinogenesis, sequelae that aggravate the underlying disease and deteriorate clinical outcome. Canalicular ATP-binding cassette (ABC) transporters, which mediate the excretion of individual bile constituents, play a key role in bile formation and cholestasis. The study of these transporters and their regulatory nuclear receptors has revolutionized our understanding of cholestatic disease. This knowledge has served as a template to develop novel treatment strategies, some of which are currently already undergoing phase III clinical trials. In this review we aim to provide an overview of the structure, function, and regulation of canalicular ABC transporters. In addition, we will focus on the role of these transporters in the pathogenesis and treatment of cholestatic bile duct and liver diseases.

Introduction

Hepatic ATP-binding cassette (ABC) transporters play a key role in cholestatic disease and are expressed at the basolateral and apical membrane of liver cells (hepatocytes). Canalicular ABC transporters are responsible for the formation of bile and secrete bile acids (ABCB11) (Gerloff et al., 1998), bilirubin (ABCC2) (Paulusma et al., 1997), phosphatidylcholine (ABCB4) (Smit et al., 1993), cholesterol (ABCG5/G8) (Berge et al., 2000), and drugs (ABCB1, ABCC2, ABCG2) across the bile canalicular membrane. ABCB11 transports bile acids against a steep (1000-fold) concentration gradient. This gradient attracts water into the bile canalicular lumen and thereby drives bile flow. Mixed micelles of phosphatidylcholine (ABCB4) and cholesterol (ABCG5/8) incorporate these bile acids and thereby mitigate their detergent effects (reviewed by Trauner et al., 2008). Other canalicular ABC transporters (mainly ABCB1, ABCC2, and ABCG2) play a key role in the biliary excretion of xenobiotics, which has important implications for drug-drug interactions and the development of multidrug resistance (reviewed by Ecker and Chiba, 2009; Keppler, 2011a). The important function of canalicular ABC transporters is underlined by their role in cholestatic disease. Hereditary and acquired ABC transporter defects may decrease bile flow, increase the biliary toxicity, and/or contribute to the development of drug-induced cholestasis (Oude Elferink et al., 2006). Basolateral ABC transporters (e.g., ABCC3 and ABCC4) transport bile acids into the blood, which protects hepatocytes from bile acid-induced damage (Keppler, 2011a). The activity of ABC transporters, in short, can either protect or damage cells of the hepatobiliary system. Their expression is consequently tightly regulated, both by nuclear receptors (NRs) at the transcriptional level and by various post-transcriptional modifications, such as insertion/retrieval of the transporter at the cell membrane (reviewed by Halilbasic et al., 2013). These regulatory mechanisms ensure bile acid homeostasis and coordinate the adaptive response to cholestatic conditions.

This review discusses the role of canalicular ABC transporters (ABCB11, ABCC2, ABCB1, ABCG2, ABCB4, ABCG5/8) in bile

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Please note that abbreviations for transporters and nuclear receptors were capitalized throughout this article when symbols were identical for human and rodents.

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ABBREVIATIONS: ABC, ATP-binding cassette; ABCB1, ATP-binding cassette, subfamily B, member 1; ABCB11, ATP-binding cassette, subfamily B, member 11; ABCB4, ATP-binding cassette, subfamily B, member 4; ABCC2, ATP-binding cassette, subfamily C, member 2; ABCC3, ATP-binding cassette, subfamily C, member 3; ABCC4, ATP-binding cassette, subfamily C, member 4; ABCG2, ATP-binding cassette, subfamily G, member 2; ABCG5/8, ATP-binding cassette, subfamily G, members 5/8; CAR, constitutive androstane receptor; CITCO, 6-(4-chlorophenyl)-imidazo [2,1-b][1,3]thiazole-5-carbaldehyde; FXR, farnesoid X receptor; GR, glucocorticoid receptor; ICP, intrahepatic cholestasis of pregnancy; IL, interleukin; LPAC, low phospholipid associated cholelithiasis syndrome; LXR, liver X receptor; MDR1, multidrug resistance protein 1, P-glycoprotein; MDR2 (rodents)/MDR3 (human), multidrug resistance protein 2 (rodents)/3 (human); norUDCA, norursodeoxycholic acid; NR, nuclear receptor; NTCP, sodium/taurocholate cotransporting polypeptide; NR, nuclear receptor; PBC, primary biliary cirrhosis; PC, phosphatidylcholine; PFIC, progressive familial intrahepatic cholestasis; PPARα, peroxisome proliferator-activated receptor alpha; PPARγ, peroxisome proliferator-activated receptor gamma; PSC, primary sclerosing cholangitis; PXR, pregnane X receptor; RARα, retinoic acid receptor alpha; RXRα, retinoid X receptor alpha; SHP, short heterodimer partner; SNP, single-nucleotide polymorphism; SULT2A1, sulfotransferase 2A1; TPN, total parenteral nutrition; UDCA, ursodeoxycholic acid; UGT1A1, UDP glucuronosyltransferase 1A1; UGT2B4, UDP glucuronosyltransferase 2B4; VDR, vitamin D receptor.

formation and cholestasis. To provide a basis for this undertaking, we will commence with a brief overview of bile acid metabolism. Subsequently, we will turn our attention to the individual canalicular transporters and review their structure, function, associated substrates, and regulation in health and disease. In the last part of the review, we will focus on the potential role of these transporters and the NRs that regulate their transcription as drug targets in cholestatic disease. Many of the studies described in this review were performed in mice, which have a significantly different bile acid pool compared with humans. The direct extrapolation of animal data to human physiology is therefore not possible without their verification in human models. Although the animal studies discussed in this review were invaluable for our understanding of bile metabolism, their interpretation thus needs careful appreciation of interspecies discrepancies.

Bile Acid Metabolism and Its Regulation

Bile acids are synthetized from cholesterol in the liver. This synthesis requires 17 enzymatic steps, of which the conversion of cholesterol into 7α-hydroxycholesterol by 7α-hydroxylase is considered to be rate limiting. Most (>99%) bile acids are directly conjugated (either with taurine or with glycine), which necessitates their active secretion (via ABCB11 and ABCC2) across the bile canalicular membrane. The secreted bile acids then enter the intestinal lumen and are efficiently (>95%) reabsorbed, mostly by the apical sodium-dependent bile acid transporter in the terminal ileum (Dawson et al., 2003). The reabsorbed bile acids return to the liver via the portal circulation, from where they are extracted by the basolateral uptake transporters of the hepatocyte. The sodium/taurocholate cotransporting polypeptide (NTCP) transports the majority (~90%) of these bile acids, whereas multispecific organic anion transporters play a comparably modest role in hepatocellular bile acid uptake (Hagenbuch and Meier, 1994; Kullak-Ublick et al., 1994).

NRs regulate the transcription of hepatic genes that are involved in bile acid homeostasis (Fig. 1; reviewed by Halilbasic et al., 2013). These receptors act as intracellular sensors and prevent the accumulation of toxic biliary compounds. Activated NRs change conformation, recruit coactivators (and/or dissociate from corepressors), and induce/repress transcription either by binding the DNA of their target genes or by interacting with other NRs. The role and function of NRs is exemplified by the farnesoid X receptor (FXR), which acts as an intracellular sensor for bile acids (Fig. 2) (Makishima et al., 1999; Parks et al., 1999; Wang et al., 1999). Bile acid–activated FXR forms a heterodimer with the retinoid X receptor (RXR), which then binds an inverted repeat-1 sequence (or other response elements) in the promoter of its target genes (Forman et al., 1995; Seol et al., 1995; Laffitte et al., 2000). The resulting gene transcription decreases hepatocellular bile acid uptake (NTCP) and synthesis (CYP7A1/CYP8B1), while promoting canalicular (ABCB11, ABCC2) and basolateral bile acid excretion in rodent and human hepatocytes (Ananthanarayanan et al., 2001; Denson et al., 2001; Gerloff et al., 2002; Kast et al., 2002; Plass et al., 2002; Eloranta and Kullak-Ublick, 2005). These effects are partly mediated by the FXR-induced activation of the short heterodimer partner (SHP), which represses the transcription of *NTCP*, *CYP7A1*, and *CYP8B1* (Fig. 1) (Brendel et al., 2002; Gupta et al., 2002; Abrahamsson et al., 2005; Kir et al., 2012). FXR also induces bile acid detoxification via *CYP3A4*, *SULT2A1*, and *UGT2B4*, which further protects the hepatocyte from bile acid–induced damage (reviewed by Zollner et al., 2006). Finally, FGF19, which is expressed in the human liver and intestine, can also be induced by FXR (Holt et al., 2003; Inagaki et al., 2005; Kim et al., 2007; Schaap et al., 2009). This last mechanism represents a negative feedback loop, which can be induced by an increased intestinal or hepatic bile acid concentration (e.g., after a meal) (Choi et al., 2006). Other NRs such as the pregnane X receptor (PXR) and the constitutive androstane receptor (CAR) are also involved in bile acid metabolism. Both receptors are best known for their role in phase I (cytochromes P450), phase II (conjugation), and phase III (transport proteins) drug elimination. PXR and CAR are, however, also activated by hydrophobic bile acids (PXR) and bilirubin (indirect activation; CAR) in rodent and human hepatocytes (Staudinger et al., 2001; Xie et al., 2001; Huang et al., 2003b). This activation induces hepatocellular bile acid excretion (ABCC2, ABCC3, ABCC4) and detoxification (CYP3A4/CYP2B10/SULT2A1) (Xie et al., 2000; Marschall et al., 2005; Chai et al., 2011, 2012) and stimulates bilirubin conjugation (UGT1A1) and excretion (ABCC2) (Huang et al., 2003b; Marschall et al., 2005). PXR also represses bile acid synthesis (via CYP7A1) (Staudinger et al., 2001). The vitamin D receptor (VDR) is activated by secondary bile acids such as lithocholic acid (Makishima et al., 2002). The impact of VDR activation on bile acid metabolism and cholestatic disease is difficult to predict, because it inhibited FXR-dependent gene transactivation in vitro, but also had antifibrotic effects in a rat model of liver fibrosis (Honjo et al., 2006; Abramovitch et al., 2011). VDR does not seem to have a significant impact on the expression of canalicular ABC transporters. Several nonbile acid activators, such as peroxisome proliferator-activated receptors (PPARs) and the glucocorticoid receptor (GR), are also involved in bile acid detoxification and elimination (Fig. 1), but an extensive discussion on their role in bile acid metabolism falls beyond the scope of this review.

ABCB11

ABCB11 acts as the canalicular bile salt export pump and transports conjugated monovalent bile acids from the hepatocyte into the bile. This transport not only protects the liver from bile acid-induced toxicity, but also represents the major driving force for (bile acid-dependent) bile flow. As the major canalicular bile acid transporter in humans, ABCB11 plays a key part in bile formation and (hereditary) cholestasis.

ABCB11 is a 160-kDa member of the B subfamily (ABCB) of ABC transporters and has a structure that consists of two nucleotide-binding and two 6-helical transmembrane domains (Fig. 3) (Kubitz et al., 2012). ABCB11, like ABCC2, ABCB4, ABCB1, and ABCG5/8, is an exclusively apical transporter. Its expression pattern is restricted to hepatocytes, which supports its role in canalicular bile acid transport and bile formation. Human ABCB11 transports conjugated/amidated monovalent bile acids (Table 1) in the following order of clearance: taurochenodeoxycholic acid > glycochenodeoxycholic acid > taurocholic acid > glycocholic acid (Hayashi et al., 2005). ABCB11 thus clears chenodeoxycholic acid, which is the most toxic of these bile acids, with the greatest efficacy (Hayashi et al., 2005; Song et al., 2011). Interestingly, some in vitro reports suggested that ABCB11 might also transport drugs (e.g., vinblastine, taxol, and pravastatin) (Childs et al., 1998; Lecureur et al., 2000; Hirano et al., 2005). The impact of ABCB11 on drug transport, however, has not been established.

A decrease in ABCB11 activity leads to bile acid accumulation and plays an important role in the pathogenesis of acquired and hereditary cholestatic disease. Prescription drugs, inflammation, and total parental nutrition (TPN), for example, can all lead to acquired cholestasis. Drugs, such as cyclosporine A, glybenclamide, rifampicin, and rifamycin, can repress ABCB11 activity via competitive inhibition. The resulting decrease in canalicular bile acid transport can lead to drug-induced cholestasis, which will generally resolve quickly after drug withdrawal (Stieger et al., 2000). Inflammation and TPN repress canalicular ABCB11 expression in rodents (Nishimura et al., 2005; Recknagel et al., 2012).

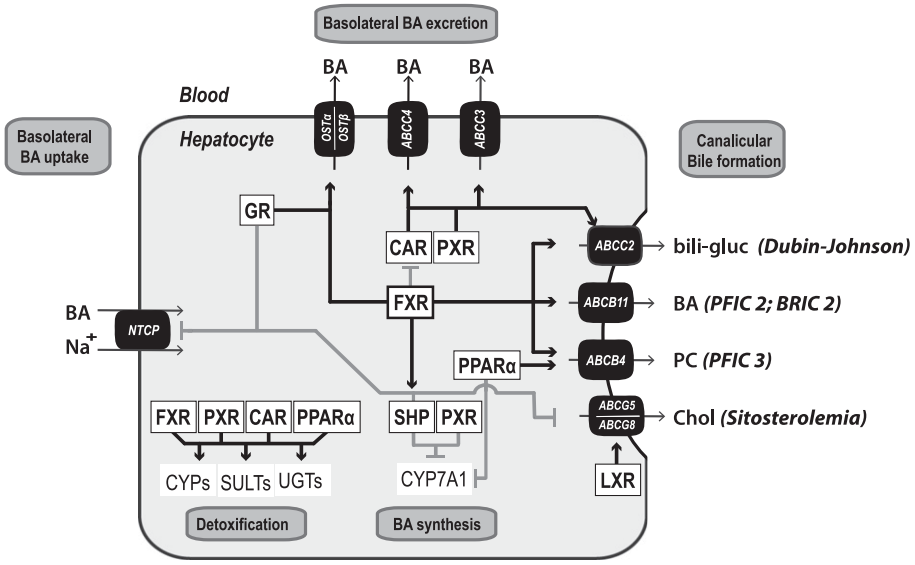

Fig. 1. Nuclear receptors as key regulators of bile homeostasis in the liver. Hepatic FXR represses bile acid uptake (NTCP) and synthesis (CYP7A1) and induces bile acid elimination (ABCB11, ABCC2, ABCC3, ABCC4) and detoxification (cytochromes P450, SULTs, UGTs). FXR also stimulates the biliary excretion of phospholipid (ABCB4) but decreases canalicular ABCG5/8 activity (via SHP). PXR and CAR induce bile acid (ABCC2, ABCC3, ABCC4) and conjugated bilirubin (ABCC2) excretion. PPARα increases ABCB4-mediated phospholipid secretion (ABCB4) and induces bile acid detoxification. LXR promotes ABCG5/8-mediated cholesterol excretion. Finally, GR decreases bile acid uptake (NTCP) and increases basoalteral bile acid excretion (OSTα/β). For simplicity, other uptake systems for organic anions and cations are not shown. Black arrows, stimulatory effects; gray lines, suppressive effects on target genes. BAs, bile acids; Bili-glu, bilirubin glucuronide; ABCB11, bile salt export pump; CAR, constitutive androstane receptor; CYP7A1, cholesterol-7a-hydroxylase, cytochromes P450, cytochrome P450 enzymes; FXR, farnesoid X receptor; GR, glucocorticoid receptor; LXR, liver X receptor; ABCB4, multidrug resistance protein 3; ABCC2, multidrug resistance-associated protein 2; ABCC3, multidrug resistance-associated protein 3; ABCC4, multidrug resistance-associated protein 4; NTCP, sodium taurocholate cotransporting polypeptide; OSTα/β, organic solute transporter α and β; PC, phosphatidylcholine; PXR, pregnane X receptor; PPARα, peroxisome proliferator-activated receptor α; PPARγ, peroxisome proliferator-activated receptor γ; SHP, small heterodimer partner; SULTs, sulfatation enzymes; UGTs, glucuronidation enzymes.

This decrease, which occurs via various (post-) transcriptional mechanisms, can contribute to the development of inflammatory/septic or TPN-induced cholestasis. *ABCB11* polymorphisms can predispose to acquired cholestatic disease, and the single-nucleotide polymorphism (SNP) rs2287622 has a relatively high prevalence in patients with drug-induced cholestasis, intrahepatic cholestasis of pregnancy, liver fibrosis, and cholangiocarcinoma (reviewed by Stieger and Beuers, 2011). Severe ABCB11 mutations can lead to the development of hereditary cholestasis, which covers a mild to severe phenotypical spectrum. Progressive familial intrahepatic cholestasis type 2 (PFIC2) leads to severe cholestasis and is generally associated with a nonfunctional ABCB11 protein (reviewed by Jacquemin, 2012). This disease usually manifests itself

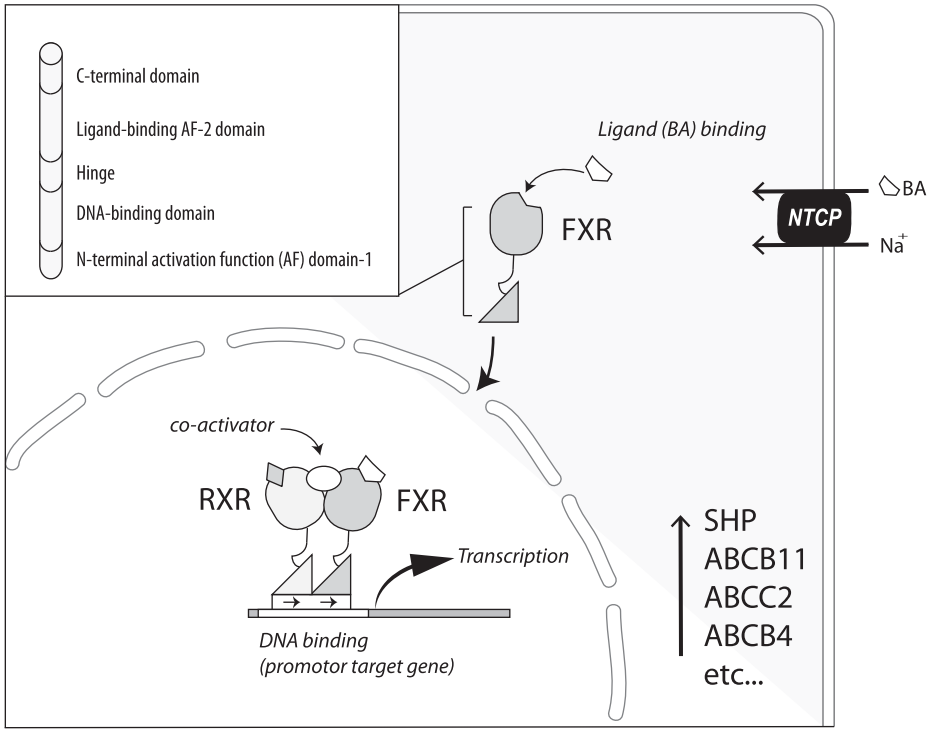

Fig. 2. The principal structure and function of nuclear receptors, as exemplified by FXR. The structure and function of NR can be exemplified by FXR. Bile acid (⬡)-activated FXR heterodimerizes with RXR, recruits coactivators/dissociates from corepressors, and induces transcription of its target genes. The upper left panel shows the general structure of a nuclear receptor, consisting of an activation function domain-2 (AF-2), a ligand-binding domain, a hinge region, a DNA-binding domain, and an AF-1. The DNA- and ligand-binding domains recognize (promoter) DNA and NR ligands, and AF-1 and AF-2 induce ligand-independent nuclear receptor transactivation.

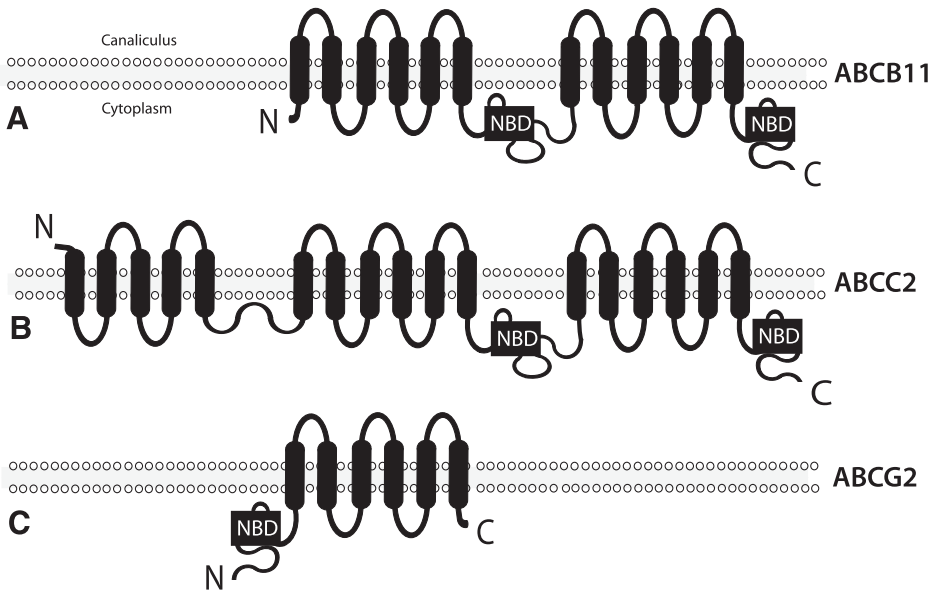

Fig. 3. The principal structure of canalicular ABC transporters. The structure of canalicular ABC transporters can consist of 1, 2, or 3 transmembrane domains (for details kindly refer to the text). The ABCB (B1, B11) and ABCG (G2, G5, G8) transporter family members mentioned in the text have comparable structures and are therefore not shown separately in this figure.

within the first 6 months of life. Patients typically suffer from cholestasis, fat malabsorption, growth retardation, and an increased risk for hepatocellular carcinoma (Knisely et al., 2006). The initial treatment usually consists of ursodeoxycholic acid (UDCA), fat-soluble vitamins (D, K), cholestyramine (for pruritus), and biliary diversion (Emond and Whitington, 1995). Most patients, however, will require liver transplantation in the first 2 decades of life. Some transplanted patients develop rebound cholestasis due to formation of anti-ABCB11 antibodies (Keitel et al., 2009). Treatment options for PFIC2 patients with a nonfunctional protein remain limited in the absence of gene therapy. Patients with residual ABCB11 activity, however, may benefit from ABCB11 activation via chaperones in the future. Treatment of MDCK cells harboring a (E297G or D482G) mutant form of ABCB11 with 4-phenylbutyrate, for example, led to an increase in apical ABCB11 incorporation (Hayashi and Sugiyama, 2007). PFIC2 patients with residual ABCB11 activity are also more likely to benefit from UDCA, because tauroursodeoxycholic acid relies on a functional protein for its transport (Gerloff et al., 1998). UDCA shifts the bile acid pool to a more hydrophilic (i.e., less toxic) composition and promotes apical ABCB11 insertion (see below), which induces choleresis (Kurz et al., 2001; Dombrowski et al., 2006). Benign recurrent intrahepatic cholestasis 2 belongs to the same phenotypical continuum as PFIC2 and is characterized by mild and self-limiting episodes of cholestasis (Lam et al., 2006). Notably, *ABCB11* knockout mice display a significantly milder phenotype compared with their human PFIC2 counterparts (Lam et al., 2005). This discrepancy could partly be attributed to the formation of less toxic polyhydroxylated bile acids in mice (Perwaiz et al., 2003). These hydrophilic bile acids could, in theory, be excreted via alternative hepatocellular bile acid transporters, such as ABCC2 and ABCB1.

The activity of ABCB11 is tightly regulated at the level of its transcription and by several posttranscriptional modifications. *ABCB11* transcription is mainly regulated by FXR, as stated above. Other transcriptional factors, however, influenced the interaction of FXR with the *ABCB11* promoter in vitro and in rodents. VDR activation, via 1,25-dihydroxyvitamin D3, inhibits FXR-induced *ABCB11* transactivation (Honjo et al., 2006). Activating signal cointegrator-2-containing complex recruitment by chenodeoxycholic acid increases FXR-induced transactivation, because this coactivator complex methylates the *ABCB11* promoter histones (Ananthanarayanan et al., 2011). Steroid receptor coactivator-2 activation by liver kinase B1 and AMP-activated protein kinase also promotes FXR-induced transactivation by acetylation of promoter histones (Chopra et al., 2011). The liver receptor homolog-1 and the oxidative stress sensor nuclear factor erythroid 2–related factor 2 finally transactivate *ABCB11* by binding to specific response elements in the *ABCB11* promoter (Weerachayaphorn et al., 2009). The rapid, short-term, adaptation of canalicular ABCB11 expression is mainly regulated at the posttranscriptional level. This regulation involves the shuttling of ABCB11 between its intracellular pool and the canalicular membrane and may be triggered by hormones (Crocenzi et al., 2003), oxidative stress (Pérez et al., 2006), hydration (Schmitt et al., 2001), and cell swelling (Häussinger et al., 1993), as demonstrated in vitro and in rodent studies. Cell swelling can occur in response to a meal and lead to a rapid canalicular insertion of ABCB11, which increases the postprandial excretion of bile acids. UDCA treatment, in addition, also increases bile flow partly via (posttranscriptional) canalicular ABCB11 insertion. The regulation of these posttranslational mechanisms involves the induction of integrins by cell swelling, which triggers focal adhesion kinase, proto-oncogene tyrosine-protein kinase, mitogen-activated protein kinases, extracellular signal-regulated kinases, and p38 mitogen-activated protein kinase (Kurz et al., 2001; Häussinger et al., 2003; Schliess et al., 2004). Tauroursodeoxycholic acid acts via the same pathway but also via the activation of various protein kinase C isoforms. Protein kinase Cα recruitment by estradiol-17β-D-glucuronoside decreases canalicular ABCB11 expression in rodents, which could partly be responsible for its cholestatic properties (Crocenzi et al., 2008). Inflammation-induced cholestasis finally can lead to a decreased ABCB11 insertion into the canalicular membrane in vitro and in rodents. Inflammatory cytokines (e.g., IL-1, IL-6), however, can also decrease *ABCB11* (and *ABCC2*) transcription by their inhibitory effect on key transcriptional networks (e.g., retinoic acid receptor-α [RARα], RXRα, FXR, PXR, CAR) (reviewed by Wagner et al., 2010) and (especially in human ABCB11) via posttranscriptional mechanisms (Elferink et al., 2004).

ABCC2

ABCC2 (multidrug resistance-associated protein 2) is expressed at critical sites of uptake and elimination and is involved in the excretion and detoxification of endo- and xenobiotics. Hepatic ABCC2 plays an important role in the canalicular excretion of glutathione and conjugated

TABLE 1

Selected endogenous and exogenous canalicular ABC transporter substrates

ABCB11	ABCC2	ABCB1	ABCG2	ABCB4	ABCG5/G8
Endogenous substrates					
Glycocholic acid[a]	Bilirubin mono- and diglucuronide[a]	Aldosterone[a]	Cholic acid[a]	Phosphatidylcholine[a]	Cholesterol[a]
Taurocholic acid[a]	Cholecystokinin-8-sulfate[a]	Cholesterol[a]	Estradiol-17β-glucuronide[a]		
Glycochenodeoxycholic acid[a]	Estradiol-17β-glucuronide[a]	Cortisol[a]	Estrone-3-sulfate[a]		
Taurochenodeoxycholic acid[a]	Estrone-3-sulfate[a]	Estradiol-17β-glucuronide[a]	Folic acid glutamates[a]		
Glycodeoxycholic acid[a]	Glutathione disulfide[a]	Estrone[a]	Glycocholic acid[a]		
Taurodeoxycholic acid[a]	Hyodeoxycholic acid glucuronide[a]	Ethinylestradiol[a]	Heme[a]		
Tauroursodeoxycholic acid[a]	Leukotriene C_4[a]	Opioid peptides[a]	Protoporphyrin IX[a]		
Taurolithocholate-3-sulfate[a]	Prostaglandin E2[a]	Short-chain phospholipids[a]	Taurocholic acid[a]		
	Taurolithocholatic acid sulfate[a]	Unconjugated bilirubin[a]	Taurolithocholic acid sulfate[a]		
	Tauroursodeoxycholic acid[a]	6α-OH-taurocholic acid	Urate[a]		
	6α-OH-taurocholic acid				
Exogenous substrates					
Calcein-AM	Acetaminophen glucuronide	Calcein-AM[a]	4-Methylumbelliferone glucuronide[a]	Digoxin[a]	24-Methylene cholesterol[a]
Pravastatin[a]	Acetaminophen glutathione	Colchicine	4-Methylumbelliferone sulfate[a]	Paclitaxel[a]	Brassicasterol[a]
Taxol	Acetaminophen sulfate	Daunorubicin[a]	Albendazole sulfoxide[a]	Vinblastine[a]	Campesterol[a]
Vinblastine	Ampicillin	Digoxin[a]	Anthracenes[a]		5α-Campestanol[a]
	Arsenite[a]	Diltiazem[a]	Anthracyclines[a]		5α-Cholestanol[a]
	Bromosulfophthalein glutathione[a]	Docetaxel[a]	Camptothecin derivates[a]		22-Dehydrocholesterol[a]
	Cadmium[a]	Doxorubicin[a]	Daunomycin[a]		Sitosterol[a]
	Carboxydichlorofluorescein-diacetate	Erythromycin[a]	Dinitrophenyl glutathione[a]		5α-Sitostanol[a]
	Ceftriaxone	Ethidium bromide[a]	Doxorubicin[a]		Stigmasterol[a]
	Dibromosulfophthalein	Etoposide[a]	E3040-glucuronide		
	Dinitrophenyl glutathione[a]	Gramicidin D[a]	Hoechst 33342[a]		
	Indomethacin glucuronide	Hoechst 33342[a]	Irinotecan (SN-38 metabolite)[a]		
	Methotrexate[a]	Indinavir	Imatinib[a]		
	Morphine glucuronide[a]	Ivermectin[a]	Lysotracker green[a]		
	Mycophenolic acid glucuronide	Losartan	Methotrexate[a]		
	Paclitaxel[a]	Methotrexate[a]	Mitoxantrone[a]		
	Phenobarbital glucuronide	Mitomycin C[a]	Nucleoside analogs[a]		
	Phenolphthalein sulfate	Opioid peptides[a]	Pheophorbide α[a]		
	2-amino-1-methyl-6-phenylimidazo [4,5b]pyridine (PhIP)	Paclitaxel[a]	PhIP[a]		
	Phytoestrogen glucuronides	Rhodamine 123[a]	Pitavastatin[a]		
	Pravastatin[a]	Ritonavir[a]	Rhodamine 123[a]		
	Probenecid[a]	Saquinavir[a]	Topotecan[a]		
	Resveratrol sulfate[a]	Teniposide[a]			
	Sulfinpyrazone[a]	Topotecan[a]			
	Vinblastine[a]	Valinomycin[a]			
	Zinc	Verapamil[a]			
		Vinblastine[a]			
		Vincristine[a]			

[a]Demonstrated in ABC human transporter studies.

bilirubin. ABCC2 mutations can cause the Dubin-Johnson-syndrome, which is characterized by a mild conjugated hyperbilirubinemia.

ABCC2 is a 190-kDa member of the C subfamily (ABCC) of ABC transporters. Its structure consists of two nucleotide-binding and three (instead of the normal two) transmembrane domains (Fig. 3). The function of the third transmembrane domain, which consists of 5 instead of 6 helices, is still being investigated (Fernández et al., 2002; Westlake et al., 2005). ABCC2 is expressed at the apical membrane of intestinal epithelial cells (Fromm et al., 2000; Sandusky et al., 2002), hepatocytes (Keppler and Kartenbeck, 1996), renal proximal tubule epithelial cells (Schaub et al., 1997, 1999), gallbladder epithelial cells (Rost et al., 2001), and placental syncytiotrophoblast cells (Keppler, 2011b). This expression pattern at major barrier sites results in a decreased uptake (i.e., bioavailability) and an increased excretion of its various endo- and exogenous substrates. Although these mechanisms protect the body, they may also decrease treatment efficacy and/or lead to the development of multidrug resistance. The development of drug resistance, however, has mainly been associated with the overexpression of other multidrug transporters (i.e., ABCB1 and ABCG2) (Gerhard Ecker, 2009; Marquez and Van Bambeke, 2011).

ABCC2 transports various amphiphilic anions but displays a preference for phase II (e.g., glucuronic acid, sulfuric acid, or glutathione conjugated) metabolites (Table 1). Its endogenous substrates include tetrahydroxylated bile acids (Megaraj et al., 2010), divalent bile acids

(Kuipers et al., 1988), glutathione (Oude Elferink et al., 1990), bilirubin glucuronosides (Paulusma et al., 1997), eicosanoids (prostaglandin E2, leukotriene C_4) (Cui et al., 1999), and conjugated steroids [estrone 3-sulfate (Kopplow et al., 2005), estradiol-17β-glucuronate (Cui et al., 1999)]. Exogenous ABCC2 substrates are mostly conjugated, either with glucuronic acid [e.g., phytoestrogens (Krumpochova et al., 2012), acetaminophen (Xiong et al., 2000), indomethacin (Kouzuki et al., 2000), morphine (van de Wetering et al., 2007)], sulfuric acid [e.g., acetaminophen (Zamek-Gliszczynski et al., 2005), resveratrol (Kaldas et al., 2003)], or with glutathione [e.g., acetaminophen (Chen et al., 2003a), bromosulfophthalein (Jansen et al., 1987), dinitrophenyl (Elferink et al., 1989)]. However, ABCC2 also transports unconjugated anionic drugs, such as pravastatin (Yamazaki et al., 1997), ampicillin (Verkade et al., 1990), and methotrexate (Hooijberg et al., 1999). In addition, it transports uncharged (vinblastine, sulfinpyrazone) (Evers et al., 2000) or positively charged (Cd^{2+} and Zn^{2+}) (Houwen et al., 1990; Dijkstra et al., 1996) substrates that require glutathione-complex formation to obtain a negative charge, which is necessary for ABCC2-mediated transport.

Hepatic ABCC2 plays an important role in the development of acquired and hereditary jaundice. Sepsis, inflammatory cholestatic disease (e.g., alcoholic hepatitis, chronic hepatitis C), TPN, and obstructive cholestasis are all associated with a decrease in canalicular ABCC2 expression in rodents (Hinoshita et al., 2001; Denson et al., 2002; Elferink et al., 2004; Nishimura et al., 2005). This decrease in ABCC2, which occurs via several (post-) transcriptional mechanisms, provides a molecular explanation for the conjugated hyperbilirubinemia that can be observed under inflammatory conditions (Hinoshita et al., 2001; Zollner et al., 2001; Denson et al., 2002). Septic hyperbilirubinemia, for example, is largely induced by a cytokine-mediated decrease in ABCC2 expression and is considered to be a poor prognostic sign in critically ill patients (Trauner et al., 1997; Recknagel et al., 2012). Hepatic ABCC2 also transports glutathione and bile acids. ABCC2-mediated glutathione transport helps to create an osmotic gradient in the bile canalicular lumen and is mainly responsible for the instigation of the bile acid–independent bile flow (Chu et al., 2006; Vlaming et al., 2006). The ABCC2-mediated transport of divalent bile acids complements the monovalent bile acid transport by ABCB11 but plays a minor role in bile flow. Animal models that lack a functional ABCC2 transporter, such as ABCC2-deficient (Wistar) rat strain rats, mutant Eisai hyperbilirubinemic (Sprague-Dawley) rats, and *ABCC2* knockout mice, fail to secrete glutathione and bilirubin into the bile (Büchler et al., 1996; Paulusma et al., 1996; Chu et al., 2006; Vlaming et al., 2006). Their phenotype is consequently characterized by a 30% decrease in bile flow and a permanent conjugated hyperbilirubinemia. The important role of ABCC2 in bilirubin metabolism is further illustrated by the Dubin–Johnson syndrome, which is caused by mutations that result in an inactive form of ABCC2. These patients are unable to excrete glucuronidated bilirubin into the bile and consequently develop a permanent isolated conjugated hyperbilirubinemia (Dubin and Johnson, 1954; Paulusma et al., 1997). ABCC2 deficiency is partly compensated by the activity of alternative transporters, which may be responsible for the absence of a severe (liver) phenotype in Dubin–Johnson patients. Basolateral ABCC3, for example, decreases various intracellular ABCC2 substrates, such as bilirubin to nontoxic levels (Konig et al., 1999; Johnson et al., 2006). *ABCC2* SNPs, which can reduce ABCC2 activity, occur in a higher frequency in patients with nonfatty alcoholic liver disease (rs17222723 and rs8187710) (Sookoian et al., 2009), intrahepatic cholestasis of pregnancy (rs3740066) (Sookoian et al., 2008), bile duct cancer (rs3740066) (Hoblinger et al., 2009), and diclofenac-induced hepatotoxicity (rs717620) (Daly et al., 2007). Several of these SNPs are also associated with altered pharmacokinetics of ABCC2 substrate drugs, such as methotrexate and pravastatin. *ABCC2* polymorphisms also lead to a decreased biliary excretion of toxic metabolites during irinotecan treatment, which protects patients from irinotecan-induced diarrhea (de Jong et al., 2007; Gradhand and Kim, 2008; Megaraj et al., 2011).

ABCC2 gene transcription is regulated by FXR, PXR, and CAR. These NRs heterodimerize with RXR after their activation and subsequently bind a shared 26-bp sequence hormone response element (ER-8) in the *ABCC2* promoter (Kast et al., 2002). FXR (e.g., chenodeoxycholic acid), PXR (e.g., rifampicin), and CAR (e.g., phenobarbital) agonists thus increased ABCC2 expression in human and rodent livers (Fardel et al., 2005). Inflammatory cholestasis, sepsis, and obstructive cholestasis can decrease ABCC2 expression by a cytokine-induced repression of transcriptional networks in vitro and in rodents (RARα, RXRα, FXR, PXR, CAR) (reviewed by Wagner et al., 2010). Bile duct ligation or lipopolysaccharide (LPS) treatment resulted in an IL-1β–mediated RARα/RXRα downregulation, which in turn decreased *ABCC2* transcription in rats (Denson et al., 2002). Oxidative stress (e.g., via toxic bile acids) can increase *ABCC2* transcription via nuclear factor erythroid 2–related factor 2 in rodents (Maher et al., 2007; Okada et al., 2008). Posttranscriptional mechanisms fine tune the canalicular ABCC2 expression. Lipopolysaccharide treatment, cytokines, estradiol-17β-D-glucuronoside, and hyperosmolar conditions all decreased the canalicular ABCC2 expression via posttranscriptional mechanisms in rodent models (Kubitz et al., 1999; Dombrowski et al., 2000; Paulusma et al., 2000; Mottino et al., 2002; Crocenzi et al., 2003; Fickert et al., 2006). These posttranscriptional modifications were associated with membrane retrieval and cytoplasmic accumulation of ABCC2, which was indicated by a "fuzzy" immunestaining pattern. A similar fuzzy pattern was observed in cholestatic patients (e.g., in primary biliary cirrhosis and obstructive cholestasis) (Zollner et al., 2001; Kojima et al., 2003).

ABCB1

ABCB1 (MDR1; MDR1a/MDR1b in rodents) protects the body from a broad variety of hydrophobic drugs and plays a key role in the development of multidrug resistance. ABCB1 also interacts with several biliary constituents (e.g., cholesterol, bile acids, phospholipids), but its contribution to bile formation and cholestasis remains to be established.

ABCB1, a 170-kDa member of the B subfamily (ABCB) of ABC transporters, consists of two nucleotide-binding and two 6-helical transmembrane domains (Fig. 3). ABCB1 is expressed at the apical membrane of intestinal epithelial cells, hepatocytes, renal tubular epithelial cells, endothelial vascular cells of the blood-brain and blood-testis barriers, and in cells of the adrenal gland, pancreas, lung, and placenta (Thiebaut et al., 1987; Sugawara et al., 1988). This expression pattern allows ABCB1 to inhibit the uptake of drugs from the intestinal lumen (bioavailability), decrease their entry in sanctuary organs, such as the brain and testes (distribution), and increase their renal and biliary elimination.

ABCB1 is a highly promiscuous transporter that interacts with nearly half of all registered pharmaceutical compounds (Nicolaou et al., 2012). ABCB1 transports mainly neutral or positively charged amphipathic compounds, although transport of negatively charged compounds (e.g., methotrexate) has been reported (Table 1) (de Graaf et al., 1996; Huang et al., 1998; Gerhard Ecker, 2009). Its unusual promiscuity has made it hard to find compounds that are not substrates. Accordingly, ABCB1 has been implicated in the transport of various endogenous compounds, such as cholesterol (Lee et al., 2013), steroids [e.g., cortisol, aldosterone, ethinylestradiol, estrone, estriol (Ueda et al., 1992; Kim

and Benet, 2004)], short-chain (not long-chain) phospholipids (van Helvoort et al., 1996; Morita et al., 2007), opioid peptides (Oude Elferink and Zadina, 2001), unconjugated bilirubin (Jetté et al., 1995; Watchko et al., 2001), and tetrahydroxylated bile acids (Megaraj et al., 2010). Most of these compounds were only investigated in vitro and/or showed a low affinity for ABCB1. For several of these substrates (e.g., phospholipids, unconjugated bilirubin, tetrahydroxylated bile acids) it consequently remains to be determined if ABCB1 actually contributes to their in vivo metabolism. Exogenous ABCB1 substrates include chemotherapeutics [e.g., paclitaxel (Fellner et al., 2002), topotecan (Li et al., 2008), etoposide (Takeuchi et al., 2006), teniposide (Vasanthakumar and Ahmed, 1989), doxorubicin (Ueda et al., 1987), vincristine (Cisternino et al., 2001), vinblastine (Cisternino et al., 2001), daunorubicin (Takeuchi et al., 2006), docetaxel (Shirakawa et al., 1999), mitomycin C (Hayes et al., 2001)], cytotoxic drugs [e.g., colchicines (Cisternino et al., 2003)], antihypertensives [e.g., losartan (Soldner et al., 1999), diltiazem (Katoh et al., 2006)], antiarrhythmics [e.g., verapamil (Soldner et al., 1999), digoxin (Pauli-Magnus et al., 2000)], antibiotics [e.g., erythromycin (Schuetz et al., 1998)], HIV-protease inhibitors [e.g., indinavir, ritonavir (Lee et al., 1998)], and various other xenobiotic compounds [rhodamine 123 (Bachmeier et al., 2005), Hoechst 33342 (Chen et al., 1993), calcein-AM (Holló et al., 1994)].

The physiologic function of ABCB1 has been extensively studied in mice. Mice possess, in contrast to humans, two genes that code for two ABCB1 proteins, namely *ABCB1a* and *ABCB1b*. Together, these proteins fulfill the same function as ABCB1 in humans. The deletion of these genes in mice did, somewhat surprisingly, not lead to a severe phenotype. *ABCB1a/ABCB1b* compound knockout mice were fertile, displayed a normal biliary composition and flow, and showed a normal life span under laboratory conditions. The absence of ABCB1a and ABCB1b, however, did result in an altered pharmacological profile of substrate drugs. This altered profile generally led to an increased bioavailability, an increased distribution volume (mainly to the brain), and a decreased renal/biliary elimination of ABCB1a/b substrates (Schinkel, 1998; Chen et al., 2003b). As a consequence, these animals displayed higher plasma and tissue (e.g., brain) levels of ABCB1a/b substrate drugs compared with their wild-type controls. Human *ABCB1* mutations and polymorphisms have also been extensively investigated and were (similarly) not associated with any severe phenotype (reviewed by Ieiri, 2012). *ABCB1* SNPs did affect the pharmacokinetic profile of several drugs, but results were equivocal and differed significantly between studies. Consequently, *ABCB1* genotype-directed drug dosing is not (yet) recommended in routine clinical practice (Wolf et al., 2011; Ieiri, 2012). *ABCB1* SNPs have also been associated with an increased susceptibility to various diseases, such as inflammatory bowel disease and colorectal cancer (Schwab et al., 2003; Andersen et al., 2009). The validity of these associations, however, remains to be established and deserves further investigation. The above-mentioned considerations do not infer that alterations in ABCB1 expression are of no consequence. Indeed, drug resistance that results from intrinsic (e.g., untreated) and acquired (e.g., drug-induced) ABCB1 overexpression remains a major problem in brain-targeted therapies and in anticancer treatment (Chan et al., 1991; Shukla et al., 2011). An increased expression of ABCB1 in tumor cells, for example, confers drug resistance by promoting the efflux of anticancer drugs (Gottesman et al., 2002; Sikic, 2006). Indeed, ABCB1 tumor overexpression has been associated with nonresponse to chemotherapy and a poor clinical prognosis in various cancers (Chan et al., 1991; Penson et al., 2004; Sikic, 2006). These considerations led to the development of ABCB1 inhibitors, which overcame drug resistance in animal models and tumor cell lines. Unfortunately, these inhibitors remained unsuccessful in clinical trials because of side effects and toxicity (reviewed by Shukla et al., 2011; Falasca and Linton, 2012). This lack of success may be due to the complexity of multidrug transport, in which the inhibition of one transporter may lead to compensatory effects that can alter drug handling and promote toxicity.

The role of ABCB1 in bile formation and cholestasis has yet to be elucidated. Bile formation seems unaffected in *ABCB1a/ABCB1b* knockout mice, as discussed above. ABCB1 is, however, significantly upregulated in the liver of cholestatic animal models and in liver specimens of patients with obstructive cholestasis, biliary atresia, and primary biliary cirrhosis (PBC) (Schrenk et al., 1993; Shoda et al., 2001; Zollner et al., 2003; Barnes et al., 2007). The reason for this upregulation remains unclear, but it might result in an increased canalicular excretion of toxins under cholestatic conditions. Interestingly, ABCB1a/b was shown to transport tetrahydroxylated bile acids in mice, albeit with a much lower affinity than ABCC2 (Megaraj et al., 2010). This transport could, as discussed in our section on ABCB11, mitigate the phenotype of *ABCB11* knockout mice. This hypothesis was supported by the observation that 1) ABCB1 was markedly upregulated in *ABCB11* knockout mice, and 2) that *ABCB11/ABCB1a/ABCB1b* compound knockout mice displayed a more severe cholestatic phenotype than single *ABCB11* knockouts (Wang et al., 2009b). ABCB1 may also protect hepatocytes against apoptosis under cholestatic conditions by exporting toxins (Sakaeda et al., 2002). Taken together, these observations support a compensatory role for ABCB1 during cholestasis. Its role in bile acid transport, however, is likely more important in mice than in humans, inasmuch as only mice are able to generate hydrophilic tetrahydroxylated bile acids as part of their adaptive response to cholestasis (Perwaiz et al., 2003).

ABCB1 transcription is mainly regulated via PXR, CAR, VDR, and FXR. PXR induced *ABCB1* transcription in the intestine, liver, and kidney. Its agonists (e.g., rifampicin) consequently decreased the intestinal uptake (bioavailability) and increased the (biliary/renal) elimination of ABCB1 ligands in healthy volunteers (Chen, 2010). CAR agonists (e.g., CITCO [6-(4-chlorophenyl)-imidazo[2,1-b][1,3] thiazole-5-carbaldehyde]) induced ABCB1 expression in brain capillary cells (Chen, 2010; Lemmen et al., 2013). VDR activation, via 1,25-dihydroxyvitamin D3, induced ABCB1 in the kidney and brain of mice (Chow et al., 2011). Chenodeoxycholic acid, a potent FXR agonist, induced ABCB1 expression in HepG2 cells (Martin et al., 2008). *FXR* knockout mice showed almost no increase in hepatic ABCB1 after bile duct ligation, which demonstrates that cholestatic upregulation of ABCB1 is largely FXR dependent in this animal model (Stedman et al., 2006). ABCB1 (post-) transcriptional regulation is certainly not the exclusive domain of these NRs. The tumor suppressor protein p53, for example, downregulates ABCB1a and ABCB1 and may influence drug resistance in cancer (Bush and Li, 2002). Rat ABCB1b is upregulated during endotoxin-induced cholestasis via tumor necrosis factor-α, which requires nuclear factor κB signaling (Ros et al., 2001). P53 actually increases ABCB1b and endotoxin treatment does not affect ABCB1a, which illustrates that the two rodent *ABCB1* genes are differentially regulated. Indeed the (post-) transcriptional regulation of human ABCB1 is highly complex and influenced by epigenetic methylation, micro-RNA expression, and various other mechanisms (reviewed by Labialle et al., 2002; Baker and El-Osta, 2004; Toscano-Garibay and Aquino-Jarquin, 2012).

ABCG2

ABCG2 (breast cancer resistance protein) is the final canalicular multidrug transporter that will be discussed in this review. Its main function is similar to that of ABCC2 and ABCB1, namely the

protection of the body against xenobiotics. ABCG2 does not seem to have a significant role in the adaptive response to cholestasis in the liver, although recent studies suggest that it is capable of bile acid transport. This transport, however, likely is more relevant in the placenta than in the liver.

ABCG2 is a 72-kDa member of the G subfamily (ABCG) of ABC transporters. Its structure consists of one N-terminal nucleotide-binding domain, and one C-terminal (6-helical) transmembrane domain (Fig. 3) (McDevitt et al., 2006; Ni et al., 2010). This structure is somewhat aberrant, because in most ABC transporters the transmembrane domain is located at the N-terminal end and the nucleotide-binding domain at the C-terminal end of the protein. ABCG2 is a half-transporter, like all members of the ABCG subfamily, and must at least dimerize to become functional. It is expressed at the apical membrane of intestinal epithelial cells (Gutmann et al., 2005), hepatocytes (Hilgendorf et al., 2007), renal tubular epithelial cells (Huls et al., 2008), endothelial vascular cells of the blood-brain and blood-testis barriers (Cooray et al., 2002; Fetsch et al., 2006), and cells of the placenta and mammary gland (Allikmets et al., 1998; Robey et al., 2011). Its expression pattern, at critical sites of uptake and elimination, resembles that of ABCB1. ABCG2 has consequently a similar effect on the bioavailability, distribution, and elimination of its ligands as ABCB1 (Vlaming et al., 2009; Agarwal et al., 2011). Because ABCG2 and ABCB1 are often colocalized and because they share many substrates, they can team up at critical barrier sites (Agarwal et al., 2011). This cooperation protects sanctuary organs, such as the brain, but may also prevent entry of chemotherapeutic drugs, which can lead to treatment failure (e.g., in brain cancer) (Agarwal et al., 2011).

ABCG2 is, like ABCB1, somewhat promiscuous when it comes to its exogenous substrates. In addition, it has been implicated in the transport of several endogenous compounds, including heme (Jonker et al., 2002), porphyrins (Jonker et al., 2002), folates (mono-, di-, and tri-glutamates of folic acid) (Lemos et al., 2009), urate (Woodward et al., 2009), sulfated steroids (Suzuki et al., 2003), and bile acids (Blazquez et al., 2012) (Table 1). Exogenous ABCG2 substrates include sulfuric acid [e.g., E3040S (Suzuki et al., 2003)]-, glucuronic acid [e.g., E3040G (Suzuki et al., 2003)]-, or glutathione-conjugated [e.g., dinitrophenyl glutathione (Suzuki et al., 2003)] compounds. ABCG2 also transports various unconjugated drugs, sometimes in cotransport with glutathione. It is, however, best known for its ability to transport chemotherapeutics, such as methotrexate (Chen et al., 2003c), topotecan (Maliepaard et al., 1999), mitoxantrone (Doyle et al., 1998), and the SN-38 metabolite of irinotecan (Maliepaard et al., 1999).

ABCG2 knockout mice did not, much like *ABCC2* and *ABCB1a/b* knockout mice, display a severe phenotype. This may well be because multidrug transporters have a considerable overlap in their substrates and sites of expression. If one gene is deleted, other transporters can compensate for its loss. A single gene deletion will therefore only have a limited phenotypic effect. *ABCG2* knockout mice did accumulate endogenous (i.e., protoporphyrin X) and dietary (i.e., pheophorbide) porphyrins, which induced protoporphyria (via protoporphyrin X) and phototoxic skin lesions (via pheophorbide) (Jonker et al., 2002). These mice also showed an increased bioavailability, an increased distribution volume (e.g., to the brain), and a decreased biliary/urinary elimination of ABCG2 substrate drugs (reviewed by Vlaming et al., 2009). *ABCG2* gene mutations and polymorphisms were (similarly) not associated with a severe phenotype in humans. *ABCG2* SNPs, however, were associated with an altered pharmacological profile of ABCG2 substrate drugs (e.g., sulfalazine, topotecan, statins) (reviewed by Ieiri, 2012). Interestingly, recent studies have demonstrated an association between *ABCG2* SNPs (e.g., rs2231142) and the development of gout (Dehghan et al., 2008; Woodward et al., 2009). These studies also identified uric acid as an ABCG2 substrate. ABCG2, like ABCB1, has been implicated to promote the efflux of anticancer drugs in tumor cell lines. Its role in drug resistance, however, remains to be established in a clinical setting, and clinical trials with ABCG2 inhibitors are currently not advisable (Falasca and Linton, 2012).

The role of ABCG2 in bile formation and cholestasis has been extensively debated. Mennone et al. (2010) failed to find a liver phenotype in bile duct-ligated or sham-operated *ABCG2* knockout mice. This result pleaded against a significant role of hepatic ABCG2 in the adaptive response to cholestasis. A recent study in pregnant *ABCG2* knockout mice by Blazquez et al. (2012), suggested that ABCG2 might affect bile acid transport in the placenta but not in the liver. This study also demonstrated bile acid transport by recombinant ABCG2 in WIF-B9/R cells, in Chinese hamster ovary cells, and in *Xenopus laevis* oocytes. Other in vitro studies have shown ABCG2-mediated bile acid transport in bacteria (Janvilisri et al., 2005), liver flukes (Kumkate et al., 2008), and transfected plasma membrane vesicles (Imai et al., 2002). Some in vitro studies, however, failed to demonstrate a role of ABCG2 in bile acid transport (Suzuki et al., 2003; Vaidya and Gerk, 2006). However, the majority of the available data from in vitro and animal studies suggests that ABCG2 is capable of bile acid transport. The importance of this transport may depend on the relative coexpression of other bile acid exporters (e.g., ABCB11, ABCC2) in the apical membrane (Mennone et al., 2010; Blazquez et al., 2012). The relative contribution of ABCG2 to bile acid transport will consequently be minimal in the liver because of to the presence of ABCB11 (and ABCC2). Placental ABCC2, however, has no (significant) coexpression of ABCB11 and may consequently play a major role in (local) bile acid transport (Patel et al., 2003).

ABCG2 transcription is regulated via CAR and PXR. CAR (phenobarbital, CITCO) and PXR (rifampicin and 2-acetylaminofluorene) ligands can thus increase ABCG2 expression in vitro (Jigorel et al., 2006; Lemmen et al., 2013). Other transcription factors can also induce *ABCG2*, and its promoter contains hypoxia, estrogen, progesterone, PPARγ, and aryl hydrocarbon receptor response elements (Ebert et al., 2005; Szatmari et al., 2006; Robey et al., 2011; To et al., 2011). Cytokines, growth factors, and micro-RNAs affected gene expression in various ways, whereas promoter methylation increased ABCG2 expression in vitro (Le Vee et al., 2009; Robey et al., 2011).

ABCB4

ABCB4 (MDR3; MDR2 in rodents) plays a key role in bile formation. Although ABCB11 transports bile acids, ABCB4 secretes phosphatidylcholine (PC). PC and cholesterol form mixed stable micelles with bile acids, which protect the biliary tree from their detergent effects.

ABCB4, a 170-kDa member of the B subfamily (ABCB) of ABC transporters, consists of two nucleotide-binding and two 6-helical transmembrane domains (Fig. 3) (Zhang, 1996). ABCB4 is predominantly expressed in the apical membrane of hepatocytes (Yoshikado et al., 2011; Pasmant et al., 2012), although low levels of mRNA transcripts have been detected in the adrenal glands, heart, striated muscles, tonsils, placenta, and brain (Smit et al., 1994; Patel et al., 2003; Augustine et al., 2005; Kim et al., 2008; Cui et al., 2009). This expression pattern supports its role as the major canalicular PC transporter in humans. ABCB4, a so-called floppase, translocates ("flops") PC from the inner to the outer leaflet of the canalicular membrane, from where it is extracted by bile acids (Smit et al., 1993). The association of PC with bile acids (and cholesterol) results in the

formation of mixed and stable micelles (Wang et al., 2009a). These micelles protect the epithelial lining of the biliary tree from bile acid–induced toxicity and phospholipid extraction (reviewed by Trauner et al., 2008). Although ABCB4 is a particularly specific PC transporter, it has a weak affinity for some ABCB1 substrate drugs (e.g., digoxin, paclitaxel, vinblastine; Table 1) (Smith et al., 2000). The clinical relevance of this transport, however, has not been established. Other drugs, such as oral contraceptives and itraconazole, can inhibit ABCB4 activity, which may result in drug-induced liver damage (Yoshikado et al., 2011; Pasmant et al., 2012).

A loss in ABCB4 function is not readily compensated and leads to severe hepatobiliary pathology in animal models and patients. *ABCB4* knockout mice are unable to excrete PC and consequently produce toxic bile. This toxicity is due to the relatively high nonmicellar ("free") bile acid concentration and leads to an increased permeability of the biliary epithelium, bile leakage, pericholangitis, periductal fibrosis, sclerosing cholangitis, and finally (in older mice) to hepatocellular carcinoma (Mauad et al., 1994; Fickert et al., 2002, 2004; Katzenellenbogen et al., 2007). The micro- and macroscopic damage observed in these animals closely resembles that of (primary) sclerosing cholangitis in humans (PSC). The impaired PC/bile acid micelle formation also decreases the canalicular extraction (i.e., secretion) and solubility of cholesterol. The latter results in the recurrent formation of cholesterol gallstones (Trauner et al., 2008). Patients with progressive familial intrahepatic cholestasis type 3 (PFIC3) are the human counterparts of *ABCB4* knockout mice. PFIC3 usually has a similar clinical presentation as PFIC2 (see *ABCB11* section) but may also present with recurrent choledocholithiasis in older children and adults (reviewed by Jacquemin, 2012). Although UDCA treatment can be helpful in the presence of a partial ABCB4 defect, hepatic transplantation will remain the only definitive therapy before gene therapy becomes available in most patients (Deleuze et al., 1996; De Vree et al., 1998). Patients with misfolding of the transporter, such as the reported PFIC3 heterozygous mutation I541F, may benefit from chaperone treatment to correct these folding defects in the future (Delaunay et al., 2009; Gautherot et al., 2012). Cyclosporine A was indeed able to restore a correct maturation of the endoplasmic reticulum sequestered I541F mutant in vitro (Gautherot et al., 2012). Less severe ABCB4 mutations can lead to the low phospholipid associated cholelithiasis syndrome (LPAC) and intrahepatic cholestasis of pregnancy (ICP). LPAC is characterized by the formation of cholesterol gallstones and may lead to progressive fibrosing cholestatic liver disease and portal hypertension (Zakim et al., 2011). ICP usually manifests in the second or third trimester of pregnancy and is associated with itching, abnormal liver biochemistry, and jaundice. Although it usually resolves spontaneously after delivery, it is associated with fetal risk (e.g., prematurity, neonatal respiratory distress syndrome) (Dixon et al., 2000). Both LPAC and ICP are treated with UDCA, which prevents gallstone formation in LPAC and improves symptoms and liver biochemistry in ICP. Bile duct ligation or partial hepatectomy only slightly enhanced ABCB4 expression in mice (Stedman et al., 2006; Csanaky et al., 2009), whereas TPN decreased ABCB4 expression in rats (Nishimura et al., 2005). Several other cellular stress conditions (e.g., endotoxin treatment) were not associated with an altered ABCB4 expression in animal studies (Vos et al., 1998).

ABCB4 regulation is still poorly understood but occurs partly via FXR and PPARα. FXR agonists (cholate, GW4064) transactivate the human *ABCB4* gene in vitro, which results in an increased maximal biliary PC secretion (Huang et al., 2003a). FXR thus regulates both biliary bile acid (ABCB11) and phospholipid (ABCB4) excretion. PPARα agonists (fibrates) also increased ABCB4 expression in human hepatocytes (Ghonem et al., 2012).

ABCG5/8

ABCG5/8 is the main sterol transporter and plays a key role in the biliary excretion of cholesterol and plant sterols (i.e., phytosterols). Mutations in the *ABCG5* or *ABCG8* gene lead to the development of sitosterolemia, which is characterized by sterol accumulation and atherosclerosis.

ABCG5 (73 kDa) and ABCG8 (76 kDa) are both members of the G subfamily of ABC transporters. Members of this transporter family are half transporters as mentioned in our section on ABCG2. ABCG5 and G8, which each consist of one nucleotide-binding and one 6-helical transmembrane domain, consequently need to combine to become functional (Fig. 3) (Graf et al., 2002). The ABCG5/8 heterodimer transports sterols (i.e., phytosterols and cholesterol; Table 1) and is expressed in the apical membrane of hepatocytes and enterocytes (Berge et al., 2000). This expression pattern allows ABCG5/8 to promote sterol excretion in the bile and to prevent sterol uptake from the intestinal lumen. *ABCG5/8* knockout mice displayed a 75% decrease in biliary cholesterol excretion, which showed a large but not exclusive role for ABCG5/8 in biliary cholesterol transport (the remaining 25% was partly transported by canalicular scavenger receptor B1) (Yu et al., 2002a; Klett et al., 2004; Wiersma et al., 2009; Dikkers et al., 2013). These mice do not display a severe cholestatic phenotype like *ABCB4* knockout mice, which indicates that mixed micelle formation remains adequate in the absence of this transporter (Yu et al., 2002a; Klett et al., 2004; Wiersma et al., 2009; Dikkers et al., 2013). Other studies in mice showed that ABCG5/8 overexpression protected against atherosclerosis. This protective effect was only present in mice that overexpressed this transporter both in the bile canaliculus and in the intestine, which illustrated the complementary effect of canalicular and intestinal ABCG5/8-mediated sterol transport (Yu et al., 2002b; Wilund et al., 2004). The role of ABCG5/8 in sterol transport was first discovered in sitosterolemia, which is characterized by an increased dietary absorption and a decreased biliary excretion of sterols (Berge et al., 2000; Lee et al., 2001). Patients with this rare inherited disease consequently accumulate phytosterols (e.g., sitosterol, stigmasterol, campesterol, 5α-cholestanol, 5α-campestanol, 5α-sitostanol, 22-dehydrocholesterol, brassicasterol, and 24-methylene cholesterol) and cholesterol in their blood and suffer from premature development of atherosclerosis (Berge et al., 2000). Because sitosterolemia is caused by mutations in the *ABCG5* or *ABCG8* gene, it was concluded that cholesterol and the above-mentioned plant sterols are ABCG5/G8 substrates. *ABCG5/8* polymorphisms, such as the common SNP rs11887534, also increase the risk of cholesterol gallstones (and lead to obstructive cholestasis), likely by increasing the biliary cholesterol content (Grünhage et al., 2007). Apart from its role in gallstone formation, ABCG5/8 does not seem to be a major contributor to cholestatic disease, as illustrated by the absence of a cholestatic phenotype in *ABCG5/8* knockout mice and sitosterolemia patients.

ABCG5/8 transcription is mainly regulated via the liver X receptor (LXR) and FXR (Janowski et al., 1996; Lehmann et al., 1997; Janowski et al., 1999; Gupta et al., 2002; Freeman et al., 2004). LXR is activated by oxysterols and promotes sterol excretion (ABCG5/8) and the conversion of cholesterol into bile acids (CYP7A1) in rodents (Gupta et al., 2002). FXR inhibits liver receptor homolog-1 (via SHP), which decreases ABCG5/8 expression in human liver and intestinal cell lines (Freeman et al., 2004). FXR also inhibits CYP7A1 and CYP8B1, which leads to a reduced bile acid synthesis (Gupta et al., 2002). FXR and LXR thus have opposite effects on ABCG5/8 and bile acid synthesis. Several other transcription factors also play a role in *ABCG5/8* transactivation. GATA-binding protein 4 (GATA4), GATA6, and hepatocyte nuclear factor 4-α synergistically induce human *ABCG5/8*

transcription in vitro (Sumi et al., 2007). Thyroid hormone also increased biliary cholesterol excretion in animal models by increasing ABCG5/8 expression, although the exact mechanism remains to be elucidated (Gälman et al., 2008; Bonde et al., 2012). Treatment with thyroid hormone and its liver specific agonists (e.g., eprotirome, sobetirome) significantly lowered cholesterol in various animal models, although its use in humans will be limited because of potential side effects and the safety and efficacy of statin treatment. Insulin resistance can, finally, increase ABCG5/8 expression in mice via disinhibition of the forkhead box O1A transcription factor by insulin (Biddinger et al., 2008).

Canalicular ABC Transporters and Their Regulatory NRs as Drug Targets

Canalicular ABC transporters and their NRs play a key role in bile formation and cholestasis. As such they are attractive targets for the treatment of cholestatic disease. We will therefore briefly discuss the effect of several important (experimental) treatment strategies on their expression.

UDCA, the only Food and Drug Administration–approved drug for cholestasis, promoted the canalicular insertion of ABCB11, ABCC2, and ABCB4 in rodents (Beuers et al., 2001; Fickert et al., 2001; Kurz et al., 2001). This posttranscriptional modification stimulated bile flow (ABCB11, ABCC2) and promoted the excretion of various biliary constituents (e.g., bile acids, glutathione, phospholipids) (reviewed by Poupon, 2012). Although UDCA has limited transcriptional effects, it also acts as a weak FXR and (after intestinal conversion to lithocholic acid) PXR agonist in in vitro and animal studies (Staudinger et al., 2001; Lew et al., 2004). The activation of these NRs increased the canalicular (e.g., ABCB11, ABCC2) and basolateral (e.g., ABCC3, ABCC4) expression of bile acid exporters (reviewed by Poupon, 2012; Halilbasic et al., 2013). UDCA has, in addition, various other beneficial effects, such as increasing the hydrophilicity of the circulating bile acid pool, cytoprotection against bile acids and cytokines, immune modulation, and anti-inflammatory effects (reviewed by Poupon, 2012). In PBC patients, UDCA combined with budesonide (but not UDCA or budesonide alone) restored the activity of cholangiocyte anion exchanger 2, which mitigated the impaired choleresis in these patients (Arenas et al., 2008). UDCA also induced the antimicrobial peptide cathelicidin in PBC patients, presumably via VDR activation (D'Aldebert et al., 2009).

The development of norUDCA, a side chain shortened UDCA analog, represents a promising new treatment strategy for cholestatic bile duct diseases. NorUDCA does not exert its primary therapeutic effects via canalicular ABC transporters, although it did increase ABCB11 activity in vitro (Kagawa et al., 2013). Nevertheless, it almost completely reversed sclerosing cholangitis in the *ABCB4* knockout mouse model for PFIC3/PSC (Fickert et al., 2006). Its suggested therapeutic mechanisms include an increased hydrophilicity of the circulating bile acid pool, protection of injured bile ducts by a bicarbonate-rich choleresis, a decreased hepatocellular bile acid load by the induction of basolateral bile acid efflux transporters and bile acid detoxification pathways (phase I and II enzymes), and various anti-inflammatory and antifibrotic properties (reviewed by Trauner et al., 2008). NorUDCA supposedly has an intrinsic capacity to undergo cholehepatic shunting, which is essential for several of its beneficial effects (e.g., biliary HCO_3^- output) (Halilbasic et al., 2009). The above-mentioned beneficial effects clearly favor its therapeutic potential, and norUDCA treatment is currently being evaluated in PBC and PSC patients.

The past years have witnessed the development of several synthetic FXR activators. These activators have a far higher affinity for FXR than natural bile acids and can be either bile acid- or non-bile acid-derived. The hepatoprotective effects of these activators have been convincingly demonstrated in animal studies. FXR activation in rodents promoted bile formation via ABCB11, ABCC2, ABCB1, and ABCB4. FXR also repressed hepatocellular bile acid uptake and synthesis and promoted bile acid elimination and detoxification, as discussed in our section on bile acid metabolism. GW4064, a non-bile acid-based FXR activator, and 6*E*-chenodeoxycholic acid (INT747), a synthetic bile acid analog, ameliorated obstructive and chemically induced cholestasis in rats (Liu et al., 2003; Fiorucci et al., 2005). INT767, another synthetic bile acid analog, mitigated biliary fibrosis and portal inflammation in the *ABCB4* knockout mouse. INT767 increased, among others, the biliary bicarbonate content in these animals, which decreased biliary toxicity (Baghdasaryan et al., 2011). FXR activation also has anti-inflammatory properties, because chenodeoxycholic acid treatment induced the expression of the antimicrobial peptide cathelicidin in the human biliary epithelium (D'Aldebert et al., 2009). Finally, FXR activation via GW4064 counteracted bacterial overgrowth in bile duct–ligated rodents (Ogata et al., 2003). FXR activation thus promotes bile formation, decreases the hepatocellular bile acid load, decreases biliary toxicity, and has anti-inflammatory and antimicrobial effects. In recent phase II clinical trials, INT747 with or without UDCA cotreatment ameliorated the biochemical markers of liver damage in PBC patients that were nonresponsive to UDCA alone. Results of a multicenter INT747 trial in UDCA-responsive PBC patients are currently awaited (Mason et al., 2010; Hirschfield et al., 2011; Kowdley et al., 2011).

PXR and CAR induce bile acid detoxification, bile acid elimination, and bilirubin glucuronidation, as discussed in our section on bile acid metabolism. Several PXR and CAR ligands have been used to treat pruritus or jaundice long before their mode of action became known. Rifampicin, a classic PXR agonist, is used to treat pruritus in cholestatic patients and ameliorated biochemical markers of liver damage in PBC patients (Bachs et al., 1989; Cançado et al., 1998; Yerushalmi et al., 1999). Rifampicin induced bile acid and bilirubin elimination via canalicular ABCC2. In addition, it induced bile acid detoxification (CYP3A4) and bilirubin conjugation (UGT1A1) in rodents (Marschall et al., 2005). Its antipruritic effect may partly involve PXR-mediated transactivation of autotaxin, a recently identified mediator of pruritus (Kremer et al., 2012). Phenobarbital, a potent CAR agonist, was used to treat neonatal jaundice in the 1960s and exerts its hypobilirubinemic effect by inducing ABCC2 and UGT1A1 (reviewed by Cuperus et al., 2009).

PPARs, finally, are fatty acid-activated NRs that play an important role in lipid homeostasis. These NRs, however, also play a role in bile formation and cholestasis. Treatment with the PPARα agonist fenofibrate increased the canalicular expression of ABCB4 in human hepatoma cells, which may be beneficial in patients with inherited ABCB4 defects (i.e., PFIC3, LPAC, and ICP) (Ghonem et al., 2012). In addition, PPARα decreased bile acid synthesis (CYP7A1) and induced bile acid detoxification (SULT2A1, UGT2B4, UGT1A3) in animal models (Patel et al., 2000; Jung et al., 2002; Barbier et al., 2003; Fang et al., 2005). The PPAR agonist bezafibrate showed beneficial effects in PBC patients in pilot trials, although these results need to be confirmed by larger randomized-controlled clinical trials (Honda et al., 2013).

Conclusion and Perspectives

Canalicular ABC transporters and their regulatory transporters play a key role in the pathogenesis and pathophysiology of cholestatic disorders. The study of these transporters has provided researchers and

clinicians with a molecular framework that allows the development of novel treatment strategies. The clinical implementation of some of these treatments (e.g., FXR agonists, norUDCA) will likely benefit cholestatic patients in the near future.

Authorship Contributions

Wrote or contributed to the writing of the manuscript: Cuperus, Claudel, Gautherot, Halilbasic, Trauner.

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