

Impaired hepatic uptake by organic anion-transporting polypeptides is associated with hyperbilirubinemia and hypercholanemia in *Atp11c* mutant mice

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Running title: Impaired hepatic uptake by Oatps in *Atp11c* mutant mice

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List of abbreviations:

BAs; bile acids, Bsep; bile salt export pump, $CL_{\text{bile, liver}}$; biliary clearance normalized by the liver concentration, $CL_{\text{bile, plasma}}$; biliary clearance normalized by circulating plasma concentration, CL_{total} ; total plasma clearance, CM; canalicular membrane, $C_{\text{ss, liver}}$; liver concentrations at steady-state, $C_{\text{ss, plasma}}$; plasma concentrations at steady-state, $E_217\beta\text{G}$; 17 β estradiol 17 β -D-glucuronide, LPMs; liver plasma membranes, Mrp2; multidrug resistance associated protein 2, NaK; Na⁺, K⁺-ATPase α 1 subunit, Ntcp; Na⁺-taurocholate co-transporting polypeptide, Oatps; organic anion transporting polypeptides, PFIC; progressive familial intrahepatic cholestasis, qPCR; quantitative PCR, SEM; standard error of the mean, TA; taurocholic acid, $V_{\text{ss, bile}}$; biliary excretion rate at steady-state,

Abstract

Biliary excretion of organic anions such as bile acids (BAs) is the main osmotic driving force for bile formation, and its impairment induces intrahepatic cholestasis. We investigated the involvement of *Atp11c* in the hepatic transport of organic anions using *Atp11c* mutant mice, which exhibit hypercholanemia and hyperbilirubinemia. Pharmacokinetic analysis following a constant intravenous infusion in *Atp11c* mutant mice showed decreased hepatic sinusoidal uptake and intact biliary secretion of [³H]-17 β estradiol 17 β -D-glucuronide ([³H]-E₂17 β G). Consistent with this result, compared with cells and membranes from control mice, isolated hepatocytes and liver plasma membranes (LPMs) from *Atp11c* mutant mice had a much lower uptake of [³H]-E₂17 β G and expression of organic anion-transporting polypeptides (Oatps), which are transporters responsible for hepatic uptake of unconjugated BAs and organic anions including bilirubin–glucuronides. Uptake of [³H]-TC into hepatocytes and expression of Na⁺-taurocholate cotransporting polypeptide in LPMs, which mediates hepatic uptake of conjugated BAs, was also lower in the *Atp11c* mutant mice. Bile flow rate, biliary BA concentration, and expression of hepatobiliary transporters did not differ between *Atp11c* mutant mice and control mice. These results suggest that *Atp11c* mediates the transport of BAs and organic anions across the sinusoidal membrane, but not the canalicular membrane, by regulating the abundance of transporters. *Atp11c* is a candidate gene for genetically undiagnosed cases of hypercholanemia and hyperbilirubinemia but not of intrahepatic cholestasis. This gene may influence the pharmacological and adverse effect of drugs because Oatps regulate their systemic exposure.

Introduction

The biliary excretion of bile acids (BAs) and glutathione from the hepatocyte is the main osmotic driving force for bile formation. Transport of BAs across the sinusoidal membrane is mediated by uptake transporters, Na⁺-taurocholate cotransporting polypeptide (Ntcp) (Hagenbuch and Meier, 1994; Hagenbuch et al., 1991) and organic anion transporting polypeptides (Oatp) (Meier and Stieger, 2002; Trauner and Boyer, 2003). After reaching the canalicular membrane (CM), monovalent taurine- and glycine-conjugated BAs (such as taurocholic acid (TC)) and sulfated BAs amidates and bile salt ethereal glucuronides (divalent) are secreted into bile by the bile salt export pump (Bsep) (Byrne et al., 2002; Gerloff et al., 1998; Hayashi et al., 2005b; Noe et al., 2002) and the multidrug resistance-associated protein 2 (Mrp2) (Akita et al., 2001; Kuipers et al., 1988; Takikawa et al., 1991), respectively, both of which are ATP-binding cassette transmembrane transporters located on the CM. Impaired transport of BAs across the CM causes intrahepatic cholestasis, a state of reduced bile flow that is an acquired or inherited syndrome, and results in hepatocellular damage because a high concentration of BAs is toxic.

One of the most severe forms of intrahepatic cholestasis is progressive familial intrahepatic cholestasis (PFIC), a heterogeneous group of inherited autosomal recessive liver diseases. This group of diseases is characterized by intrahepatic cholestasis and jaundice in the first year of life and progression to severe cholestasis with sustained intractable itching, jaundice, watery diarrhea, and failure to thrive, which eventually leads to liver failure and death before adulthood (Davitt-Spraul et al., 2009; Morotti et al., 2011). PFIC is subdivided based on the serum GGT level and the causal genes (Davitt-Spraul et al., 2009). *ATP8B1* and *ABCB11* have been identified as the genes responsible for PFIC associated with a normal GGT level (Bull et al., 1998; Strautnieks et al., 1998). However, about one-third of affected individuals with a normal GGT level have no mutations in either gene (Davitt-Spraul et al., 2010). In PFIC patients with mutations in *ABCB11*

encoding BSEP, biliary BAs secretion is impaired because of the compromised expression of BSEP and/or abolished transport activity of BSEP (Hayashi et al., 2005a; Wang et al., 2002). ATP8B1 is a member of the P4 subfamily of P-type adenosine triphosphatases (P4-ATPases) and translocates aminophospholipid from the outer leaflet to the inner leaflet in lipid bilayer of biological membranes (Paulusma et al., 2008; Ray et al., 2010; Takatsu et al., 2014). It has been suggested that a deficiency in ATP8B1 causes secondary suppression of BSEP-mediated BAs excretion into bile by disrupting the well-organized aminophospholipid asymmetry in the CM (Paulusma et al., 2009; Paulusma et al., 2006) or through mass action related to the decreased expression of BSEP mRNA (Chen et al., 2004).

Considering these underlying mechanisms, we have begun to search for agents that have therapeutic potency in patients with mutations in *ATP8B1* and *ABCB11*. We have published experimental and clinical evidence that 4-phenylbutyrate, a drug used to treat ornithine transcarbamylase deficiency, has an additional pharmacological effect that increases the expression of BSEP on the CM (Hayashi and Sugiyama, 2007) and improves liver function and/or pruritus in these PFIC patients (Hasegawa et al., 2014; Naoi et al., 2014). The development of therapeutic methods to treat other PFIC patients and understanding of the mechanism underlying intrahepatic cholestasis caused by inherited genetic defects require the identification of other genes that are causally associated with PFIC in the remaining 30% of patients with a normal GGT level.

Recently, two independent groups have constructed mutant mice that have inherited an N-ethyl-N-nitrosourea-induced point mutation in *Atp11c* (Siggs et al., 2011a; Yabas et al., 2011) that encodes a P4-type ATPase and functions as an aminophospholipid flippase (Segawa et al., 2014; Takatsu et al., 2014; Yabas et al., 2011). These mutant mice developed cell-intrinsic arrest of adult B lymphopoiesis and presented with anemia and hyperbilirubinemia (Siggs et al., 2011a; Yabas et al., 2014; Yabas et al., 2011). Subsequent detailed analysis of hyperbilirubinemia involving bone marrow transplantation and biochemical

testing indicated that the hyperbilirubinemia derived from a deficiency in the function of *Atp11c* in nonhematopoietic cells. *Atp11c* mutant mice showed elevated total plasma BAs and bilirubin levels, but normal GGT level, compared with control mice (Siggs et al., 2011b). Considering that *Atp11c* is expressed predominantly in the liver (Siggs et al., 2011b), in the present study, we used *Atp11c* mutant mice to examine whether *ATP11C* could be the causal gene of PFIC associated with a normal GGT level. The influence of *Atp11c* deficiency on hepatobiliary transport was evaluated *in vivo* using a constant intravenous infusion of [³H]-TC and [³H]-17 β estradiol 17 β -D-glucuronide ([³H]-E₂17 β G) into *Atp11c* mutant mice and subsequent pharmacokinetic analysis and *in vitro* biological, histological, and transport functional experiments using livers from the mutant mice.

Materials and Methods

Reagents and antibodies

[³H]-TC (2 Ci/mmol) and [³H]-E₂17 β G (55 Ci/mmol) were obtained from PerkinElmer Life Sciences (Boston, MA). Antibodies against *Atp11c*, *Bsep*, and *Ntcp* were purchased from Abcam (Cambridge, MA). Anti-Mrp2, and Na⁺, K⁺-ATPase α 1 subunit (NaK) antibodies were obtained from Santa Cruz Biotechnology (Santa Cruz, CA). Antisera to Mrp3, Oatp1b2, and Oatp1a4 were raised in rabbits as described previously (Hirohashi et al., 2000; Ose et al., 2010; Sasaki et al., 2004). All other chemicals were of analytical grade.

Mice

The mouse strain with an *Atp11c*^{emptyhive} allele, which contains an X-linked N-ethyl-N-nitrosourea-induced point mutation in *Atp11c* on a pure C57BL/6J background

(C57BL/6J-*Atp11c*^{m1Btr}/Mmjax) (Siggs et al., 2011a; Siggs et al., 2011b), was obtained from the Mutant Mouse Regional Resource Center (www.mmrrc.org). This strain was maintained by breeding of hemizygous male mice (*Atp11c*^{emptyhive/Y}) with heterozygous female mice (*Atp11c*^{emptyhive/+}). At 9-14 weeks of age, the mice were fasted for 12 h and used for the experiments.

Genotyping of offspring was performed using genomic DNA isolated from tail biopsies. The *Atp11c*^{emptyhive} allele has a 2113C>T mutation in *Atp11c* that confers resistance to restriction by Mbol to *Atp11c*. A partial sequence (359 base pairs) of *Atp11c*, which included the mutated sites in the *Atp11c*^{emptyhive} allele, was amplified using PCR involving 5'-TGAGCTACAGCACTCAGCAGC-3' (forward) and 5'-TTGGAAAAGGCGGCAGGCATAGC-3' (reverse) as primers. The samples were digested by Mbol for 1 h at 37°C, and analyzed by electrophoresis. The products from male control (*Atp11c*^{+Y}) mice and female control (*Atp11c*^{+/+}) mice were digested into two bands of 242 and 117 base pairs, whereas those from male hemizygous (*Atp11c*^{emptyhive/Y}) mice and female homozygous (*Atp11c*^{emptyhive/emptyhive}) mice were detectable as a single band of 359 base pairs (Figure 1A). All three bands were observed in the products from female heterozygous (*Atp11c*^{+/emptyhive}) mice.

All animals were maintained under standard conditions with a reversed dark–light cycle and were treated humanely. Food and water were available ad libitum. The studies reported in this manuscript were carried out in accordance with the guidelines provided by the Institutional Animal Care Committee (Graduate School of Pharmaceutical Sciences, The University of Tokyo, Tokyo, Japan).

Analysis of serum, liver, and bile composition

Biochemical testing of serum was outsourced to Oriental Yeast Co. (Tokyo, Japan). Lipids and BAs were extracted from serum, liver, and bile using the Bligh-Dyer method (Bligh and Dyer, 1959) and then

subjected to enzymatic measurement of BAs concentration (Wako Pure Chemical Industries, Tokyo, Japan).

***In vivo* infusion study in mice**

Male mice (9-14 weeks old) were fasted for 12 h and then subjected to an *in vivo* infusion study using [³H]-TC and [³H]-E₂17βG as described (Hayashi et al., 2012b; Hayashi and Sugiyama, 2007; Hirano et al., 2005). [³H]-TC or [³H]-E₂17βG in saline was infused through the jugular vein cannula at a rate of 500 and 13.3 pmol/min/kg for 60 min, respectively. Blood and bile specimens were obtained at specified times. The radioactivity associated with the plasma, bile, and liver was measured in a liquid scintillation counter (LS 600SC; Beckman, Fullerton, CA) as described previously (Hayashi et al., 2012b; Hayashi and Sugiyama, 2007).

Pharmacokinetic analysis.

The total plasma clearance (CL_{total}), biliary clearance normalized by circulating plasma concentration (CL_{bile, plasma}), and biliary clearance normalized by the liver concentration (CL_{bile, liver}) were calculated from the equations $CL_{total} = I/C_{ss, plasma}$, $CL_{bile, plasma} = V_{ss, bile}/C_{ss, plasma}$, and $CL_{bile, liver} = V_{ss, bile}/C_{ss, liver}$, respectively, where *I* represents the infusion rate (pmol/min/kg), *C*_{ss, plasma} represents the steady-state plasma concentrations (nM), *V*_{ss, bile} represents the steady-state biliary excretion rate (pmol/min/kg), and *C*_{ss, liver} represents the average steady-state hepatic concentration (pmol/g liver) (Hayashi et al., 2012b; Hayashi and Sugiyama, 2007). The steady-state plasma concentrations (*C*_{ss, plasma}) was determined as the mean of the plasma concentration of [³H]-TC or [³H]-E₂17βG at 30, 45, and 60 min. The steady-state biliary excretion rate at steady-state (*V*_{ss, bile}) was determined as the mean of the biliary excretion rate for [³H]-TC or [³H]-E₂17βG from 30 to 45 min and from 45 to 60 min. *C*_{ss, liver} was determined as the average hepatic concentration of [³H]-TC or [³H]-E₂17βG at

the end of the in vivo experiment.

Uptake study using isolated hepatocytes

Hepatocytes were isolated from *Atp11c*^{+Y} and *Atp11c*^{emptyhive/Y} mice using the collagenase perfusion method (Yamazaki et al., 1993), suspended in Krebs–Henseleit buffer, and adjusted to 2.0×10^6 cells/ml. The hepatocyte suspensions were prewarmed at 37°C for 3 min and then subjected to the uptake assay as described previously (Hirano et al., 2004). The uptake of [³H]-TC and [³H]-E₂17βG into hepatocytes at the designed time points was evaluated by measuring the amount of intracellular [³H]-TC or [³H]-E₂17βG.

Western blot analysis

Liver plasma membranes (LPMs) was prepared from *Atp11c*^{+Y} and *Atp11c*^{emptyhive/Y} mice, loaded to the wells of 7 or 10% SDS-PAGE gel with a 3.75 % stacking gel, and then subjected to Western blot analysis as described previously (Hayashi et al., 2012a; Hayashi et al., 2012b; Hayashi and Sugiyama, 2007; Mizuno et al., 2015). Immunoreactivity was detected with an ECL Prime Western Blotting Detection Reagent (Amersham Biosciences, Piscataway, NJ). The intensity of the band indicating each protein was quantified using Multi Gauge software (v.2.0; Fujifilm, Tokyo, Japan).

Determination of mRNA levels.

Total RNA from the liver specimens of mice was isolated using ISOGEN II (Nippon Gene, Tokyo, Japan) according to the manufacturer's instructions. Reverse transcription was performed with ReverTra Ace qPCR RT Master Mix with gDNA Remover (Toyobo, Tokyo, Japan). The mRNA level for each protein were measured by real-time quantitative PCR (qPCR) using a LightCycler 480 system II (Roche Diagnostics,

Mannheim, Germany) as described previously (Hayashi et al., 2012b; Hayashi and Sugiyama, 2007; Naoi et al., 2014). The following primer sequences were used: 5'-CTGTCATCAATGTGGGCAAC-3' (forward) and 5'-CTGTTTCCATGCTGATGGTG-3' (reverse) for *Ntcp*, 5'-TAGCTTGCCTCCAGTATGCCTT-3' (forward) and 5'-ACAGGCCAAATGCTATGTATGC-3' (reverse) for *Oatp1a1*, 5'-CAAGCTTTCTCCCTGCACTCTT-3' (forward) and 5'-TCCTTCGCAGTGAGCTTCATT-3' (reverse) for *Oatp1a4*, 5'-AGCAATGATCGGACCAATCCT-3' (forward) and 5'-AACCCAACGAGCATCCTGA-3' (reverse) for *Oatp1b2*, and 5'-AGAACATCATCCCTGCATCC-3' (forward) and 5'-CACATTGGGGGTAGGAACAC-3' (reverse) for *Gapdh*. Gene expression for each reaction was normalized by the internal control (*Gapdh*).

Immunohistochemistry

The liver was removed from *Atp11c*^{+/-Y} and *Atp11c*^{emptyhiv/Y} mice, cut into small pieces, embedded in OCT compound (Sakura Finetek, Torrance, CA), and frozen in liquid nitrogen. Ten-micrometer-thick sections were prepared from the frozen sections using a cryostat (Leica CM 1950; Leica, Solms, Germany), mounted onto cover glasses (Matsunami Glass Ind. Ltd., Osaka, Japan), air-dried, fixed in 4% paraformaldehyde/PBS for 10 min, permeabilized in 0.1% saponin/PBS for 10 min, blocked with 3% BSA/PBS for 30 min, and stained with primary antibodies for 2 h and then with the appropriate Alexa Fluor-conjugated secondary antibodies for 1 h. These staining procedures were performed at room temperature. The specimens were mounted with VECTASHIELD mounting medium (Vector Laboratories Inc., Burlingame, CA) and then visualized by confocal microscopy using a Leica TCS SP5 II laser scanning confocal microscope.

Statistical analysis

Experiments were repeated at least three times, and the data are presented as mean \pm standard error of the mean (SEM). *p*-values between two variables were calculated at the 95% confidence level using unpaired Student's *t* tests. The data were analyzed using Prism software (GraphPad Software, La Jolla, CA).

Results

Expression of Atp11c in LPMs from mice

LPMs were prepared from *Atp11c*^{+Y} and *Atp11c*^{emptyhiv/Y} mice and analyzed by Western blot analysis. The immunosignal derived from the antibody against Atp11c was observed as two bands, about 120 and 90 kDa, in LPMs from *Atp11c*^{+Y} mice, but was undetectable in those from *Atp11c*^{emptyhiv/Y} mice (Figure 1B). The smaller band of Atp11c could be produced by caspase-mediated cleavage (Segawa et al., 2014). As reported previously, the liver function tests showed markedly elevated concentrations of total and direct bilirubin and total BAs, and normal activity of GGT in the plasma of *Atp11c*^{emptyhiv/Y} mice (Siggs et al., 2011a) (Table 1). Moderate but significant increases in ALT, AST, ALP, and LAP were observed in *Atp11c*^{emptyhiv/Y} mice.

Hepatobiliary transport of [³H]-TC and [³H]-E₂17βG in *Atp11c*^{emptyhiv/Y} mice

The constant intravenous infusion study with [³H]-TC, a typical BA that is taken up predominantly into hepatocytes by Ntcp and excreted into bile by Bsep, showed that the *C*_{ss, plasma} (plasma concentrations at steady-state), *C*_{ss, liver} (liver concentrations at steady-state), and *V*_{ss, bile} (biliary excretion rate at steady-state) for [³H]-TC did not differ significantly between *Atp11c*^{+Y} and *Atp11c*^{emptyhiv/Y} mice (Figure 2A, C and Table 2).

Consequently, the CL_{total} , $CL_{bile, plasma}$, and $CL_{bile, liver}$ for [3H]-TC, which represents its disappearance from the body, vectorial transport from the sinusoidal space to the canaliculus through hepatocytes, and hepatobiliary transport across the canalicular membrane, respectively, did not differ significantly between *Atp11c*^{+Y} and *Atp11c*^{emptyhiv/Y} mice (Table 2). The bile flow rate during the infusion assay with [3H]-TC was almost the same in the *Atp11c*^{+Y} and *Atp11c*^{emptyhiv/Y} mice and was constant in both mice strains (Figure 2E).

[3H]-E₂17 β G undergoes vectorial transport through Oatps and Mrp2, which mediate the hepatic uptake of unconjugated BAs (Meier et al., 1997; van de Steeg et al., 2010) and biliary excretion of sulfated BAs amidates and BAs ethereal glucuronides (divalent) (Akita et al., 2001; Kuipers et al., 1988; Takikawa et al., 1991), respectively. To gain further insight into the hepatobiliary transport of BAs, [3H]-E₂17 β G was infused intravenously into *Atp11c*^{+Y} and *Atp11c*^{emptyhiv/Y} mice. The $C_{ss, liver}$ and $V_{ss, bile}$ of [3H]-E₂17 β G did not differ significantly between these mice (Figure 2D and Table 3), whereas the $C_{ss, plasma}$ of [3H]-E₂17 β G was 2.1-fold higher in *Atp11c*^{emptyhiv/Y} mice than in *Atp11c*^{+Y} mice (Figure 2B and Table 3). The bile flow rate during the infusion assay with [3H]-E₂17 β G was almost the same in the *Atp11c*^{+Y} and *Atp11c*^{emptyhiv/Y} mice and was constant in both mice (Figure 2F). Consequently, the CL_{total} and $CL_{bile, plasma}$ for [3H]-E₂17 β G were about 50 and 60% lower in *Atp11c*^{emptyhiv/Y} mice than in *Atp11c*^{+Y} mice (Table 3). By contrast, the $CL_{bile, liver}$ for [3H]-E₂17 β G did not differ significantly between these mice. These results suggest that *Atp11c*^{emptyhiv/Y} mice exhibited decreased hepatic uptake, but with normal biliary excretion of E₂17 β G and unconjugated BAs. Consistent with these results, the bile flow rate and biliary concentrations of BAs did not differ between *Atp11c*^{+Y} and *Atp11c*^{emptyhiv/Y} mice (Table 4).

Uptake of [3H]-TC and [3H]-E₂17 β G into hepatocytes from *Atp11c*^{emptyhiv/Y} mice

To confirm the decreased hepatic uptake of [3H]-TC and [3H]-E₂17 β G in *Atp11c*^{emptyhiv/Y} mice,

hepatocytes were isolated from *Atp11c*^{+/-} and *Atp11c*^{emptyhiv/-} mice and subjected to an uptake study. Time-dependent uptake of [³H]-TC and [³H]-E₂17βG into the hepatocytes from both mice was observed, but was markedly decreased in the presence of 100 μM unlabeled compounds (Figure 3A and B). The saturable component of the hepatic uptake for [³H]-TC and [³H]-E₂17βG, which was calculated from the slope of the hepatic uptake between 0.5 and 2 min, was compromised substantially in the hepatocytes from *Atp11c*^{emptyhiv/-} mice. Its value for [³H]-TC and [³H]-E₂17βG in the hepatocytes from *Atp11c*^{emptyhiv/-} mice was 18% and 6% of that in cells from *Atp11c*^{+/-} mice (Figure 3C and D), suggesting decreased function of the hepatic transporters responsible for uptake of BAs and bilirubin-glucuronides in *Atp11c*^{emptyhiv/-} mice.

Hepatic expression of BAs transporters in *Atp11c*^{emptyhiv/-} mice

Consistent with results of the *in vitro* uptake study using the isolated hepatocytes, analysis of LPMs by Western blot analysis showed markedly decreased expression of the sinusoidal transporters responsible for BAs uptake, Oatp1b2, Oatp1a4, and Ntcp, in *Atp11c*^{emptyhiv/-} mice (Figure 4A). NaK, another sinusoidal membrane protein, was unaffected in *Atp11c*^{emptyhiv/-} mice, suggesting that the role of Atp11c in the maintenance of the expression of sinusoidal membrane proteins is relatively specific for Oatps and Ntcp. In contrast to the altered expression of sinusoidal transporters for BAs uptake, the abundance of Bsep and Mrp2, both of which mediate biliary excretion of BAs across the CM, did not differ between mice. Together with the finding that *Atp11c*^{+/-} and *Atp11c*^{emptyhiv/-} mice had similar expression level of Mrp3, which mediates the basolateral efflux of BAs and bilirubin-glucuronides and is upregulated by hepatic accumulation of bile constituents, this result is consistent with the intact CL_{bile, liver} for [³H]-TC and [³H]-E₂17βG and normal bile flow rate and biliary BAs concentration in *Atp11c*^{emptyhiv/-} mice (Table 2–4).

mRNA expression of hepatic BAs transporters was measured using qPCR and normalized by that of

Gapdh. The mRNA expression levels of Oatp1b2, Ntcp, and Bsep were about 20% lower in *Atp11c*^{empty/hivc^Y} mice than in *Atp11c*^{+^Y} mice (Figure 4B). However, this difference is unlikely to explain the markedly decreased expression of Oatp1b2 and Ntcp.

The immunohistochemical analysis of liver frozen sections showed basolateral localization of Atp11c in hepatocytes (Figure 4C). The immunosignal was undetectable in specimens from *Atp11c*^{+^Y} mice.

Discussion

PFIC, a heterogeneous group of inherited autosomal recessive liver diseases, is attributed to the impaired transport of BAs across the CM of hepatocytes (Chen et al., 2004; Hayashi et al., 2005a; Paulusma et al., 2009; Wang et al., 2002). The causal gene of PFIC with the normal GGT is unidentifiable in about 30% of affected individuals (Davit-Spraul et al., 2010). *Atp11c* mutant mice present with a similar phenotype to PFIC (Siggs et al., 2011a; Yabas et al., 2014; Yabas et al., 2011). To explore whether *Atp11c* is a candidate gene that can explain genetically undiagnosed PFIC associated with the normal GGT level, in the current study, we analyzed the effects of Atp11c deficiency on the vectorial transport of BAs across the hepatocytes in *Atp11c* mutant mice. Unexpectedly, *Atp11c* mutant mice showed normal vectorial transport of [³H]-TC across hepatocytes, but decreased hepatic sinusoidal uptake and intact biliary secretion of [³H]-E₂17βG (Tables 2 and 3). This result can be explained by two observations: (1) the much lower expression of Oatps, including Oatp1b2 and Oatp1a4, which are sinusoidal transporters for the hepatic uptake of BAs and organic anions, and (2) the unaffected expression of Bsep and Mrp2, which are canalicular transporters for the biliary excretion of BAs, in *Atp11c* mutant mice compared with control mice (Figure 4A). *Slco1a/1b* cluster knockout mice exhibit hypercholanemia and hyperbilirubinemia because of

compromised hepatic uptake of BAs and reuptake of conjugated bilirubin (van de Steeg et al., 2010); therefore the reduced function of Oatps, but not of BSEP and MRP2, is probably responsible for the hypercholanemia and hyperbilirubinemia observed in *Atp11c* mutant mice. This suggests that *Atp11c* may be a causal gene responsible for genetically undiagnosed cases of hypercholanemia and hyperbilirubinemia, such as in Rotor syndrome without mutations in *SLCO1B1* and *SLCO1B3*, but not for cases of PFIC.

Oatps mediate hepatic uptake of a wide variety of structurally-unrelated compounds including clinically used drug such as HMG-CoA reductase inhibitors (statins), angiotensin II receptor blockers (sartans), and angiotensin converting enzyme (ACE) inhibitors, and thereby regulate their dispositions (Giacomini et al., 2013; International Transporter et al., 2010). Genetic polymorphisms and drug-drug interactions that significantly alter the function of OATPs affect the systemic exposure of their substrates, which causes increased pharmacological effects and adverse reactions such as statin-induced myotoxicity (Giacomini et al., 2013; Group et al., 2008; International Transporter et al., 2010). Therefore, the results of the current study imply implications of *Atp11c* in drug disposition and thereby in its pharmacological and adverse effects. To our knowledge, this is the first report to suggest the association of P4-ATPases with disposition, pharmacological action, and toxicity of drugs. Several coding SNPs in *Atp11c* have been reported in the dbSNP database hosted by NCBI. If these influences on function and expression of *Atp11c* are confirmed, *Atp11c* should receive more attention in the attempt to improve drug development and to overcome interindividual variations in medical therapy.

It remains unknown why the basolateral expression of Oatps and Ntcp is markedly reduced in *Atp11c* mutant mice. One possible mechanisms is that *Atp11c* functions to maintain the well-organized aminophospholipid asymmetry of the basolateral membrane, as is the case of ATP8B1, which translocates phosphatidylserine from the outer leaflet to the inner leaflet at the hepatocanalicular membrane and thereby

contributes to making it a rigid, liquid-ordered membrane (Paulusma et al., 2008; Paulusma et al., 2006). Disruption of membrane fluidity because of defective Atp11c function might alter the dynamics of Oatps and Ntcp on the basolateral membrane, which may destabilize and facilitate their degradation and thereby reducing the expression of these transporters on the basolateral membrane. This hypothesis is supported by the basolateral localization of Atp11c in hepatocytes (Figure 4C) and its function at the plasma membrane of cultured cells in the translocation of aminophospholipids into the inner leaflet (Segawa et al., 2014; Takatsu et al., 2014; Yabas et al., 2011). Alternatively, Atp11c may affect the trafficking of transport vesicles containing Oatps and Ntcp to the basolateral membrane as has been shown for Atp8a1 and P4-ATPases of *Saccharomyces cerevisiae* and *Caenorhabditis elegans* (Chen et al., 2010; Lee et al., 2015; Liu et al., 2008). It has been suggested that these P4-ATPases form the membrane curvature and/or recruit membrane fission protein through the unidirectional transport of phospholipids from the luminal leaflet to the cytosolic leaflet in the organelles in which they localize, which helps to generate transport vesicles. Although Atp11c localizes predominantly on the plasma membrane in HeLa cells (Takatsu et al., 2011), its minor distribution to other organelle such as the Golgi apparatus and endosome in hepatocytes may influence the budding of transport vesicles containing Oatps and Ntcp to the basolateral membrane. Future research to identify the intracellular localization of Atp11c in hepatocytes will provide further insight into the role of Atp11c in the regulation of the basolateral expression of Oatps and Ntcp.

In conclusion, we have demonstrated that Atp11c is indispensable to maintaining the appropriate expression level of Oatps and is thereby involved in the hepatic uptake of BAs and organic anions, including conjugated bilirubin, across the sinusoidal membrane. These results suggest that *Atp11c* is a candidate gene that may be responsible for genetically undiagnosed cases of hypercholanemia and hyperbilirubinemia but not of PFIC. Our results are consistent with the recent preliminary results of Naik et al., which suggested

Oatp1b2 contributes to hyperbilirubinemia and hypercholanemia in *Atp11c* mutant mice (Naik et al., 2015). *Atp11c* may influence disposition, pharmacological effect, and toxicity of drugs because Oatps mediate the hepatic uptake of many drugs and consequently regulate their systemic exposure. Future research with global analysis to identify membrane proteins whose expression is affected by *Atp11c* provides further insight into the regulatory mechanism of the sinusoidal membrane proteins by *Atp11c* and expands the understanding of the physiological and pharmacological importance of *Atp11c*.

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Authorship contributions

Participated in research design: Hayashi

Conducted experiments: Matsuzaka

Performed data analysis: Matsuzaka, Hayashi, and Kusuvara

Wrote or contributed to the writing of the manuscript: Hayashi and Kusuvara

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Footnote

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Figure legends

Figure 1. Genotype analysis of *Atp11c* knockout mice.

(A) Genotype analysis of mice that inherited the wild-type and *Atp11c*^{empty/hive} allele. A partial sequence in *Atp11c* was amplified by PCR involving genomic DNA prepared from the mice, digested by MboI, and subjected to electrophoretic analysis. (B) *Atp11c* expression in liver. LPMs (10 µg) was prepared from *Atp11c*^{+Y} and *Atp11c*^{empty/hive/Y} mice and analyzed by Western blot analysis. The data shown in A and B are representative result of more than two independent experiments. *Atp11c*^{empty/Y}; *Atp11c*^{empty/hive/Y}.

Figure 2. Plasma concentration and biliary excretion rate of [³H]-TC and [³H]-E₂17βG during constant intravenous infusion into *Atp11c*^{+Y} and *Atp11c*^{empty/hive/Y} mice.

[³H]-TC (A, C, E) and [³H]-E₂17βG (B, D, F) were infused intravenously into *Atp11c*^{+Y} and *Atp11c*^{empty/hive/Y} mice at a rate of 500 or 13.3 pmol/min/kg for 60 min. Plasma concentrations at the designed time points (A, B) and biliary excretion rate (C, D) and bile flow rate (E, F) for the indicated time segments were measured. Each point represents the mean ± SEM of more than three mice. *, p<0.05, **, p<0.01. *Atp11c*^{empty/Y}; *Atp11c*^{empty/hive/Y}.

Figure 3. Uptake of [³H]-TC and [³H]-E₂17βG into isolated hepatocytes prepared from *Atp11c*^{+Y} and *Atp11c*^{empty/hive/Y} mice.

The uptake of [³H]TC (20 nM) (A) and [³H]-E₂17βG (3 nM) (B) for 0.5 and 2 min into the isolated hepatocytes from the livers of *Atp11c*^{+Y} (white) and *Atp11c*^{empty/hive/Y} (black) mice was measured at 37°C in the absence (circles) or presence (squares) of 100 µM unlabeled compounds. The uptake amount per minute of [³H]-TC (C) and [³H]-E₂17βG (D) in the hepatocytes was calculated from the results shown in (A, B). Representative

results of two independent experiments are shown. Each point (A, B) and bar (C, D) represents the mean \pm SEM of quadruplicate determinations. *, $p < 0.05$, **, $p < 0.01$. *Atp11c*^{emp/Y}; *Atp11c*^{emptyhiv/Y}.

Figure 4. Hepatic expression of BAs transporters in liver.

(A) Protein expression. Upper image, LPMs (10 μ g) was prepared from the liver of *Atp11c*^{+Y} and *Atp11c*^{emptyhiv/Y} mice and subjected to Western blot analysis. A representative result of three independent experiments is shown. Lower image, quantification of the amount of each transporter in LPMs. The band intensity was quantified as described in Materials and Methods. Each bar represents the mean \pm SEM of three independent experiments. **, $p < 0.01$; ***, $p < 0.001$; a.u.; arbitrary unit. (B) mRNA expression. RNA prepared from the liver of *Atp11c*^{+Y} and *Atp11c*^{emptyhiv/Y} mice was analyzed by qPCR as described in Materials and Methods. Expression of each transporter was normalized by that of Gapdh. Each bar represents the mean \pm SEM of three independent experiments. *, $p < 0.05$; a.u.; arbitrary unit. (C) Localization of Atp11c in the liver. Frozen liver sections from *Atp11c*^{+Y} and *Atp11c*^{emptyhiv/Y} mice were subjected to immunohistochemistry as described in Materials and Methods. The lower and upper images are specimens from *Atp11c*^{+Y} and *Atp11c*^{emptyhiv/Y} mice, respectively. A typical image from each mouse is shown. Bar, 100 μ m. *Atp11c*^{emp/Y}; *Atp11c*^{emptyhiv/Y}.

Table

Table 1. Serum biochemistry				
Parameters	<i>Atp11c</i> ^{+/-Y} (n=6)	<i>Atp11c</i> ^{emptyhiv/-Y} (n=12)	P value (significance)	
TP (g/dL)	4.8 ± 0.1	4.7 ± 0.2	7.8E-01	
ALB (g/dL)	3.1 ± 0.1	3.1 ± 0.1	9.4E-01	
AST (IU/L)	102 ± 13	177 ± 21	3.4E-02	*
ALT (IU/L)	30.8 ± 3.1	102 ± 18	1.9E-03	**
ALP (IU/L)	315 ± 15	484 ± 34	4.7E-04	***
LDH (IU/L)	709 ± 84	852 ± 68.9	2.3E-01	
GGT (IU/L)	3 >	3 >	N.D.	
T-CHO (mg/dL)	104 ± 2	106 ± 7	7.7E-01	
F-CHO (mg/dL)	26.2 ± 1.5	33.9 ± 3.6	6.9E-02	
E-CHO (mg/dL)	78.5 ± 3	72.9 ± 3.9	3.6E-01	
TG (mg/dL)	28.5 ± 6	24.9 ± 6.2	7.2E-01	
PL (mg/dL)	202 ± 5	184 ± 16	2.8E-01	
T-BIL (mg/dL)	0.06 ± 0.01	1.1 ± 0.2	2.5E-04	***
D-BIL (mg/dL)	0.01 >	0.8 ± 0.2	N.D.	
TBA (μmol/L)	10.7 ± 6.4	79.6 ± 13.5	3.5E-04	***

TP; total protein, ALB; albumin, AST; aspartate aminotransferase, ALT; alanine aminotransferase, ALP; alkaline phosphatase, LDH; lactate dehydrogenase, GGT; gamma-glutamyl transferase, T-CHO; total cholesterol, F-CHO; free cholesterol, E-CHO; esterified cholesterol, TG; triglyceride, PL; phospholipid, T-BIL; total bilirubin, D-BIL; direct bilirubin, TBA; total bile acids
N.D.; not determined. *, P<0.05, **, P<0.01, ***, P<0.001

Table 2. Pharmacokinetic parameters of [³H]TC during constant infusion into *Atp11c*^{+/-Y} and *Atp11c*^{emptyhiv/-Y}

Parameters	<i>Atp11c</i> ^{+/-Y} (n=4)	<i>Atp11c</i> ^{emptyhiv/-Y} (n=3)	P value
C _{ss, plasma} (nM)	10.1 ± 0.9	10.5 ± 1.3	0.81
C _{ss, liver} (pmol/g liver)	35.6 ± 4.8	33.6 ± 2.0	0.72
V _{ss, bile} (pmol/min/kg)	428 ± 37	432 ± 46	0.95
CL _{tot} (ml/min/kg)	43.6 ± 7.2	33.7 ± 4.8	0.34
CL _{bile, plasma} (ml/min/kg)	37.3 ± 4.6	38.6 ± 1.8	0.82
CL _{bile, liver} (ml/min/kg)	10.2 ± 1.4	13.9 ± 1.2	0.17

Table 3. Pharmacokinetic parameters of [³H]E₂17βG during constant infusion into Atp11c^{+/-Y} and Atp11c^{emptyhiv/-Y}

Parameters	Atp11c ^{+/-Y} (n=3)	Atp11c ^{emptyhiv/-Y} (n=3)	P value
C _{ss, plasma} (nM)	0.488 ± 0.075	1.01 ± 0.10	0.013*
C _{ss, liver} (pmol/g liver)	2.95 ± 0.38	3.58 ± 0.13	0.19
V _{ss, bile} (pmol/min/kg)	14.2 ± 2.0	14.6 ± 0.6	0.85
CL _{tot} (ml/min/kg)	27.9 ± 5.1	13.7 ± 1.5	0.050*
CL _{bile, plasma} (ml/min/kg)	23.0 ± 2.9	13.8 ± 1.1	0.040*
CL _{bile, liver} (ml/min/kg)	3.87 ± 0.37	3.76 ± 0.25	0.82

Table 4. Measurement of bile flow rate and biliary BA concentrations			
Parameters	<i>Atp11c</i> ^{+/-} (n=9)	<i>Atp11c</i> ^{emptyhiv} (n=11)	P value
Bile flow rate (μ L/min/kg)	65.9 \pm 11.7	61.0 \pm 3.1	0.69
BA concentrations (mM)	139 \pm 14	140 \pm 10	0.94

Figure 1.

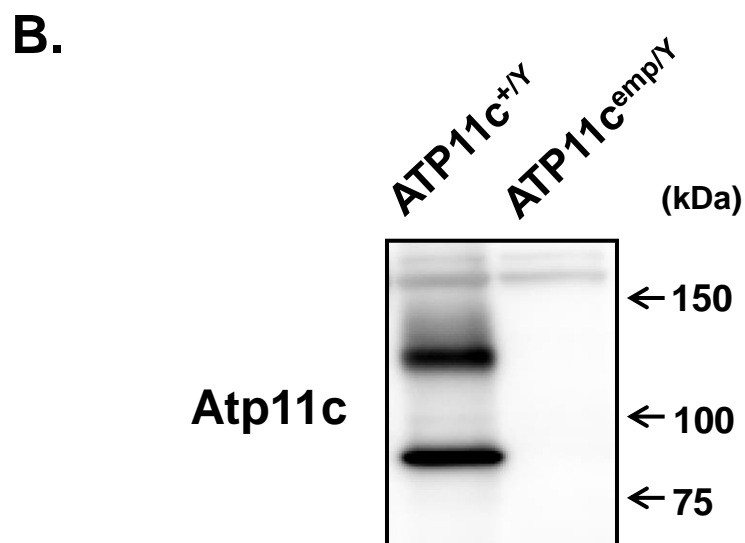
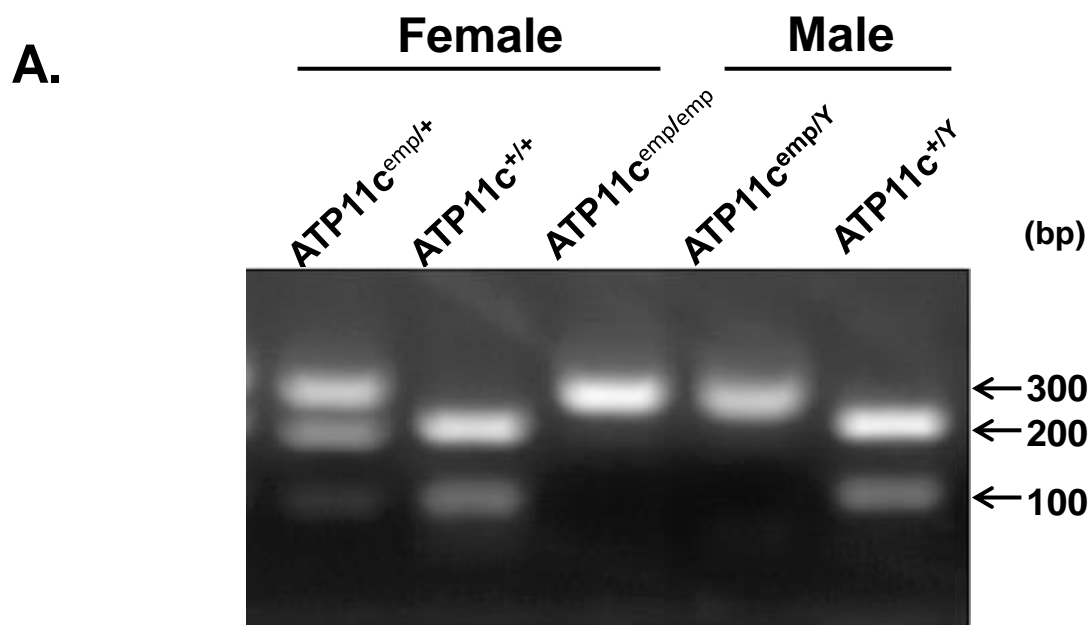


Figure 2.

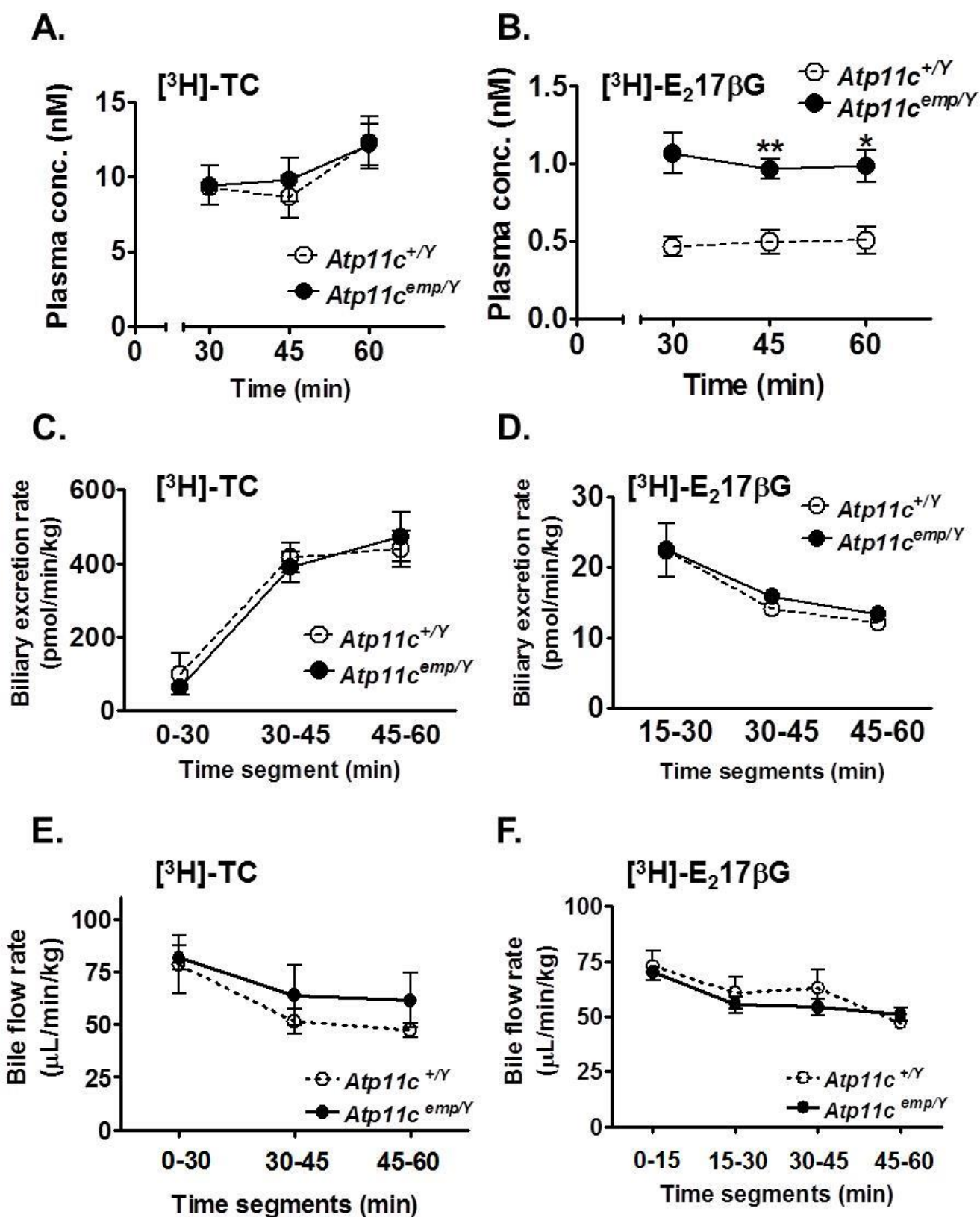


Figure 3.

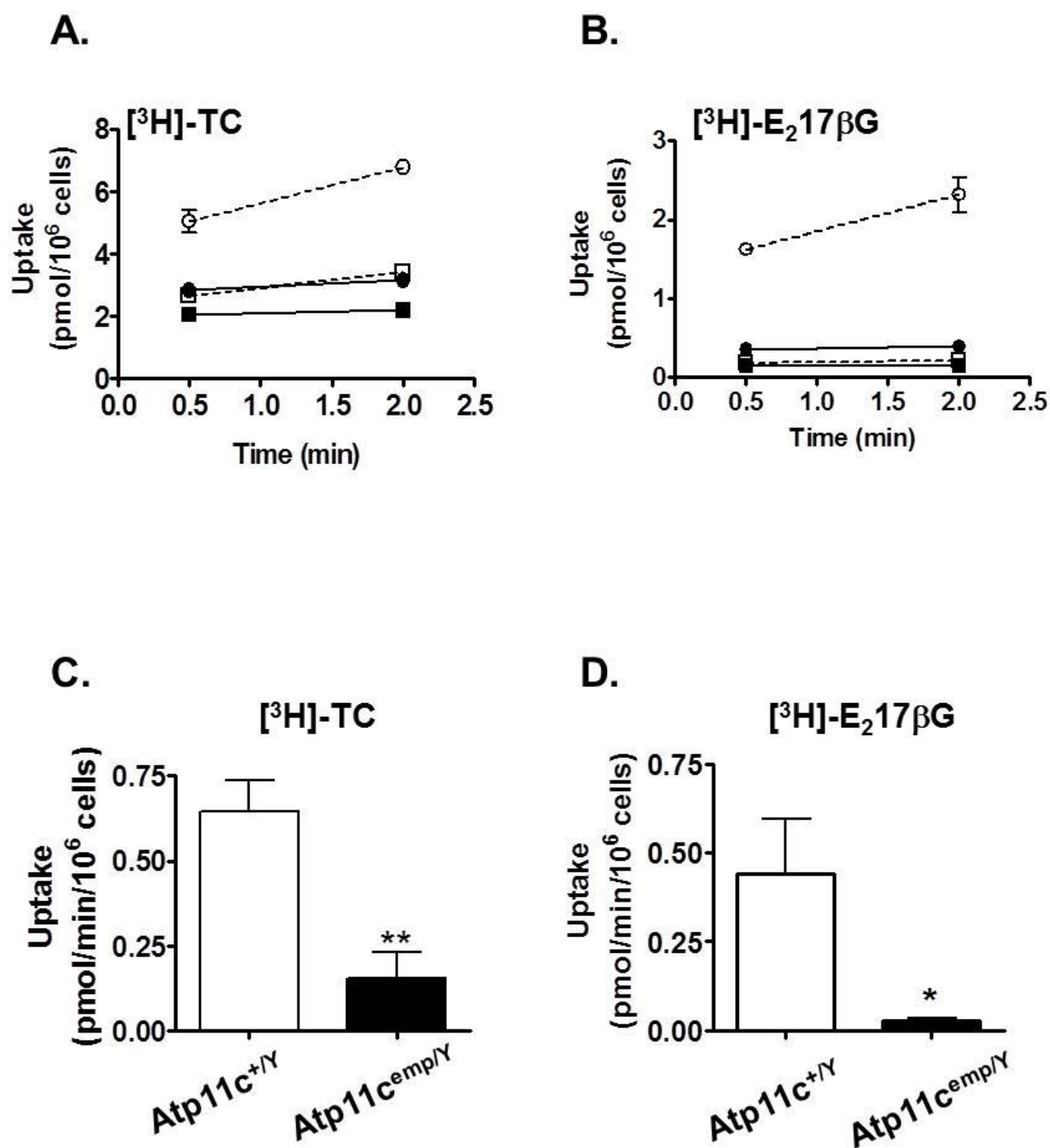


Figure 4.

A.

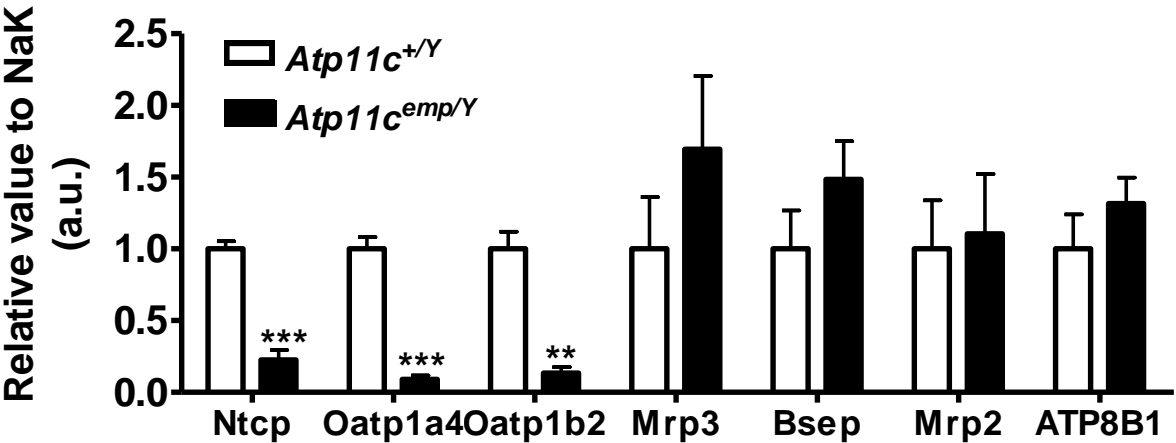
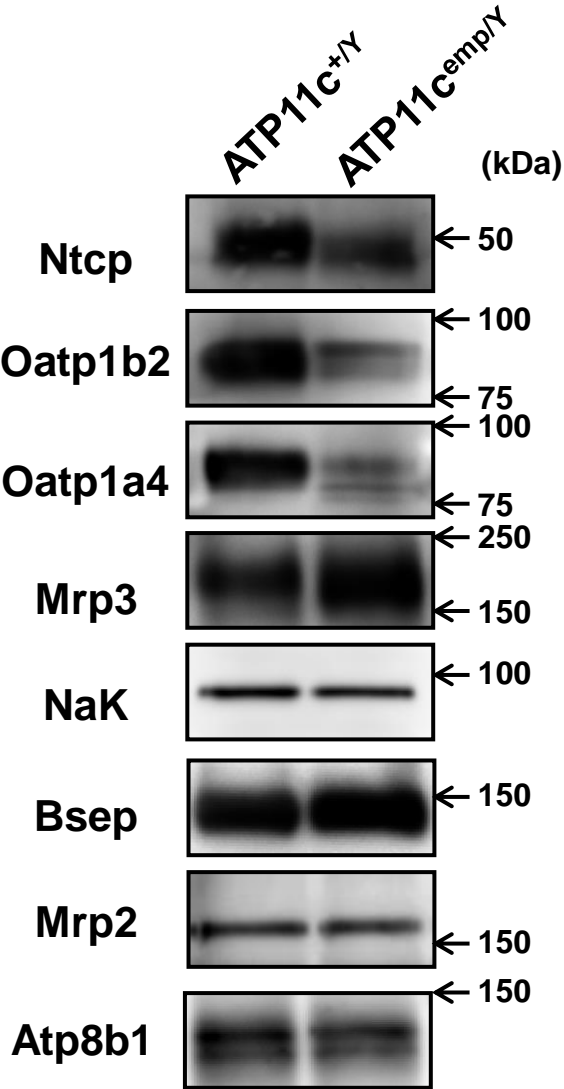
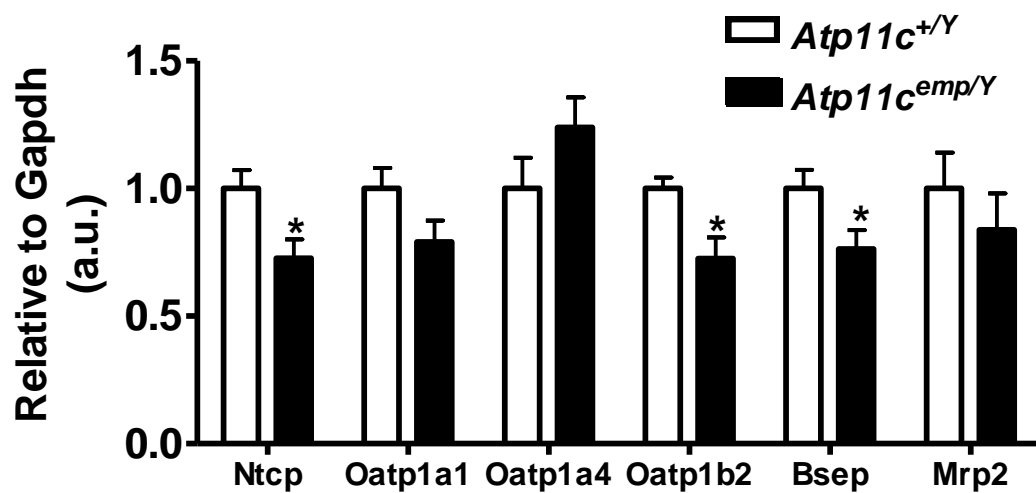


Figure 4.

B.



C.

