Received: 06 April 2022 | Revised: 11 August 2022 | Accepted: 13 August 2022

DOI: 10.1002/hep.32735

ORIGINAL ARTICLE

OPEN

Genetic predisposition to porto-sinusoidal vascular disorder: A functional genomic-based, multigenerational family study

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Abstract

Background and Aims: Porto-sinusoidal vascular disorder (PSVD) is a group of liver vascular diseases featuring lesions encompassing the portal venules and sinusoids unaccompanied by cirrhosis, irrespective of the presence/absence of portal hypertension. It can occur secondary to coagulation disorders or insult by toxic agents. However, the cause of PSVD remains unknown in most cases. Hereditary cases of PSVD are

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Abbreviations: BL, bulge loop; DEG, differentially expressed gene; FCHSD1, FCH and double SH3 domains 1; FCHSD1^{WT}, wild-type FCHSD1; FXR, farnesoid X receptor; HL, hairpin loop; HSC, hepatic stellate cell; HUVEC, human umbilical vein endothelial cell; MBL, multibranched loop; mLST8, MTOR-associated protein, LST8 homolog; mTOR, mechanistic target of rapamycin; NCPH, noncirrhotic portal hypertension; PHT, portal hypertension; PKLR, pyruvate kinase L/R; PPI, protein–protein interaction; PSVD, porto-sinusoidal vascular disorder; SP, stacked pair.

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Funding information
Weill Cornell Medicine-Qatar, Grant/Award Number: BMRP

exceptionally rare, but they are of particular interest and may unveil genetic alterations and molecular mechanisms associated with the disease.

Approach and Results: We performed genome sequencing of four patients and two healthy individuals of a large multigenerational Lebanese family with PSVD and identified a heterozygous deleterious variant (c.547C > T, p. R183W) of FCH and double SH3 domains 1 (*FCHSD1*), an uncharacterized gene, in patients. This variant segregated with the disease, and its pattern of inheritance was suggestive of autosomal dominant with variable expressivity. RNA structural modelling of human *FCHSD1* suggests that the C-to-T substitution at position 547, corresponding to $FCHSD1^{R183W}$, may increase both messenger RNA (mRNA) and protein stability and its interaction with MTOR-associated protein, LST8 homolog, a key protein of the mechanistic target of rapamycin (mTOR pathway). These predictions were substantiated by biochemical analyses, which showed that $FCHSD1^{R183W}$ induced high *FCHSD1* mRNA stability, overexpression of FCHSD1 protein, and an increase in mTORC1 activation. This human *FCHSD1* variant was introduced into mice through CRISPR/Cas9 genome editing. Nine out of the 15 mice carrying the human $FCHSD1^{R183W}$ variant mimicked the phenotype of human PSVD, including splenomegaly and enlarged portal vein.

Conclusions: Aberrant FCHSD1 structure and function leads to mTOR pathway overactivation and may cause PSVD.

INTRODUCTION

Porto-sinusoidal vascular disorder (PSVD; also previously described as idiopathic noncirrhotic portal hypertension [NCPH], hepatoportal sclerosis, idiopathic portal hypertension [PHT], obliterative portal venopathy, and incomplete septal cirrhosis) is an underrecognized vascular liver disease of unknown etiology and is clinically characterized by features of PHT, which some patients do not exhibit at the time of diagnosis, in the absence of a causative disease such as liver cirrhosis, occlusion of the extrahepatic portal vein/hepatic vein, blood disease, parasitic disease, granulomatous liver disease, or congenital hepatic fibrosis.[1,2] PSVD showcases a wide spectrum of liver histopathological abnormalities that cause an impairment of blood microcirculation in the liver, including portal and perisinusoidal fibrosis, sinusoidal dilatation, and regenerative changes in hepatocytes.[1,2] One of the main histopathological features of the disease is the obliteration of the small intrahepatic branches of the portal vein.[3] Although the cause of PSVD remains elusive, several contributing factors have been considered, including immunological and hematological disorders, drug toxicity, and infections.

The disease has a worldwide distribution, but it is more common in developing countries, especially those with lower socioeconomic groups. In 1980, it caused 30%–40% of instances of PHT cases in Japan and the Indian subcontinent but recently has caused only 5% or less.[4,5] It may account for 3%–5% of instances of in Western nations, and the patients tend to be older (50–69 years) than those in Japan (40–59 years) and India (30–49 years).[1,6] However, PSVD is probably underdiagnosed or misdiagnosed because its clinical presentation closely mimics that of cryptogenic cirrhosis.[5] The lack of pathognomonic clinical and laboratory findings makes histological examination of liver tissue samples critically important to achieve a definite diagnosis of PSVD.[7]

Familial cases of PSVD are exceptionally rare; only 27 multiplex families having PSVD running in their heredity have been reported in the literature.[2–5] The identification of the PSVD-causing genes and their functions may provide tremendous insight into the pathogenesis of the disease and open up new areas of investigation. A definite genetic component of PSVD has not yet been identified; both autosomal dominant and recessive inheritance have been proposed. Recently, several candidate genes for PSVD were suggested by applying exome or whole-genome sequencing,[8–11] but no direct evidence or functional studies have been provided to corroborate these findings.

By using a multifaceted and comprehensive approach, this study aimed to identify the genetic alterations responsible for PSVD.

METHODS

Study subjects

Members of a large multiplex Lebanese family with PSVD participated in the study. Written informed consent was obtained from each person included in the study, and the study protocol conforms to the ethical guidelines of the 1975 Declaration of Helsinki as reflected in a priori approval by the Saint Joseph University of Beirut's Ethical Committee on Clinical Investigation. The initial clinical diagnosis and liver histology, in all five patients (including the deceased one) with PSVD, were performed at the Hotel-Dieu de France Hospital in Beirut, Lebanon. Further clinical investigation, liver biopsies, and treatment of the surviving four patients were conducted in France at the Hôpital Charles Nicolle, Rouen, and Hôpital Beaujon, Clichy.

Genetic and biochemical analysis

Peripheral blood samples were collected from six members (four patients and two unaffected members), and genomic DNA was extracted using QIAamp DNA Maxi Blood Kits (Qiagen). Whole-genome sequencing was performed using a HiSeq 2500 sequencer (30× average coverage) at Illumina (San Diego). Paired-end libraries were generated from 1 µg of genomic DNA with the Illumina TruSeq DNA PCR-Free Sample Preparation Kit. Genomic DNA was sheared using the Covaris system (Woburn), and the isolated DNA fragment ends were blunt ended, A-tailed, and ligated using sequencing adaptors with index sequences. Excess adapters and enzymes were removed using AMPure beads (Beckman Coulter Genomics). Indexed libraries were size-selected to the 350-bp range with bead-based capture, and the concentration of amplifiable fragments was determined applying quantitative polymerase chain reaction quantifications (relative to sequencing libraries with a known concentration). Normalized libraries were clustered on a c-BOT machine, and 125-bp paired-end sequencing was performed using a HiSeq 2500 system.

Quality control of the Fastq files was performed using FastQC (v0.7.12) (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/). The reads were then aligned to the reference human genome, build GrCh37, using BWA-MEM aligner: 0.7.12-r1039.[12] Genome analysis toolkit (GATK) haplotype caller was used for variant calling on individual samples. The GATK genotype genomic variant call format option was used for joint calling across individual samples. Variant calling was performed using the recommended best practices in GATK, version 3.7. Joint variant file was further subjected to GATK variant quality score recalibration (VQSR).[13] The annotation of variants was performed by using SnpEff (version: 4.3r, GRCh37.75 Reference Build) and dbNSFP 3.0.[14] Ingenuity Variant Analysis (http://ingenuity.com) was used to filter out variants as follows: (i) variants with low call quality (< 20), low coverage (< 10), and failing VQSR filter and those present in a low complexity region; (ii) variants with allele frequencies more than 1% in public database, including 1000 Genomes project and ExAC project, were excluded unless established as a pathogenic variant; (iii) a de novo dominant inheritance model was selected; and (iv) only nonsynonymous, frameshift, nonsense, and splice-site variants, which could be potentially deleterious based on functional predictions by sorting intolerant from tolerant (SIFT), Polyphen, and Mut Taster, were selected.[15–17] To verify the presence of the FCH and double SH3 domains 1 (*FCHSD1*) variant, identified by genome sequencing, Sanger sequencing was carried out on the six samples. Details are provided in Supplementary Information.

The liver cell line HepG2 and endothelial cell line human umbilical vein endothelial cell (HUVEC), both of which express low levels of FCHSD1, were used to assess the functional effect of the FCHSD1 variant. Details of the *FCHSD1* messenger RNA (mRNA) structure modelling, FCHSD1-mLST8 docking, insertion of *FCHSD1* in lentiviral vector, and *FCHSD1* expression in human hepatocyte HepG2 cells; western blotting; and immunoprecipitation are provided in Supplementary Information.

Fchsd1-R181W knock-in mice

A C57BL/6 mouse model with the R181W variant of the *Fchsd1* gene in mice, corresponding to R183W at the human *FCHSD1* locus, was generated at Cyagen Biosciences, Inc. The guide RNA (target sequence: TCTGGAGGCTGGTCCGAGAATGG, matches reverse strand) against the mouse *Fchsd1* gene, donor oligo-containing R181W (CGG to TGG) variant sites, and Cas9 mRNA were coinjected into fertilized mouse eggs to generate targeted knock-in offspring. F0 founder animals were identified by polymerase chain reaction followed by sequence analysis (primer sequence and sequencing results are shown in Supplementary Information), which were bred with wild-type mice to test germline transmission and F1 animal generation. Crossing F1 heterozygotes generated five homozygotes and eight heterozygotes. All F2 mice and two F1 heterozygotes were used to observe the effects of the *mFchsd1* variant, especially the phenotypic and biochemical changes.

Formalin-fixed paraffin-embedded tissues were used for evaluation of pathological changes after hematoxylin and eosin staining. All mice were housed in the animal facility of Ruijin Hospital (Shanghai Jiao Tong University School of Medicine); the animal care and experimental procedures complied with the guidelines on the care and use of laboratory animals were approved by the Ethical Committee and Animal Experiments at Ruijin Hospital, Shanghai Jiao Tong University School of Medicine. More details on clustered regularly interspaced palindromic repeats/CRISPR-associated protein 9 (CRISPR/Cas9) genome editing in mice and phenotype assessment are provided in Figure S1.

Statistical analysis

Statistically analysis was performed using GraphPad Prism 8. Unpaired Student's *t* tests were performed for comparison of two groups, and two-tailed $p < 0.05$ was considered statistically significant. Two-way analysis of variance was performed for comparison of mean difference of two groups and $p < 0.05$ was considered statistically significant.

RESULTS

Clinical characteristics of the patients

The pedigree of the family with PSVD is shown in Figure 1A. Six members were recruited between June 5, 2014, and November 12, 2015, and the study was done from May 2, 2017, to November 5, 2021. The patterns of inheritance were consistent with autosomal dominant disease with variable expressivity. All affected members fulfilled the clinical and histopathological criteria for PSVD (Table S1, Figure 1B and Figure S2). Portal vein thrombosis and Budd–Chiari syndrome were excluded from all affected family members. Further investigations including general metabolites screening were also performed to rule out

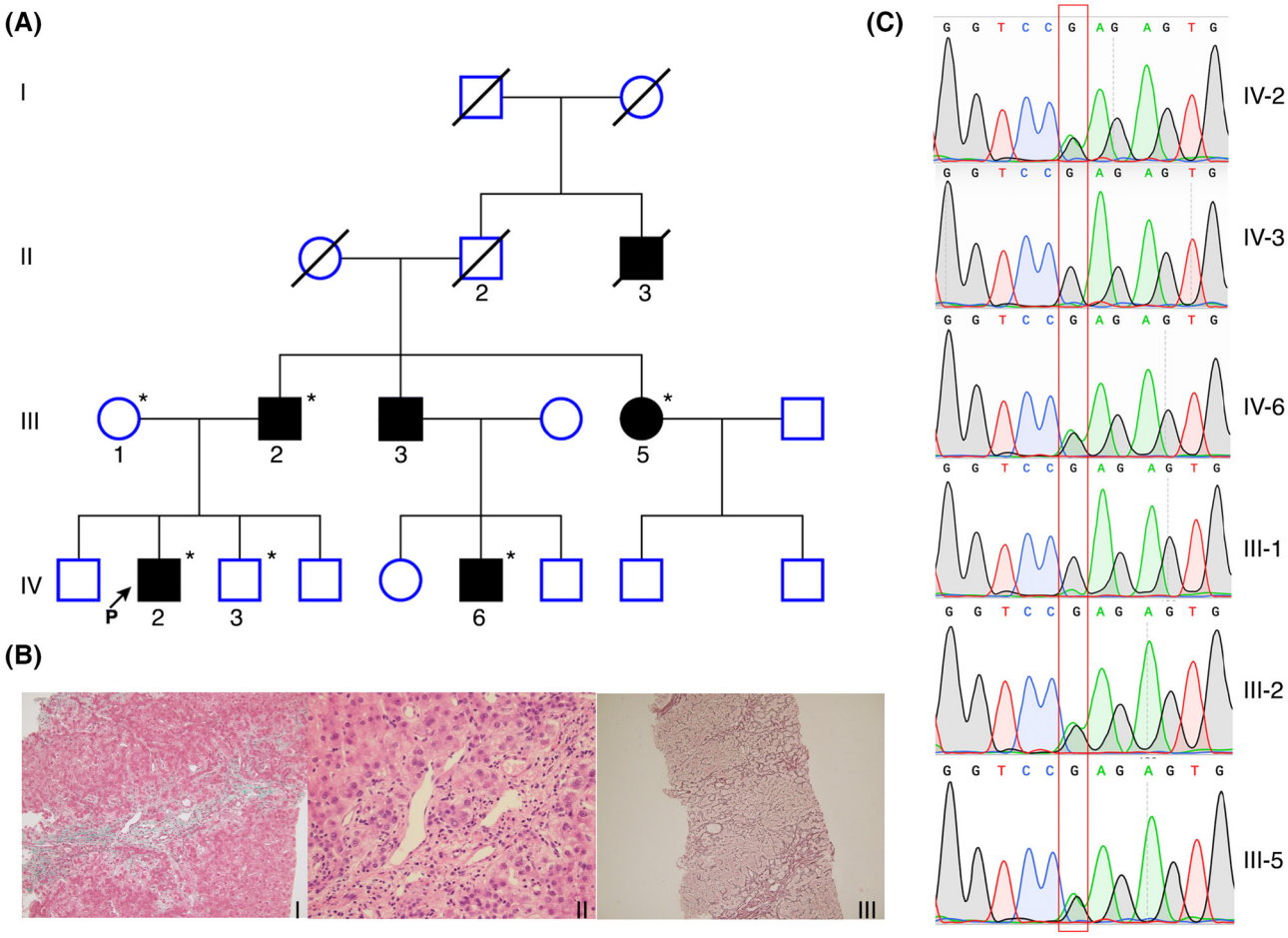

FIGURE 1 Pedigree chart of the family and the proband's liver histopathology analysis. (A) Autosomal dominant inheritance pattern of family members with idiopathic noncirrhotic portal hypertension. *The participants had their genomic DNA analyzed by whole-genome sequencing. (B) Proband's (IV-2) liver histopathology. I: Masson stain showing septal fibrosis (×200); II: Aberrant vessels in portal tracts (hematoxylin and eosin, ×400); III: Reticulin stain showing features of nodular regenerative hyperplasia (×100). (C) Chromatogram of Sanger sequencing results of chr5: 141028548-141028559. The red box labels the chromatogram at chr5: 141028553.

metabolic diseases. Hepatic viral markers (hepatitis B virus, hepatitis C virus, and hepatitis A virus) and autoimmune liver markers were negative.

The proband (IV-2) is a 15-year-old boy born to a nonconsanguineous Lebanese family. He was born at term after uncomplicated pregnancy, labor, and delivery. Physical examination at birth demonstrated weight, height, and circumferences within normal ranges. His past clinical history was unremarkable until the age of 8 years, when he was diagnosed with acute lymphoblastic leukemia, which was treated with an intrafamilial bone morrow allograft. Subsequently, the patient achieved complete remission. At 13 years, he presented with recurrent gastroesophageal variceal hemorrhage. Upper gastrointestinal endoscopy revealed grade III esophageal varices and PHT. Gastroesophageal bleeding was managed with a distal splenorenal shunt. Extensive evaluation (infectious, metabolic, toxic, and hematological) did not reveal a cause for the liver disease. Serum liver function test results were normal. Liver histology showed portal fibrosis, abnormal portal venules, numerous arterial structures, regenerative nodular changes, perisinusoidal fibrosis, and abnormal spacing of the central venous structures (Figure 1B). Hepatocytes appeared in cell thick cords. No evidence of cirrhosis, inflammatory liver disease, biliary lesions, or steatosis was found. Based on the histological and clinical findings, the patient was diagnosed with PSVD.

The proband's father (III-2), a 52-year-old man, had his first episode of gastroesophageal variceal hemorrhage at the age of 35. Liver ultrasonography showed an enlarged spleen and a normal-sized liver with venous collaterals adjacent to the portal vein, compatible with PHT. No signs of cirrhosis or portal vein thrombosis were observed. Liver histology demonstrated changes consistent with those observed in the PSVD group. A repeat liver histology at the age of 42 years for suspected hepatocellular carcinoma revealed similar findings.

The proband's paternal aunt (III-5) was initially diagnosed with hepatic polyadenomatosis at the age of 36 years and then diagnosed with PSVD at the age of 45 years. Liver histology revealed changes consistent with those observed in the PSVD group.

The proband's father reported that his brother (III-3) was affected by PSVD, but no clinical or histological evidence was provided. The proband's cousin (IV-6) was diagnosed with PSVD at the age of 15 after presenting clinical and histological changes consistent with PSVD.

The proband's paternal granduncle (II-3) was diagnosed with PSVD, and his liver histology revealed a portal tract with angiomatosis, aberrant blood vessels, sinusoidal dilatation, and nodular regenerative hyperplasia. This patient (II-3) died of PHT complications.

Genome sequencing and the search of candidate genes

With the assumption of an autosomal dominant inheritance model, chosen in accordance with the PSVD segregation pattern in the family, we searched for variants that occurred de novo in all four patients but were absent in the two unaffected members. Of the 11 variants identified, none were identified in genes previously reported to be associated with PSVD, and only two were predicted to be pathogenic: a nucleotide substitution c.1456C > T, predicted to result in the amino acid substitution p.(Arg486Trp) in pyruvate kinase L/R (*PKLR*), and another nucleotide substitution c.547C > T, predicted to result in the amino acid substitution p.(Arg183Trp) in *FCHSD1* (NM_033449.3) (Table S2). *PKLR* variants caused pyruvate kinase deficiency, an autosomal recessive disease. Because none of our patients with PSVD were homozygous for the *PKLR* variant or showed any clinical symptoms related to pyruvate kinase deficiency (Online Mendelian Inheritance in Man no. 266200), we retained *FCHSD1* as the unique candidate gene associated with PSVD running in this family. The R183W substitution in FCHSD1 is predicted to be damaging by PolyPhen-2 and deleterious by SIFT. The identified variant c.547C > T in *FCHSD1* (Chr5: 141028553G > A) was absent in more than 14,000 genomes of the Qatar Genome Program dataset[18] and rarely found in gnomAD2.1/3.1,[19] with a maximum allele frequency = 0.00003563. This finding supports the deleterious effects of this variant, as predicted by computing tools. Sanger sequencing confirmed the de novo occurrence of the identified *FCHSD1* variant in all four patients with PSVD but not in two healthy subjects (Figure 1C).

The variant c.541C > T in *FCHSD1* affects its expression

The region of the FCHSD1 protein surrounding amino acid position 183 is highly conserved across species, and arginine at position 183 is absolutely conserved across mammals (Figure S3), suggesting that it is critical for the individual's biological fitness. FCHSD1 expression was consistently low in liver tissue in the Human Protein Atlas, the Genotype Tissue Expression Project, and the Functional ANnoTation Of the Mammalian genome 5 datasets (https://www.proteinatlas.org/ENSG00000197948-FCHSD1/tissue). Ectopic expression of the wild-type *FCHSD1* (*FCHSD1*^{WT}) and *FCHSD1*^{R183W} variants in HepG2 cells and human endothelial HUVEC cells resulted in high expression levels of FCHSD1 in cells transfected with *FCHSD1*^{R183W} compared with those transfected with *FCHSD1*^{WT} (Figure 2A). Treatment with actinomycin D, which inhibits new RNA synthesis, but not the treatment

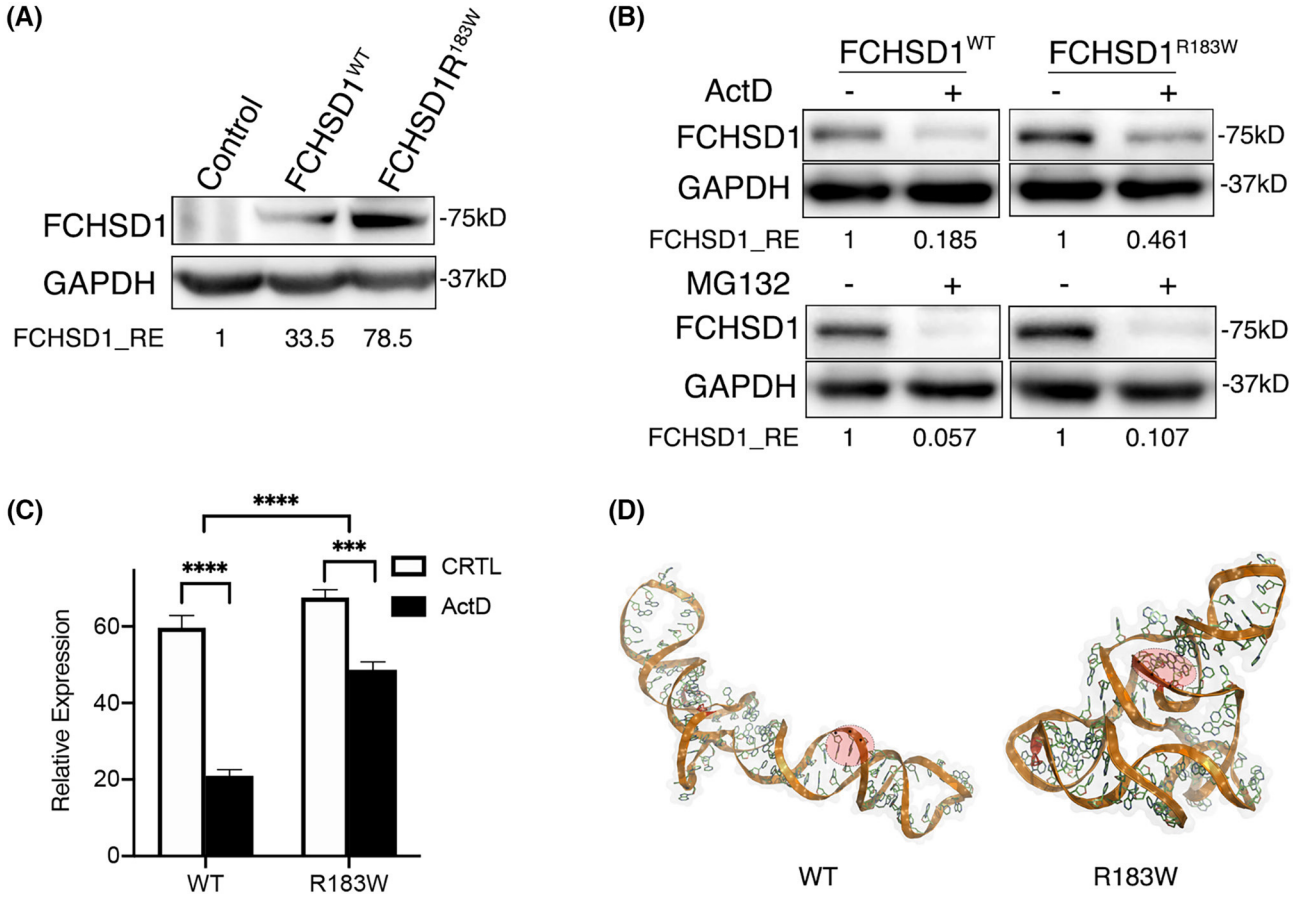

FIGURE 2 The effect of C > T mutation on FCH and double SH3 domains 1 (FCHSD1) expression. (A) The protein level of FCHSD1 in HepG2 cells (control) and HepG2 cells with overexpressed wild-type (WT) FCHSD1 (FCHSD1^{WT}) and R183W mutant FCHSD1 (FCHSD1^{R183W}). The FCHSD1 protein was revealed by anti-FCHSD1 antibody. (B) The protein level of FCHSD1 in FCHSD1^{WT} and FCHSD1^{R183W} HepG2 cells with/without overnight treatment of actinomycin D (ActD; 1 μm) or MG132 (1 μm). (C) The mRNA levels of FCHSD1 in FCHSD1^{WT} and FCHSD1^{R183W} HepG2 cells with/without ActD treatment for 6 h. ***$p < 0.001$; ****$p < 0.0001$. (D) Predicted morphological differences of the short RNA sequence of WT and R183W FCHSD1. The nucleobases are represented as green sticks, and the folded single strand is represented as gray transparent surface and orange cartoons. 3′ and 5′ ends are colored in red. The triplet of nucleobases containing the point mutation is framed in red, and the position is indicated with asterisks. (A–C) Representative data from one of at least two independent experiments. The relative expression of FCHSD1 to GAPDH is the normalized ratio of integrated density measured by ImageJ.

with MG132, which inhibits protein degradation, had different effect on the protein level of FCHSD1 in HepG2 cells transfected with *FCHSD1^{R183W}* compared with those transfected with *FCHSD1^{WT}*, suggesting that the expression difference might be regulated at the RNA level (Figure 2B). Treatment of HepG2 cells with antimycin D showed that mRNA of *FCHSD1*^{R183W} were more resistant to the drug treatment than that of *FCHSD1*^{WT} (Figure 2C). Similar results were also observed at both protein and mRNA levels in HUVEC cells (Figure S4A,B). The secondary structures in the RNA, decomposed into nearest-neighbor loops, of both *FCHSD1*^{WT} and *FCHSD1*^{R183W} are shown in Figure S5, and the top 10 predictions are listed in Table S3. A comparison of the secondary structures and hydrogen bond pseudoknots revealed several differences between *FCHSD1*^{WT} and *FCHSD1*^{R183W}. For instance, owing to the presence of uracil in *FCHSD1*^{R183W}, the stacked pair (SP)2 and two hairpin and bulge loops (hairpin loop [HL]1 and bulge loop [BL]2) split into two paired nucleobases (SP2 and SP3), two harpin loops (HL1 and HL2), and one multibranched loop (MBL; MBL2). Similarly, the top-scoring hydrogen bond pseudoknotted structures displayed structural rearrangements. This is the case of the HL1, which changes into a new structure containing an MBL2, SP2, SP3, HL1, and HL2. Notably, the hydrogen bond interactions between MBL1 and MBL2 involve the rare variant nucleobase U49. Additionally, the RNA tridimensional structure of the wild type was morphologically different, with a more elongated shape than that of the rare variant (Figure 2D). In addition, a significant decrease in the solvent-accessible solvent area was observed in the rare variant of *FCHSD1* compared with that in the wild type (17879 Å2 vs. 20490 Å2). These data indicate that the rare variant could make the predicted RNA structure less accessible to the solvent and, hence, to regulatory proteins that bind to it.

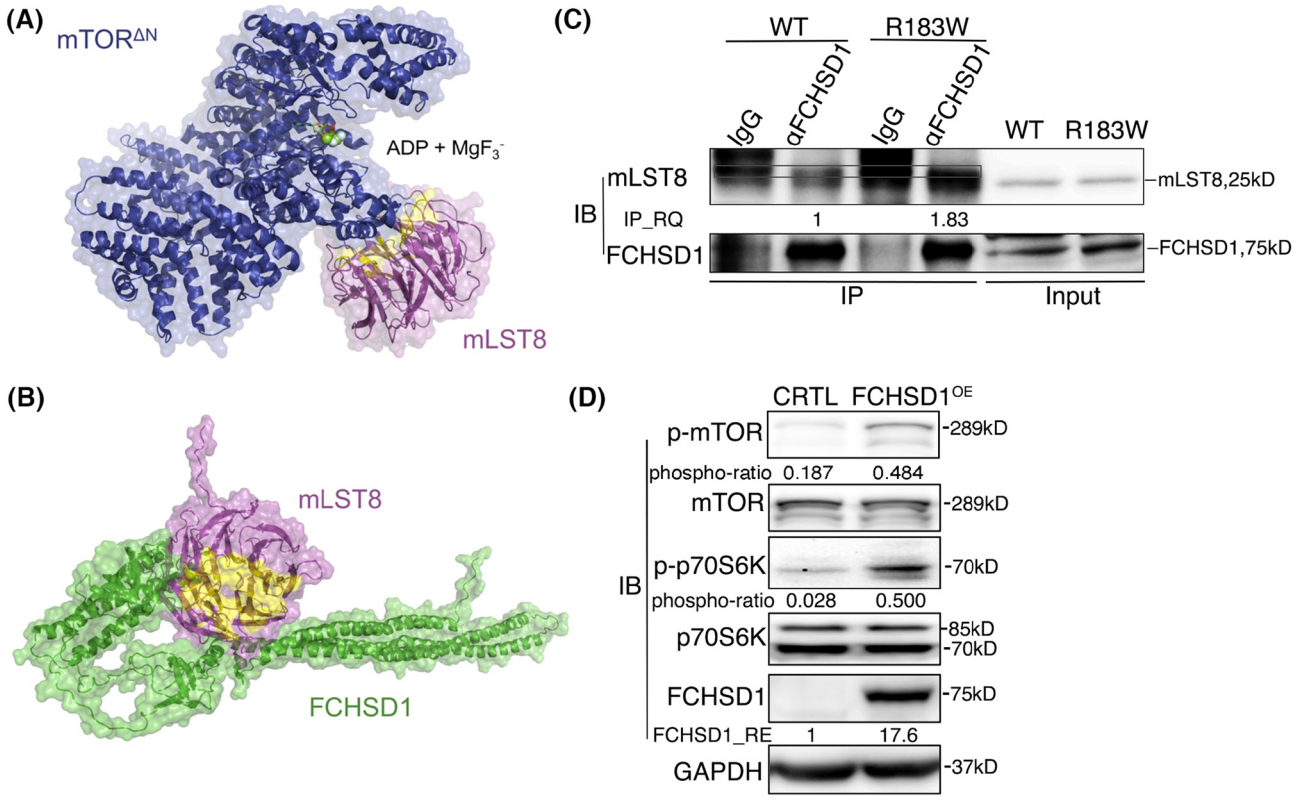

FIGURE 3 FCH and double SH3 domains 1 (FCHSD1) binds to MTOR-associated protein, LST8 homolog (mLST8) and activates mechanistic target of rapamycin (mTOR) signaling. Protein–protein docking analysis shows that mLST8 interacts with mTOR1 and FCHSD1 and form two specific protein–protein interfaces. (A) Crystal structure of mLST8 (magenta surface) in its conformation activating mTOR1 (green surface, Protein Data Bank identifier: 4JSN). Protein–protein interface is represented as yellow surface. (B) Proposed docking model between FCHSD1 and mLST8 represented in green and magenta surfaces respectively. Yellow residues binding mTOR have the same coloring scheme as in (A). (C) Coimmunoprecipitation (IP) analysis of mLST8 and wild-type (WT) FCHSD1 (FCHSD1^{WT}) or FCHSD1^{R183W}. The gray box indicates an unspecific band in all four IP lanes. The relative quantification (RQ) of immunoprecipitated mLST8 to FCHSD1 is the normalized ratio of integrated density measured by ImageJ. (D) The phosphorylation of mTOR Ser2448 and p70S6 kinase Thr389 in HepG2 (CRTL) and FCHSD1 overexpressed (FCHSD1^{OE}) HepG2 cells. The phosphorylation ratio equals (phosphor-signal/GAPDH-signal)/(total-signal/GAPDH-signal). (C, D) Representative data from one of at least two independent experiments. IB, immunoblot.

FCHSD1 is involved in mTOR signaling

To gain insight into the function of FCHSD1, we analyzed its binding proteins listed in the protein–protein interaction (PPI) database and expanded our analysis to its well-defined *Drosophila* orthologue, the Nervous Wreck (Nwk). One of the Nwk-interacting proteins is fly Lst8, which is homologous to mammalian mLST8 (a mechanistic target of rapamycin [mTOR]–associated protein). mLST8 is a key subunit of mammalian target of rapamycin complex (mTORC)1/2 that binds to mTOR directly and increases its kinase activity. Strong preclinical evidence of mTOR inhibitor has been shown for the treatment of PHT.[20,21] To investigate the possibility of an interaction between human FCHSD1 and mLST8, we performed protein docking experiments. The most populated cluster contained 44 conformations with center and lowest weighted scores of −965 and −1178, respectively. The proposed docking model showed that the mLST8 subunit in the mTORC1 complex formed the protein–protein interface with FCHSD1 (Figure 3A,B). A close-up inspection of this interface revealed a tight network of interactions distributed across the two clusters (Figure S6). The first cluster includes mainly electrostatic interactions, such as Glu-451 with Arg-115, Arg-380 with Asp-160, Arg-357 with Asp-205, and Arg-98 with Glu-374. By contrast, the second cluster displayed hydrogen bond interactions, such as Arg-71 with Pro-167, Gln-164 with Glu-289, Leu-283 with Glu-163, Val-277 with Gln-209, Arg-67 with Pro-212, and Lys-213.

To validate the observations deduced from in silico PPI analysis, we immunoprecipitated FCHSD1 in HepG2^{FCHSD1WT} and HepG2^{FCHSD1R183W} cells. Both FCHSD1^{WT} and FCHSD1^{R183W} bound to mLST8. The FCHSD1^{R183W} protein showed strong binding to mLST8 (Figure 3C). In agreement with the structural analysis, western blotting showed higher levels of FCHSD1 protein in HepG2^{FCHSD1R183W} than in HepG2^{FCHSD1WT}. Overexpression of FCHSD1 correlated with enhanced mTOR phosphorylation (Figure 3D).

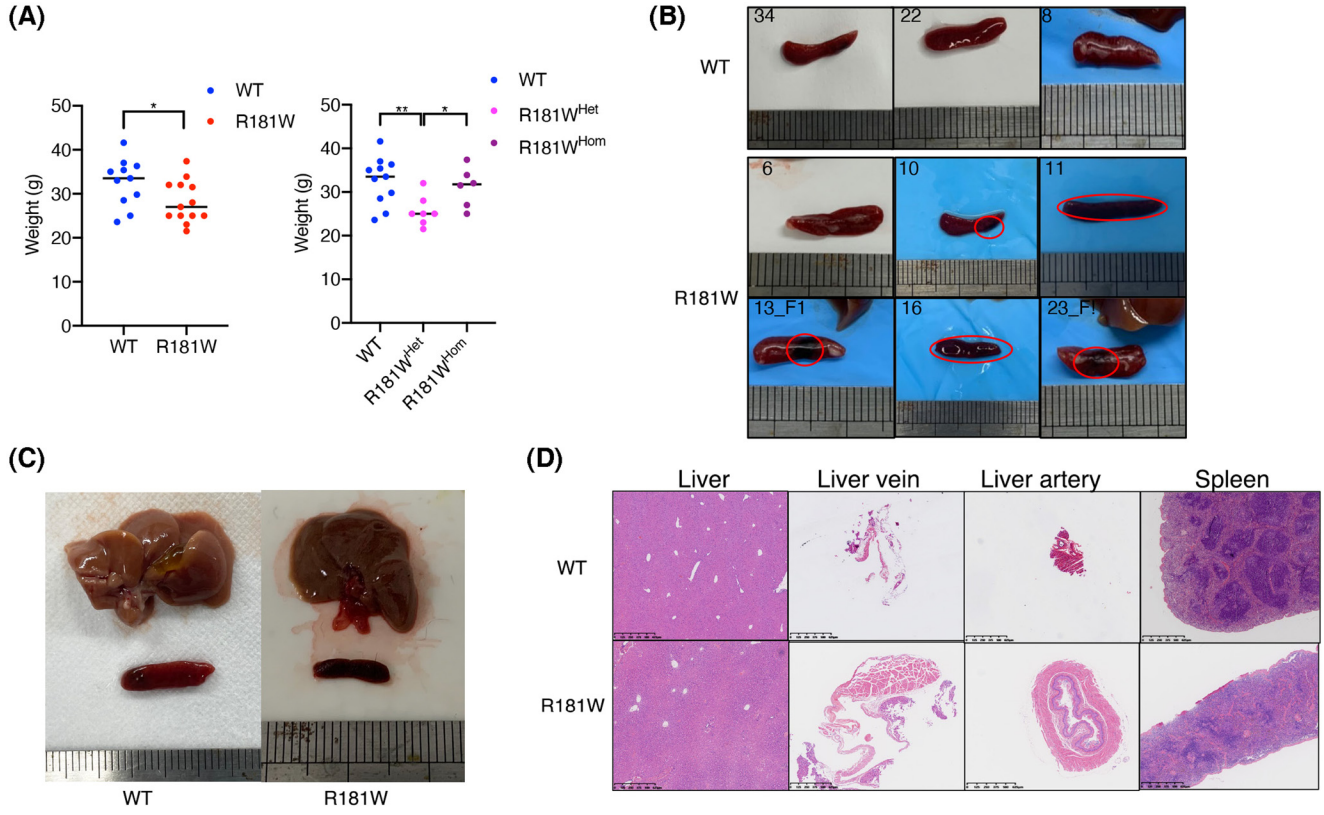

FIGURE 4 The characterization of R181W knock-in mice. (A) The body weight comparison between wild-type (WT) and R181W knock-in mice at age 24 weeks. Het: heterozygote; Hom: Homozygote. *$p < 0.05$; **$p < 0.01$. (B) Representative images of liver and spleen of R181W knock-in mice and WT mice. (C) Dissected livers and spleens of WT mouse and R181W carrier sacrificed at 44 weeks. (D) Hematoxylin and eosin staining of liver, portal vein, liver artery, and spleen of WT mouse and R181W carrier with enlarged portal vein sacrificed at 44 weeks.

FCHSD1 variant knock-in mice mimic the phenotype of human PSVD

Ten heterozygous and five homozygous mice containing the human *FCHSD1*^{R183W} variant were obtained using CRISPR/Cas9 genome editing. No spontaneous death was observed in either group of 11 mice (maintained until the 24 weeks) or in four mice maintained (until 44 weeks). Compared with the wild-type mice, the genetically engineered mice were more likely to have lower body weight at 24 weeks (Figure 4A, left; Table S4). The heterozygotes showed significantly lower body weight compared with the wild-type or the homozygotes (Figure 4A, right). Overall, out of the 15 genetically engineered mice, nine *FCHSD1*^{R183W} carriers (7 heterozygotes and 2 homozygotes) showed PSVD-like symptoms; eight mice, sacrificed at 24 weeks, were found to have an enlarged spleen or blood clot on the spleen (Figure 4B and Figure S7A), which are typical features of PHT. Histological analysis of the liver did not reveal any obvious pathological abnormalities (Figure S8); however, we observed an overexpression of the Fchsd1 protein and an increase in p70 S6 kinase phosphorylation, which indicates the activation of mTOR in the spleen cells of these mice (Figure S7B). Another carrier of the *FCHSD1*^{R183W} variant (mouse 14, Table S4), showed phenotypic abnormalities including lethargy and low body weight. When the mouse was sacrificed at 44 weeks of age, enlargement of the portal vein was observed and established by histological analysis (Figure 4C,D). Noteworthy, this male mouse had significantly lower body weight compared with the other mice (Table S4). An increased Fchsd1 protein level and phosphorylation of mTOR and p70 S6 kinase were noticed in its liver and spleen cells (Figure S7C). Next, regardless of the presence of liver cirrhosis, we examined the expression of molecular markers of pathological alterations associated with PHT in liver tissues. Only endothelial activation markers significantly increased or tended to increase in the R181W variant carriers; in contrast, inflammation, angiogenesis, fibrogenesis, and necroinflammation markers did not significantly increase in these animals (Figure S9). We carried out RNA sequencing and examined differentially expressed genes (DEGs) in liver specimens from wild-type mice and R181W variant carriers to assess the impact of this variant on gene expression (Table S5, Figure S10A,B). The metabolic pathways such as steroid hormone production, retinol metabolism, and xenobiotics biodegradation are prominent in the DEGs (Figure S10C,D). The maintenance of the liver's primary functions,

including as metabolism, detoxification, and vitamin storage, involves each of these pathways. The liver transcriptome results strongly suggest that this variant has a pathogenic role in liver disease.

DISCUSSION

Our study revealed the structure and function of *FCHSD1*, an uncharacterized gene, associated with the inheritance of PSVD in a large multigenerational family.

In agreement with previous reports,[8,22] the *FCHSD1*^{R183W} variant identified in this family segregated with PSVD in an autosomal dominant pattern. Interestingly, the affected members expressed different PSVD symptoms, thus reflecting the variable expressivity of the disease within this family. Our findings, hence, strongly imply the gain-of-function mutation of *FCHSD1* as a potential underlying etiology of PSVD.

Variant analyses are commonly used to support the diagnosis and management of hereditary diseases. More often, the assessment of variant effects involves the dysfunction of the gene product; however, the disease-causing variants may also affect protein expression through mRNA instability. RNA secondary structures regulate elongation, termination, and translation initiation in both eukaryotic and prokaryotic cells. Thus, mutations in highly conserved regions may have deleterious effects on these biological functions. For example, the substitution of adenine to guanine in CAGUGU, a highly conserved motif in the 5′-untranslated region of the ferritin light chain results in hereditary hyperferritinemia-cataract syndrome.[23] This mutation prevents the formation of a crucial harpin which ensures the recognition and interaction between the RNA and the iron-responsive element-binding protein at low iron concentrations.[23] Similarly, our in silico *FCHSD1*_RNA structure analyses showed that the *FCHSD1*^{R183W} variant causes a change in both the secondary and tridimensional structures of *FCHSD1*_RNA. Consequently, the mRNA folding may be altered, leading to an increase in its thermodynamic stability and eventually in its protein overproduction. Altered mRNA stability has been strongly implicated in the manifestation of various human diseases.[24,25] In addition to mRNA stability, its translation represents another fundamental regulation for gene expression. Recent studies have underscored the role of transfer RNA variation in mRNA degradation.[26] The strong binding found between FCHSD1^{R183W} protein and the mTOR-associated protein, mLST8, could be explained by the loss of the positive charge on the side chain of arginine in FCHSD1^{R183W}, resulting in the release of FCHSD1 from being anchored to the negatively charged phospholipid membrane, which may make FCHSD1 more accessible to mLST8.

The current treatment for PHT often adopts treatment for common high blood pressure and nonselective beta blockers.[27] However, only a subset of patients exhibited a hemodynamic response,[28] which might be detrimental to some patients. Thus, novel therapies are urgently needed.[29] A characteristic of PSVD is enlargement of lymph vessels,[30] which was observed in a rat model of PHT and was underlain by activated mTOR signaling.[20] Polymorphisms in *CD73* and xanthine oxidase genes, both of which are mTOR pathway genes, determined the risk of NCPH in patients with HIV.[31] mTOR blockade achieved superior results in NCPH rats, with a significant decrease in portal pressure and spleen size.[20,21] Collectively, these findings suggest a critical role of mTOR signaling in the molecular pathogenesis of PSVD. Furthermore, mTOR signaling contributes to the development of experimental pulmonary arterial hypertension.[32] Our crystal structure elucidates mLST8's binding site in close proximity of the kinase catalytic pocket[33] and further reveals an intricate complex of other subunits. The stabilization of protein–protein complexes follows very precise rules of oligomerization and is a subject of great interest in drug discovery; however, it remains challenging to achieve. Examples of PPI stabilizers include 14-3-3 and their partners, ubiquitin/E2 enzymes and ARF1/Sec7. The proper formation of these interfaces is driven by both shape and electrostatic charge complementarity.[34] Similarly, the protein–protein interface, as presented in our proposed docking model, displays a dense network of polar interactions. Consequently, this might stabilize the mLST8 conformation downstream in the complex with mTORC1. Recently, loss-of-function mutation of *FCHSD1* was shown to ameliorate chronic obstructive pulmonary disease in a mouse model.[35] *FCHSD1*^{R183W} is a gain-of-function variant for mTOR signaling, which is consistent with the observation in PHT. Alternatively, steroidal farnesoid X receptor (FXR) agonist was effective in both NCPH and cirrhotic PHT experimental models.[36] FXR is an emerging, highly potential therapeutic target for chronic liver disease. FXR activation has been proposed as a biomarker of mTOR inhibition.[37,38] These data demonstrate that the mTOR signaling pathway plays a central role in the etiology of PSVD, and mTOR pathway antagonists could be potent anti-PHT therapeutics.

We only observed 60% (9 of 15) of our CRISPR/Cas9 mice—those showing symptoms of human PSVD until 20 months after birth. The low penetrating variant in mice could be explained by the genetic difference between humans and mice and by the late onset and the incomplete penetrance of this idiopathic disease in humans. FCHSD1 level is barely detectable in human hepatic or endothelial cells; however, *Fchsd1* is considerably expressed in murine hepatic or endothelial cells. Hence, a mouse model of mTOR hyperactivation other than the

mFCHSD1 gene model is warranted to verify the role of mTOR in PSVD.

Lymphoid tissues including lymph node, spleen, and bone marrow displayed high levels of FCHSD1 expression (link: t.ly/oLoR), and infiltrating liver immune cells (vascular endothelial cells and T cells) as well as hepatic stellate cells (HSCs) do express significant levels of FCHSD1 (link: t.ly/BqA3). The development of PVSD has been linked to the infiltration of immune cells in the liver.[36] Moreover, our liver transcriptomic data demonstrated that immune system genes were differently enriched in R181W carriers. Thus, this variation in FCHSD1 expression may reflect an increase in the infiltration of inflammatory cells in the tissue surrounding porto-sinusoidal venules and further contributes to the progression of PSVD. Dysfunction in lipid metabolism may also play a role in PSVD etiology. Our transcriptomic analysis, showing that the top enriched DEGs are involved in lipid metabolism, is consistent with the reported results of a transcriptomic study of a human PSVD cohort.[39] In addition, retinol metabolism is another enriched Kyoto Encyclopedia of Genes and Genomes pathway in our transcriptomic data. HSCs, which are found in the perisinusoidal region, have the capacity to store vitamin A and control sinusoidal circulation. Vitamin A levels have been associated with PVSD, regardless of the presence of cirrhosis.[40,41] Therefore, it is possible that this FCHSD1 mutation causes HSCs to have a dysfunctional vitamin A metabolism, which contributes to the progression of PSVD.

In summary, our study provides insights into the mechanism mediating the development of PSVD and support the use of mTOR inhibitors as a potential PSVD treatment. Furthermore, our animal model suggests a long disease course in the PSVD genetic model and motivates further studies to identify the environmental factors that influence PSVD progression.

AUTHOR CONTRIBUTIONS

Lotfi Chouchane and Jingxuan Shan conceived and designed the study. Jingxuan Shan, Pu Li, Aziz Chouchane, Sirin W Abuaqel, and Murugan Subramanian performed the biochemical analyses. Deepak Karthik, Ramzi Temanni, Chadi Saad, and Hamdi Mbarek processed the whole-genome data. Pu Li, Huiying Hua, Chun Pan, and Xixi Chen performed analyses on the mouse model. André Megarbane, Cesar Yaghi, Cybel Mehawej, and Eliane Chouery recruited the family and accessed and verified the clinical data. Aziz Chouchane and Sami Remadi reviewed the histopathology reports. Atilio Reyes Romero and Alexander Dömling performed the structure prediction and docking analyses. Lotfi Chouchane wrote the first draft of the manuscript with contributions from all authors. Lotfi Chouchane, Jingxuan Shan, Aziz Chouchane, and André Megarbane performed a literature search and interpreted the data. Lotfi Chouchane supervised and coordinated this study. The corresponding author had full access to all data in the study and had final responsibility for the decision to submit for publication.

ACKNOWLEDGMENTS

We are grateful to the family members who contributed to this study which was supported by the Biomedical Research Program at Weill Cornell Medicine-Qatar.

FUNDING INFORMATION

This work was supported by the Biomedical Research Program funded by Weill Cornell Medicine-Qatar.

CONFLICT OF INTEREST

All the authors declare no competing interests.

DATA AVAILABILITY STATEMENT

All the variants reported here have been submitted to LOVD website (https://www.lovd.nl). All the RNA sequencing data have been deposited to National Center for Biotechnology Information Gene Expression Omnibus.

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How to cite this article: Shan J, Megarbane A, Chouchane A, Karthik D, Temanni R, Romero AR, et al. Genetic predisposition to porto-sinusoidal vascular disorder: a functional genomic-based, multigenerational family study. Hepatology. 2023;77:501–511. https://doi.org/10.1002/hep.32735