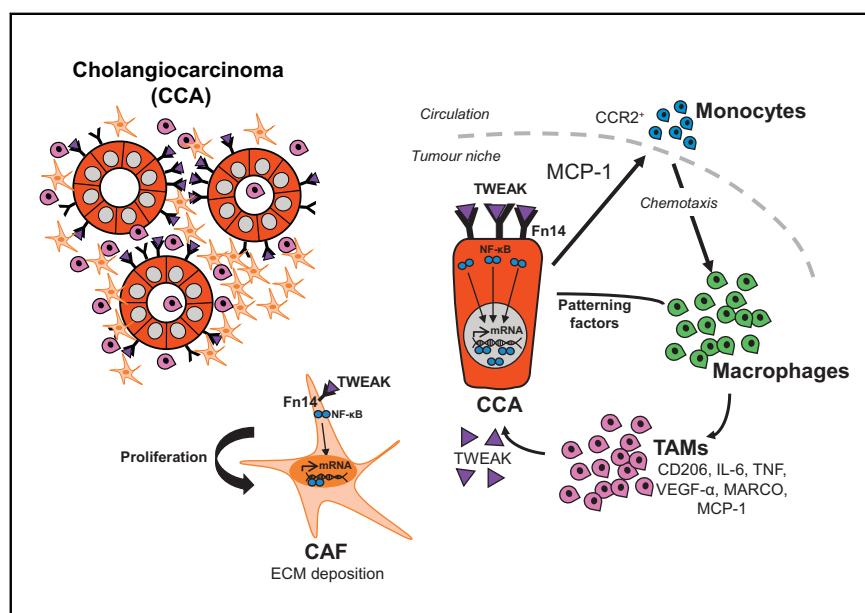


TWEAK/Fn14 signalling promotes cholangiocarcinoma niche formation and progression

Graphical abstract



Highlights

- Fn14 is upregulated on tumour cells and CAFs, and TWEAK is expressed by TAMs in human CCA.
- TWEAK/Fn14 are progressively upregulated during rodent tumour development.
- TWEAK/Fn14 signalling induces TAM accumulation via TWEAK-inducible MCP-1 chemotaxis which can be blocked *in vivo*.
- TWEAK-inducible factors from tumour cells pattern macrophages to a TAM-like phenotype.
- TWEAK overexpression in experimental tumour formation drives CAF proliferation, collagen deposition and increases macrophages in mice.

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Lay summary

Cholangiocarcinoma is an aggressive, chemotherapy-resistant liver cancer. Interactions between tumour cells and cells that form a supportive environment for the tumour to grow are a source of this aggressiveness and resistance to chemotherapy. Herein, we describe interactions between tumour cells and their supportive environment via a chemical messenger, TWEAK and its receptor Fn14. TWEAK/Fn14 alters the recruitment and type of immune cells in tumours, increases the growth of cancer-associated fibroblasts in the tumour environment, and is a potential target to reduce tumour formation.

TWEAK/Fn14 signalling promotes cholangiocarcinoma niche formation and progression

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Background & Aims: Cholangiocarcinoma (CCA) is a cancer of the hepatic bile ducts that is rarely resectable and is associated with poor prognosis. Tumour necrosis factor-like weak inducer of apoptosis (TWEAK) is known to signal via its receptor fibroblast growth factor-inducible 14 (Fn14) and induce cholangiocyte and myofibroblast proliferation in liver injury. We aimed to characterise its role in CCA.

Methods: The expression of the TWEAK ligand and Fn14 receptor was assessed immunohistochemically and by bulk RNA and single cell transcriptomics of human liver tissue. Spatio-temporal dynamics of pathway regulation were comprehensively analysed in rat and mouse models of thioacetamide (TAA)-mediated CCA. Flow cytometry, qPCR and proteomic analyses of CCA cell lines and conditioned medium experiments with primary macrophages were performed to evaluate the downstream functions of TWEAK/Fn14. *In vivo* pathway manipulation was assessed via TWEAK overexpression in NICD/AKT-induced CCA or genetic *Fn14* knockout during TAA-mediated carcinogenesis.

Results: Our data reveal TWEAK and Fn14 overexpression in multiple human CCA cohorts, and Fn14 upregulation in early TAA-induced carcinogenesis. TWEAK regulated the secretion of factors from CC-SW-1 and SNU-1079 CCA cells, inducing polarisation of proinflammatory CD206⁺ macrophages. Pharmacological blocking of the TWEAK downstream target chemokine monocyte chemoattractant protein 1 (MCP-1 or CCL2)

significantly reduced CCA xenograft growth, while TWEAK overexpression drove cancer-associated fibroblast proliferation and collagen deposition in the tumour niche. Genetic *Fn14* ablation significantly reduced inflammatory, fibrogenic and ductular responses during carcinogenic TAA-mediated injury.

Conclusion: These novel data provide evidence for the action of TWEAK/Fn14 on macrophage recruitment and phenotype, and cancer-associated fibroblast proliferation in CCA. Targeting TWEAK/Fn14 and its downstream signals may provide a means to inhibit CCA niche development and tumour growth.

Lay summary: Cholangiocarcinoma is an aggressive, chemotherapy-resistant liver cancer. Interactions between tumour cells and cells that form a supportive environment for the tumour to grow are a source of this aggressiveness and resistance to chemotherapy. Herein, we describe interactions between tumour cells and their supportive environment via a chemical messenger, TWEAK and its receptor Fn14. TWEAK/Fn14 alters the recruitment and type of immune cells in tumours, increases the growth of cancer-associated fibroblasts in the tumour environment, and is a potential target to reduce tumour formation.

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Introduction

Cholangiocarcinomas (CCAs) are aggressive hepatic malignancies, typically adenocarcinomas morphologically resembling hepatobiliary epithelium, expressing cytokeratin (CK)7 and CK19 but not CK20 or Hep-Par1.^{1–3} CCA occurs at all regions of the biliary tree and is classified according to anatomical location; intrahepatic (iCCA; 20%), perihilar (50–60%) or distal (20–30%).^{3,4} CCA remains clinically challenging because of late-stage presentation, chemotherapy resistance, and high post-surgery

Keywords: Cholangiocarcinoma; Liver cancer; TWEAK; Fn14; Tumour-associated macrophage; Cancer-associated fibroblast.

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recurrence.³ Consequently, 5-year survival rates remain below 25%.⁵

CCA develops a characteristic thick, fibrous stroma composed of α -smooth muscle actin (α SMA)-expressing cancer-associated fibroblasts (CAFs), tumour-associated macrophages (TAMs), neutrophils and vascular endothelial cells.³ Stromal cells interact with neoplastic ducts via several signals including Wnt,^{6,7} Notch,^{8,9} platelet-derived growth factor,^{10,11} stromal-derived factor-1/C-X-C chemokine receptor type-4^{12,13} and numerous cytokines, to support growth, evasion of apoptosis and promote metastatic progression via modulation of AKT and ERK pathways.^{13–15} CD14⁺/CD16⁺ peripheral blood monocytes are elevated in patients,¹⁶ and are recruited to tumour areas, where they differentiate into TAMs.^{17,18} TAM infiltration is correlated with tumour recurrence, metastasis and decreased survival.^{17,19} Fluorescently tagged bone marrow-derived macrophages comprise the majority of CD206⁺ TAMs in a rat CCA model, and secrete tumour-feeding Wnt ligands.⁷ Ablating TAMs significantly reduces tumour formation, highlighting the importance of macrophage-derived factors in maintaining CCA.⁷

The tumour necrosis factor (TNF)-like weak inducer of apoptosis (TWEAK)/fibroblast growth factor-inducible 14 (Fn14) pathway acts by activating NF- κ B/MAPK/PI3K/AKT downstream signalling²⁰ to regulate proliferation, survival, inflammation and angiogenesis. TWEAK is ubiquitously expressed by macrophages in the adult liver, with signalling modulated by dynamic regulation of Fn14 during injury and repair.^{20,21} TWEAK initiates non-hepatocyte-mediated regeneration via canonical NF- κ B-induced cholangiocyte proliferation^{21,22} and drives fibrosis-mediating hepatic stellate cell proliferation within the injury niche.²³ TWEAK-expressing macrophages were recently identified as key drivers of fibrosis, controlling Fn14⁺ HSC proliferation in human cirrhotic liver.²⁴ TWEAK also stimulates proliferation of hepatocellular carcinoma (HCC) cell lines,²⁵ potentiating a role in liver cancer growth.

We hypothesised that the principal role of TWEAK during chronic liver disease and CCA development may be 2-fold: (i) to act as a canonical NF- κ B pathway-driven mitogen controlling neoplastic duct and CAF proliferation and (ii) to induce NF- κ B-driven chemotaxis-associated signalling during the establishment, maintenance and progression of CCA. We demonstrate that the TWEAK/Fn14 pathway is increasingly expressed during multi-species CCA development, regulating proliferation, migration and polarisation of cells, including macrophages and CAFs in the tumour niche, establishing TWEAK/Fn14 signalling as a novel, therapeutically targetable driver of CCA development.

Materials and methods

Study approval

Animal experiments were approved by the University of Edinburgh animal ethics committee with U.K. Home Office approval (70/7847, 70/8150, P231C5F81) or performed according to the Australian code for the care and use of animals for scientific purposes at Curtin University (AEC_2014_29). Retrospectively collected specimens were obtained from the National Health Service Lothian Scottish Academic Health Sciences Collaboration BioResource and healthy liver from the Edinburgh Medical Research Council Sudden Death Tissue Bank (10/H0716/3). Human blood was collected under ethical approval from the University of Edinburgh (15-HV-013). All human tissue samples were collected with informed consent.

For further details regarding the materials and methods used, please refer to the CTAT table and [supplementary information](#).

Results

TWEAK and Fn14 upregulation in multi-species CCA

We assessed Fn14 expression in archival CCA samples and interrogated publicly available mRNA expression data to ascertain whether the TWEAK/Fn14 pathway was overexpressed in CCA, and to define cell type interactions of ligand and receptor. In a cohort of pathologically confirmed human iCCA cases, Fn14 was highly expressed by malignant epithelia, localising at the surface of these cells. Lower expression was observed in bile ducts in surrounding areas of non-tumour liver tissue, with diffuse staining in hepatocytes. Fn14 was identifiable in endothelial cells within portal triads. Positive stromal cell staining consistent with CAFs was observed in a subset of samples (Fig. 1A). Quantification confirmed increased Fn14 expression in CCA vs. non-CCA areas (Fig. 1B), corroborated by interrogation of publicly available transcriptomic data. In a single cell RNA-sequencing dataset (GSE125449²⁶), *Fn14* was mainly expressed by malignant cells, and subsets of CAFs and hepatic progenitor cells (HPCs). TWEAK expression was mainly observed in a subset of TAMs in iCCA (Fig. 1C). *Fn14* and TWEAK were significantly upregulated in tumour tissue vs. non-involved liver in the TCGA-Chol cohort (Fig. S1A) and in a microarray dataset (GSE26566²⁷ Fig. S1B).

We then assessed the distribution of Fn14 in PanCK⁺ tumour epithelia and α SMA⁺ CAFs in an iCCA tissue microarray, where 42.50% of tumour cells (n = 83 samples containing PanCK⁺ cells) and 62.64% of CAFs (n = 79 samples containing α SMA⁺ CAFs) expressed Fn14 (Fig. 1D). We observed a greater proportion of Fn14⁺ CCA cells in well-differentiated (grade 1) vs. poorly differentiated (grade 3) iCCAs, but no association between tumour grade and the proportion of Fn14⁺ CAFs (Fig. 1D). No association was observed between TNM stage and proportion of Fn14⁺ cells (Fig. S1C), supported by assessment of TCGA-Chol samples with respect to TNM stage (Fig. S1D).

Since archival human tissue samples represent end-stage CCA, we performed time course analyses to observe the temporal relationship of TWEAK/Fn14 expression to CCA development using rodent models of thioacetamide (TAA)-mediated injury (Fig. 2A). Histological examination of Fn14-stained serial sections by a specialist liver histopathologist found that Fn14 was readily identifiable in dysplastic biliary lesions and early CCA (10–18 weeks; Fig. S2A). Like human data, Fn14 was observed at the cell surface of biliary lesions/CCA cells, some endothelial cells and transiently in damaged hepatocytes (Fig. S2). Fn14 was transiently upregulated in PanCK⁺ ducts and surrounding damaged hepatocytes at 10 weeks (Fig. 2B and Fig. S2A), which reduced as injury progressed and more PanCK⁺ cells were detected. As malignancy developed, subsets of PanCK⁺ cells expressing Fn14 emerged. Fn14 expression continued in CCA epithelia but not in non-malignant ducts (Fig. 2B and Fig. S2B). Biphasic Fn14 expression was mirrored transcriptionally, peaking at 10 and 20 weeks of TAA treatment. TWEAK mRNA increased steadily over the time course (Fig. 2C). Transcripts of the pro-fibrotic markers collagen type 1 α 1, transforming growth factor- β 1 (TGF- β 1), tissue inhibitors of metalloproteinases (*Timp1*, *Timp2*) and matrix metalloproteinases (*MMP2*, *MMP9*) exhibited a comparable biphasic expression (Fig. S3).

We assessed expression of TWEAK ligand and Fn14 receptor in a transgenic model of CCA induction, where CCA develops

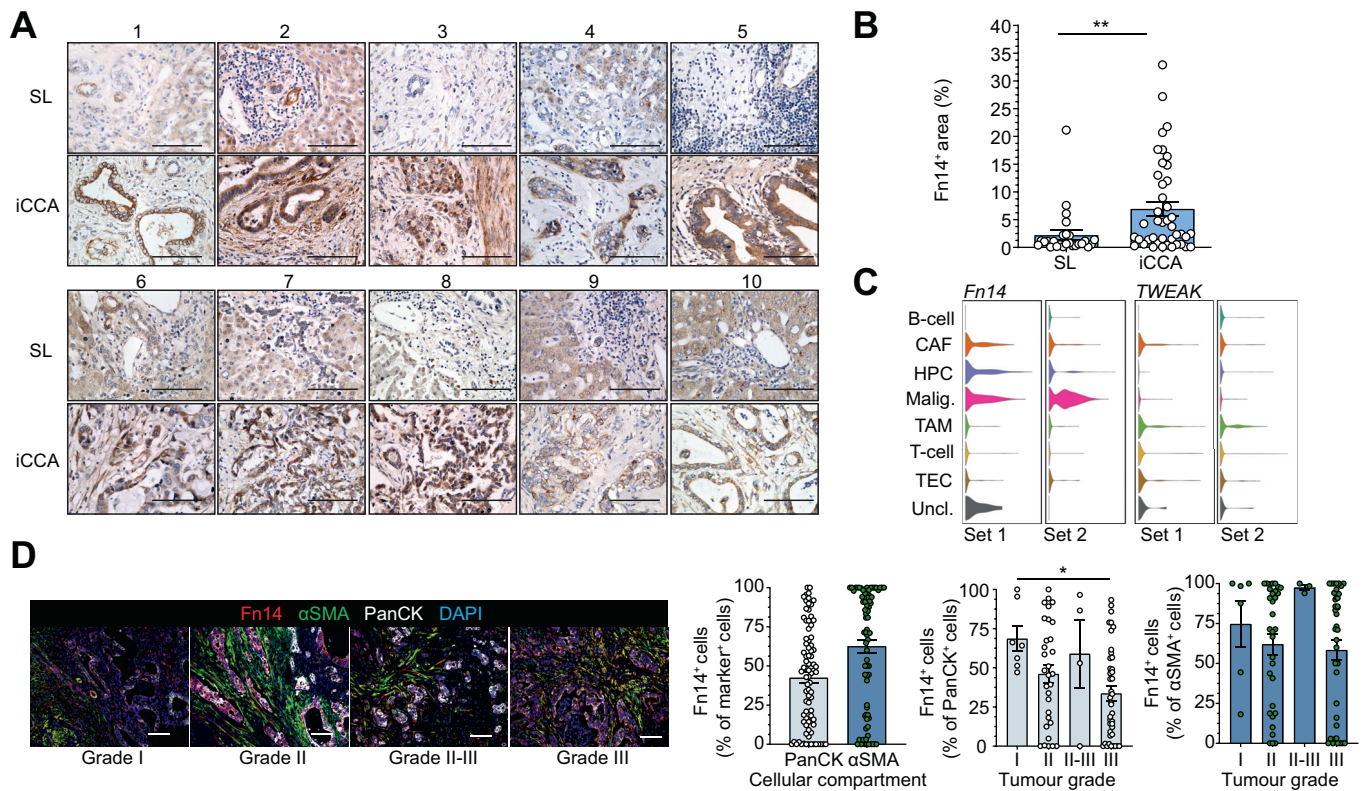


Fig. 1. TWEAK/Fn14 expression in iCCA. (A) Fn14 immunohistochemistry in archival paraffin sections of patient-matched iCCA vs. non-involved areas of SL (n = 42 iCCA vs. n = 26 SL) (B) Quantification of Fn14 immunostaining (Mann-Whitney *U* test). (C) Single cell RNA-sequencing data of iCCA (GSE125449; n = 5 per cohort). Cell types: B-cells, CAFs, HPCs, Malig., TAMs, T cells, TECs, undefined. (D) Staining of Fn14 (red) in tumour cells (PanCK; white) and CAFs (α SMA; green) in an iCCA tissue microarray. Nuclei are stained with DAPI (blue). Proportion of Fn14⁺ tumour cells (n = 84) and CAFs (n = 74) by tumour grade (Kruskal-Wallis test with Dunn's multiple comparison test). Data are mean \pm SEM. **p* < 0.05, ***p* < 0.01. Scale bars represent 100 μ m. CAFs, cancer-associated fibroblasts; HPCs, hepatic progenitor cells; iCCA, intrahepatic cholangiocarcinoma; Malig., malignant cells; SL, surrounding liver; TAMs, tumour-associated macrophages; TECs, tumour endothelial cells;

during TAA treatment in livers with CK19-inducible Cre-recombinase driven p53-deficiency, but not in mice with at least 1 functional p53 allele (Fig. 2D²⁸). TAA-treated K19-p53^{fl/fl} mice significantly increased TWEAK and Fn14 mRNA (Fig. 2E) and Fn14 protein levels (Fig. 2F) during CCA formation, compared to mice without CCA (p53^{WT/het}).

These data associate the transition of normal duct epithelium to iCCA with upregulation of the TWEAK/Fn14 pathway and suggest a potential function during development and maintenance in multi-species CCA.

TWEAK/Fn14 modulates NF- κ B-regulated cytokine/chemokine secretion in CCA cells

To assess the function of TWEAK/Fn14 in CCA epithelia, we studied the effects of recombinant human TWEAK (rhTWEAK) treatment in 4 well-characterised iCCA cell lines, all expressing cell surface Fn14 (Fig. S4A). TWEAK stimulation uniformly induced canonical p65 NF- κ B phosphorylation, processing of non-canonical NF- κ B p100 to p52 in CC-SW-1 and SNU-1079 cells (Fig. 3A), and stimulated nuclear translocation of p65 in CCA cells (Fig. 3B). Despite consistent rhTWEAK-mediated NF- κ B activation in all cell lines, only SNU-1079 and HuH-28 cells displayed a mitogenic response to rhTWEAK (Fig. 3C).

NF- κ B regulates a variety of proinflammatory and pro-fibrogenic responses in liver disease.²⁹ Since a key element of

CCA development is the formation of a stimulatory, pro-tumorigenic niche, we investigated TWEAK-induced gene expression changes in CCA cells. We observed TWEAK-inducible mRNA expression of monocyte chemoattractant protein 1 (MCP-1; 3/4 cell lines), (C-X3-C motif) ligand 1 (CX3CL1; 3/4 cell lines), interleukin (IL)-6 (1/4 cell lines), IL-8 (3/4 cell lines), macrophage colony-stimulating factor (M-CSF; 3/4 cell lines) and granulocyte macrophage colony-stimulating factor (GM-CSF; 2/4 cell lines) (Fig. 3D). To determine pathway specificity, we assessed TWEAK-inducible gene expression in the presence and absence of inhibitors of canonical or non-canonical NF- κ B signalling in CCA vs. HCC cells. Generally, TWEAK-induced gene expression was subdued by canonical NF- κ B inhibition in CCA lines. IL-6 was inhibited by both inhibitors, whereas CX3CL1 and M-CSF were not affected by either inhibitor in CC-SW-1 cells. Likewise, CX3CL1 expression was not affected by either inhibitor in HuH-28 cells. TWEAK-induced gene expression was not observed in HepG2 HCC cells (Fig. S4B).

We observed significantly increased TWEAK-induced secretion of MCP-1 (all cell lines), IL-8 (2/4 cell lines) and GM-CSF (all cell lines) into the cell culture medium (Fig. 3E). We also characterised proteins present in conditioned medium from PBS- or TWEAK-treated cells by mass spectrometry. Secreted proteins that were present in both PBS- and TWEAK-treated conditioned medium, or in TWEAK-treated conditioned medium alone, were

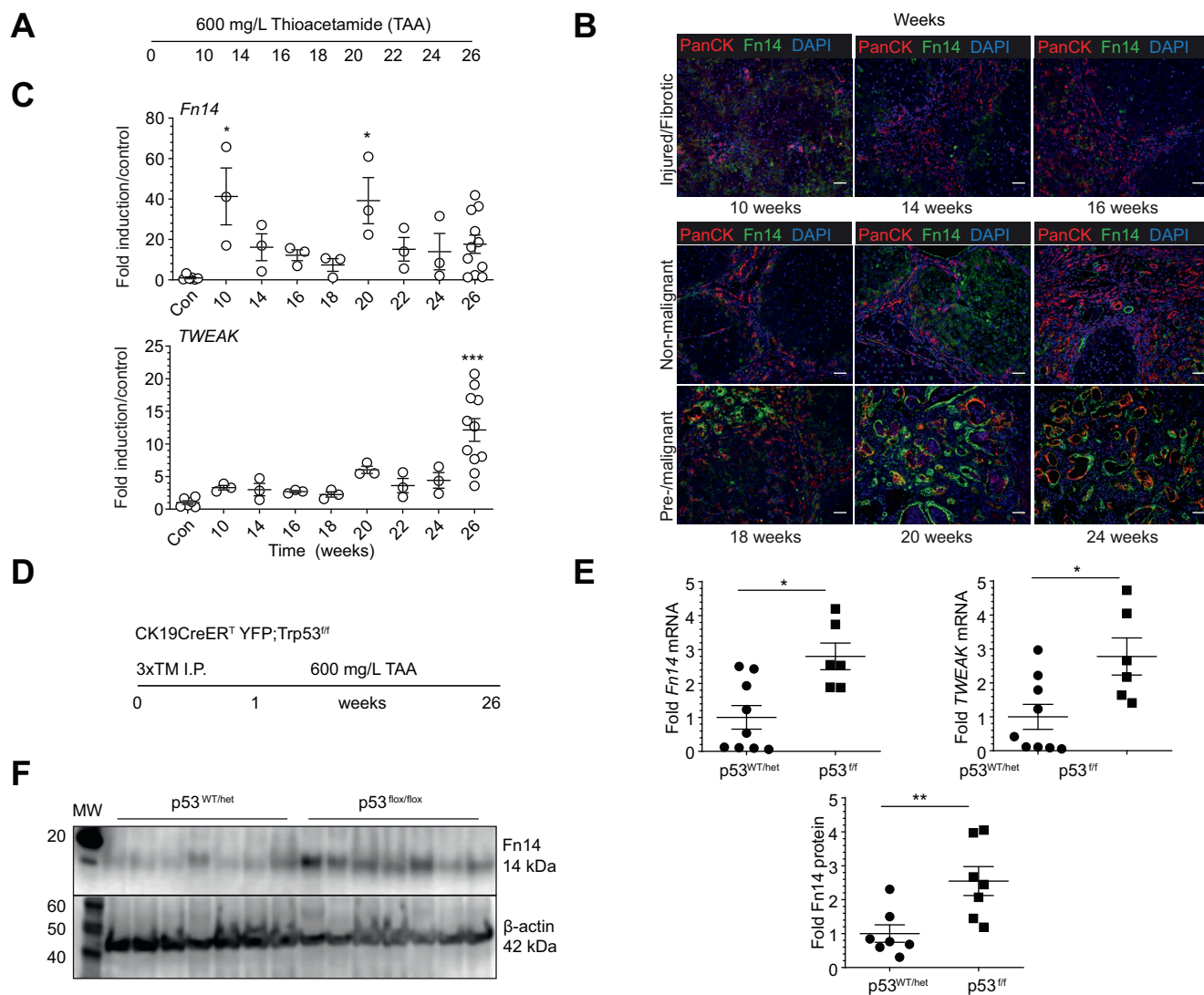


Fig. 2. TWEAK/Fn14 upregulation in rodent CCA. (A) Schematic of TAA treatment of rats to induce CCA. (B) Dual immunofluorescence reveals Fn14⁺ (green) tumour epithelia (PanCK⁺; red). (C) mRNA expression of *Fn14* and *TWEAK* in a time course of TAA treatment in rats (n = 3 to 11; Kruskal-Wallis with Dunn's post-test) (D) Schematic of TAA treatment of Krt19-CreERTR26-eYFPp53^{flx/het/wt} mice to induce CCA. (E) mRNA expression of *Fn14* and *TWEAK* in Krt19-CreERTR26-eYFPp53^{fl/WT} or Krt19-CreERTR26-eYFPp53^{WT/WT} (p53^{wt/het}; no CCA, n = 9) vs. Krt19-CreERTR26-eYFPp53^{flx/flx} (p53^{fl/fl}; CCA, n = 6; Mann-Whitney U test). (F) Protein expression of Fn14 in mouse p53^{wt/het} vs. p53^{flx/flx} mice (n = 7 each; unpaired t-test). Data are mean ± SEM. *p<0.05, **p<0.01, ***p<0.001. Scale bars represent 50 μm. CCA, cholangiocarcinoma; TAA, thioacetamide.

assessed for protein-protein interactions and 'biological process' gene ontology enrichment (Figs. S5-8). Several gene ontology terms associated with the development of a pro-tumour micro-environment were enriched in TWEAK-conditioned medium, including extracellular matrix development (extracellular matrix organisation), blood vessel development (angiogenesis, blood vessel remodelling/development) and immune modulation (regulation of leukocyte/macrophage chemotaxis, immune system process, immune response) in a cell line-specific manner.

These cell line-specific results classified the investigated Fn14⁺ iCCA lines as TWEAK-high responder (CC-SW-1 and SNU-1079) and TWEAK-low responder cell lines (CC-LP-1 and HuH-28) and provided evidence that TWEAK/Fn14 may play a role in the development of CCA by orchestrating the surrounding niche via localised NF-κB-mediated chemokine/cytokine secretion.

TWEAK-induced CCA-derived factors regulate macrophage biology

TAMs play a critical role in providing pro-proliferative and pro-survival factors in CCA.⁷ Since TWEAK induces the secretion of several proinflammatory proteins in CCA cells, we investigated whether any of these TWEAK-induced, CCA-derived secreted proteins could affect macrophage phenotypes. To model the effect of TWEAK in CCA-induced patterning of macrophages in the CCA niche, we isolated human peripheral blood monocytes (Fig. S9A), differentiated these cells into macrophages (human monocyte-derived macrophages [HMDMs]) and subjected them to (a) PBS-supplemented basal medium vs. (b) TWEAK-supplemented basal medium, to assess the direct effects of TWEAK on HMDMs; or to (c) conditioned medium from PBS-treated CCA cell lines vs. (d) conditioned medium from TWEAK-treated CCA cell lines, to measure the indirect effects of

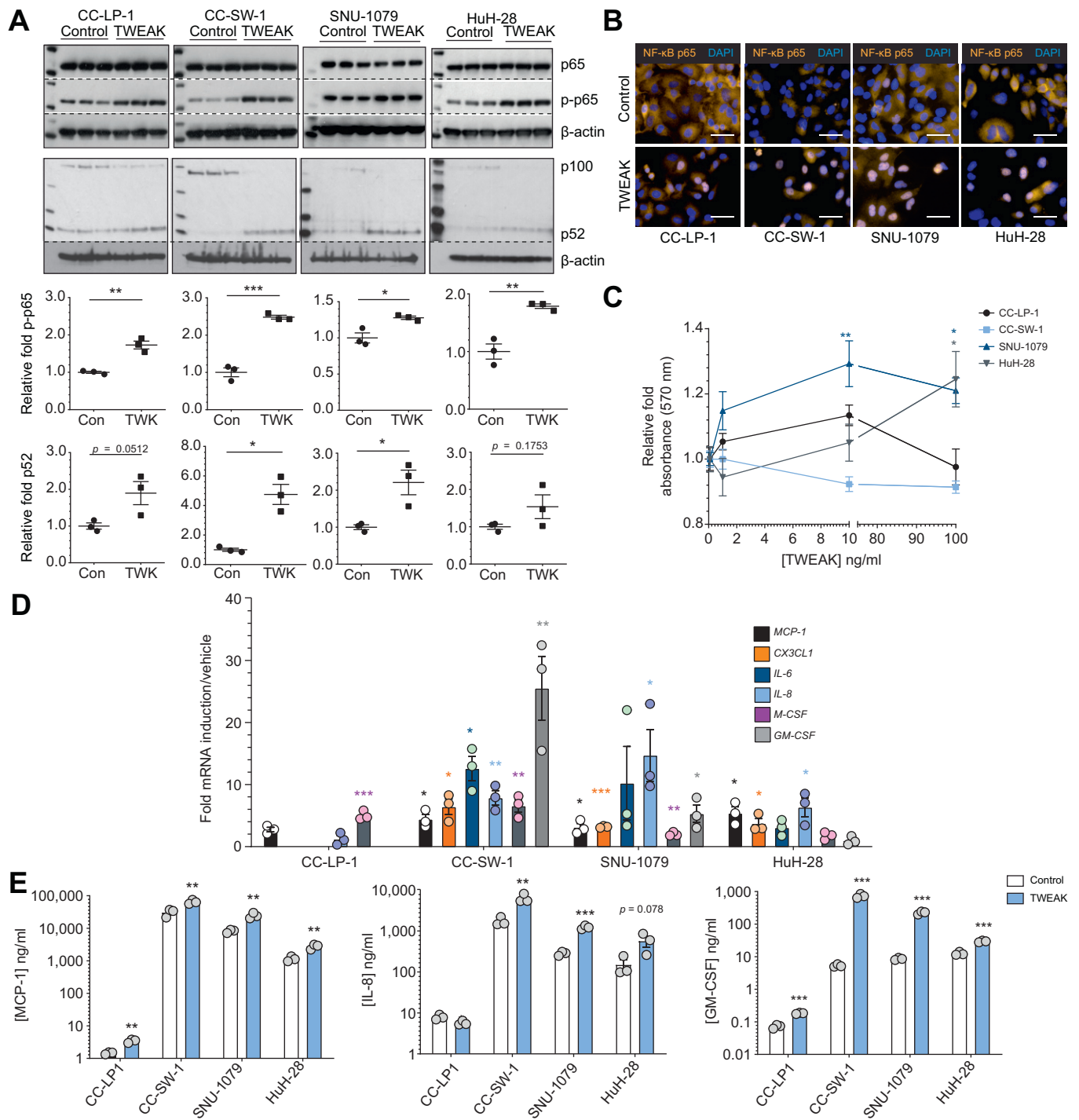


Fig. 3. TWEAK signalling drives NF-κB pathway activation and protein production. (A) TWEAK-dependent modulation of NF-κB pathway proteins in CCA cells and quantification of NF-κB protein expression 2 h-post rhTWEAK exposure. (B) Localisation of NF-κB p65 subunit in CCA cell lines after TWEAK treatment. (C) MTT assay in CCA lines following 72 h treatment with increasing dose of rhTWEAK. (D) TWEAK-dependent mRNA expression in CCA lines following 6 h rhTWEAK treatment. (E) Protein immunoassay of secreted proteins from CCA lines treated with PBS or rhTWEAK. Data are mean ± SEM. Unpaired t-test (n = 3) or one-way ANOVA with Dunnett's post-test (MTT assay; n = 6); * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Scale bars represent 50 μm. CCA, cholangiocarcinoma; rhTWEAK, recombinant human TWEAK.

TWEAK in HMDMs via TWEAK-induced protein secretion in the CCA cell lines.

HMDM differentiation was confirmed by 25F9 expression (Fig. S9B). Treatment with conditioned medium from TWEAK-

stimulated TWEAK-high responder CCA lines (CC-SW-1 and SNU-1079) significantly increased cell surface expression of a TAM-associated marker, CD206, in HMDMs. No significant difference was observed when conditioned medium from TWEAK-

low responder CCA lines (CC-LP-1 and HuH-28 cells) was used (Fig. 4A), suggesting that TWEAK-induced factors from some CCA cells can induce macrophage polarisation. We also assessed mRNA expression of several cytokines, chemokines, growth factors and receptors. HMDMs expressed 154- to 733-fold less *Fn14* mRNA than CCA/HCC cell lines (Fig. S9C) and did not modulate gene expression when treated with TWEAK alone (Fig. 4B). Few genes were differentially regulated in HMDMs exposed to conditioned medium from the TWEAK-low responder CCA cells (*MMP-2* in TWEAK-conditioned medium from CC-LP-1 cells, and *TWEAK* and *CD163* mRNA in TWEAK-conditioned medium from HuH-28 cells). However, expression of several key transcripts was induced in HMDMs treated with TWEAK-conditioned medium from CC-SW-1 and SNU-1079 cells. *IL-6* was upregulated in TWEAK-conditioned medium from both cell lines (82.6-fold and 105.2-fold), as was *TIMP-1*

(4.5-fold and 4.3-fold). In CC-SW-1 conditioned medium-patterned cells, we observed additional upregulation of *CD80* (2.8-fold), *M-CSF* (6.2-fold) and *TNF* (3.9-fold). SNU-1079-patterned cells responded with additional upregulation of *MCP-1* (4.0-fold) and vascular endothelial growth factor-alpha (*VEGF- α* ; 4.5-fold). We also assessed 2 surface markers associated with TAMs; triggering receptor expressed on myeloid cells 2 (*TREM-2*) and macrophage receptor with collagenous structure (*MARCO*). All populations expressed *TREM-2*, and SNU-1079-patterned cells upregulated *MARCO* (18.1-fold; Fig. 4B).

MCP-1 is upregulated in CCA and affects macrophage accumulation in the tumour niche

MCP-1 was the most abundant TWEAK-inducible protein produced by CCA cell lines (Fig. 2). In addition, MCP-1 was

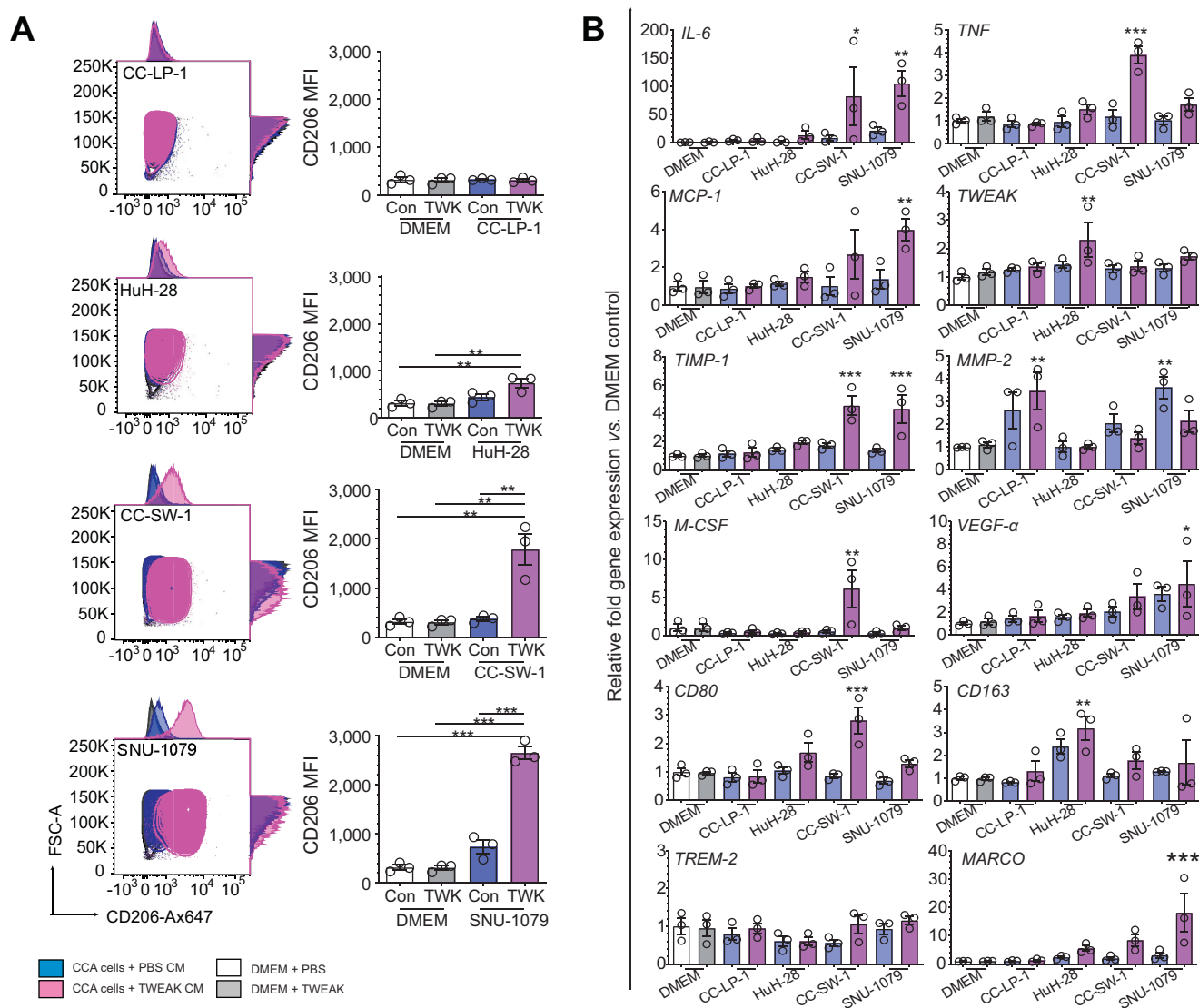


Fig. 4. CCA-derived TWEAK-inducible factors drive macrophage patterning. (A) Cell surface CD206 expression (MFI) in HMDMs treated with CM from PBS- or TWEAK-treated CCA cells (One-way ANOVA with Tukey's post-test; $n = 3$). (B) mRNA expression in HMDMs treated with CM from PBS- or TWEAK-treated CCA cells ($n = 3$). Fold changes expression was calculated compared to control DMEM with PBS (DMEM+PBS) and analysed using one-way ANOVA with Dunnett's multiple comparison test. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Data are mean \pm SEM. CCA, cholangiocarcinoma; CM, conditioned medium; HMDM, human monocyte-derived macrophage; MFI, mean fluorescence intensity.

upregulated in macrophages by TWEAK-inducible factors produced by CCA cells (Fig. 4). We therefore further investigated MCP-1 expression in CCA to link *in vitro* observations to human disease. In analysis of a single cell RNA-sequencing dataset (GSE125449²⁶), MCP-1 mRNA was expressed by CAFs, and subsets of tumour cells, HPCs and TAMs, while its cognate receptor

C-C chemokine receptor type 2 (CCR2) was mainly expressed in TAMs and T cells (Fig. S10A). We observed increased MCP-1 immunostaining in archival human iCCA in tumour epithelia and widespread expression in stromal cells, compared to a subset of paired non-involved surrounding liver areas (Fig. 5A), confirmed by pixel analysis (Fig. 5B).

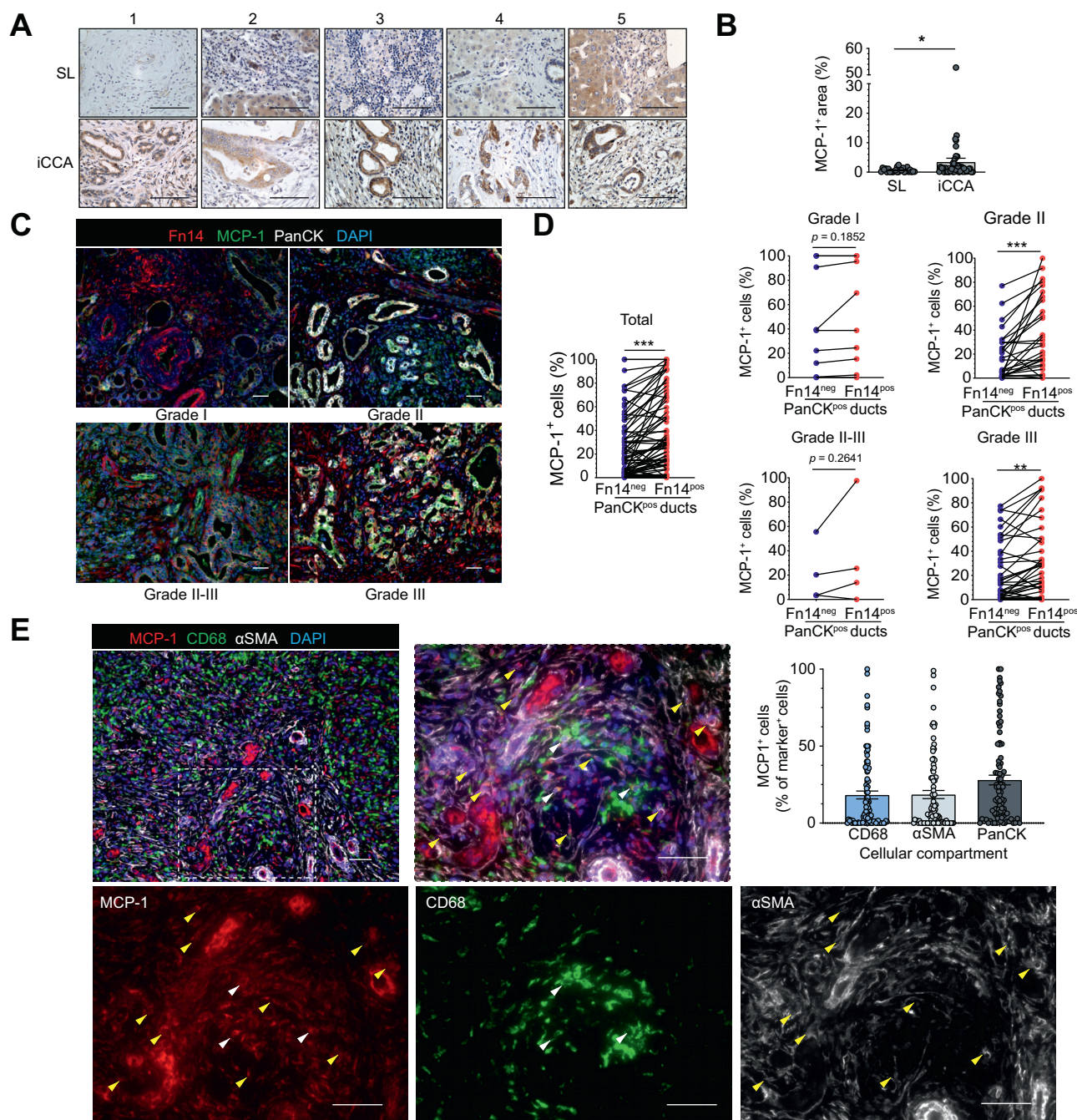


Fig. 5. MCP-1 expression in CCA. (A) MCP-1 immunohistochemistry in archival paraffin sections of patient-matched iCCA vs. adjacent non-involved SL areas. (B) Digital pixel analysis of sections (n = 42 iCCA vs. n = 26 SL; Mann-Whitney U test). (C) Staining of tumour liver tissue from an iCCA tissue microarray (n = 89) with PanCK (white), Fn14 (red), MCP-1 (green). Nuclei are stained with DAPI (blue). (D) Analysis of total distribution of MCP-1⁺ cells in Fn14^{neg} and Fn14^{pos} subsets of PanCK^{pos} tumour cells in individual CCA tissues or stratified with respect to tumour grade (Wilcoxon matched-pairs signed rank test). (E) Assessment of distribution in MCP-1⁺ cells (red) in CD68⁺ macrophages (green) and αSMA⁺ CAFs (white). Nuclei are stained with DAPI (blue). Data are mean ± SEM. *p < 0.05, **p < 0.01, ****p < 0.0001. Scale bars represent 100 μm. CAFs, cancer-associated fibroblasts; CCA, cholangiocarcinoma; iCCA, intrahepatic cholangiocarcinoma; SL, surrounding liver.

Next, we assessed the co-regulation of the TWEAK/Fn14 pathway and MCP-1 expression in CCA epithelia. We stratified PanCK⁺ epithelial tumour cells into Fn14⁺ and Fn14⁻ subsets, assessed the distribution of MCP-1⁺ cells in iCCA and further assessed these data with respect to tumour grade (Fig. 5C).

Importantly, MCP-1 expression was proportionally higher in Fn14⁺ vs. Fn14⁻ iCCA ducts in this cohort (Fig. 5D; n = 89). When stratified by tumour grade, this distribution was maintained in moderately differentiated grade 2 tumours ($p < 0.0001$, n = 32;) and poorly differentiated grade 3 tumours ($p = 0.0014$, n = 44;

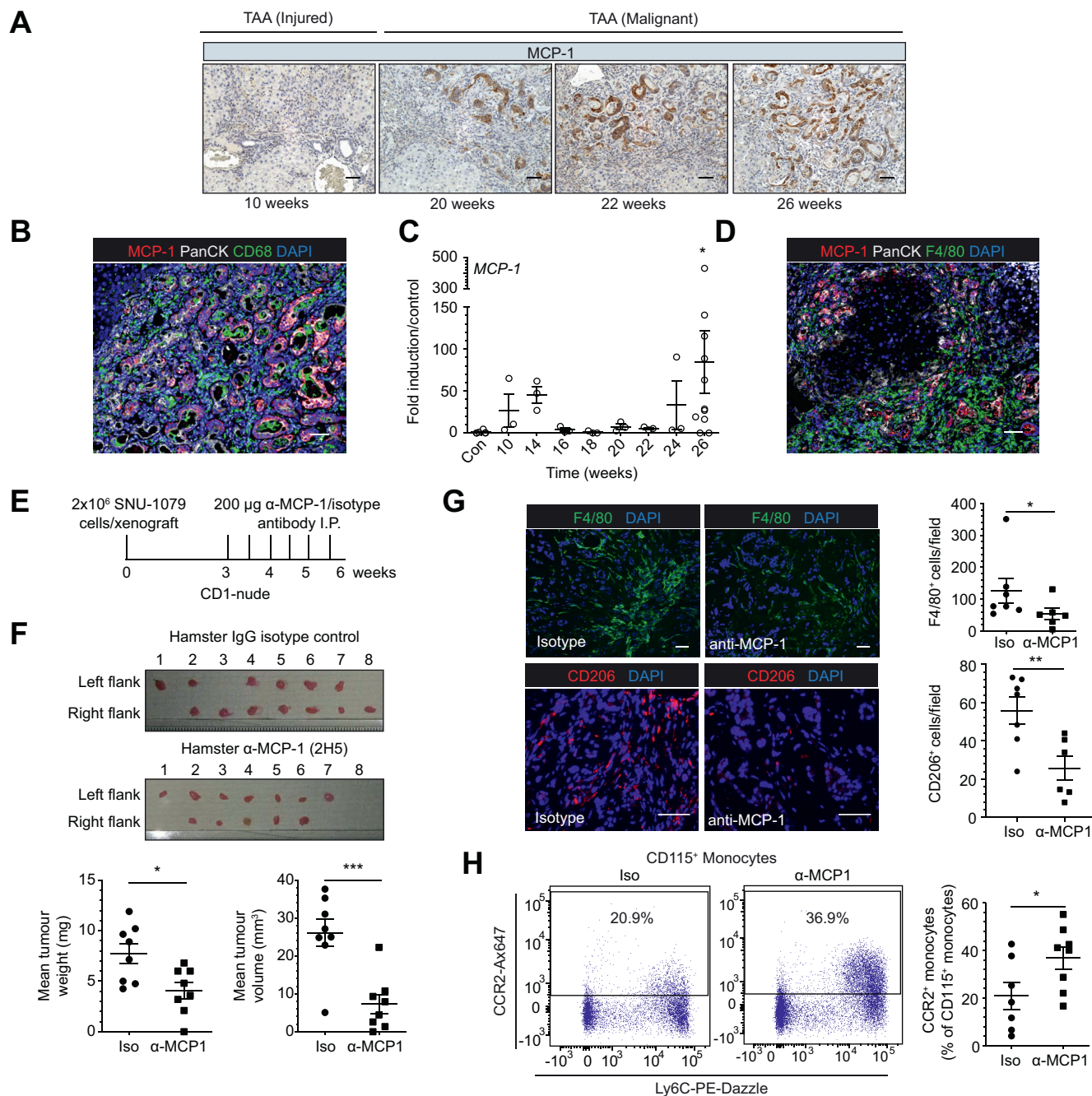


Fig. 6. MCP-1 in rodent CCA. (A) MCP-1 immunohistochemistry in liver from rats administered TAA for 10 weeks (injured, pre-malignant) up to 26 weeks. (B) Triple immunofluorescence reveals MCP-1⁺ tumour epithelia (PanCK⁺) with interspersed macrophage infiltration (CD68) in rat CCA. (C) mRNA expression of *MCP-1* in a time course of TAA treatment in rats (n = 3-11 per timepoint; Kruskal-Wallis test with Dunn's post-test). (D) Triple immunofluorescence reveals MCP-1⁺ tumour epithelia (PanCK⁺) with interspersed macrophage infiltration (F4/80⁺) in Krt19-CreERT26-eYFPp53^{Fl/Fl} mice administered TAA for 26 weeks to induce CCA. (E) Schematic of xenograft experiments. (F) SNU-1079 xenografts in CD-1 nude mice treated with control or anti-MCP-1 antibody (n = 8 per group; unpaired t-test). (G) Macrophage marker (F4/80, CD206) staining of SNU-1079 xenografts (n = 7 isotype vs. n = 6 treated with anti-MCP-1; Mann-Whitney U test). (H) Analysis of peripheral blood monocytes of xenografted CD-1 nude mice (n = 7 isotype vs. n = 8 anti-MCP-1 treated; unpaired t-test). Data are mean ± SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Scale bars represent 50 µm. CCA, cholangiocarcinoma; TAA, thioacetamide.

Fig. 5D). This preferential distribution of MCP-1⁺ cells to Fn14⁺ tumour epithelia was also observed in our cohort of archival sections from patients with iCCA and another commercially available CCA tissue microarray (Fig. S10B), suggesting an active TWEAK/Fn14/MCP-1 axis in a significant proportion of CCAs across 3 independent cohorts.

We further assessed MCP-1 protein expression in 2 key components of the tumour niche; TAMs (CD68⁺) and CAFs (α SMA⁺). MCP-1 was expressed by 18.26% of CD68⁺ TAMs and 18.52% of CAFs compared to 27.98% of malignant epithelia in this cohort of tumours (n = 88-90; Fig. 5E). Having confirmed MCP-1 upregulation in clinical samples, we explored the temporal modulation and functional significance of MCP-1 upregulation during CCA development in rodent models.

In rat CCA, small clusters of MCP-1⁺ cells were detected during early tumour development (Fig. 6A). MCP-1 was expressed specifically in PanCK⁺ epithelia in tumour niches containing large areas of accumulated TAMs (CD68⁺; Fig. 6B). MCP-1 mRNA also

exhibited the bi-phasic expression observed for *Fn14*, increasing again after peak *Fn14* expression was observed during tumour formation (Fig. 6C). MCP-1 was also expressed by CCA tumour cells in our previously described transgenic TAA CCA model²⁸ (Fig. 6D), suggesting a critical, conserved role for MCP-1 during multi-species CCA development.

To investigate the functional role of MCP-1 in recruiting macrophages to the CCA niche, we performed pharmacological blocking experiments using SNU-1079-generated human CCA cell xenografts (Fig. 6E). Mice receiving multiple injections of anti-MCP-1 antibody formed significantly smaller tumours (Fig. 6F), with 2.3-fold fewer intratumoural F4/80⁺ macrophages (Fig. 6G), and 2.2-fold fewer CD206⁺ macrophages (Fig. 6G), compared to control antibody-treated xenografts. We observed significantly more circulating MCP-1 receptor (CCR2⁺) monocytes in anti-MCP-1-treated animals (Fig. 6H). Although subcutaneous xenografts do not recapitulate the entire liver microenvironment, they enable modelling of interactions

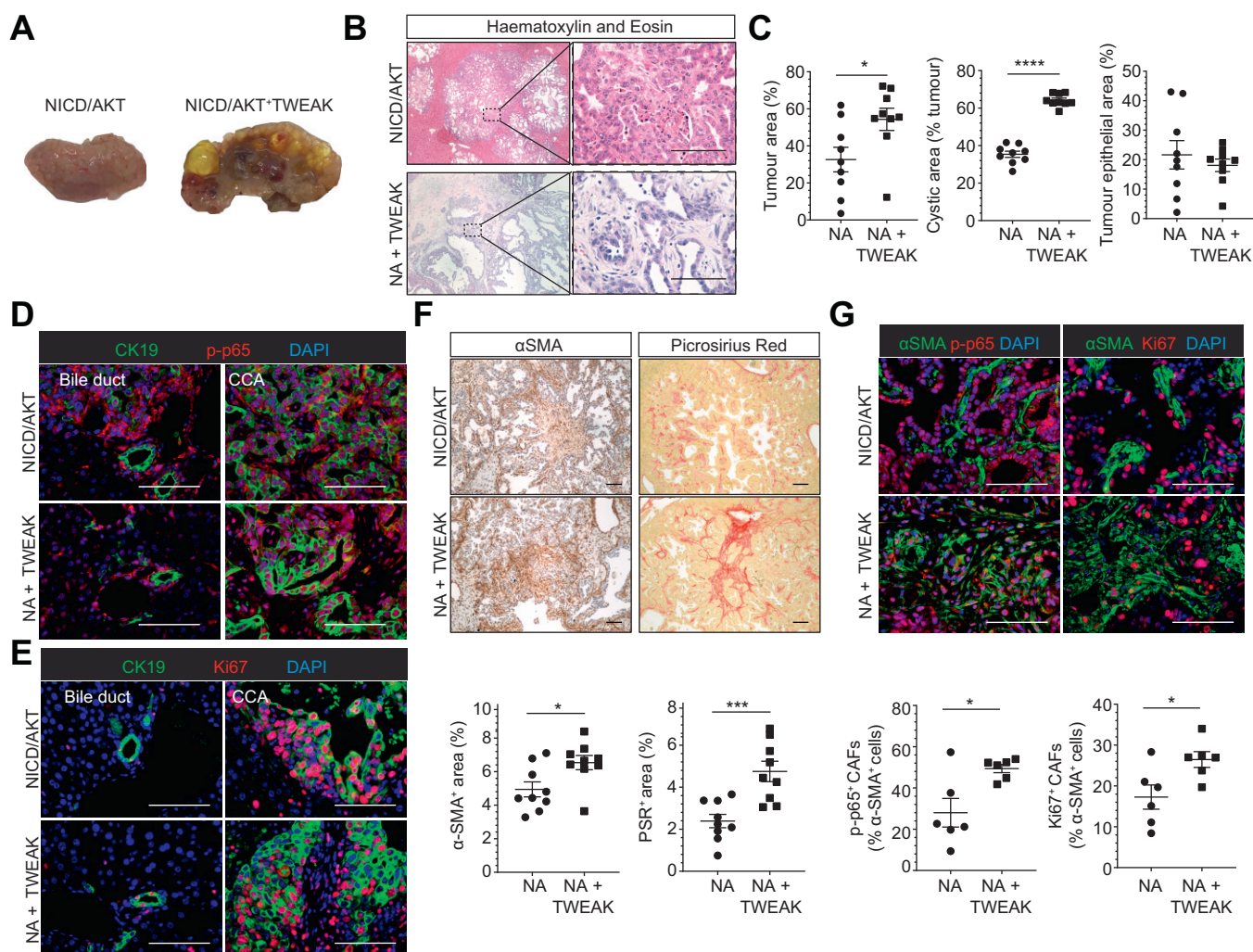


Fig. 7. TWEAK drives CAF proliferation in CCA. CCA was induced in mice with overexpression of Notch intracellular domain and AKT (NICD/AKT) with effects of TWEAK overexpression (NICD/AKT+TWEAK) assessed. (A) Gross morphology of livers. (B) Haematoxylin & eosin-stained liver sections. (C) Tumour area (Mann-Whitney *U* test) and cystic and tumour epithelial area quantification. (D) Staining of biliary tissue (CK19) and phosphorylated NF-kB p65 (p-p65) in normal and CCA areas. (E) Staining of biliary tissue and proliferation marker (Ki67). (F) Quantification of CAF (α SMA⁺) area and collagen deposition (Picrosirius red staining). (G) Staining of CAF (α SMA) and p-p65 or proliferation marker (Ki67). Data are mean \pm SEM. **p*<0.05, ****p*<0.001, *****p*<0.0001. Unpaired t-test unless otherwise stated. Scale bars represent 100 μ m. CAF, cancer-associated fibroblast; CCA, cholangiocarcinoma.

between circulating immune cells and human CCA cells. Thus, these data provide key functional context on the role of MCP-1 expression in CCA, with *in vivo* evidence that recruitment of TAMs occurs via chemoattraction of CCR2⁺ monocytes.

TWEAK signalling modulation affects tumour formation *in vivo*

To characterise the effects of TWEAK on CCA tumour development, we used a previously described system of NICD and AKT overexpression in hepatocytes to induce CCA in 6 weeks (combination referred to as NICD/AKT³⁰). We compared tumours in this model to NICD/AKT tumours overexpressing TWEAK (combination referred to as NICD/AKT+TWEAK). The construct used to overexpress TWEAK also expressed red fluorescent protein, facilitating concurrent assessment of the localisation of TWEAK-overexpressing cells (Fig. S11A). Macroscopic white, cyst-like lesions were observed on the surface of NICD/AKT livers (Fig. 7A and Fig. S12A), analogous to previously published observations.³⁰ TWEAK overexpression produced striking alterations in the appearance of livers, with sizeable bile-containing cysts observed on the surface (Fig. 7A, Fig. S12B).

Microscopic histological characterisations of tumours using blinded assessment by an independent, specialist liver histopathologist revealed features that were consistent with this model³⁰ tumours consisted of multifocal nodular lesions, often coalescing, precluding quantification of tumour number. Tumours were variably cystic and micropapillary epithelial neoplasms with cytological epithelial features in keeping with malignancy, with TWEAK overexpression increasing the cystic content of these tumours (Fig. 7B, Fig. S11B). Formal observer-independent quantification of tumour elements showed that TWEAK overexpression increased the total tumour area and cystic percentage of tumours (Fig. 7C). The tumour epithelial area was not altered by TWEAK overexpression (Fig. 7C). Accordingly, CK19⁺ epithelium with active, nuclear localisation of phosphorylated NF- κ B p65 in either bile duct or CCA tissue was similar in both conditions (Fig. 7D), and most CCA cells were proliferating (Ki67⁺; Fig. 7E), presumably as a result of AKT overexpression.³⁰ We did not find an association between the tumour cystic grade and the proportion of Fn14⁺ cells in CCA cells or CAFs in patient tissues (Fig. S13).

Complementing our xenograft results, we observed increases in innate immune cells with TWEAK overexpression, including CD11b⁺ monocyte/neutrophils that clustered within the tumour niche in cystic tumour areas (Fig. S11C), and a 2-fold increase in CD206⁺ macrophage numbers (Fig. S11C), as well as upregulation of GM-CSF in the liver and plasma (Fig. S11D).

TWEAK overexpression also significantly affected the CAF subcompartment of the CCA niche, previously shown to express Fn14⁺ in patient ICCAs (Fig. 1). We detected a 1.32-fold increase in the α SMA⁺ CAF area and the Picosirius red-positive collagen area in NICD/AKT+TWEAK tumours (Fig. 7F). TWEAK activation of canonical NF- κ B signalling, demonstrated by an increased proportion of CAFs expressing nuclear phospho-p65 (Fig. 7G), has previously been shown to drive hepatic stellate cell proliferation in chronic liver injury.²³ We observed a 1.53-fold increase in proliferating Ki67⁺/ α SMA⁺ CAFs in TWEAK-overexpressing CCAs (Fig. 7G).

Having established novel roles of TWEAK in inflammatory and fibrogenic niche development in CCA, critical components of a tumour-permissive environment,³¹ we assessed TAA-mediated

chronic liver disease in homozygous *Fn14* knockout mice compared to wildtype *Fn14*-expressing littermate controls (Fig. S14A). Following 6 months of TAA injury, significant macroscopic tumour formation was observed in *Fn14* wildtype mice (12/12 animals with 1 or multiple tumours; 2, <2 mm; 9, 2–5 mm, 1, >5 mm diameter), while 1/9 *Fn14* knockout mice displayed an early tumour of less than 2 mm in diameter (Fig. S14B). Concomitant with tumour inhibition in *Fn14* knockout mice, we observed a reduction in PanCK⁺ cells as well as F4/80⁺ and CD206⁺ macrophages (Fig. S14C, 14 D). MCP-1, GM-CSF, IL-6 and KC/Gro remained at steady-state levels in 6-month TAA-treated mice (Fig. S14E). These data support our hypothesis that TWEAK/Fn14 signalling supports hepatic tumour development by playing a pivotal role in niche establishment during chronic liver injury.

Discussion

During chronic liver injury, macrophage-produced TWEAK drives proliferation of Fn14⁺ cholangiocytes (to initiate hepatic regeneration^{21,22,32}) and α SMA⁺ myofibroblasts (affecting extracellular matrix deposition in damaged liver areas by regulating their cell numbers^{23,24}). Macrophages comprise the majority of the inflammatory cell infiltrate in the CCA stroma,^{15–17,19} providing key signals (such as Wnt ligands) to induce growth and apoptosis resistance,^{6,7} as well as cytokines (including IL-6, TNF and TGF- β 1) to promote metastatic progression.^{15,17} We hypothesised that TWEAK/Fn14-induced downstream signalling represents a significant pathway, supporting CCA growth and maintenance.

Through corroboration of transcriptomic data from multiple independent CCA patient cohorts and characterisation of patient samples, we demonstrated upregulation of Fn14 in CCA, on tumour epithelial cells and CAFs, compared to non-involved liver tissue. Significantly, a subset of TWEAK-expressing TAMs localised within the CCA niche, suggesting interplay between ligand-expressing niche and receptor-expressing tumour/niche via TWEAK/Fn14, potentiating therapeutic targeting. We demonstrated that TWEAK/Fn14 pathway elements are progressively upregulated in rodent CCA tissues. Previous studies reported proliferation of biliary epithelial, and HCC cells, in response to TWEAK.^{21,22,25,32} We explored the effects of TWEAK in CCA lines and found that TWEAK modulated NF- κ B signalling in all investigated CCA cell lines, but not HepG2 HCC cells. However, this signal led to cell line-specific cellular responses, suggesting more complex functions for TWEAK/Fn14 signalling in CCA.

In chronic injury, NF- κ B controls the expression of a multitude of chemokines and growth factors that regulate liver inflammation and repair, including MCP-1,³³ while aberrant expression of NF- κ B pathway components results in spontaneous liver fibrosis and eventual HCC in genetic mouse models.^{34–36} Although TWEAK-responsive NF- κ B pathway activation was seen in all CCA cell lines we assessed, we did not observe consistent proliferative effects, as reported in other liver cell types.^{21,22,25} In response to TWEAK stimulation, CCA cells secreted proinflammatory chemokines and growth factors, suggesting TWEAK can regulate CCA niche development. We further explored the functional role of MCP-1, which drives inflammatory macrophage recruitment to sites of liver injury via its receptor CCR2.^{37,38} Disrupting MCP-1/CCR2 has proven effective in inhibiting TAM accumulation and tumour development in pre-clinical HCC models.^{39,40} We observed *in vitro* TWEAK-inducible

MCP-1 expression and detected MCP-1 in tumour cells in multi-species CCA. MCP-1 inhibition reduced SNU-1079 xenograft size, with accumulation of CCR2⁺ monocytes in peripheral blood and decreased TAMs, providing evidence for an MCP-1-mediated macrophage recruitment to the tumour niche by CCA cells. Further support for this axis having a functional role is provided by our data from TAA-treated *Fn14* knockout mice, which displayed significantly reduced macrophages and drastically inhibited or delayed tumorigenesis.

We also report a novel function of TWEAK in the liver in driving the secretion of factors from CCA cells that alter macrophage phenotype. CCA cells actively educated macrophages towards a TAM-like phenotype, expressing a mixture of classically activated and alternative activation markers, as well as upregulating molecules involved in matrix remodelling.¹⁸ In TWEAK-high responsive CCA cell lines (SNU-1079 and CC-SW-1), we observed an increased ability to pattern macrophages towards a TAM-like 'M2-skewed' phenotype with CD206 and proinflammatory gene expression including IL-6, TNF and MCP-1, reminiscent of TAMs observed in CCA.^{7,17,19} Additionally, CCA-patterned macrophages also upregulated the scavenger receptor MARCO, a marker of immunosuppressive TAMs in many tumour types.⁴¹ Data from progressive CCA in rats demonstrated that *Fn14* and MCP-1 upregulation is co-regulated early in CCA development. Furthermore, TWEAK overexpression in CCA promoted a dramatic alteration in tumour phenotype by inducing expansion of collagen-producing CAFs, which express *Fn14* in a significant proportion of patient ICCAs. By driving inflammatory chemokine production, altering macrophage phenotype via crosstalk with CCA epithelia and promoting fibroblastic growth within the CCA microenvironment via a direct action of TWEAK on CAF proliferation, upregulation of TWEAK/*Fn14* signalling appears to be an early driver, promoting the development of a niche that supports tumour growth. Our data using genetic knockout or antibody inhibition of TWEAK downstream events highlight the potential for clinically relevant therapeutic targeting. A humanised antibody against TWEAK, RG7212, is currently being investigated for its efficacy in treating late-stage *Fn14*⁺ solid tumours in malignancies including colorectal cancer, melanoma and a cohort of 3 patients with CCA, with antibody treatment well-tolerated. Notably, one of the desired actions of antibody treatment is to reduce serum MCP-1 levels.^{42,43}

In addition to affecting the CAF and TAM niche compartments, we also report TWEAK-induced secretion of molecules involved in blood vessel development and angiogenesis from CCA cell lines. Macrophages patterned by TWEAK-inducible factors from SNU-1079 cells also upregulated *VEGF-α* mRNA. Significantly, VEGF-A and VEGF-C from CAFs are important mediators of lymphangiogenesis in CCA,⁴⁴ which is correlated with poor patient outcomes.⁴⁵ We also observed some vascular *Fn14* expression in rat and human CCA. TWEAK can stimulate endothelial cell proliferation, following *Fn14* upregulation in response to VEGF-A and FGF-2.⁴⁶ Given our *in vitro* proteomic and macrophage patterning results, combined with observation in patient samples, there is future scope to ascertain the role of TWEAK/*Fn14* signalling in metastatic progression by acting directly on the endothelium, and indirectly via secretion of proteins from tumour cells, tumour-conditioned TAMs and CAFs, which promote tumour progression via pathways such as VEGF-A and VEGF-C.

Our study provides a detailed and novel mechanistic framework of how the TWEAK/*Fn14* pathway is involved in building a tumour-permissive niche, acting on TAMs and CAFs in CCA, which both drive chemotherapy resistance.⁴⁷ Given the significant proportion of patients with CCA exhibiting aberrant upregulation of *Fn14*, targeting TWEAK/*Fn14* may provide avenues to interrupt epithelial-stromal crosstalk to create novel therapeutics for a cancer where effective treatments are urgently required.

Abbreviations

α SMA, α -smooth muscle actin; CAF, cancer-associated fibroblast; CCA, cholangiocarcinoma; CCR2, C-C chemokine receptor type 2; CK, cytokeratin; CX3CL1, (C-X3-C motif) ligand 1; *Fn14*- fibroblast growth factor-inducible 14; GM-CSF, granulocyte macrophage colony-stimulating factor; HCC, hepatocellular carcinoma; HMDM, human monocyte-derived macrophage; HPC, hepatic progenitor cell; ICCA, intrahepatic CCA; IL, interleukin; MARCO, macrophage receptor with collagenous structure; MCP-1, monocyte chemoattractant protein 1; M-CSF, macrophage colony-stimulating factor; MMP, matrix metalloprotease; NICD, Notch intracellular domain; SDF, stromal-derived factor; TAA, thioacetamide; TAM, tumour-associated macrophage; TCGA, The Cancer Genome Atlas; TGF- β 1, transforming growth factor- β 1; TIMP, tissue inhibitors of metalloproteases; TNF, tumour necrosis factor; TREM-2, triggering receptor expressed on myeloid cells-2; TWEAK, TNF-like weak inducer of apoptosis.

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Conflict of interest

S.J.F. is supported by funds from Wellcome Trust UK, Medical Research Council, UKRMP and Syncona Ltd.

Please refer to the accompanying ICMJE disclosure forms for further details.

Authors' contributions

Conceptualisation and design (B.D., E.J., S.F.-G., R.V.G., L.B., J.T.P., S.J.F.). Data generation (B.D., E.J., S.F.-G., T.K., J.G.-T., T.-Y. M., A.M.K., L.B., R.V.G., A.R., D.K.), Data analysis and interpretation (B.D., J.G.-T., T.K., L.B., R.V.G., L.C., E.O.D., A.M.K., P.S.-L., J.T.P., S.J.F.). Manuscript preparation (B.D., J.T.P., S.J.F.). Review and editing (B.D., J.T.P., J.K.O., G.A.R., S.J.F.). Funding acquisition (J.T.P., J.K.O., G.A.R., S.J.F.).

Data availability statement

Mass spectrometry data was deposited on the MassIVE repository (<https://massive.ucsd.edu/ProteoSAFe/static/massive.jsp>, accessible at Proteome Exchange (<http://www.proteomexchange.org/>; Accession: PXD015317). All other data are available upon reasonable request.

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Supplementary data

Supplementary data related to this article can be found online at <https://doi.org/10.1016/j.jhep.2020.11.018>.

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Author names in bold designate shared co-first authorship

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