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RETRACTED: MicroRNA-21 Plays Multiple Oncometabolic Roles in the Process of NAFLD-Related Hepatocellular Carcinoma via PI3K/AKT, TGF- β , and STAT3 Signaling

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Simple Summary: The PTS signaling (PI3K/AKT, TGF- β , and STAT3 Signaling) networks, regulated by microRNA-21, play roles in lipogenic factor regulation, tumor suppressor modulation and oncogenic activation. Our zebrafish model recreates the development of hepatocellular carcinoma (HCC) due to nonalcoholic fatty liver disease (NAFLD) concerning the physiological, metabolic, and histological aspects similar to that of human NAFLD-related HCC (NAHCC). Thus, microRNA-21 is critical in the pathogenesis of NAHCC, and serves as a novel therapeutic target in NAHCC progression.

Abstract: MicroRNA-21 (miR-21) is one of the most frequently upregulated miRNAs in liver diseases such as nonalcoholic fatty liver disease (NAFLD) and hepatocellular carcinoma (HCC). However, mechanistic pathways that connect NAFLD and HCC remain elusive. We developed a doxycycline (Dox)-inducible transgenic zebrafish model (LmiR21) which exhibited an upregulation of miR-21 in the liver, which in turn induced the full spectrum of NAFLD, including steatosis, inflammation, fibrosis, and HCC, in the LmiR21 fish. Diethylnitrosamine (DEN) treatment led to accelerated liver tumor formation and exacerbated their aggressiveness. Moreover, prolonged miR-21 expression for up to ten months induced nonalcoholic steatohepatitis (NASH)-related HCC (NAHCC). Immunoblotting and immunostaining confirmed the presence of miR-21 regulatory proteins (i.e., PTEN, SMAD7, p-AKT, p-SMAD3, and p-STAT3) in human nonviral HCC tissues and LmiR21 models. Thus, we demonstrated that miR-21 can induce NAHCC via at least three mechanisms: First, the occurrence of hepatic steatosis increases with the decrease of *ptenb*, *pparaa*, and activation of the PI3K/AKT pathway; second, miR-21 induces hepatic inflammation (or NASH) through an increase in inflammatory gene expression via STAT3 signaling pathways, and induces liver fibrosis through hepatic stellate cell (HSC) activation and collagen deposition via TGF- β /Smad3/Smad7 signaling pathways; finally, oncogenic activation of Smad3/Stat3 signaling pathways induces HCC. Our LmiR21 models showed similar molecular pathology to the human cancer samples in terms of initiation of lipid metabolism disorder, inflammation, fibrosis and activation of the PI3K/AKT, TGF- β /SMADs and STAT3 (PTS) oncogenic signaling pathways. Our findings indicate that miR-21 plays critical roles in the mechanistic perspectives of NAHCC development via the PTS signaling networks.

Keywords: microRNAs; hepatic steatosis; steatohepatitis; fibrogenesis; liver cancer

1. Introduction

Nonalcoholic fatty liver disease (NAFLD) manifests as a multistep disorder, beginning from a simple liver steatosis to severe forms of nonalcoholic steatohepatitis (NASH) and cirrhosis, with associated high risk of hepatocellular carcinoma (HCC) [1]. The progression of NAFLD-related HCC (NAHCC) is a more complex process, caused by several risk factors, such as genomic instability, obesity, or diabetes [2]. Deregulated microRNAs (miRNAs) may be involved in the pathogenesis of NAFLD [3] and HCC [4]. The miR-21 gene is highly conserved in vertebrates [5] and is found in the peripheral blood, bone marrow, liver, lung, kidney, intestine, colon, and thyroid [6]. miR-21 is upregulated in many biological processes, including inflammation, fibrosis, and cancer [7]. Increasing evidence has also demonstrated the importance of miR-21 in several liver diseases [5].

Previous studies have shown that miR-21 relies on a complex lipogenic transcription network to regulate lipogenesis in hepatocytes. miR-21 promotes hepatic lipid accumulation by interacting with several factors, such as sterol regulatory element binding protein (SREBP1) [8], fatty acid binding protein 7 (*FABP7*) [9], and 3-hydroxy-3-methylglutaryl-coenzyme A reductase (*HMGCR*) [10]. Lack of hepatic miR-21 is sufficient to prevent hepatic steatosis and fatty acid uptake [11]. miR-21 is upregulated in the livers of the low-density lipoprotein receptor (LDLR)-deleted mice showing liver inflammation and silencing of the miR-21 using antagomir-21 reduced hepatic inflammation and fibrosis [12]. Additionally, miR-21 contributes to cell injury, inflammation and fibrosis, through the inhibition of peroxisome proliferator activated receptor alpha (*PPAR- α*) signaling pathway [13]. These studies suggest that miR-21 has a central role in liver inflammation induced by steatosis.

MiR-21 is also known to be an oncomir that functions by increasing cell proliferation and invasion, and by inhibiting cellular apoptosis [14]. MiR-21 has been shown to be globally overexpressed in multiple neoplasms and to promote cancer cell proliferation, migration, and survival [15,16]. MiR-21 has also been linked with inflammation-related cancers, in which its expression is stimulated by inflammatory factors such as interleukin 6 (IL-6) [17], signal transducer and activator of a transcription 3 (STAT3)-dependent mechanism [18], and transforming growth factor (TGF- β) through the SMADs signaling cascade [19]. MiR-21 is also involved in carcinogenesis by targeting tumor suppressor mRNAs, such as tropomyosin 1 [20], programmed cell death 4 (*PDCD4*) [21], and phosphatase and tensin homolog (*PTEN*) [22]. In fact, miR-21 is one of the most commonly studied miRNAs in HCC [23,24].

In line with the aforementioned studies, miR-21 may therefore be implicated at different steps of the NAFLD progression into HCC: first, early onset of lipid accumulation and steatosis in hepatocytes [13], second, inflammation and/or fibrosis [25] and eventually, HCC [26]. However, relatively few reports have studied the involvement of miR-21 in NAFLD and NAHCC [8]. Thus, an appropriate animal model, which is pathologically similar to human NAHCC remains to be established with multistep profiles of the histological features of lesions and precise mechanisms regarding the role of miR-21 in the pathogenesis of NAHCC characterized.

In recent years, the zebrafish has been widely used as a model organism for cancer research [27,28]. Hence, in this study, we aimed to examine the time profiles of miR-21 expression and its target genes during NAHCC genesis using the zebrafish model, LmiR21, which was established in our laboratory.

2. Materials & Methods

2.1. Generation and Maintenance of LmiR21 Transgenic Zebrafish

The transgenic zebrafish lines, LmiR21 [*Tg(fabp10a-Tet^{on}-2A-ZsGreen:mCherry-miR-21)*], which show liver specific expression of mCherry and have miR-21 driven by the *fabp10a* promoter, and AmiR21 [*Tg(β -Act-Tet^{on}-2A-ZsGreen:mCherry-miR-21)*], which shows inducible global miR-21 expression under the control of β -action promoter [29], were maintained in a controlled environment with a 14/10-h light-dark cycle at 28 °C. All

lines were maintained in compliance with Institutional Animal Care and Use Committee (IACUC) guidelines.

2.2. Doxycycline (Dox) Treatment

The embryos as well as juvenile adult zebrafish were treated with Dox at 25 µg/mL (Sigma) in six-well plates and 3-L tanks, respectively, and the water was changed daily.

2.3. Patients and Samples

Twenty paraffin-embedded and HCC liver tissue specimens from the primary tumors of patients were obtained from the specimen bank of Chang Gung Memorial Hospital, Taiwan. The Human Research Ethics Committee (the approval numbers of Institutional Review Board: 201700777B0 & 201700777B0C101) approved the research protocol.

2.4. MiRNA Target Prediction

TargetScan Home Page [30] and miRBase Home Page [31] were used to predict the putative targets of miR-21.

2.5. Quantitative Reverse Transcription PCR (RT-qPCR) for Mature miR-21 Quantification

Zebrafish total RNA were extracted using TRIzol reagent (Invitrogen, CA) or the RNeasy Mini Kit (Qiagen) and reverse transcribed using the first-strand cDNA synthesis kit (Fermentas, Lithuania). Real-time RT-PCR was performed using the StepOne Real-Time PCR System (Applied Biosystems). The genes and corresponding primer sequences are listed in Table S1.

2.6. In Situ Hybridization (ISH)

The gene-specific probes were cloned by PCR into a pGEM-T Easy TA cloning vector (Promega) using the primers listed in Table S2. Antisense probes were synthesized by in vitro transcription using DIG RNA Labeling Kit (SP6/T7) (Roche Applied Science). ISH was performed as previously described [29].

2.7. Biochemical Analyses of Zebrafish Liver Lipids

Biochemical analyses of zebrafish liver lipids were performed as previously described [32].

2.8. Western Blot Analysis

Total hepatic proteins from homogenized liver tissue were analyzed by Western blotting as previously described [32,33]. The membrane was incubated in the following antibodies: PTEN (1:1000, Cell Signaling 138G6), p-AKT (1:2000, Cell Signaling D9E), SMAD7 (1:1000, R&D Systems MAB2029), p-SMAD3 (1:2000, Abcam ab52903), p-STAT3 (1:1000, MBL International D128-3), PPAR alpha (1:1000, Abcam ab215270), and Gapdh (1:10000, GeneTex GTX100118). Protein levels were detected by using a horseradish peroxidase (HRP)-conjugated secondary antibody (1:5000, Jackson ImmunoResearch Labs AB_10015289 or AB_2313567) and peroxidase-catalyzed chemiluminescence (Millipore WBKLS0100).

2.9. Biochemical Analyses of Zebrafish Liver Lipids

Levels of free cholesterol, cholesterol esters (CE) and lipid peroxidation (malondialdehyde, MDA) in the liver, determined by assay kits (Sigma-Aldrich MAK043 and MAK085). Concentrations of triglycerides (TG) were measured as previously described [34]. For ROS (reactive oxygen species) measurement. ROS generation was determined in zebrafish liver homogenates by DCFDA/H2DCFDA—Cellular ROS Assay Kit (Abcam ab113851).

2.10. Chemical Carcinogenesis

For this study, 21 days postfertilization (dpf) zebrafish were maintained in 3 L of water containing 100 ppm diethylnitrosamine (DEN; Sigma Chemical Co, St Louis, MO, USA) for

three days (day 22 to 25), and with 25 µg/mL Dox for three months. Fish were sacrificed in the first, third, and ninth month post-treatment for histology analysis by hematoxylin and eosin (H&E), Masson's trichrome, and Picrosirius red (PSR) staining.

2.11. Histology and Immunohistochemistry

Oil red O (ORO) staining and microscopy were performed as previously described [32,33]. The tissue sections were incubated in the following antibodies: PTEN (1:200, Cell Signaling 138G6), p-AKT (1:100, Cell Signaling D9E), SMAD7 (1:500, R&D Systems MAB2029), p-SMAD3 (1:250, Abcam ab52903), p-STAT3 (1:250, MBL International D128-3), and PCNA (1:1000, Santa Cruz Biotechnology sc-7907). BrdU staining was performed by using a BrdU in situ detection kit (BD Biosciences, San Jose, CA, USA). Masson's trichrome and PSR was performed using Masson's Trichrome kit (Sigma-Aldrich #HT15-1KT), and Picro Sirius Red Stain Kit (Abcam ab150681), respectively.

2.12. Statistical Analysis

All data are provided as the mean ± standard error of the mean (SEM). Statistical analysis was performed with analysis of variance (ANOVA) followed by Bonferroni post-tests. All analyses were performed using GraphPad Prism 8.0 software (GraphPad, San Diego, CA, USA). A value of $p < 0.05$ was considered statistically significant.

3. Results

3.1. Generation of Transgenic LmiR21 Zebrafish Lines

To generate stable inducible expression of the mCherry-fused miR-21 in zebrafish liver, we used the β -Act-Tet^{on}-2A-ZsGreen:mCherry-miR-21 (Figure S1A) and *fabp10a*-Tet^{on}-2A-ZsGreen:mCherry-miR-21 construct (Figure 1A) to produce the germline-transmitting transgenic zebrafish lines, AmiR21[Tg (β -Act-Tet^{on}-2A-ZsGreen:mCherry-miR-21)] and LmiR21[Tg (*fabp10a*-Tet^{on}-2A-ZsGreen:mCherry-miR-21)], respectively. The AmiR-21 line had miR-21 inducible globally (Figure S1B,C), and the LmiR21 lines had miR-21 inducible locally in the liver (Figure 1B). The transgenic lines showed high ZsGreen signals without doxycycline treatment (−Dox), whereas both of ZsGreen and mCherry signals were detected in Dox treatment groups only (+Dox) (Figure 1C and Figure S1B).

Several transgenic zebrafish were identified by the presence of strong red fluorescence signals in the liver (Figure 1C) or whole body (Figure S1B) of transgenic larvae, and the miR-21 expression was confirmed by RT-qPCR (Figure 1B and Figure S1C). The LmiR21#1 + Dox larva expressed slightly higher levels of the miR-21 (Figure 1B) and mCherry-miR-21 protein (Figure 1C) than those in the control fish, LmiR21 − Dox and WT (wild type). At the larval stage, the AmiR-21 + Dox showed no discernible phenotypic changes in the two founder lines compared to that in the WT (data not shown). However, the time of onset of liver hyperplasia, hepatomegaly (Figure 1D), and the liver size were determined by measuring the volume of ZsGreen-expressing livers using 2D-dimensional images (Figure 1D). The liver size of LmiR21#1 + Dox at 48 and 72 h postfertilization (hpf) larvae increased by approximately 175% and 230%, respectively, compared to that in 7dpf LmiR21#1 − Dox (Figure 1D). PCNA immunohistochemical staining showed active cell proliferation in LmiR21#1 + Dox livers compared with that in the control fish (Figure 1E), indicating that miR-21 induction enhances hepatocyte proliferation.

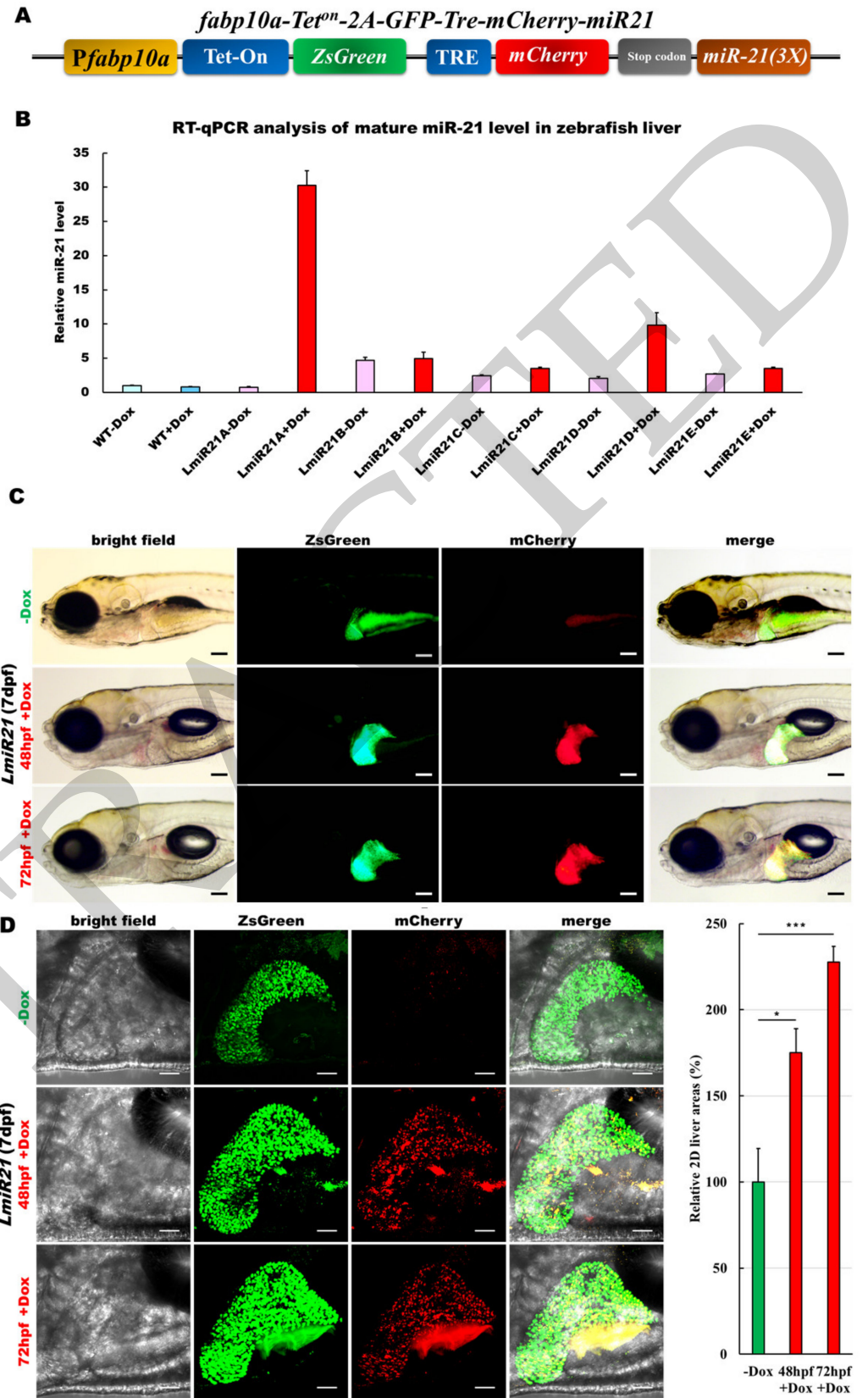


Figure 1. Cont.

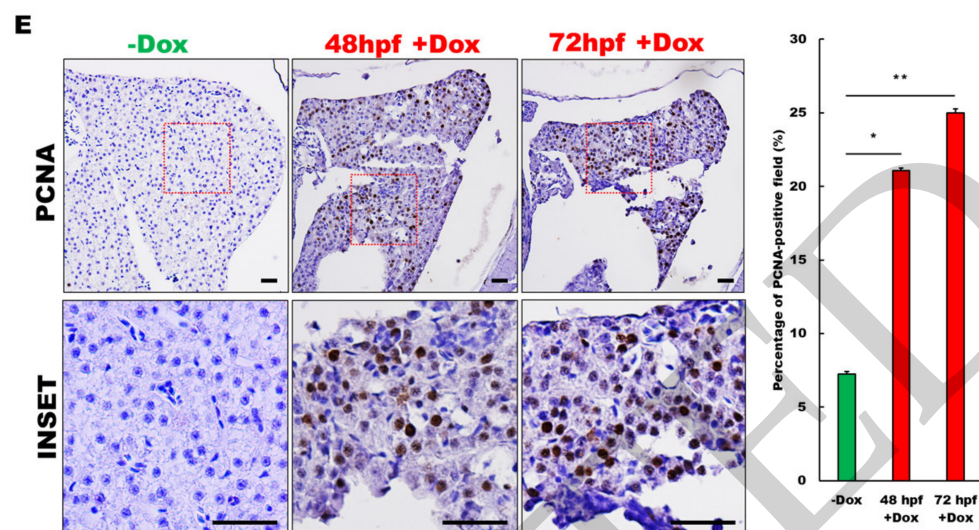


Figure 1. Generation of a liver specific and inducible microRNA (miR)-21 transgenic zebrafish. (A) Schematic diagram of the DNA construct used to generate LmiR21 [*Tg(fabp10a-Tet^{on}-2A-ZsGreen:mCherry-miR-21)*] transgenic zebrafish. *Fabp10a* promoter drives expression of ZsGreen and tetracycline-inducible transcription factor (Tet-on/off), which controls mCherry and miR-21 expression. (B) Relative quantification of miR-21 expression using (RT-qPCR) analysis. LmiR21#1-5+doxycycline (Dox) represent five independent transgenic lines. Control: wild-type (WT)-Dox and LmiR21#1-5-Dox zebrafish. (C) Liver-specific inducible miR-21 expression in the LmiR21#1 7 days post fertilization (dpf). Transgenic larvae were treated with 25 $\mu\text{g}/\text{mL}$ Dox from 48 or 72 h post fertilization (hpf) to 7 dpf. Scale bar: 100 μm . (D) Left: images of zebrafish liver; right: 2D measurements of liver area using ImageJ. Scale bar: 50 μm . (E) Representative photomicrographs of IHC detection of cell proliferation marker-PCNA in zebrafish liver (Left). Scale bar: 50 μm ; Statistical analysis of the percentage of PCNA-positive field. Statistically significant differences from –Dox group were denoted by * ($p < 0.05$), ** ($p < 0.01$) and *** ($p < 0.001$) for panel D and E.

3.2. Effects of Hepatic miR-21 Expression on Early Onset of Liver Steatosis

MiR-21 has been reported to play an important role in the pathogenesis of NAFLD [35]; hence, we examined lipid metabolism in the LmiR21 liver. ORO staining of whole mount LmiR21 + Dox larvae showed more severe liver steatosis than in the controls (Figure 2A), indicating a higher percentage of ORO stained liver than the controls (Figure 2A). LmiR21 + Dox larvae also showed substantial lipid accumulation (Figure 2B, left) and histological staining showed the abnormal shape of lipid vacuoles in hepatocytes compared to the controls (Figure 2B, right). We then examined whether the early onset steatosis phenotypes would progress into NAFLD in adults. Approximately 50% of the LmiR21 + Dox fish at 4 months post fertilization (mpf) began to reveal yellow and greasy livers in both males and females (Figure 2C). The hepatic triglyceride (TG) and cholesterol of LmiR21 + Dox was significantly greater than the controls (Figure 2D). Furthermore, histopathologic examination revealed that LmiR21 + Dox developed NAFLD as determined by H&E (Figure 2E, left), ORO (Figure 2E, right), Masson's trichrome (Figure 2F, left) and PSR staining (Figure 2F, right); this was not observed in the controls. These data suggest that miR-21 overexpression can induce hepatic steatosis in both larvae and adults.

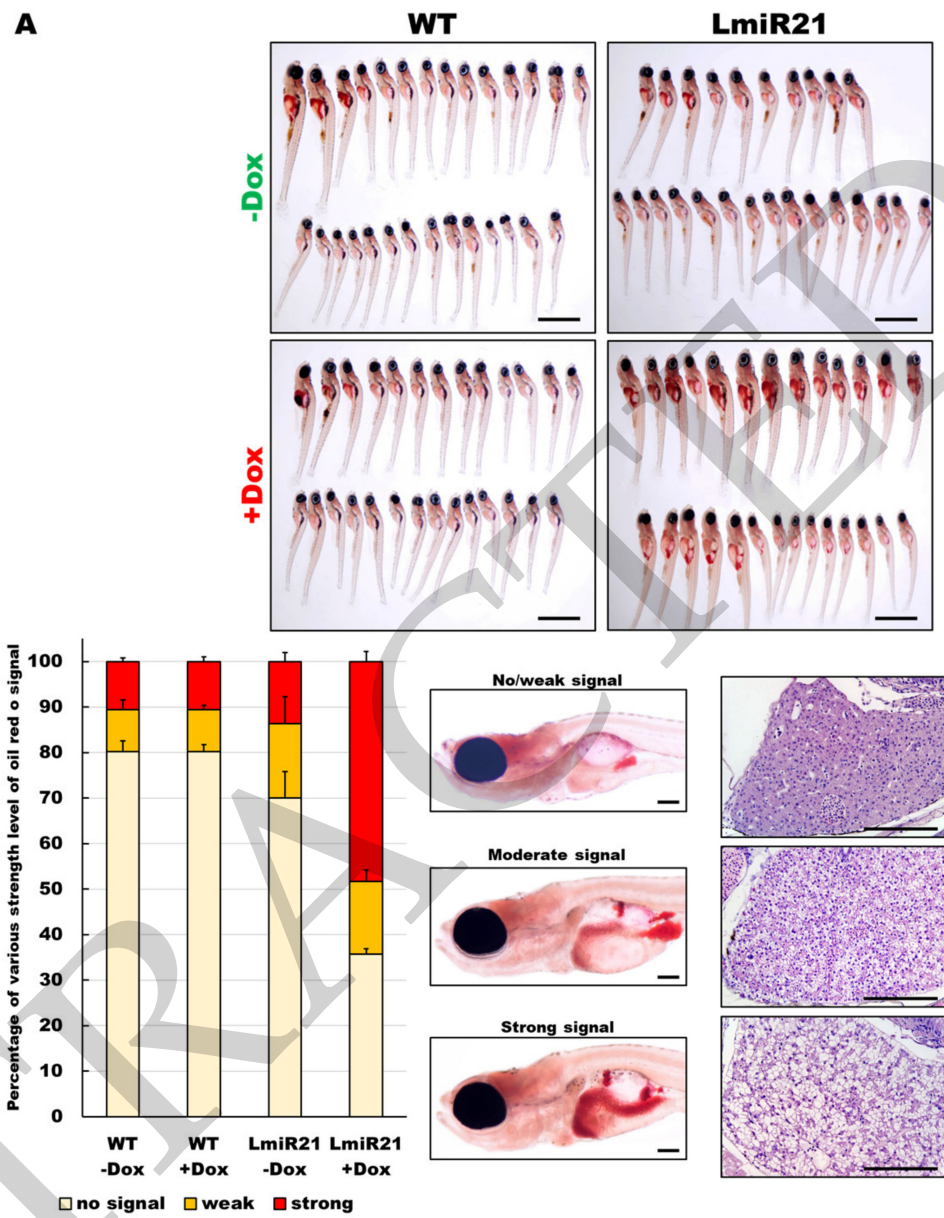


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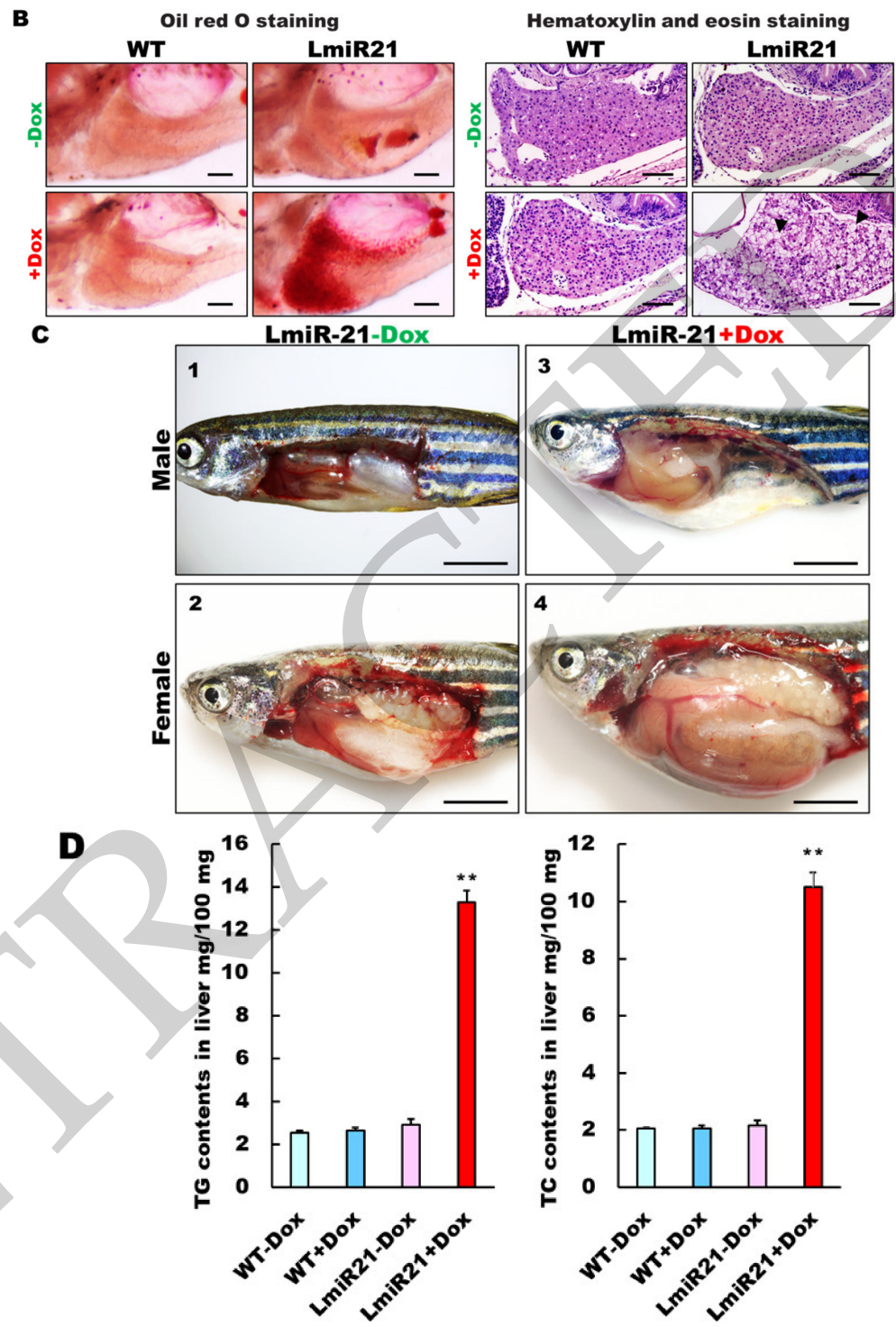


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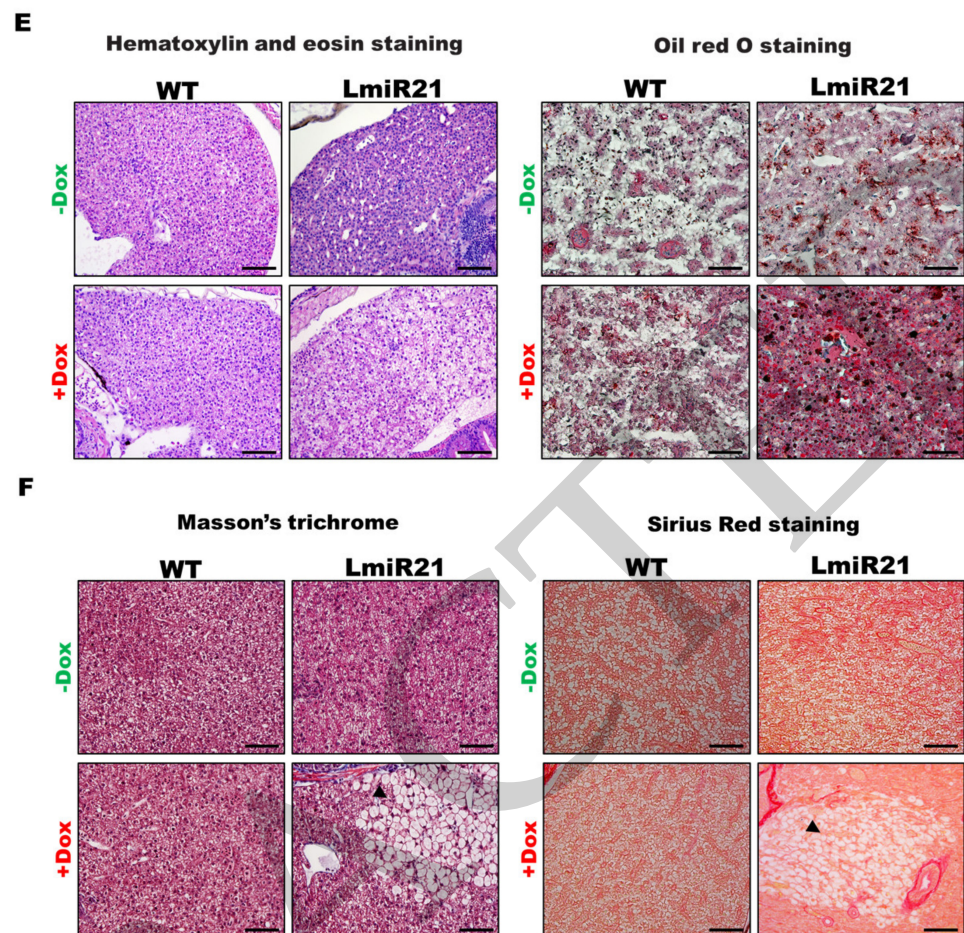


Figure 2. Characterization of hepatic steatosis in LmiR21 larvae and adult. **(A)** Whole-mount oil-red O (ORO) staining of WT \pm Dox and LmiR21 \pm Dox larvae at 21 dpf. Lipid contents in livers and swim bladders were stained by ORO (up). Scale bar: 2 mm. Percentages of WT \pm Dox and LmiR21 \pm Dox larvae with weak, moderate and strong levels of hepatic steatosis at 21 dpf (down). Scale bar: 200 μ m. **(B)** Representative ORO images of liver in 21 dpf larvae (left). Scale bar: 500 μ m. Hematoxylin-eosin (H&E) staining of livers at 21 dpf LmiR21 + Dox larvae show abnormally shaped hepatocytes with lipid vacuoles (arrows) compared with that in the controls at the same stage. Scale bar: 100 μ m. (right). **(C)** Gross liver phenotypes at 4 months post fertilization (mpf) LmiR21 \pm Dox. Normal hepatic morphology is clearly composed of lobes in LmiR21 – Dox adult (panels 1,2). Liver hyperplasia with yellow and greasy phenotypes in LmiR21 + Dox adult liver (panels 3,4). Scale bar: 5 mm. **(D)** Triglyceride (TG) and total cholesterol (TC) in the livers is greater in LmiR21 + Dox than in the controls ($n = 3$). Statistically significant differences from LmiR21 – Dox were denoted by ** ($p < 0.01$). **(E)** H&E staining of liver tissue from WT \pm Dox and LmiR21 \pm Dox at 4 mpf depicting morphological changes resulting from accumulation of microvesicular steatosis. Scale bar: 50 μ m. (left). ORO staining of liver cryosections from WT \pm Dox and LmiR21 \pm Dox adults at 4 mpf. Scale bar: 50 μ m. An abundance of lipid accumulation is observed in LmiR21 + Dox compared to that in controls. (right). **(F)** Representative liver sections showing ballooned hepatocytes (large arrow) and lipid vacuoles (star) with Masson's trichrome (left), and Picrosirius red (right). Scale bar: 50 μ m.

3.3. MiR-21 Targets *ptenb* and *pparaa* in Hepatocytes, which Leads to Hepatic NAFLD Progression

To identify the potential targets of miR-21 that might contribute to the NAFLD phenotypes, we used the prediction programs TargetScan to analyze two potential targets of miR-21, phosphatase and tensin homolog b (*ptenb*) and peroxisome proliferator-activated receptor alpha a (*pparaa*) (Figure 3A, left). Whole mount ISH showed miR-21 significantly repressed expression of *ptenb* and *pparaa* mRNA in AmiR21 + Dox as compared to that

in Amir21 – Dox (Figure 3A, right). This was reflected in the RT-qPCR data, which also showed that increased levels of miR-21 results in decreased expression of *ptenb* and *pparaa* mRNA (Figure 3B). Western blot analyses also showed that protein levels of Ptenb and Pparaa were dramatically downregulated in LmiR21 + Dox compared to that in controls (Figure 3C and Figures S4–S7). These data suggest that miR-21 may inhibit post-transcriptional *ptenb* and *pparaa* expression by targeting its 3' untranslated (UTR) region. *Ptenb* and *pparaa* are involved in de novo lipogenesis and oxidative status in the liver, and are thus implicated in NAFLD development [13,36]. Examination of miR-21 mediated hepatic lipogenic gene expression revealed that *ptenb* was suppressed in LmiR21 + Dox compared with that in the controls, and a concomitant increase in levels of acetyl-CoA carboxylase (*acaca*), carbohydrate-responsive element-binding protein (*chrebp*), sterol regulatory element-binding transcription factor 1 (*srebp1*), sterol regulatory element-binding transcription factor 2 (*srebp2*), and peroxisome proliferator-activated receptor gamma (*ppar-γ*) genes were detected in the former group (Figure 3D). A decreased expression of β -oxidation genes was also detected in response to *pparaa* suppression in LmiR21 + Dox than in controls (Figure 3D). Higher levels of hepatic oxidative stress, malondialdehyde (MDA), and H_2O_2 in mitochondria were also detected in LmiR21 + Dox than in controls (Figure 3E). Collectively, these results demonstrate that *ptenb* and *pparaa* are strong targets of miR-21 and have a synergetic effect on NAFLD development (Figure 3F).

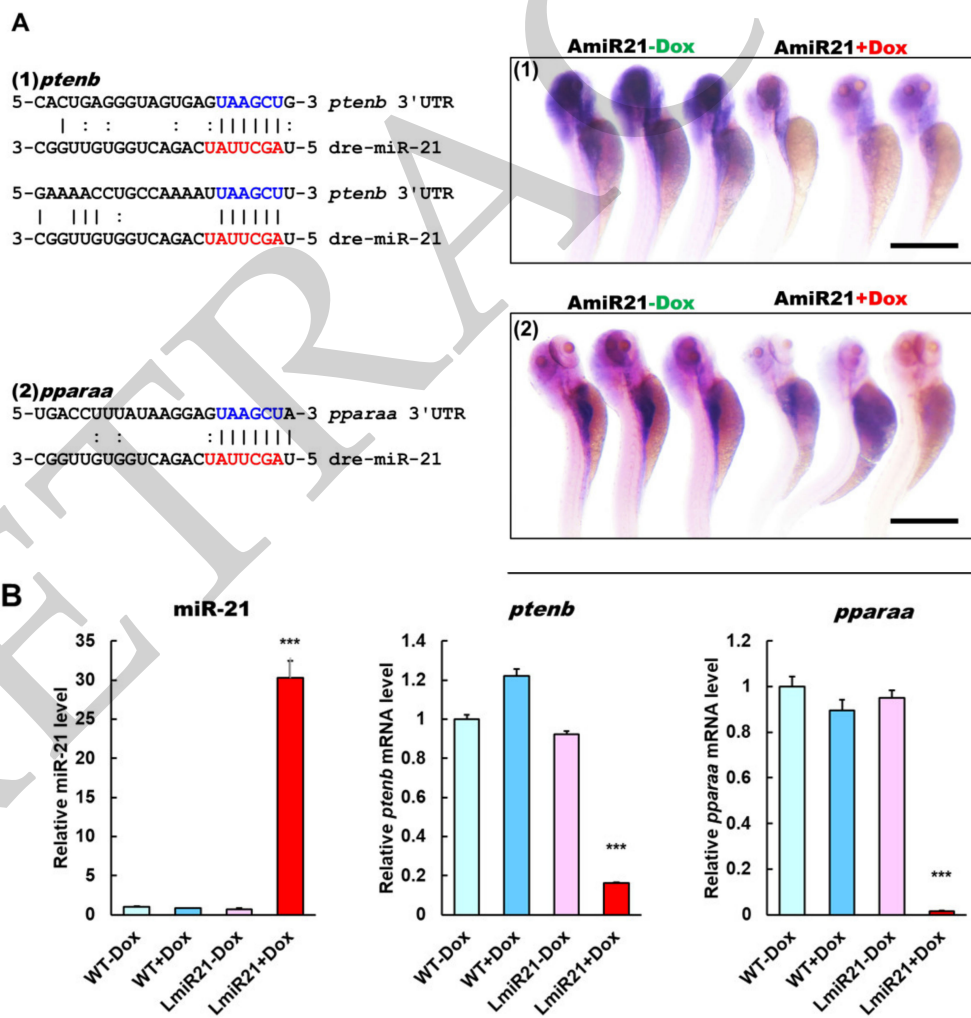


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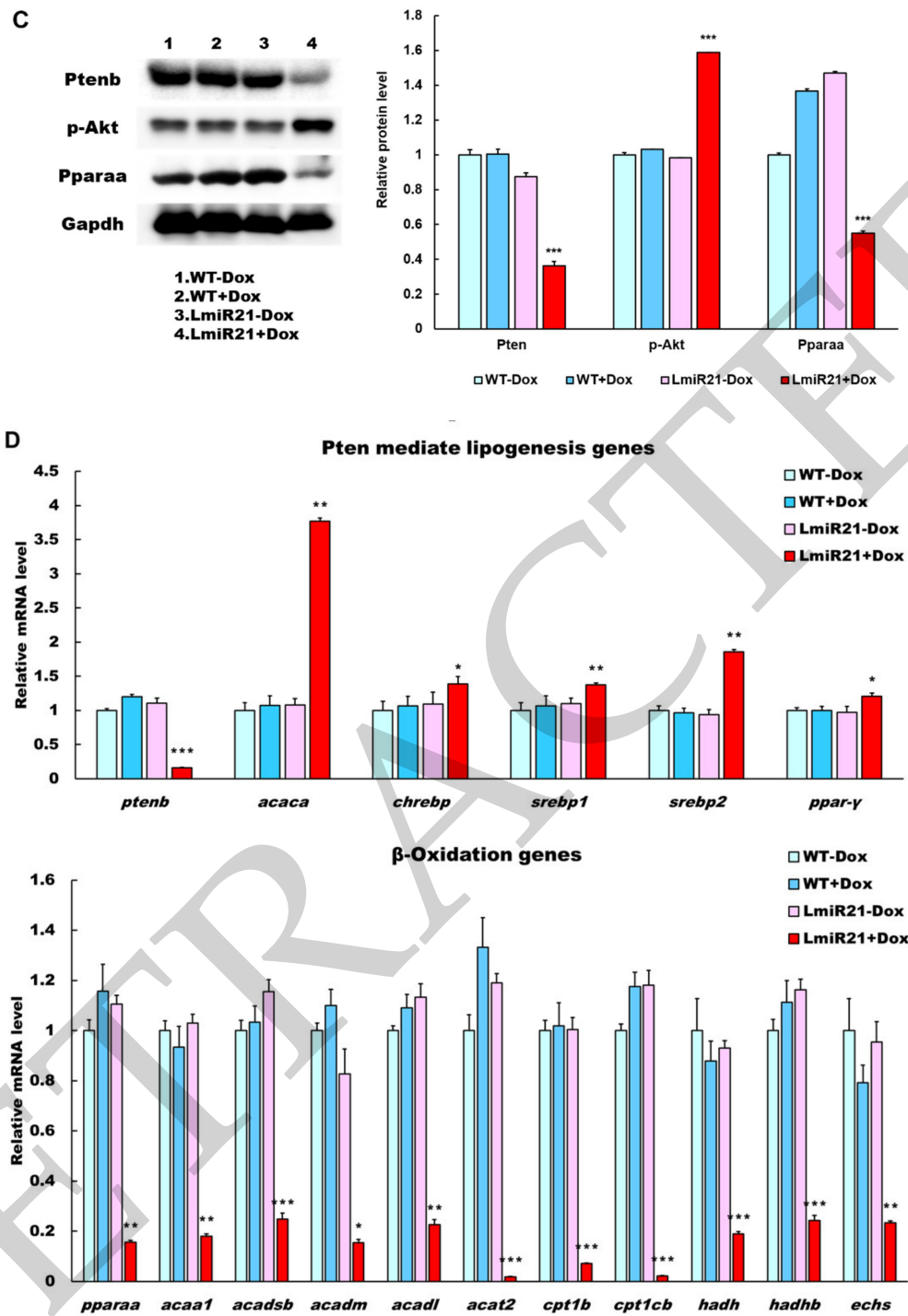


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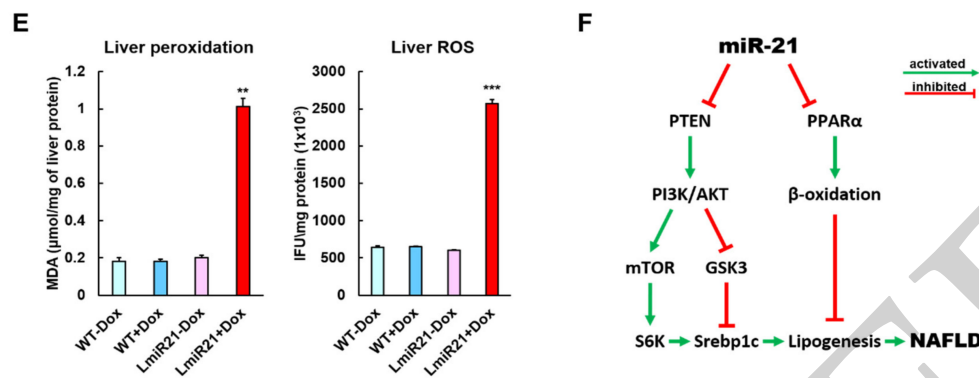
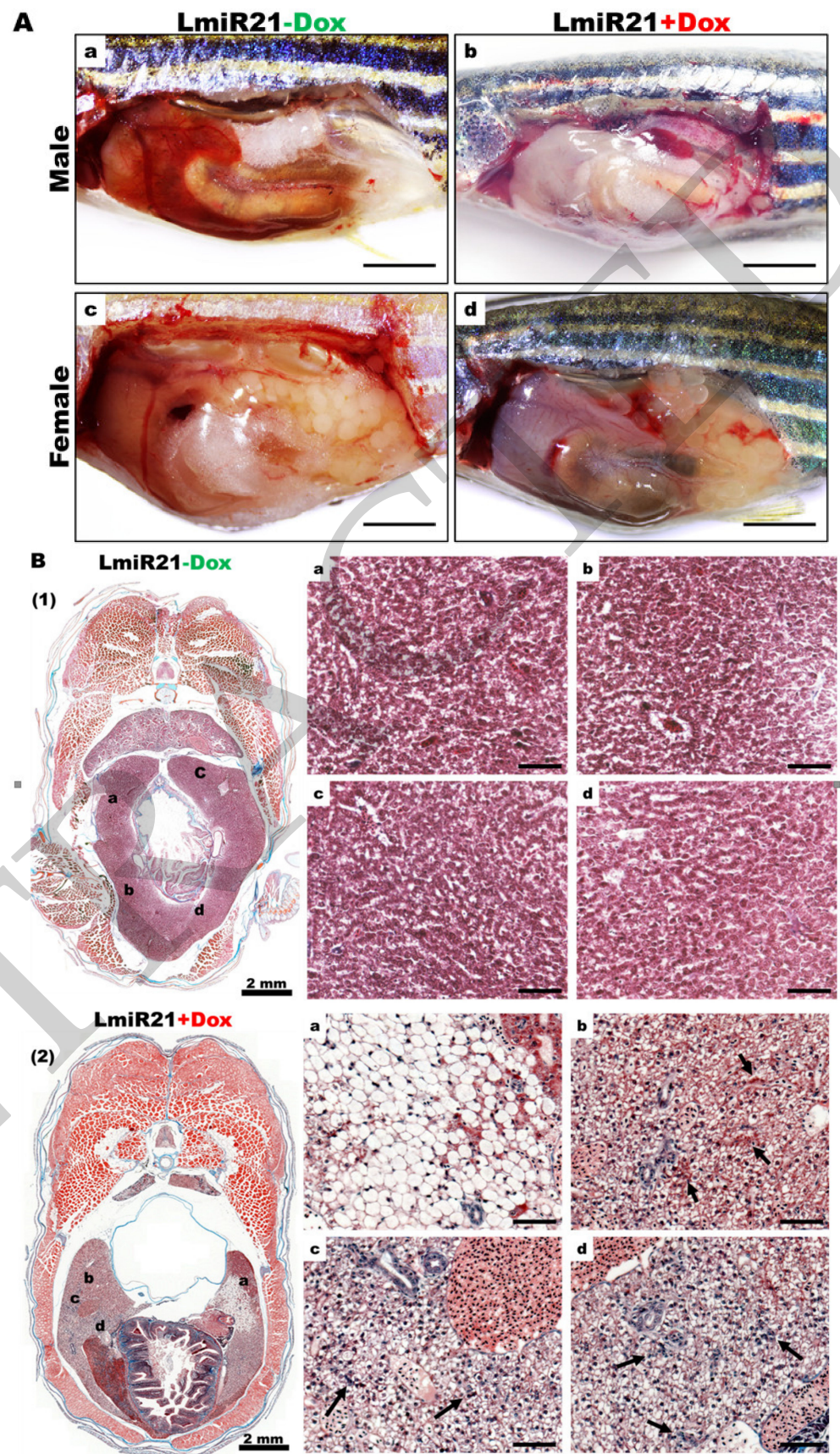


Figure 3. MiR-21 targets *ptenb* and *pparaa* levels in hepatocytes, which leads to nonalcoholic fatty liver disease (NAFLD) progression. (A) Schematic alignment between the mature miR-21 seed sequence (red) and (1) *ptenb*, (2) *pparaa* mRNA target sequence (blue) at the 3'-UTR. Perfect matches are indicated by a line, and G:U pairs by a colon. (left). Whole mount in situ hybridization (ISH) assays demonstrate that miR-21 significantly represses in vivo expression of (1) *ptenb* and (2) *pparaa* mRNA in AmiR + Dox, compared to that in AmiR-Dox (right). Scale bar:1 mm. (B) MiR-21 expression in the livers of WT ± Dox and LmiR21 ± Dox at 4 mpf. mRNA expression levels of *ptenb* and *pparaa* mRNA liver of WT ± Dox and LmiR21 ± Dox at 4 mpf. (C) Western blot images (left) and quantitative data (right) of Ptenb, Pparaa and p-Akt in the livers of WT ± Dox and LmiR21 ± Dox at 4 mpf. (D) Increased expression of lipogenic genes in response to *pten* suppression was greater in LmiR21 + Dox than controls ($n = 3$). Decreased expression of genes involved in fatty acid β -oxidation in response to *pparaa* suppression was greater in LmiR21 + Dox than controls ($n = 3$). (E) Levels of hepatic oxidative stress, MDA, and H_2O_2 in hepatic mitochondria is also greater in LmiR21 + Dox than in the controls ($n = 3$). (F) Bilateral-factorial effects of miR-21 in NAFLD acceleration. Statistically significant differences from LmiR21 – Dox were denoted by * ($p < 0.05$), ** ($p < 0.01$) and *** ($p < 0.001$) for panels B–E.

3.4. Effects of miR-21 Expression on NASH

MiR-21 upregulation has been found in various tissue inflammatory conditions [19] in human patients and experimental models with NASH [37]; thus, we examined hepatic inflammation in LmiR21 fish. Approximately 70% of the 6 mpf LmiR21 + Dox displayed a pale red liver (Figure 4A). Histopathologic examination revealed increased Mallory–Denk bodies (MDBs) with ballooning hepatocytes and lobular inflammation, which are characteristic hallmarks of NASH, and were frequently observed in the livers of the 6 mpf LmiR21 + Dox compared to that in LmiR21 – Dox (Figure 4B).



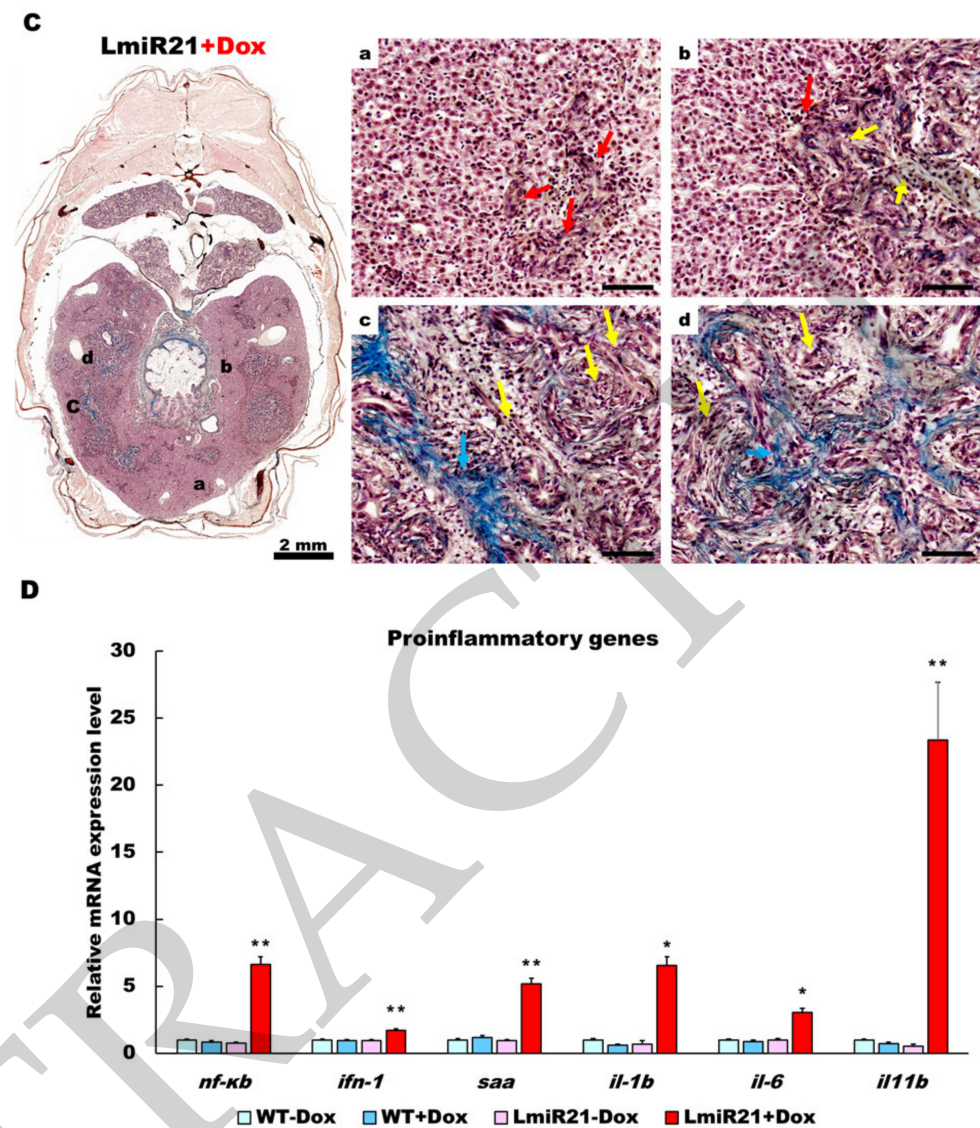


Figure 4. Development of nonalcoholic steatohepatitis (NASH) phenotypes in LmiR-21 zebrafish at 6 mpf. (A) Gross liver images of (a) LmiR21 – Dox male, (b) LmiR21 + Dox male, (c) LmiR21 – Dox female, (d) LmiR21 + Dox female. Scale bar: 3 mm. (B) Representative images of Masson's trichrome staining of steatohepatitis in livers of (1) LmiR21 – Dox (insets a-d) and (2) LmiR21 + Dox; Insets: (a) hepatocyte ballooning, (b) Mallory-Denk bodies (MDBs) are indicated by arrows, and (c,d) lobular inflammation is indicated by arrows. Scale bar: 50 µm. (C) Representative images of Masson's trichrome staining of fibrotic liver tissue from LmiR21 + Dox; Insets: (a,b) MDBs concomitant with fibrosis (red arrows) and scar tissue associated with liver fibrosis (yellow arrows) and (c,d) lobular inflammation concomitant with blue collagen (blue arrows). Scale bar: 50 µm. (D) Induction of proinflammatory gene expressions in response to inflammation was significantly greater in LmiR21 + Dox than in controls ($n = 3$). Statistically significant differences from LmiR21 – Dox were denoted by * ($p < 0.05$), ** ($p < 0.01$).

The early onset of fibrosis observed in 6 mpf LmiR21 + Dox, was also evidenced by using the Masson's trichrome stain that revealed increased MDBs in hepatocytes and scar tissue concomitant with fibrosis and lobular inflammation (Figure 4C). Induction of nuclear factor- κ B (*nf-kb*), interferon-1 (*ifn-1*), serum amyloid A (*saa*), interleukin-1b (*il-1b*), *il-6*, and *il-11b* was observed in response to inflammation in LmiR21 + Dox when compared with controls (Figure 4D). Cholestasis and cholangitis were also observed in the 6 mpf LmiR21 + Dox (Figure S2).

These results together indicate that hepatic miR-21 expression leads to the development of NASH and early stage liver fibrosis.

3.5. MiR-21 Targets *smad7* and *ptenb* in Hepatocytes to Sequentially Progress Advanced Fibrosis

We identified *smad7* as another potential target of miR-21 (Figure 5A), which can contribute to the development of NASH or fibrotic phenotypes in LmiR-21. Decreased *smad7* and *ptenb* expression has been reported in the activation of hepatic stellate cells during rat liver fibrosis [25,38]. Whole mount ISH assays showed that miR-21 significantly repressed expression of *smad7* mRNA of AmiR + Dox compared to that in AmiR-21 – Dox (Figure 5A). Furthermore, quantitative analyses showed that mRNA and protein levels of *smad7* and *ptenb* were dramatically downregulated in 8 mpf LmiR21 + Dox compared to that in LmiR21 – Dox (Figure 5B,C and Figures S8–S11). Histopathologic examination revealed advanced fibrosis such as portal, periportal, bridging fibrosis, and cirrhosis the characteristic hallmarks of NASH, which were frequently observed in the livers of 8 mpf LmiR21 + Dox compared with that in LmiR21 – Dox (Figure 5D). We then determined whether LmiR21 + Dox could directly affect activated HSC (aHSC) and fibrogenesis. *Smad7* and *ptenb* were suppressed in LmiR21 + Dox compared with that in controls, with a concomitantly increased expression of hepatic α -smooth muscle actin (α -*sma*), collagen type 1 alpha 1 (*col1a1*), connective tissue growth factor (*ctgfa*), matrix metalloproteinase 9 (*mmp9*), tissue inhibitors of metalloproteinases 2a (*timp2a*), lysyl oxidase a (*loxa*), chitinase acidic.3 (*chia.3*), laminin subunit beta 2 (*lamb2*) and vimentin (*vim*) mRNA levels (Figure 5E). Collectively, these data suggest that miR-21 may inhibit post-transcriptional *smad7* and *ptenb* expression levels by targeting its 3' UTR, thereby suggesting that they are strong targets of miR-21 having a synergetic effect on advanced fibrosis progress via the TGF- β signaling pathway (Figure 5F).

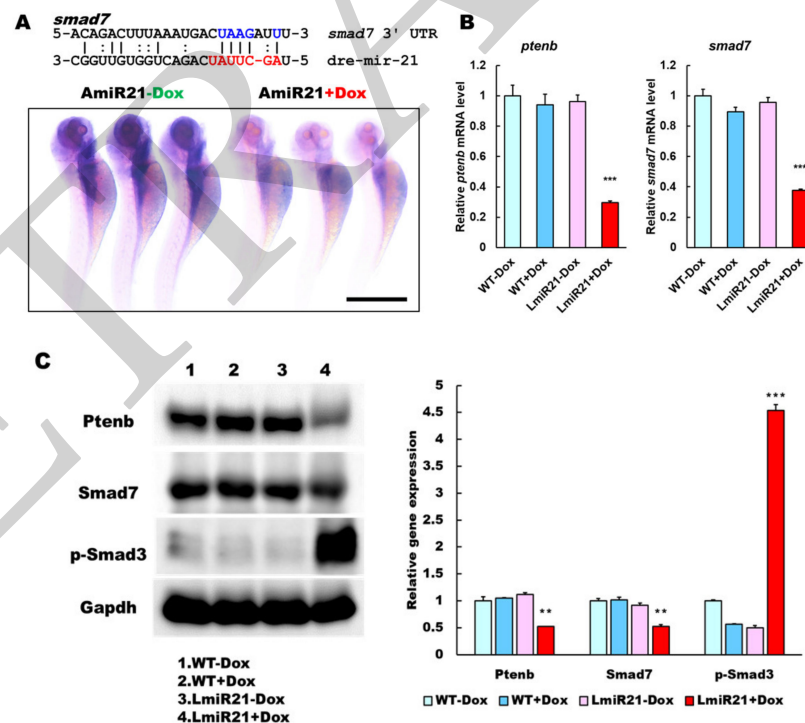


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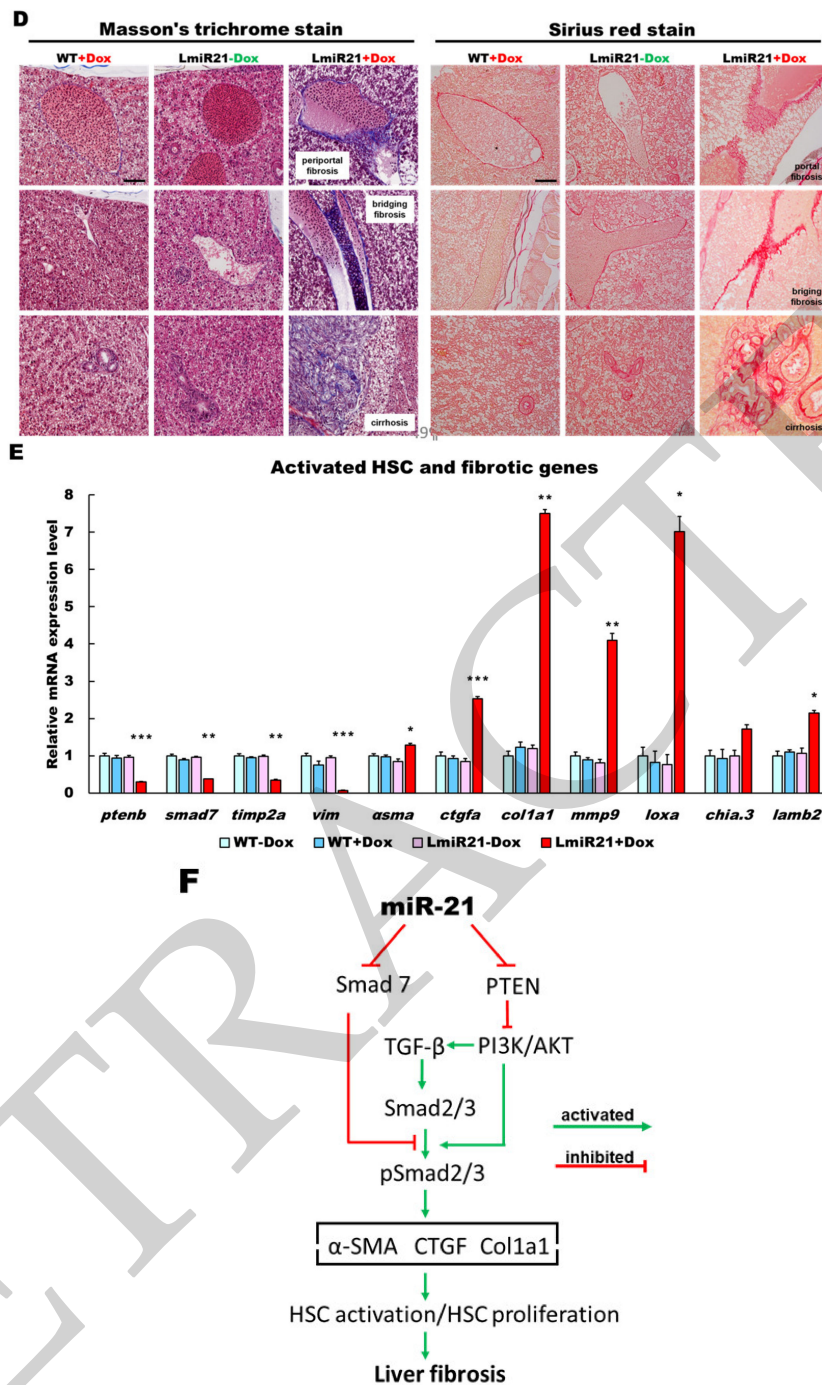


Figure 5. MiR-21 targets *smad7* and *ptenb* in hepatocytes and leads to fibrogenesis. (A) Schematic alignment between the mature miR-21 seed sequence (red) and the *smad7* mRNA target sequence (blue) at the 3-UTR. Perfect matches are indicated by a line, and G:U pairs by a colon. Whole mount in situ hybridization assays show significant repression of *smad7* mRNA by miR-21 in AmiR+Dox, as compared to AmiR21 – Dox . Scale bar: 1 mm. (B) RT-qPCR analysis of *smad7* and *ptenb* mRNA expression in the liver of WT ± Dox and LmiR21 ± Dox fish at 8 mpf. (C) Representative Western blots of Smad7 and PTEN in livers of WT ± Dox and LmiR21 ± Dox at 8 mpf. (D) Representative images of Masson’s trichrome and Picrosirius red staining of liver tissue from WT±Dox and LmiR21 ± Dox at 8 mpf depicting the individual components of advanced fibrosis (as indicated): portal and periportal fibrosis, bridging fibrosis and cirrhosis. Scale bar: 50 µm. (E) Increased expression of HSC and fibrotic genes in response to Smad7 and PTEN suppression was significantly greater in LmiR21 + Dox at 8 mpf than controls ($n = 3$). (F) Bilateral-factorial effects of miR-21 in fibrogenesis activation. Statistically significant differences from LmiR21 – Dox are denoted by * ($p < 0.05$), ** ($p < 0.01$) and *** ($p < 0.001$) for panels B, C and E.

3.6. LmiR21 Is Highly Sensitive to both DEN-Induced Liver Fibrosis and Carcinogenesis

As no obvious hepatic neoplastic changes, except NAFLD phenotypes were observed in LmiR-21 until nine mpi (months post induction), we examined its oncomir functions. We induced accelerated hepatocarcinogenesis in the liver of LmiR-21 + Dox fish by treatment with DEN, a hepatotoxic chemical that causes chronic liver damage and carcinogenesis. The LmiR21s were then examined at one, three, and nine months post DEN treatment (Figure 6A–D).

Only a few cases of lobular inflammation and early fibrosis at three months post DEN-treatment were observed in LmiR21 + Dox compared to that in the controls (Figure 6B–D). However, 27.50% of LmiR-21 + Dox showed steatosis and hepatitis at three months post DEN-treatment, with atypical NAFLD features being clearly displayed, including steatosis, hepatocellular ballooning, and lobular inflammation compared to that in the liver architecture of controls (Figure 6B–D, Table 1). Intrahepatic cholangiocarcinoma (IHCC) and HCC progression were observed in 10% and 22.50% of LmiR21 + Dox at three months post DEN-treatment (Figure 6B, Table 1). Surprisingly, the LmiR21 + Dox showed dramatic NAFLD progression at nine months with 63.33% showing steatosis, 43.67% showing fibrosis (Figure 6C,D), 43.33% showing IHCC and 73.33% showing HCC (Figure 6B–D, Table 1). Additionally, 3.33–6.67% of the control fish at nine months post DEN-treatment developed steatosis and 10.00–13.33% developed HCC; no fibrosis and IHCC were observed (Table 1). PCNA and BrdU stained cells were detected in the one-, three-, and nine-month-post DEN-exposed LmiR21 + Dox livers (Figure S3), indicating that miR-21 enhances hepatocyte proliferation during carcinogenesis. Together, these results indicated that LmiR21 fish were more susceptible to DEN-induced liver fibrosis and carcinogenesis.

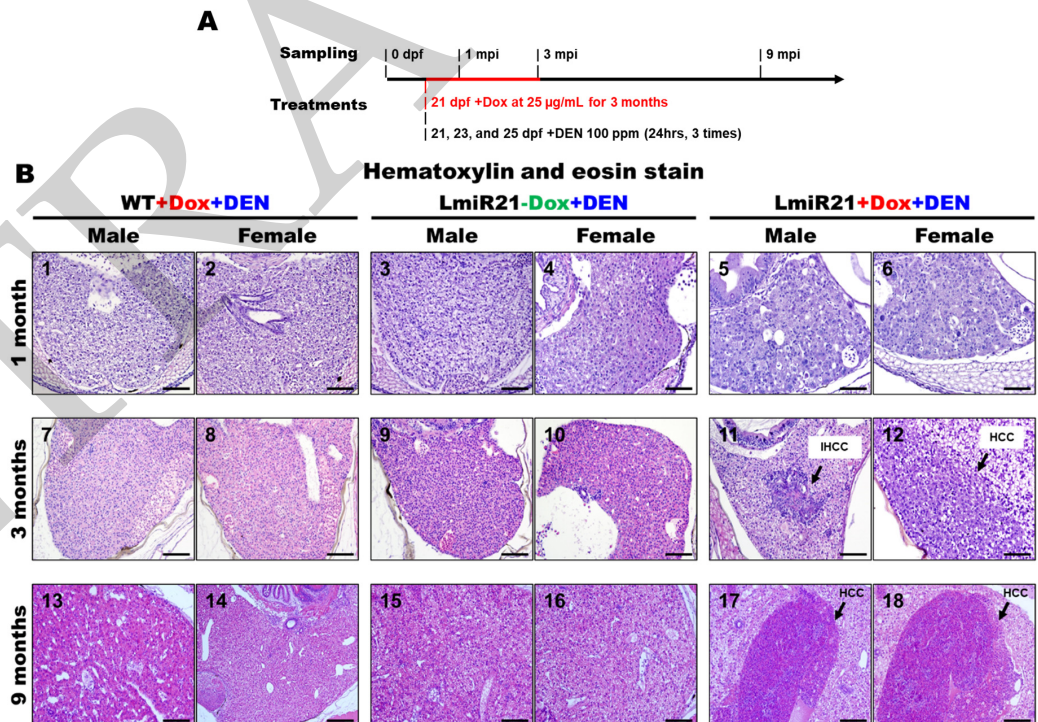


Figure 6. Cont.

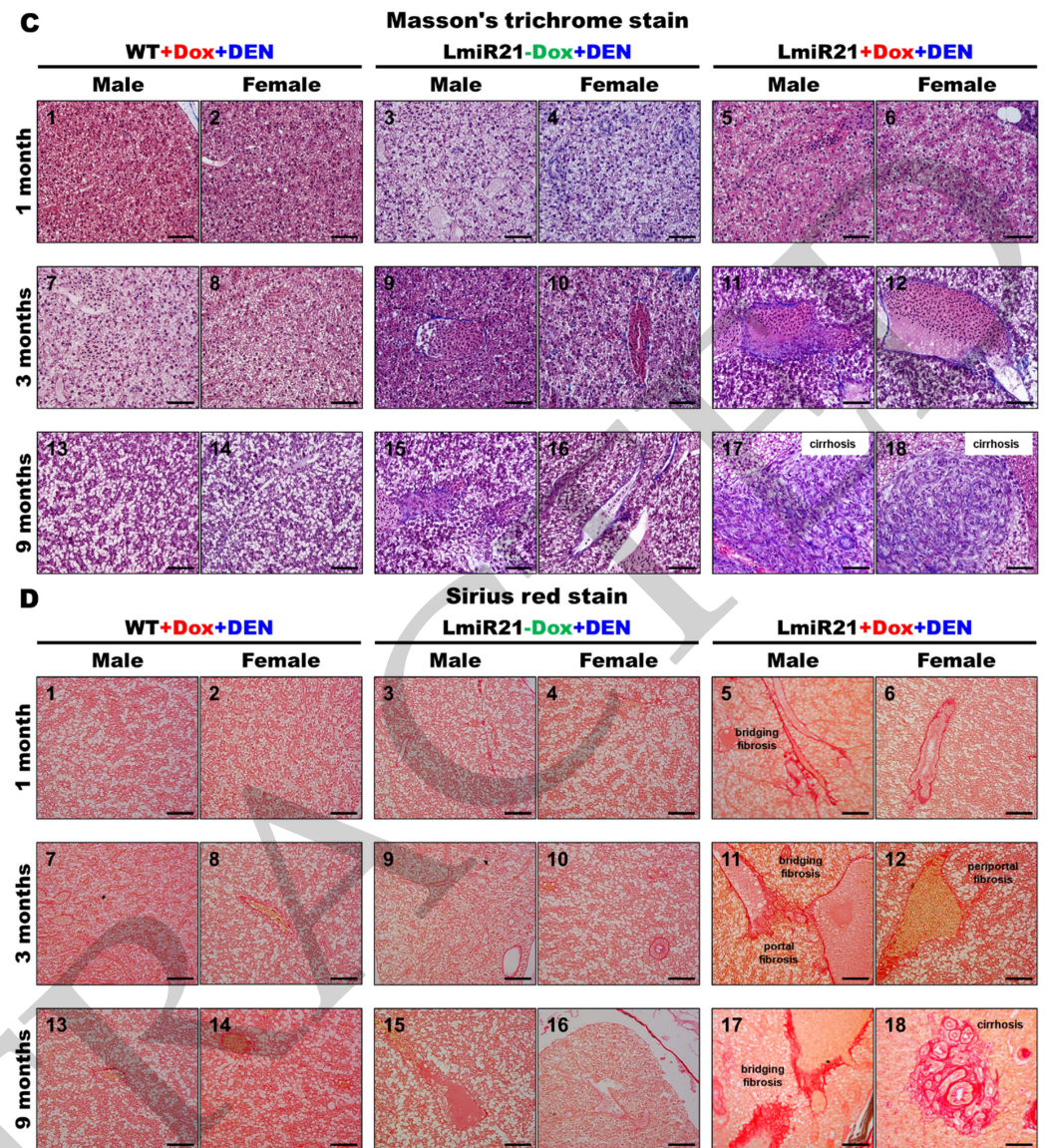


Figure 6. Increased susceptibility of LmiR21 zebrafish to diethylnitrosamine (DEN)-induced liver fibrosis and carcinogenesis. (A) Experimental design of three independent DEN treatments and doxycycline (Dox) dosing. (B) Representative images of livers with microscopic tumors identified following hematoxylin & eosin staining (indicated with arrows) one, three, and nine months after DEN treatment. Scale bar: 100 μm . (C) Representative images of livers with microscopic injuries identified by Masson's trichrome staining at one, three, and nine months after DEN treatment. Scale bar: 50 μm . (D) Representative images of livers with microscopic injuries identified by Sirius red staining at one, three, and nine months after DEN treatment. Scale bar: 50 μm .

Table 1. Incidents in the livers of DEN-treated zebrafish.

		DEN	DOX	Total Fish	% of Fish with Fatty Liver	% of Fish with HCC	% of Fish with IHCC	% of Fish with Fibrosis
3 mpi	LmiR21	+	+	40	27.50 (11/40)	22.50 (9/40)	10.00 (4/40)	0
	LmiR21	+	−	40	0	0	0	0
	WT	+	+	30	0	0	0	0
9 mpi	LmiR21	+	+	30	63.33 (19/30)	73.33 (22/30)	43.33 (13/30)	46.67 (14/30)
	LmiR21	+	−	30	6.67 (2/30)	10.00 (3/30)	0	0
	WT	+	+	30	3.33 (1/30)	13.33 (4/30)	0	0

mpi: months post DEN/Doxycycline induction.

3.7. Chronic Effects of Hepatic miR-21 Expression on NAHCC

As LmiR-21 + Dox fish showed marked activation by oncogenic protein modification and accelerated HCC, we analyzed whether the LmiR21 liver was predisposed to cancer development from the start. By monitoring LmiR21 + Dox at 10 mpf, a fraction of fish that developed HCC was observed not earlier than 9 mpf, with the distinct phenotypes such as liver hypoplasia and pale color (Figure 7A). The main hepatic vessels were observed in both LmiR21 ± Dox, while the reticular vessels were only observed in LmiR-21 + Dox liver due to hepatic angiogenesis (Figure 7B). Histopathological examination revealed the development of steatohepatitis, fibrosis concomitant with HCC from Lmi-R21 + Dox liver along with clear NAHCC (Figure 7C,D). H&E stain revealed tumor-bearing livers accompanied by lobular inflammation, MDBs (Figure 7C, panel 2) and Masson's trichrome stain revealed that tumor-bearing livers accompanied by fibrosis (Figure 7D, panel 2) and cirrhosis (Figure 7D, panel 3) was observed in LmiR21 + Dox compared to that in Lmi-R21 − Dox (Figure 7C,D panel 1). Furthermore, 70% male and 50% female LmiR21 fish (at least ten months old) showed evidence of NAHCC with inflammation and fibrosis, respectively.

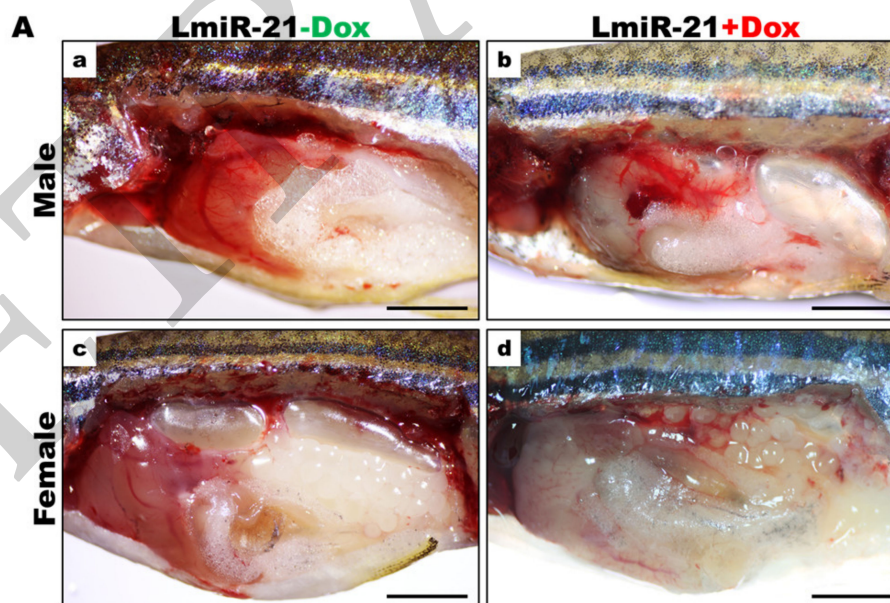


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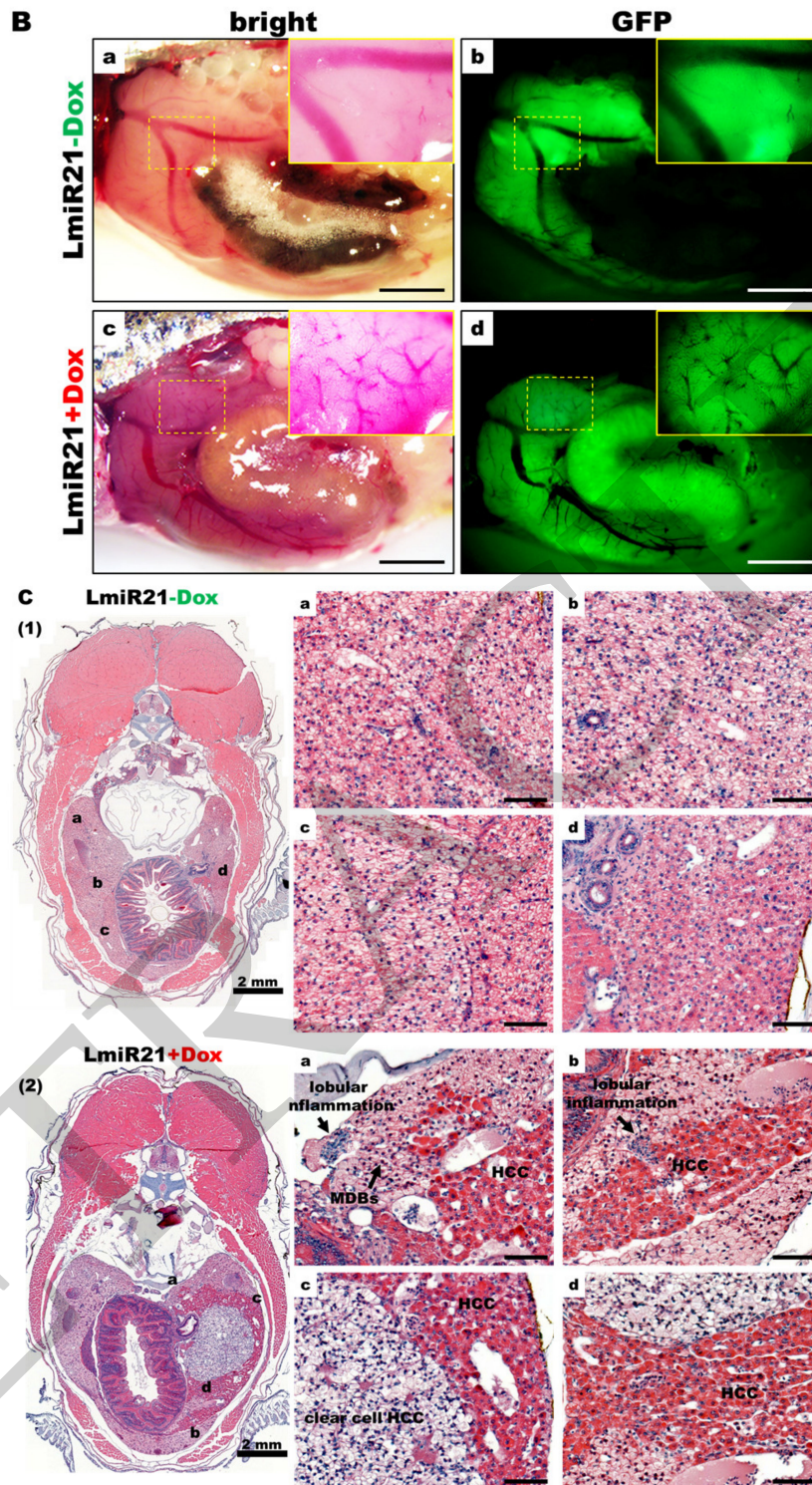


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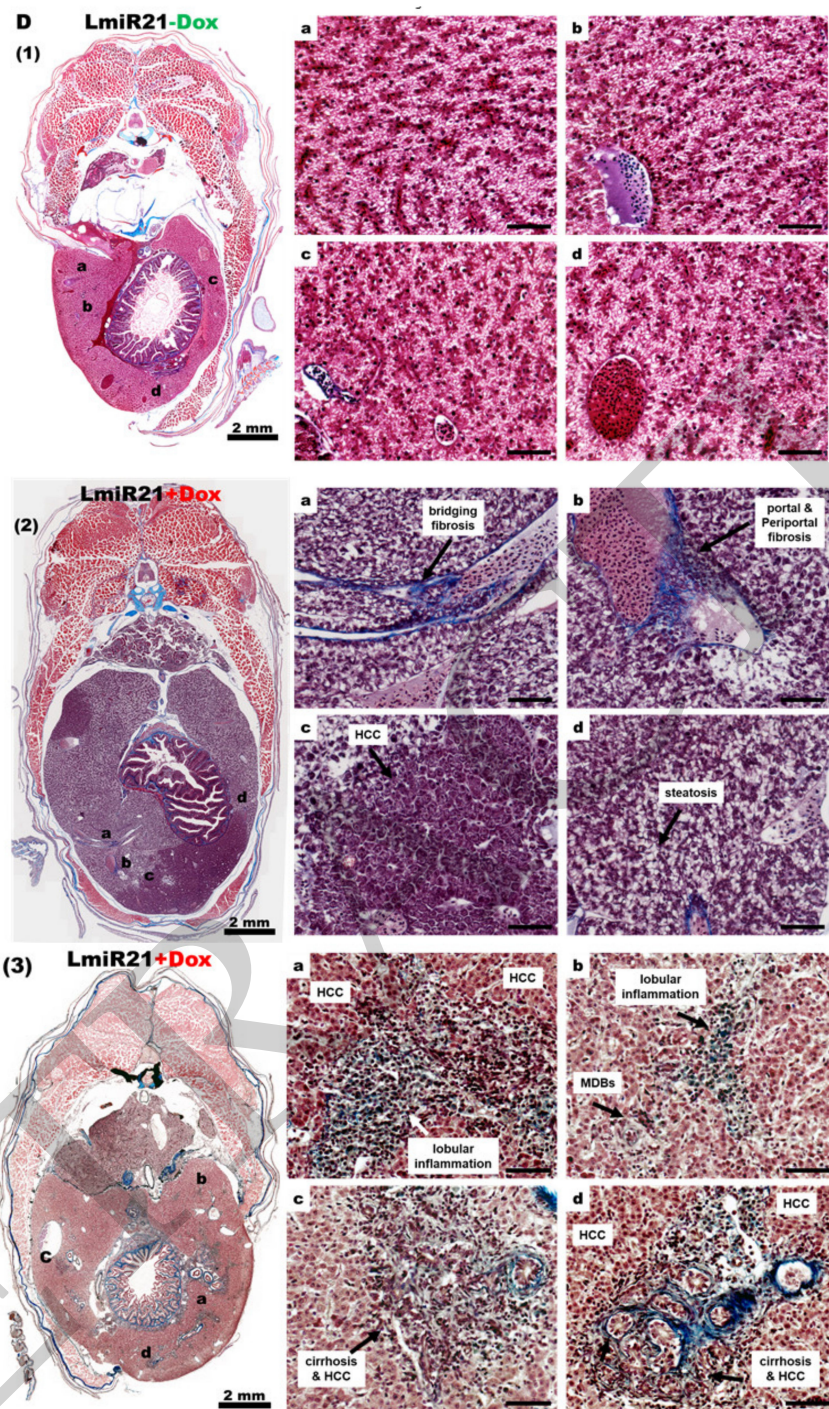


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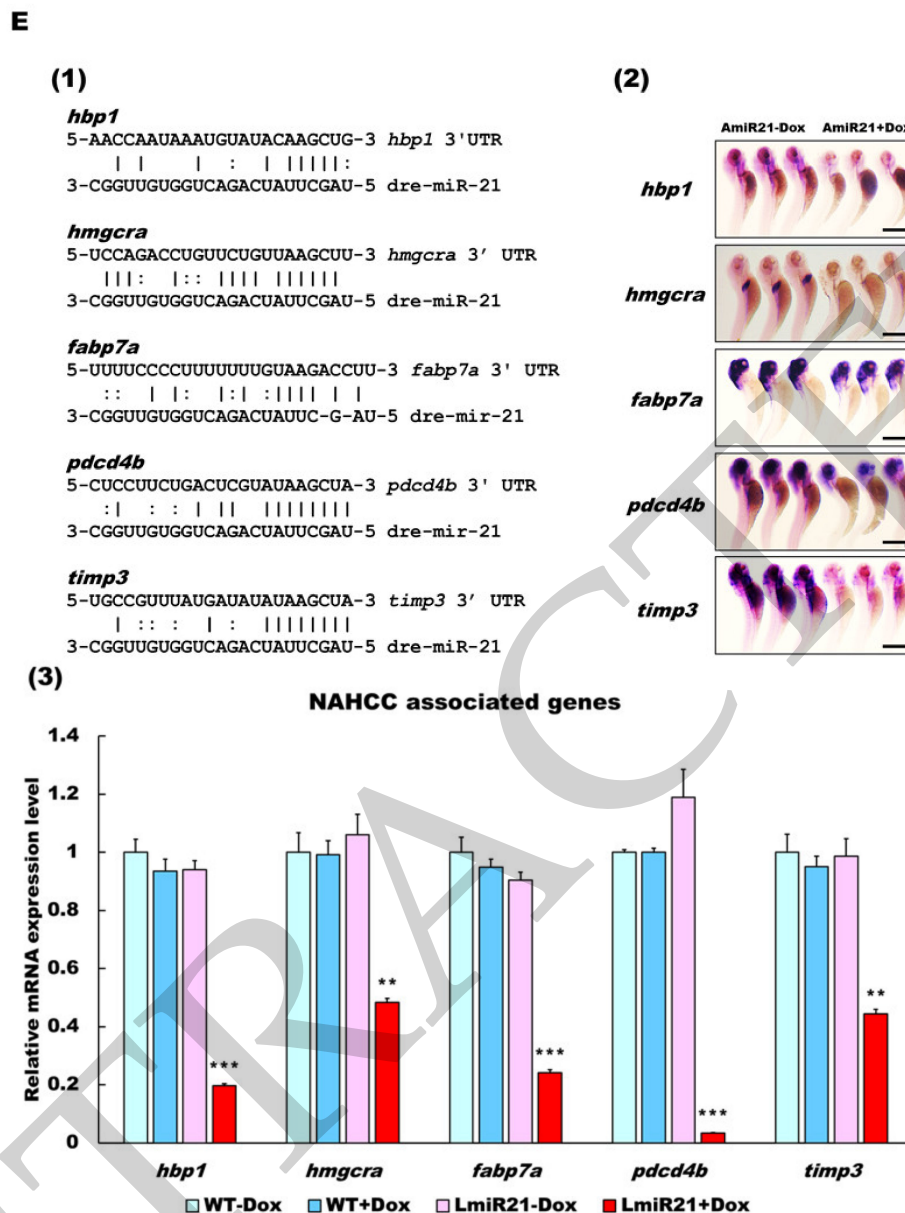


Figure 7. LmiR21 zebrafish develop nonalcoholic hepatocellular carcinoma (NAHCC) phenotypes at 10 months post fertilization (mpf). (A) Gross liver images from (a) LmiR21 – Dox male, (b) LmiR-21 + Dox male, (c) LmiR21 – Dox female, and (d) LmiR21 + Dox female. Scale bar: 3 mm. (B) Microscopic views of angiogenesis in livers from bright field: (a) LmiR21 – Dox (c) LmiR21 + Dox and corresponding GFP fluorescence images (b) LmiR21 – Dox (d) LmiR21 + Dox. Scale bar: 2 mm. (C) Hematoxylin & eosin stained livers from (1) LmiR21 – Dox (insets a–d) (2) LmiR21 + Dox (insets a–d) of steatohepatitis concomitant with HCC: hepatocyte ballooning, Mallory–Denk bodies (MDB), lobular inflammation and HCC (indicated by arrows). Scale bar: 50 μ m. (D) Masson’s trichrome stained livers of (1) LmiR21 – Dox (insets a–d), (2) LmiR21 + Dox (insets a–d) indicative of steatohepatitis, portal and periportal fibrosis concomitant with HCC and (3) LmiR21 + Dox (insets a–d) indicative of steatohepatitis, advanced fibrosis (cirrhosis) concomitant with HCC. Scale bar: 50 μ m. (E) Analysis of selected miR-21 targeted NAHCC associated genes: HMG-box transcription factor 1 (*hbp1*), 3-hydroxy-3-methylglutaryl-CoA reductase (*hmgcr*), fatty acid binding protein 7a (*fabp7a*), programmed cell death 4b (*pdcd4b*), and tissue inhibitors of metalloproteinases 3 (*timp3*). (1) Schematic alignment between the mature miR-21 seed sequence and the mRNA target sequence at the 3' UTR. (2) Whole mount in situ hybridization assays demonstrate that miR-21 significantly represses expression of NAHCC associated genes in AmiR21 fish. Scale bar: 1 mm. (3) RT-qPCR analysis of the NAHCC associated genes mRNA expression in the liver of WT \pm Dox and LmiR21 \pm Dox at 10 mpf. Statistically significant differences from LmiR21 – Dox were denoted by ** ($p < 0.01$) and *** ($p < 0.001$).

In addition, ingenuity pathway analysis (IPA) revealed the altered expression of genes involved in triglyceride biosynthesis and commonly associated with NAFLD and HCC, such as HMG-box transcription factor 1, 3-hydroxy-3-methylglutaryl-CoA reductase, fatty acid binding protein 7, programmed cell death 4b, and tissue inhibitors of metalloproteinases 3 (Figure 7E). These genes were previously downregulated in NAHCC development [5] and carry an miR-21 complementary binding site in the 3'UTR (Figure 7E, panel 1). Whole mount ISH demonstrated that miR-21 significantly repressed the expression of mRNAs of the aforementioned genes in AmiR + Dox compared with that in AmiR-Dox (Figure 7E, panel 2). RT-qPCR analyses also showed that their mRNA levels were dramatically downregulated in LmiR21 + Dox compared to that in LmiR21 – Dox at 10 mpf (Figure 7E, panel 3). These data suggest that long-term hepatic miR-21 expression can successfully induce NAHCC within ten months in zebrafish.

3.8. The Activation of PI3K, TGF- β and STAT3 (PTS) Signaling Networks in LmiR21 Zebrafish Is Relevant to Human Nonviral HCCs

To explore the regulatory role of miR-21 in the signaling pathways of NAHCC and IHC, Western blot and RT-qPCR analysis were used to detect the expression of PI3K/Akt, TGF- β /Smad3 and Stat3 (PTS) signaling pathway-related proteins in the livers of LmiR21 fish. A dramatic increase of p-Akt positive hepatocytes and a slight increase in p-Smad3 and p-Stat3 positive hepatocytes were observed in the 10 mpf LmiR21 + Dox compared to that in LmiR21 – Dox livers (Figure 8A). A dramatic decrease of Ptenb and Smad7 positive hepatocytes were observed in LmiR21 + Dox compared to that in clear LmiR21 – Dox hepatocytes (Figure 8A). Molecularly, significant increases in p-Akt, p-Smad3 and p-Stat3 were detected in LmiR21 + Dox and a significant inhibition of Ptenb and Smad7 in control fish (Figure 8B and Figures S11–S17).

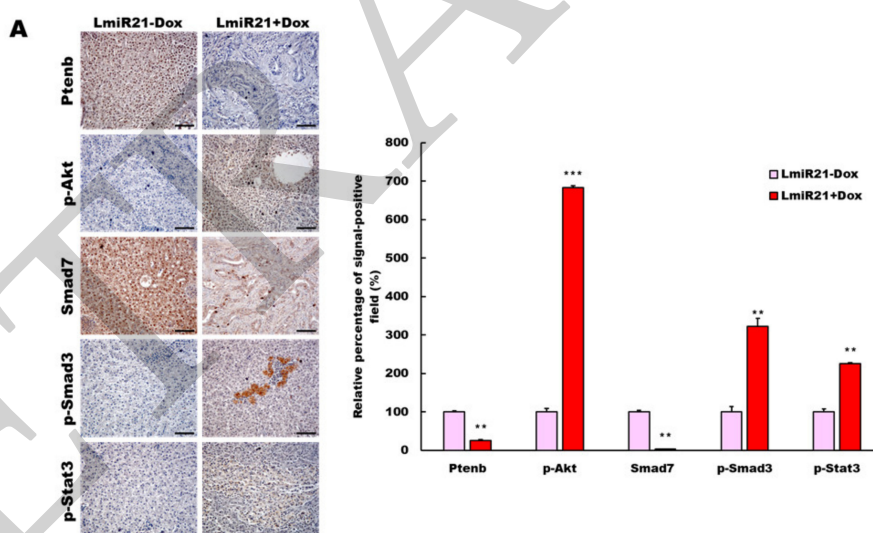


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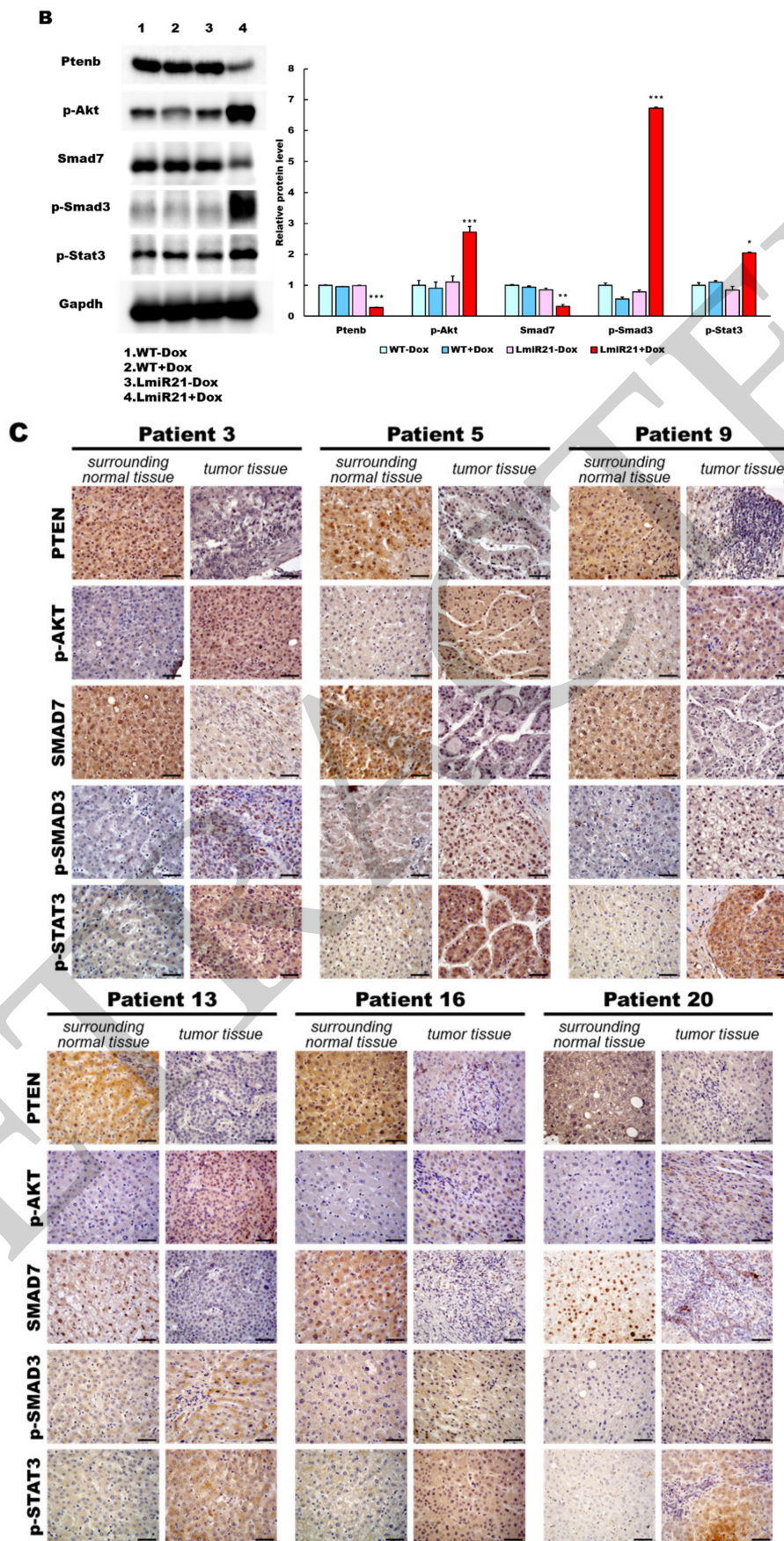


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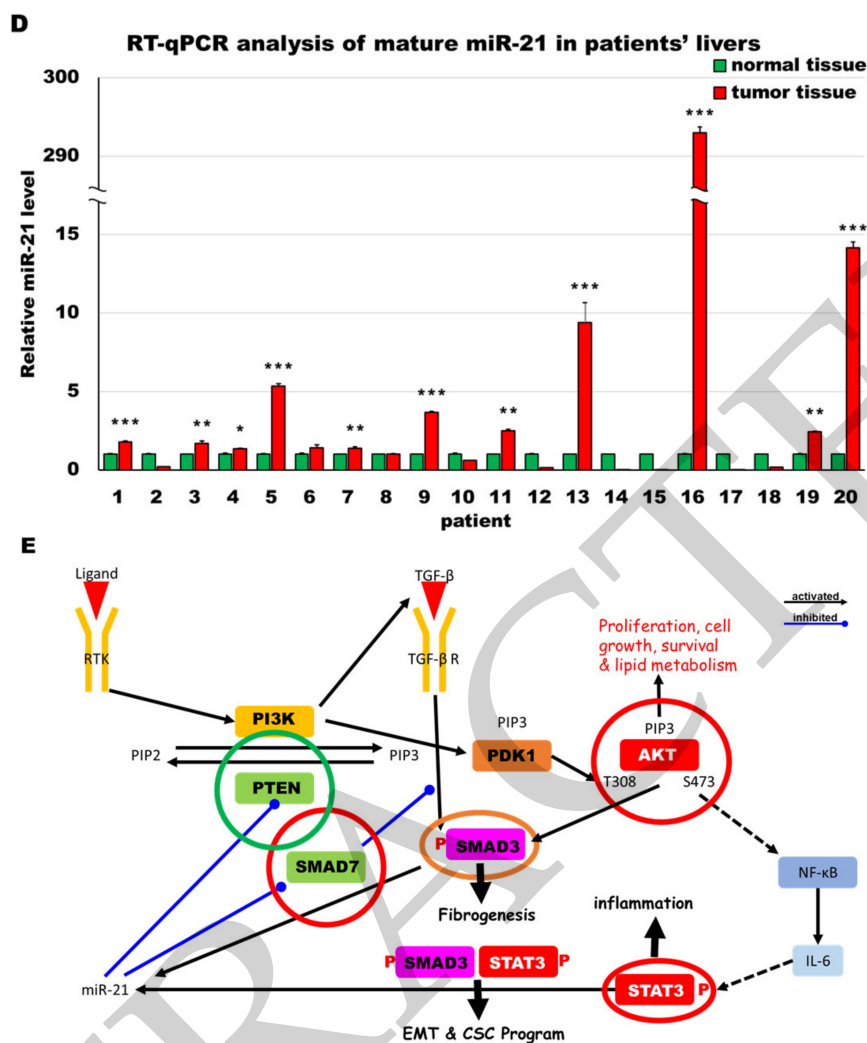


Figure 8. MiR-21 expression shows a direct correlation with activation of PI3K, TGF- β and STAT3 (PTS) signaling network proteins in LmiR21 zebrafish and human nonviral hepatocellular carcinomas (HCC). (A) Expression patterns of Ptenb, p-Akt, Smad7, p-Smad3 and p-Stat3 in 10 mpf LmiR21 \pm Dox liver samples after immunohistochemical (IHC) staining. Scale bar: 50 μ m. Positive signal areas per field were quantified. (B) Western blot images (left) and quantitative data (right) of PTS signaling regulatory protein in 10 mpf LmiR21 \pm Dox liver. (C) Human nonviral HCC samples ($n = 20$) were subjected to IHC of PTEN, p-AKT, SMAD7, p-SMAD3 and p-STAT3 expression. Scale bar: 50 μ m. (D) miR-21 expression profiles in the surrounding normal and liver cancer tissues from nonviral HCC patients ($n = 20$) were analyzed by RT-qPCR. Positive correlation of miR-21 with PTS signaling regulatory genes in 60% of the nonviral HCC samples were observed. (E) Proposed mechanism by which miR-21 links the NAHCC development. MiR-21 mediates a newly discovered PI3K/Akt, TGF- β /Smad3 and Stat3 (PTS) signaling loop and feed forward loop involving Smad3/Stat3 dependent on miR-21 expression. (Abbreviations: \rightarrow : activated, $\rightarrow\bullet$: inhibited) Statistically significant differences from LmiR21 – Dox were denoted by * ($p < 0.05$), ** ($p < 0.01$) and *** ($p < 0.001$) for panels A, B and D.

To validate the involvement of PTS networks in human HCC tissues, IHC was performed using serial sections from non-hepatitis A, B or C related human HCC tissues (Figure 8C). We validated the miR-21 expression in human nonviral HCC specimens to establish its expression levels ($n = 20$) (Figure 8D). Human HCC samples with different expression levels of miR-21 from nonviral HCC patients were examined for PTEN, p-AKT, SMAD7, p-SMAD3 and p-STAT3 expression. As shown in Figure 8C, PTEN and SMAD7 were observed in the surrounding tissue, and nuclear p-AKT, p-SMAD3 and p-STAT3 were observed in tumor cells, suggesting nuclear translocation post phosphorylation (Figure 8C). HCC patients with high miR-21 expression and PTS proteins showed similar expression levels to LmiR-21 + Dox fish (Figure 8A,C). Interestingly, correlation between miR21 and

p-Akt, p-Smad3 and p-Stat3 showed the positive trend with NAHCC progression. Combined, these results suggest that miR-21 induces NAHCC via the PTS signaling networks in both LmiR-21 fish and humans (Figure 8E).

4. Discussion

NAHCC progression is a complex and multistep process. Currently, proposed mechanisms describe genetic, metabolic, immunologic, and endocrine pathways that lead to HCC [2]. In this study, we investigated the effect of miR-21 expression in NAFLD-related HCC in a zebrafish model-LmiR21, which mimics hepatocellular carcinoma development caused by NAFLD/NASH. We discovered a signature of genes, which were consistently deregulated in LmiR21 fish and human samples, validating our transgenic line as a good model system by mimicking key features of HCC progression with a background of NAFLD. We have also shown regulatory signaling networks of miR-21 in NAHCC progression.

NAFLD/NASH plays a critical role in HCC progression [2]. Until now, only a few studies focused on miRNA expression in human NAHCC. miR-223 depletion induced a full spectrum of NAFLD in mice including steatosis, inflammation, fibrosis, and HCC in long-term high-fat-diet fed mice [39]. Downregulation of miR-122 was also shown in a NASH mouse model, indicating its direct role in NAHCC [40]. MiR-221 transgenic mice are characterized by steatohepatitis, which resembles the human NASH [41]. Although increasing evidence has demonstrated the role of miR-21 in several types of liver diseases [12], only one study indicates the potential association between NAFLD, HCC and miR-21 via the interaction with the Hbp1-p53-Srebp1c pathway [8]. However, these models are dissimilar to human NASH in that they involve gene knockout and lack in progressive fibrosis. Importantly, most models do not develop HCC with concurrent hepatic fibrosis or NASH. NAHCC onset should be triggered by NAFLD progressively and not by only oncogenic activation. In addition, key regulators/pathways responsible for NAHCC remain largely unknown. In this study, we developed a transgenic zebrafish model-LmiR21, in which long-term hepatic expression of miR-21 induced sequential development of fatty liver, steatohepatitis, fibrosis and HCC with concurrent cirrhosis, thereby mimicking human NAHCC, all of which are in agreement with other models mimicking human HCC progression due to long-term miR-21 expression.

Our results revealed that 73.33% of LmiR21 zebrafish developed HCC at 9 months post DEN treatment compared to that in the controls (10.00–13.00%) that were only DEN treated, supporting our hypothesis that miR-21 plays a major role in malignancy and cancer progression. These results are in line with a study on miR-21 in HCC patients (5), further corroborating our findings (Figure 6, Table 1). In addition, LmiR21 showed that pathways and key proteins also activated in human NAHCC with corresponding histologic phenotypes (Figures 7 and 8).

Progressive miR-21 upregulation was detected in mouse liver disease models [5] of NAFLD or HCC, in which strikingly similar genes were identified as in our transgenic model (Figure 7E). We demonstrated that miR-21 had at least three molecular and pathophysiological ways of NAHCC development. The first way is via increased hepatic lipogenesis through a decrease in hepatic levels of various proteins (Ptenb, Pparaa and Smad7), identified as potential miR21 target genes in NAFLD progression (Figures 3 and 5). We also showed that in both human HCC biopsies and LmiR21 + Dox fish, an inverse expression between miR-21 expression and the PTS regulatory proteins Ptenb, p-Akt, Smad7, P-Smad3 and p-Stat3 was observed (Figure 8A–C), which are also involved in fatty acid synthesis and metabolism. [42]. STAT3 plays an important role in liver inflammation and cancer [18]. Accordingly, the second mechanism by which miR-21 can induce NASH is via an increase in hepatic inflammatory gene expression via the STAT3 signaling pathway and liver fibrosis through HSC activation and collagen deposition via the TGF- β /Smad3/Smad7 signaling pathways (Figures 4 and 5). Junk et al. proposed that epithelial-mesenchymal transition (EMT) and cancer stem cells (CSC) could be induced via a STAT3/SMAD3 gene transcription [43]. High p-AKT, p-SMAD3 and p-STAT3 expression

in both LmiR21 + Dox and human HCC biopsies was associated with high miR-21 expression (Figure 8A–C). MiR-21 inhibits *PTEN* that causes an increase in AKT phosphorylation, which upregulates the downstream signaling genes of AKT that are required for tumor formation and increases the phosphorylation of STAT3 (p-STAT3); this gene network promotes hepatic lipid accumulation. In addition, miR-21 inhibits *SMAD7*, which increases SMAD3 phosphorylation (p-SMAD3), which in turn activates the TGF- β signaling pathway, and triggers fibrosis; this gene network promotes fibrogenesis. p-SMAD3 and p-STAT3 can together feedback to increase the miR-21 expression, and also cooperate with each other to activate the downstream signaling genes of EMT and CSC; this gene network promotes carcinogenesis. Thus, the third way to induce HCC is through oncogenic activation of SMAD3/STAT3 signaling pathways. The LmiR21 transgenic line is therefore similar to human NAHCC in terms of activation of oncogenic pathways, resulting in metabolic status, lipid abnormalities, progressive fibrosis and HCC (Figure 8E).

MicroRNA-21 was upregulated in different stages of NAHCC [5,44]. Dysregulated miR-21 could be a biomarker and is more easily detected in blood [45,46]. With the development of microRNA silencing and antagomiRs techniques, using antimiRs as anticancer drugs provides effective therapeutic strategies in mammalian models [47,48]. MicroRNA-21 could be a novel therapeutic target in different stages of NAHCC.

5. Conclusions

In conclusion, our studies emphasize the intriguing idea of PTS signaling networks and their roles in lipogenic factor regulation, tumor suppressor modulation and oncogenic activation. The tight regulation of these proteins defines the phenotypes and transcriptional profiles observed in LmiR21 transgenic zebrafish and by human nonviral HCCs. Our model recreates the development of HCC due to NAFLD with respect to the physiological, metabolic, and histological aspects similar to those of human NAHCC. Our findings, combined with other studies, indicate that miR-21 plays a critical role in the pathogenesis of NAHCC, and thus serves as a fitting model to identify therapeutic targets in NAHCC progression.

Supplementary Materials: The following are available online at <https://www.mdpi.com/2072-6694/13/5/940/s1>, Figure S1: Generation of a global and inducible microRNA (miR-21) transgenic zebrafish, AmiR21 lines, Figure S2: Development of severe cholestasis is dependent on the levels of miR-21 expression. Macroscopic images of a cholestatic liver obtained from 6 mpf LmiR21 + Dox are shown. Scale bar: 3mm, Figure S3: Detection of the proliferative activity of cells in in zebrafish liver. Detection of the proliferative activity of cells in in the livers of WT + Dox and LmiR21 \pm Dox at 1-,3-, and 9-months post diethylnitrosamine (DEN)-treatment using immunohistochemical staining of PCNA and BrdU, then counterstain the nuclei with haematoxylin. Arrows indicate examples of the PCNA and BrdU immunopositive cells indicative of proliferating cells. Scale bar = 50 μ m, Figure S4: Western blot original image of Ptenb in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 4 mpf, Figure S5: Western blot original image of p-Akt in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 4 mpf, Figure S6: Western blot original image of Pparaa in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 4 mpf, Figure S7: Western blot original image of GAPDH in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 4 mpf, Figure S8: Western blot original image of Ptenb in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 8 mpf, Figure S9: Western blot original image of Smad7 in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 8 mpf; Figure S10: Western blot original image of p-Smad3 in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 8 mpf, Figure S11: Western blot original image of Gapdh in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 8 mpf, Figure S12: Western blot original image of Ptenb in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 10 mpf, Figure S13: Western blot original image of p-Akt in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 10 mpf, Figure S14: Western blot original image of Smad7 in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 10 mpf, Figure S15: Western blot original image of p-Smad3 in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 10 mpf, Figure S16: Western blot original image of p-Stat3 in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 10 mpf, Figure S17: Western blot original image of Gapdh in zebrafish livers of WT \pm Dox and LmiR21 \pm Dox at 10 mpf, Table S1: Primer sequences used for quantitative RT-PCR, Table S2: Primer sequences used for in situ hybridization probes.

Author Contributions: G.M.H. and K.-Y.Y. designed the experiments and C.-Y.L. (Chi-Yu Lai) wrote the manuscript. C.-Y.L. (Chi-Yu Lai) and K.-Y.Y. performed the majority of the experiments presented in the paper. Y.-W.H., H.-H.L. and C.-Y.L. (Chiu-Ya Lin) designed and performed the zebrafish work. J.-R.C. and C.-C.H. examined a series of images demonstrating the pathologic findings and pathological image analysis in the paper. All authors have read and agreed to the published version of the manuscript.

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Institutional Review Board Statement: This study was conducted in accordance with the Declaration of Helsinki, and the protocol was approved by the Chang Gung Medical Foundation Institutional Review Board (IRB number: 201700777B0).

Informed Consent Statement: Informed consent was obtained from all subjects involved in the study.

Data Availability Statement: The data presented in this study are available in Supplementary Materials here.

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Conflicts of Interest: The authors declare no conflict of interest.

Abbreviations

<i>acaca</i>	acetyl-CoA carboxylase
<i>chrebp</i>	carbohydrate-response element-binding protein
DEN	diethylnitrosamine; Dox, doxycycline
dpf	days post fertilization
<i>fabp7a</i>	fatty acid binding protein 7 a
<i>hbp1</i>	HMG-box transcription factor 1
HCC	hepatocellular carcinoma
<i>hmgcr</i>	3-hydroxy-3-methylglutaryl-CoA reductase
hpf	hours post fertilization
HSC	hepatic stellate cell
IHCC	intra-hepatic cholangiocarcinoma; mpf, months post fertilization
mpi	months post induction
NAHCC	NAFLD-related HCC;
NASH	non-alcoholic steatohepatitis
ORO	Oil Red O
<i>pdc4b</i>	programmed cell death 4 b
<i>pparaa</i>	peroxisome proliferator-activated receptor alpha (α) a
<i>ppar-γ</i>	peroxisome proliferator-activated receptor gamma (γ)
<i>ptenb</i>	phosphatase and tensin homolog deleted on chromosome ten b
<i>srebp1</i>	sterol regulatory element binding protein 1
<i>tim3</i>	tissue inhibitors of metalloproteinases 3

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