

METABOLIC AND STEATOHEPATITIS

Strain dependence of diet-induced NASH and liver fibrosis in obese mice is linked to diabetes and inflammatory phenotype

Geoffrey C. Farrell¹, Auvro R. Mridha¹, Matthew M. Yeh², Todor Arsov¹, Derrick M. Van Rooyen¹, John Brooling¹, Tori Nguyen¹, Deborah Heydet¹, Viviane Delghingaro-Augusto³, Christopher J. Nolan³, Nicholas A. Shackel⁴, Susan V. McLennan⁵, Narci C. Teoh¹ and Claire Z. Larter¹

¹ Liver Research Group, Australian National University Medical School at The Canberra Hospital, Garran, ACT, Australia

² Department of Pathology, University of Washington, Seattle, WA, USA

³ Department of Endocrinology, Canberra Hospital, Garran, ACT, Australia

⁴ Centenary Institute, Camperdown, NSW, Australia

⁵ Department of Endocrinology, Royal Prince Alfred Hospital, Camperdown, NSW, Australia

Keywords

cytokines – fibrosis – growth factors – Non-alcoholic steatohepatitis – strain difference

Abbreviations

ALT, alanine transaminase; CTGF, connective tissue growth factor; ELISA, enzyme-linked immunosorbent assay; GWAS, genome-wide association studies; H&E, haematoxylin and eosin; HCC, hepatocellular carcinoma; HF, high fat; IFN- γ , Interferon- γ ; IL, Interleukin; MCP-1, monocyte chemoattractant protein-1; MMP, matrix metalloproteinase; NAFLD, non-alcoholic fatty liver disease; NAS, NAFLD activity score; NASH, non-alcoholic steatohepatitis; NOD, non-obese diabetic; PDGF α , platelet-derived growth factor α ; PNPLA3, patatin-like phospholipase domain containing 3; SREBP-2, sterol regulatory element binding protein-2; T2D, Type 2 diabetes; TGF- β , transforming growth factor- β ; TNF- α , tumour necrosis factor- α ; WT, Wild type; α -SMA, α -Smooth muscle actin.

Correspondence

Professor Geoff Farrell, MD, FRACP
Liver Research Group, Australian National University Medical School
Level 5, Building 10 The Canberra Hospital
Yamba Drive, Garran, ACT 2605, Australia
Tel: +612 6244 2473
Fax: +612 6244 3235
e-mail: geoff.farrell@anu.edu.au

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Abstract

Background & Aims: Obese *Alms1* mutant (*foz/foz*) NOD.B10 mice develop diabetes and fibrotic NASH when fed high-fat (HF) diet. To establish whether diabetes or obesity is more closely associated with NASH fibrosis, we compared diabetic *foz/foz* C57BL6/J with non-diabetic *foz/foz* BALB/c mice. We also determined hepatic cytokines, growth factors and related profibrotic pathways. **Methods:** Male and female *foz/foz* BALB/c and C57BL6/J mice were fed HF or chow for 24 weeks before determining metabolic indices, liver injury, cytokines, growth factors, pathology/fibrosis and matrix deposition pathways. **Results:** All *foz/foz* mice were obese. Hepatomegaly, hyperinsulinemia, hyperglycaemia and hypoadiponectinaemia occurred only in *foz/foz* C57BL6/J mice, whereas *foz/foz* BALB/c formed more adipose. Serum ALT, steatosis, ballooning, liver inflammation and NAFLD activity score were worse in C57BL6/J mice. In HF-fed mice, fibrosis was severe in *foz/foz* C57BL6/J, appreciable in WT C57BL6/J, but absent in *foz/foz* BALB/c mice. Hepatic mRNA expression of TNF- α , IL-12, IL-4, IL-10 was increased (but not IFN- γ , IL-1 β , IL-17A), and IL-4:IFN- γ ratio (indicating Th-2 predominance) was higher in HF-fed *foz/foz* C57BL6/J than BALB/c mice. In livers of HF-fed *foz/foz* C57BL6/J mice, TGF- β was unaltered but PDGF α and CTGF were increased in association with enhanced α -SMA, CD147 and MMP activity. **Conclusions:** In mice with equivalent genetic/dietary obesity, NASH development is linked to strain differences in hyperinsulinaemia and hyperglycaemia inversely related to lipid partitioning between adipose and liver. Diabetes-mediated CTGF-regulation of MMPs as well as cytokines/growth factors (Th-2 cytokine predominant, PDGF α , not TGF- β) mobilized in the resultant hepatic necroinflammatory change may contribute to strain differences in NASH fibrosis.

Among patients with non-alcoholic fatty liver disease (NAFLD), 25–40% have type 2 diabetes (T2D), an additional 15–25% previously undiagnosed diabetes on oral

glucose tolerance testing and/or a family history of T2D (1–3), and there is a three to four fold risk of developing diabetes within 3 years of NAFLD diagnosis.

Furthermore, insulin resistance and glucose intolerance are associated with a higher risk of fibrotic progression in NAFLD (4, 5). Experimentally, diabetes worsens fibrosis progression in dietary steatosis (6). While NAFLD is attributable to over-nutrition and under-activity (1, 2), not all over-weight/obese people develop NAFLD; an additional factor of individual susceptibility is required. Family studies, comparisons of NAFLD frequency between ethnic groups, and genome-wide association studies (GWAS) indicate that genetic predisposition underlines such individual susceptibility to NAFLD (7, 8), and also its severity (9). Some of these genetic polymorphisms influence bodily lipid partitioning and/or pathways of lipolysis or lipogenesis (*PNPLA3*) (7, 9). It also seems likely that genetic predisposition to diabetes predisposes to NAFLD, particularly its pathological more severe form of non-alcoholic steatohepatitis (NASH), and to NAFLD-related fibrotic progression (3).

In humans, rare single gene mutations profoundly alter appetite regulation, leading to obesity complicated by diabetes and NAFLD. Examples include defects in leptin, the leptin receptor and the Alström gene product (*ALMS1*). The latter causes Alström syndrome, a childhood obesity syndrome complicated by T2D, premature cardiovascular disease and cirrhosis (10, 11). Rodents with defective appetite regulation are widely used in diabetes and NAFLD research and include leptin-deficient *ob/ob* mice, and *db/db* mice and *fa/fa* rats with leptin receptor mutations. We have characterized *Alms1* mutant (*foz/foz*) NOD.B10 mice which likewise develop obesity, insulin resistance, hyperglycaemia/T2D, hypercholesterolaemia and hypertension (metabolic syndrome) (12–14). Feeding *foz/foz* mice high-fat (HF) diet containing 0.2% cholesterol accentuates metabolic complications that cause transition of steatosis to NASH with fibrosis (14, 15). *Alms1* locates to the anchoring site (basal body) of primary cilia (10, 13), and *foz/foz* mice exhibit at weaning a reduction in number of hypothalamic neurons that bear a primary cilium, in association with profound leptin resistance (13). The founder line of *foz/foz* mice was from a colony of non-obese diabetic (NOD) mice. If the only effect of the *Alms1* mutation is on appetite regulation, *foz/foz* mice of any strain should develop obesity, and it will be the strain response to obesity which determines the severity of resulting fatty liver disease. Those strains in which insulin resistance, metabolic syndrome and type 2 diabetes occur (as in human NASH) will develop NASH; those without insulin resistance and its metabolic complications will develop simple steatosis but not NASH. Conversely, if *Alms1* influences cellular factors operating in the pathogenesis of NASH, such as adipose differentiation, hepatic lipid handling and inflammatory recruitment, all *foz/foz* mice will develop the same pathological phenotype of NAFLD.

To test which of the above propositions is correct, we back-crossed the *Alms1* mutation onto C57BL6/J mice, which are known to develop diet-induced insulin

resistance, and onto BALB/c mice, which are refractory to obesity-related diabetes (16). The finding of equivalent weight gain between strains confirms the central role of *Alms1* mutation on appetite dysregulation and resultant obesity. However, we found diametric differences in NASH fibrotic severity between HF-fed *foz/foz* C57BL6/J and BALB/c mice, which corresponded to marked differences in bodily fat distribution (adipose vs. liver), serum adiponectin, hyperinsulinaemia and glucose tolerance. Because of conflicting human data on the relative susceptibility of males and females to NAFLD, we also conducted the present studies on both male and female mice. We then explored whether the observed metabolic changes could influence fibrogenesis directly via connective tissue growth factor (CTGF), a protein responsive to diabetes and other metabolic factors. Finally, we assessed whether the Th-1 cytokine-modulated transforming growth factor (TGF)- β pathway, the Th-2 or Th-17 profibrotic pathways are involved in NAFLD-related fibrosis in these models.

Materials and methods

Animals and dietary regimens

Animal experiments were approved by the ANU Animal Ethics Committee. The *Alms1* 11-base pair truncating mutation (*foz*) was identified by 4% agarose gel electrophoresis of PCR products, as described (12). This allows heterozygotes, homozygous normal and *foz/foz* mice to be identified (12). Using heterozygous (*foz/+*) founder NOD.B10 mice (12), the *foz* mutation (i.e. *foz/+* mice) was bred into BALB/c and C57BL6/J mice over 8 generations to yield *foz/+* BALB/c or C57BL6/J mice that were, in turn, used to breed *foz/foz* mice of each strain. From 6 week age, groups ($n = 4–10$) of male or female *foz/foz* or littermate wild type (WT) C57BL6/J or BALB/c mice were fed either HF diet (23% fat, 45% carbohydrate, 20% protein, 0.19% cholesterol w/w; Specialty Feeds, Western Australia) or chow (Gordon's Speciality Stock-feed, New South Wales) for 24 weeks. Animals were fasted 4 h to determine blood glucose, anesthetized, blood, liver and adipose harvested. All animals tolerated the dietary regimen well and there was no mortality.

Assessment of liver injury and liver histology

Serum alanine aminotransferase (ALT) levels, histology of haematoxylin and eosin (H&E) stain liver sections [steatosis, ballooning, necroinflammatory and NAFLD activity score (NAS)] (14, 17), and Sirius red staining to determine fibrosis by image analysis quantification were as described (15).

Estimation of serum proteins and insulin resistance

Serum insulin (Millipore, Billerica, MA, USA), adiponectin, leptin, tumour necrosis factor-alpha (TNF)- α

and monocyte chemoattractant protein (MCP)-1 were measured by enzyme-linked immunosorbent assays (ELISA) (R&D Systems, Minneapolis, MN, USA). Insulin resistance (IR) was calculated from the product of fasting serum insulin and blood glucose (homeostatic assessment model, HOMA-IR) as follows: HOMA-IR = fasting blood glucose (mmol/L) \times fasting serum insulin (mU/L) divided by 22.5.

Quantification of hepatic gene expression

For genes mentioned in results, semi-quantitative real-time PCR was performed (15) using primer sequences in Table S1.

Hepatic proteins

Expression of specific hepatic proteins was determined by Western immunoblot (antibody details provided on request) (14). Chemiluminescence images were captured, quantified, normalized to HSP-90 and presented relative to respective chow-fed WT strain controls.

Immunofluorescence staining

OCT-embedded liver sections were fixed with methanol/acetone and blocked with 3% BSA. Primary antibodies were applied, sections washed and fluorescent-labelled secondary antibodies added.

Matrix Metalloproteinase (MMP)

Total MMP activity was quantified by a commercial kit (Anaspec, Fremont, CA, USA). Gelatin zymography and *in situ* zymography were performed by established methods (18, 19). As negative control, MMP-specific activity was blocked with 10 mM 1,10-phenanthroline.

Statistical analyses

Data (mean \pm SEM) were analysed by either one-way or two-way analysis of variance (ANOVA), followed by *post hoc* analysis using Bonferroni's multiple comparison test.

Results

Changes in body and tissue weights, and equivalent steatosis between strains

After 24 week, HF-fed *foz/foz* BALB/c and *foz/foz* C57BL6/J male mice were similarly obese (Fig. 1A), with <15% difference in body weight between groups by diet, genotype and strain. Similar data were noted in females (Fig. S1A). However, bodily fat distribution differed dramatically between the 2 strains of obese mice. White adipose tissue (WAT) expansion (as peri-epididymal fat weight) was >50% greater in *foz/foz* BALB/c than *foz/foz* C57BL6/J males (Fig. 1B), and >three-fold (periovarian

WAT) in females (Fig. S1B); there were similar (and proportional) changes in subcutaneous WAT (data not shown). Conversely, hepatomegaly occurred in *foz/foz* C57BL6/J mice (fed HF or chow) as well as in HF-fed male WT C57BL6/J (Fig. 1C; Fig. S1C). The hepatomegaly observed in *foz/foz* C57BL6/J mice was attributable to steatosis, as indicated by the greasy pale macroscopic appearance (not shown) and grade 3 steatosis score (Fig. 1D; Fig. S1D). As reported by others (6), we also observed severe steatosis in HF-fed WT C57BL6/J mice, and it was conspicuous (albeit not causing hepatomegaly) in *foz/foz* BALB/c mice (Fig. 1D; Fig. S1D).

Metabolic and inflammatory complications of obesity occur in C57BL6/J but not BALB/c mice

A striking feature of our earlier work in HF-fed *foz/foz* NOD.B10 mice is hyperinsulinaemia and early onset diabetes (12, 14, 15). As shown in Fig. 1E (Supplementary Fig. SE for females), HF feeding cause minimal (if any) increases in fasting serum insulin in WT C57BL6/J or BALB/c mice of either strain. On the other hand, *foz/foz* C57BL6/J mice fed chow or HF diet, but not *foz/foz* BALB/c mice, exhibited five- to 20-fold-increases in fasting serum insulin compared with corresponding WT mice (Fig. 1E; Fig. S1E). The metabolic significance of hyperinsulinaemia in *foz/foz* C57BL6/J mice was evident by fasting hyperglycaemia, which exceeded 8 mmol/L (diabetes) in these 2 groups (Fig. 1F; Fig. S1F) reflecting insulin resistance as indicated by the increase in HOMA-IR (Fig. 1G; Fig. S1G). HF-fed *foz/foz* C57BL6/J (and also chow-fed *foz/foz* C57BL6/J female) but not HF-fed *foz/foz* BALB/c mice also develop hypercholesterolaemia (Fig. 1H; Fig. S1H). Consistent with these metabolic complications of obesity, both chow and HF-fed *foz/foz* C57BL6/J mice exhibited significant falls in serum adiponectin compared with *foz/foz* BALB/c counterparts (Fig. 1I; Fig. S1I). Conversely, both strains of *foz/foz* mice showed the increase in serum leptin expected direct proportional to body weight (data not shown).

NAFLD is more severe in HF-fed *foz/foz* C57BL6/J than BALB/c mice

In male mice, serum ALT exceeded 300 U/L in HF-fed *foz/foz* C57BL6/J mice compared to ca. 100U/L in HF-fed *foz/foz* BALB/c, chow-fed *foz/foz* C57BL6/J and HF-fed WT C57BL6/J mice (Fig. 2A). A similar and more pronounced pattern of ALT changes was observed in females (Fig. S2A). The severity of hepatocellular ballooning (Fig. 2B) and necroinflammatory scores (Fig. 2C) were broadly similar to ALT in male mice, but ballooning and necroinflammatory change were also evident in female HF-fed *foz/foz* BALB/c mice (Fig. S2B, 2C). The NAFLD Activity Score (NAS) was 5–6 in HF-fed *foz/foz* C57BL6/J male and female mice (Fig. 2D; Fig. S2D), and 4–5 in HF-fed WT C57BL6/J mice, and in female, but not male HF-fed *foz/foz* BALB/c mice,

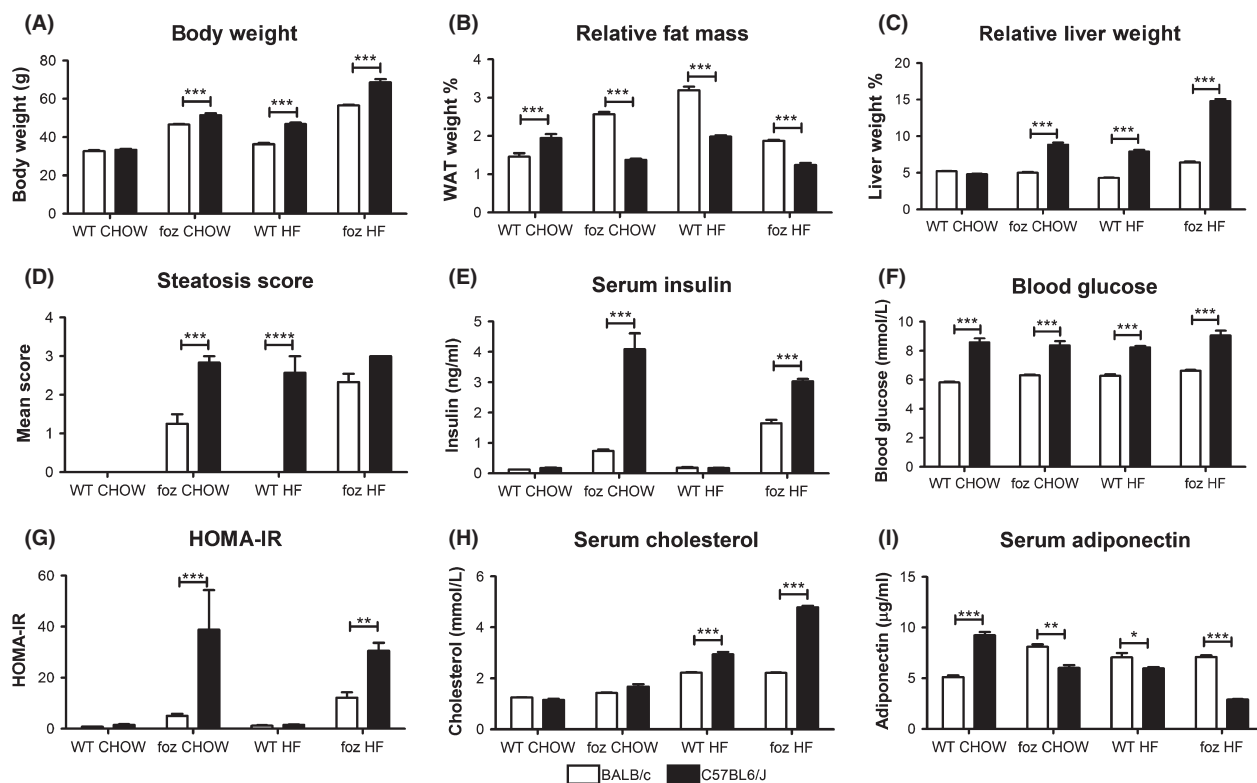


Fig. 1. Body weight, tissue weights, steatosis and metabolic complications of obesity in male *foz/foz* and WT C57BL6/J and BALB/c mice. (A) After 24 weeks of HF feeding WT and *foz/foz* C57BL6/J mice weighed slightly more than corresponding BALB/c mice. (B) In *foz/foz* and HF-fed WT mice, WAT mass was greater in BALB/c than C57BL6/J, but (C) hepatomegaly occurred only in HF-fed *foz/foz* C57BL6/J mice. (D) Steatosis was observed in both *foz/foz* strains (irrespective of diet) and HF-fed WT C57BL6/J mice. (E) Serum insulin increased markedly in *foz/foz* C57BL6/J mice, and (F) fasting blood glucose was higher in C57BL6/J mice compared to BALB/c counterparts. (G) HOMA-IR increased in C57BL6/J but not BALB/c mice. (H) Hypercholesterolaemia occurred in HF-fed *foz/foz* C57BL6/J mice, but not in BALB/c counterparts. (I) Serum adiponectin levels fell in chow and HF-fed *foz/foz* C57BL6/J mice compared to BALB/c counterparts. Data are mean \pm SEM, * $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$ and **** $P \leq 0.0001$, by two-way ANOVA with Bonferroni's test (same animals as in Table 1).

corresponding to the presence of definite or borderline NASH in these groups, as appraised by global assessment of liver pathology (Table 1, Fig. 2G; Fig. S2G). While the pattern of elevated serum MCP-1 levels resembled the NAS (Fig. 2E vs. Fig. 2D), serum TNF- α levels were highly variable, and below detection in many animals in all groups (not shown).

Liver fibrosis occurs in C57BL6/J but not in BALB/c mice

Appreciable fibrosis (Sirius red staining) occurred only in HF-fed *foz/foz* or WT C57BL6/J mice of either gender (Fig. 2F, 2H; Fig. S2F, 2H). It was most severe in HF-fed *foz/foz* C57BL6/J mice (both genders), but absent in HF-fed *foz/foz* (and WT) BALB/c mice (Fig. 2H; Fig. S2H). The differences between groups are most evident by Sirius red densitometry (Fig. 2F; Fig. S2F).

Hepatic cytokine and growth factor expression

BALB/c mice are not inherently refractory to hepatic fibrosis. Actually, for some forms of liver injury they are

particularly prone to fibrotic responses and this has been attributed to a Th2-weighted cytokine response in this strain, particularly IL-4. In the present studies, only TNF- α (Fig. 3A) and IL-12 (Fig. 3B) transcripts among Th-1 cytokines were increased in livers of HF-fed WT and *foz/foz* C57BL6/J mice compared with BALB/c counterparts, with no change in interferon (IFN)- γ (Fig. 3C) or IL-1 β (Fig. 3D) or in Th-17-related IL-17A (Fig. 3E) and IL-13 (data not shown). On the other hand, there was an important increase in IL-4 mRNA in HF-fed *foz/foz* C57BL6/J vs. BALB/c mice (Fig. 3G), and broadly similar changes in IL-10 mRNA (Fig. 3F). In addition, HF-fed *foz/foz* C57BL6/J mice showed an increase in the ratio of IL-4 to IFN- γ mRNA, which was not altered in BALB/c mice (Fig. 3H).

The key profibrotic factor TGF- β is partly regulated by TNF- α ; despite a variable increase in hepatic TNF- α mRNA (Fig. 3A), hepatic TGF- β expression appeared similar in all groups (Fig. 3I, M). Conversely, platelet-derived growth factor (PDGF)- α expression increased in all C57BL6/J mice with NAFLD fibrosis, but not in corresponding BALB/c mice (Fig. 3J, M). CTGF is

Table 1. Liver histology of male mice revealed NASH in HF-fed *foz* C57BL6/J, but not BALB/c mice

Strain	Group	<i>n</i>	Normal	NAFLD not NASH	Borderline NASH	Definite NASH
BALB/c	WT CHOW	4	4 (100%)	0	0	0
	<i>foz</i> CHOW	8	7 (87.5%)	1 (12.5%)	0	0
	WT HF	4	4 (100%)	0	0	0
	<i>foz</i> HF	6	2 (33%)	4 (67%)	0	0
C57BL6/J	WT CHOW	4	4 (100%)	0	0	0
	<i>foz</i> CHOW	6	0	0	2 (33%)	4 (67%)
	WT HF	7	1 (14%)	2 (28.5%)	2 (28.5%)	2 (28.5%)
	<i>foz</i> HF	4	0	0	1 (25%)	3 (75%)

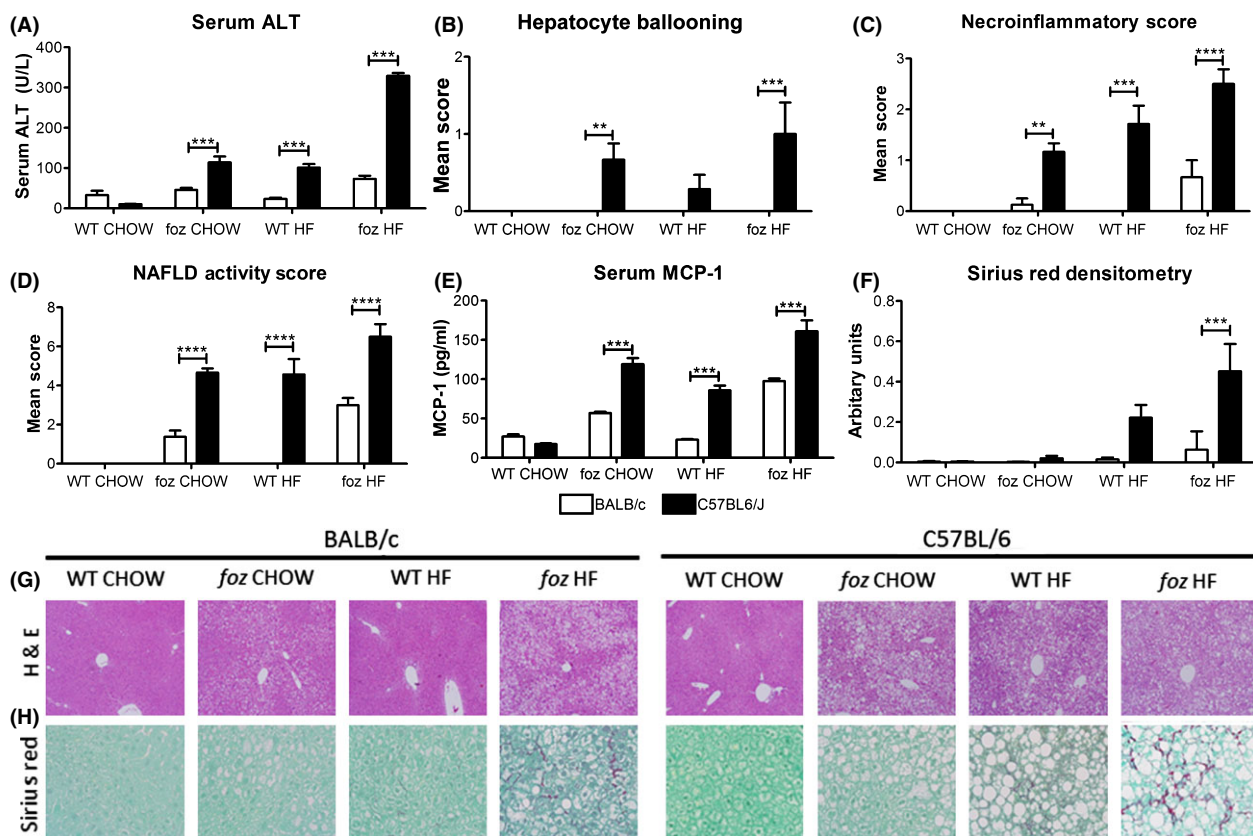


Fig. 2. Steatohepatitis occurs in both strains of HF-fed *foz/foz* male mice, whereas liver fibrosis occurs in HF-fed *foz/foz* C57BL6/J but not in BALB/c mice. (A) Serum ALT was higher in HF-fed *foz/foz* C57BL6/J mice compared to other groups. (B) Hepatocyte ballooning, (C) necroinflammatory changes, and (D) NAFLD activity score (NAS) were all increased in HF-fed WT and *foz/foz* C57BL6/J mice and in HF-fed *foz/foz* BALB/c mice. (E) Increases in serum MCP-1 were similar to NAS. (F) Densitometry analysis of Sirius red stain was highest in HF-fed *foz/foz* C57BL6/J. Representative images of (G) liver histology by haematoxylin and eosin (H&E) stain and (H) collagen deposition by Sirius red stain. Data are mean \pm SEM * P \leq 0.05, ** P \leq 0.01, *** P \leq 0.001, **** P \leq 0.0001 and ***** P $<$ 0.0001, by two-way ANOVA with Bonferroni's test (same animals as in Table 1).

regulated by glucose and insulin-like growth factors; values increased two-fold in HF-fed *foz/foz* C57BL6/J livers (Fig. 3K, B (P $<$ 0.001), and this was strongly associated with Sirius red densitometry (Fig. 2F), enhanced α -smooth muscle actin (SMA) (Fig. 3L, M), and collagen-1 α mRNA (not shown).

CD147-mediated effects on MMP activity in *foz/foz* C57BL6/J mice with fibrosis

In other work, some of us have shown that CTGF activation is associated with fibrotic progression in a nutritional model of steatohepatitis (HF-fed WT C57BL6/J

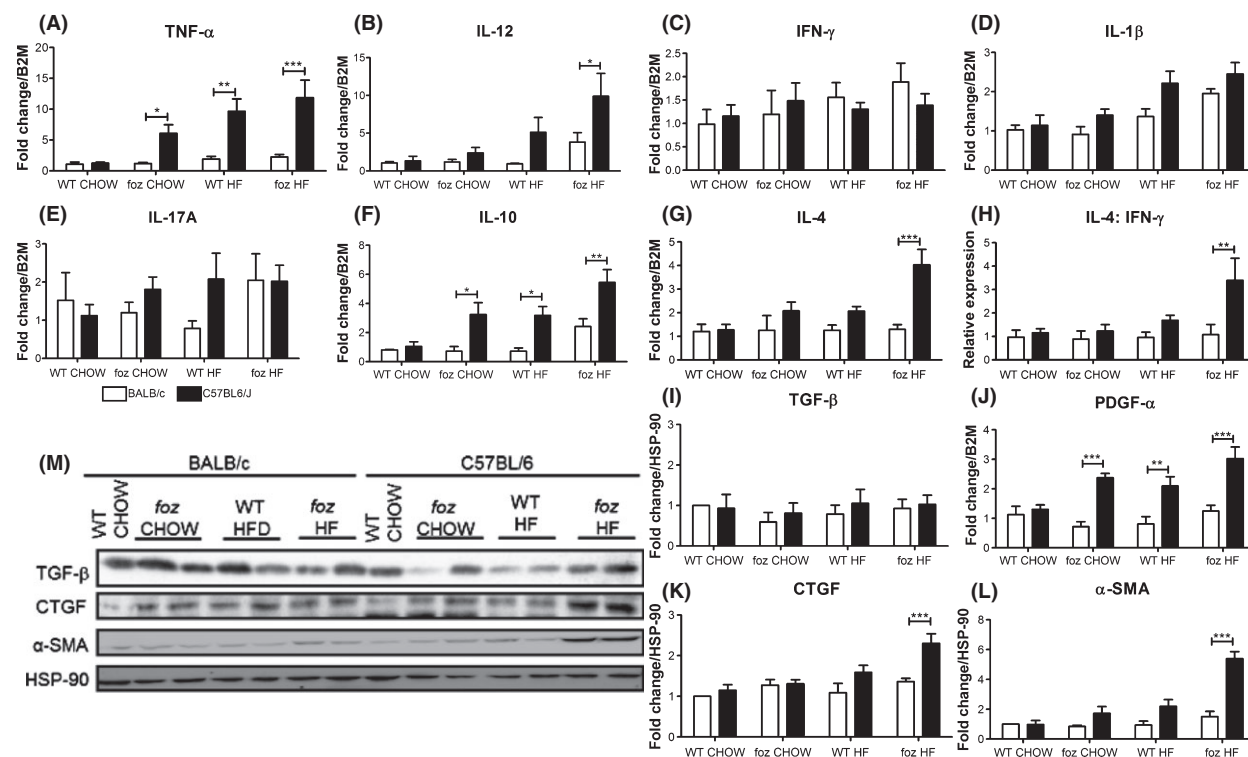


Fig. 3. Selective changes in Th-1 and Th-2 cytokines, PDGF α , CTGF and α -SMA expression in HF-fed *foz/foz* C57BL/6J mice vs. corresponding BALB/c mice. Hepatic mRNA expression of Th-1 cytokines (A) TNF- α and (B) IL-12 were increased in HF-fed *foz/foz* C57BL/6J compared with BALB/c mice, but (C) IFN- γ and (D) IL-1 β were unaltered. Th-17 related (E) IL-17A was unaltered across all groups/strains. Th-2 cytokines (F) IL-10 and (G) IL-4 were markedly increased in HF-fed *foz/foz* C57BL/6J compared to BALB/c mice, so that (H) the IL4: IFN- γ was increased HF-fed *foz/foz* C57BL/6J, compared to BALB/c mice. (I) TGF- β levels were unaltered, but (J) PDGF α , (K) CTGF, and (L) α -SMA expression were significantly higher in HF-fed *foz/foz* C57BL/6J than in BALB/c mice. (M) Representative Western Blots are shown for TGF- β , CTGF, α -SMA and HSP-90 (as loading control). Data are mean \pm SEM * P \leq 0.05, ** P \leq 0.01 and *** P \leq 0.001, by two-way ANOVA with Bonferroni's test (same animals as in Table 1).

mice) when streptozotocin was administered to cause diabetes (6). If diabetes is responsible for CTGF-induced liver fibrosis in NASH, we would expect that the pronounced increase in CTGF observed in HF-fed *foz/foz* C57BL/6J (but not in similarly fed *foz/foz* BALB/c mice) (Fig. 3K, 3M) would be associated with congruent profibrotic pathways. CD147 is secreted by hepatocytes and regulates MMP activity (20). In this study, we showed that increased CTGF expression in *foz/foz* C57BL/6 mice is associated with increased expression of CD147 around hepatocytes (Fig. 4A), and we confirmed a close relationship between CD147 expression and *in situ* MMP activity (Fig. 4B). The basis of such MMP activation was revealed by the anticipated effects of increased CD147 (Fig. 4C, D) in HF-fed *foz/foz* C57BL/6J mice, including increased total MMP activity (Fig. 4E), and expression of MMP-2 and -9 (Figs. 4F, 4G and 4H).

Discussion

The severity of NAFLD is worse in diabetes (1–4), with more progression to NASH, cirrhosis and HCC, while

the possibility that “diabetes genes” separately influence NASH fibrosis has been raised by observations in families (3). In earlier study in *foz/foz* (*Alms1* mutant) mice, we employed the NOD.B10 strain, which is genetically prone to diabetes. In such animals, serum insulin reaches very high levels and we have shown that this drives SREBP-2-mediated dysregulation of hepatocyte cholesterol metabolism (2, 12) that is central to the lipotoxic pathogenesis of NASH (15, 18). In the same model, we have also shown that dietary (21) and pharmacological strategies that improve insulin sensitivity, thereby lowering serum insulin, improve NAFLD severity and liver fibrosis (22–24).

The first major finding of this study was that NAFLD is more severe, with higher NAS and clear evidence of NASH, in HF-fed *foz/foz* C57BL/6J mice than in corresponding *foz/foz* BALB/c mice. Like NOD.B10 mice, *foz/foz* C57BL/6 mice develop insulin resistance with hyperinsulinaemia and diabetes whereas *foz/foz* BALB/c mice do not. The differences were most clear-cut in males as female *foz/foz* BALB/c mice developed some ballooning and necroinflammatory change as well as steatosis. However, an even more important and highly

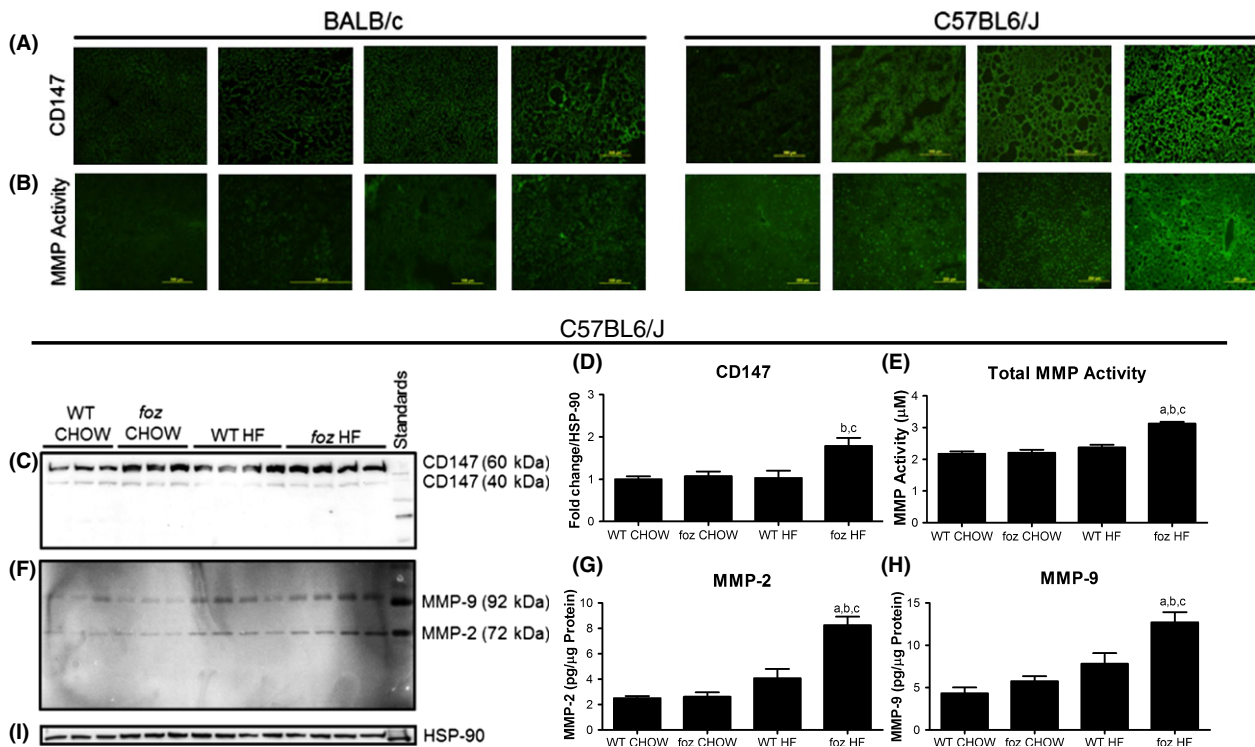


Fig. 4. Hepatic expression of CD147 and MMPs were increased in HF-fed male *foz/foz* C57BL6/J but not BALB/c mice. (A) Immunofluorescent staining of CD147 increased around hepatocytes in HF-fed *foz/foz* C57BL6/J, but not BALB/c mice, (B) increased MMP activity by *in situ* zymography in HF-fed *foz/foz* C57BL6/J mice, (C and D) CD147 expression increased in HF-fed *foz/foz* C57BL6/J mice. Similar patterns for (E) total MMP activity, (F, G and H) MMPs-2 and -9. (I) HSP-90 loading control. Data are mean \pm SEM $P \leq 0.05$ significantly different from ^aWT CHOW, ^b*foz* CHOW, ^cWT HF, by one-way ANOVA with Bonferroni's test (same animals as in Table 1).

reproducible difference was that *foz/foz* C57BL6/J develop substantial NAFLD-related fibrosis but *foz/foz* BALB/c mice do not. It should be noted that BALB/c mice are not refractory to hepatic fibrosis caused by non-metabolic factors, such as toxins (25, 26) and schistosomiasis (27), in fact BALB/c mice are actually the most susceptible mouse strain to CCl_4 injury and fibrosis (28). Furthermore, C57BL6/J mice *without* the *foz/foz* defect also develop hepatic fibrosis in the presence of NASH, as shown by some of us earlier (6) and confirmed here. It is therefore clear that the observed strain-dependent difference in fibrotic severity of NAFLD is not because of a direct effect of the *Alms1* mutation in mediation of liver fibrosis. Instead, it must be because of the differing metabolic context (insulin resistance, diabetes) and/or the more severe necroinflammatory response to liver injury caused by disordered bodily lipid partitioning.

Strain-specific differences in susceptibility to diet-induced NAFLD/NASH are well known. Among 10 different mouse strains, hepatic triglyceride levels are actually highest in BALB/c, moderate in C57BL6/J and lowest in SWR strains (29). In the present experiments, steatosis was similar in *foz/foz* C57BL6/J and BALB/c mice (both genders), but hyperinsulinaemia, hyper-

glycaemia and hypoadiponectinaemia were conspicuous only in C57BL6/J, not in BALB/c mice. BALB/c mice appear to form WAT more efficiently than C57BL6/J (or NOD.B10) mice (2, 15), and this may be a protective mechanism against hepatic accumulation of toxic lipid molecules that cause liver injury in NASH and which contribute to insulin resistance. However, there did not appear to be strain-specific differences in patterns of adipose distribution, such as the relative limitation of subcutaneous adipose with expansion of visceral adipose that is found in humans with NASH (1, 2).

The second important finding of this study is that the appetite defect in *foz/foz* mice, recently attributed to a defect in hypothalamic neuronal cilia stability (13), results in excessive weight gain independent of background strain and minimally influenced by gender. Thus, at the end of the 24-week feeding experiments, chow or HF-fed male *foz/foz* C57BL6/J mice weighed only slightly more than their BALB/c counterparts, while *foz/foz* C57BL6/J and BALB/c females were of similar weight. Despite this, *foz/foz* C57BL6/J mice develop hyperinsulinaemia and diabetes, whereas the similarly obese HF-fed *foz/foz* BALB/c mice do not. Thus, genetic differences between the C57BL6/J and BALB/c strains determine onset of insulin resistance and diabetes as

obesity occurs. The strain-dependent fall in serum adiponectin is further evidence that metabolic disease in obese mice depends on variables other than the *Alms1* mutation which leads to obesity.

In addition to the metabolic differences, it is possible that the observed strain differences in NAFLD-related fibrogenesis could be partly because of differences in the necroinflammatory activity of NASH, because serum ALT levels were higher in HF-fed *foz/foz* C57BL6/J than corresponding BALB/c mice, and hepatomegaly was more pronounced. Inflammation can involve platelet activation, and it is noteworthy that the profibrogenic PDGF α was expressed only in C57BL6/J livers with NAFLD. It is also possible that the immunophenotype of liver inflammation differs between C57BL6/J and BALB/c mice with NAFLD (30). In the present studies, circulating levels of the macrophage chemokine, MCP-1, implicated in hepatic fibrogenesis (31) were increased in C57BL6/J mice with NASH compared with their BALB/c counterparts, while hepatic TNF- α mRNA levels (but not serum levels) followed a similar strain-selective pattern. While hepatic expression of several cytokines increased in C57BL6/J mice with NASH (TNF- α , IL-12, IL-4, IL-10), others were not increased (IFN- γ , IL-1 β , IL-17A, IL-13). Furthermore, the balance reflected by the IL-4: IFN- γ ratio was Th-2 weighed, not Th-1 or Th-17. This has previously been noted to indicate a higher probability of liver fibrosis (30). On the other hand, it is notable that hepatic expression of the profibrogenic growth factor TGF- β , which is responsive to Th-1 cytokines, did not differ between C57BL6/J and BALB/c mice.

In addition to the changes in PDGF α and Th-2 weighted cytokines, we consider that a cogent explanation for fibrotic differences between C57BL6/J and BALB/c mice with NAFLD is that the divergent metabolic differences between strains effects CTGF expression. Hyperglycaemia, insulin-like growth factors and integrin interactions are among the factors known to increase CTGF expression (32). CTGF regulates fibrosis in skin, heart, kidney and lungs, while hepatic (and serum) CTGF expression increases in NASH (33). The low levels of CTGF expressed by hepatocytes are increased by liver injury, and increases in serum and liver CTGF levels have been reported in several models of liver fibrosis (34, 35). CTGF activates survival pathways in hepatic stellate cells (HSCs) and induces expression of α -SMA and type I collagen (35), strongly supporting a role for CTGF in hepatic fibrogenesis. It was previously thought that CGTF stimulation depended on TGF- β , but TGF- β -independent regulatory pathways have now been identified (36, 37). For instance, MMPs bind a CTGF enhancer element to increase CTGF expression (36). In this respect, it is possible that CD147, a plasma membrane glycoprotein (20) which we found activated in HF-fed *foz/foz* C57BL6/J but not *foz/foz* BALB/c mice with NASH, may play a role shifting the balance towards MMP production and activation.

In summary, all strains of *Alms1* mutant (*foz/foz*) mice develop equivalent obesity, but there are striking strain-dependent responses to obesity. BALB/c mice appear to form WAT more efficiently than C57BL6/J (or NOD.B10) mice (2, 15) and this may protect them from the metabolic complications of obesity, such as insulin resistance and NASH. Thus, while *foz/foz* C57BL6/J develop hyperinsulinaemia, diabetes, hypercholesterolaemia, hypo adiponectinaemia and severe NAFLD, *foz/foz* BALB/c mice fed the same HF diet are metabolically normal and have less severe NAFLD. The strain-dependent metabolic differences observed between C57BL6/J and BALB/c mice influence development of steatohepatitis, more so in male than female mice. There were also differences in circulating MCP-1, hepatic PDGF α expression, and Th-2 weighted hepatic cytokine expression related to differences in severity of liver inflammation between the two strains. However, Th-1 regulated TGF- β failed to explain the major differences observed in NASH fibrosis, which was severe in HF-fed *foz/foz* C57BL6/J mice, moderate in their chow-fed *foz/foz* or HF-fed WT counterparts, and virtually absent in HF-fed *foz/foz* BALB/c mice. Conversely, hyperinsulinaemia and hyperglycaemia were associated with increased hepatic expression of CTGF that interacts with CD147-mediated regulation of MMP activity via MMP-2 and -9. These important differences between mouse strains in NASH fibrosis that are seemingly related to metabolic factors provide an experimental model to consider factors which counter insulin resistance, such as moderately vigorous regular exercise (38) as well as the pharmacological agents studied earlier (22–24), as approaches to prevent liver fibrosis in NASH.

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Supporting information

Additional Supporting Information may be found in the online version of this article:

Table S1. List of primers sequences.

Fig. S1. Body weight, tissue weights, steatosis and metabolic determinants of obesity in female *foz/foz* and WT C57BL6/J and BALB/c mice.

Fig. S2. In female mice steatohepatitis occurs in both

strains of HF-fed *foz/foz* mice, whereas liver fibrosis occurs in HF-fed *foz/foz* C57BL6/J, but not in BALB/c mice.

Fig. S3. Method for back-crossing *Alms1* (*foz*) mutation from founder NOD.B10 strain onto BALB/c background (method for C57BL6/J was identical).

Fig. S4. Intraperitoneal glucose tolerance testing (IP-GTT) of wildtype (WT) C57BL/6 mice fed 26–30 weeks either chow or the same high-fat diet (HF), as used in this study.

Fig. S5. Intraperitoneal glucose tolerance testing of *foz/foz* and WT BALB/c mice fed the same high-fat diet (HF), as used in this study for 8 weeks (the mice are 11 weeks of age).