Lactate transport inhibition therapeutically reprograms fibroblast metabolism in experimental pulmonary fibrosis

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# Abstract

# Keywords

# Introduction

Idiopathic pulmonary fibrosis (IPF) is a chronic and progressive lung disease with high mortality and limited therapeutic options. IPF affects approximately 150,000 patients in the U.S. with a median survival of 3-5 years (1–3). Currently approved pharmacotherapies for IPF are limited to the antifibrotics pirfenidone and nintedanib that slow, but do not stop, disease progression (4, 5), leaving lung transplantation as the only option available to eligible patients with progressive disease. The limited efficacy of antifibrotic therapies emphasizes the need for novel therapeutic approaches targeting different features of IPF pathobiology.

Accumulating evidence suggests that metabolic reprogramming may be one such therapeutic vulnerability in IPF (6, 7). Lung fibrosis is driven by the excessive deposition of extracellular matrix by myofibroblasts (3). Fundamental changes in myofibroblast metabolism support myofibroblast differentiation and extracellular matrix production (8–12). In particular, increased glycolysis and lactate production have been observed in IPF myofibroblasts *ex vivo* and following TGF-β1 (TGFβ)-induced myofibroblast differentiation *in vitro* (8, 9, 13, 14). These metabolic changes are critical for fibrogenesis, as small molecule inhibitors of glucose uptake, glycolysis, and lactate fermentation prevent myofibroblast differentiation *in vitro* and attenuate pulmonary fibrosis in animal models (8–10, 13, 15, 16). Unfortunately, low target affinities, poor specificity, narrow therapeutic indices, and common genetic resistance have all hampered the translation of these investigational compounds for clinical use (17–19). Moreover, the molecular mechanisms by which these metabolic inhibitors attenuate the myofibroblast differentiation transcriptional program remain unclear. In order to leverage metabolic therapies for IPF, more targeted and better characterized drugs must be developed.

Toward this end, we sought to characterize the effects of a novel metabolic approach - inhibition of lactate transport - on myofibroblast differentiation and experimental pulmonary fibrosis. Lactate must be secreted to sustain glycolysis in myofibroblasts. A family of monocarboxylate transporters (MCT1-4) maintains lactate homeostasis and small molecule inhibitors of these transporters have been under active clinical development for oncologic applications where glycolytic reprogramming also features prominently in disease pathobiology (20, 21). Importantly, compared to previously investigated inhibitors of glycolysis, MCT inhibitors exhibit favorable pharmacologic profiles and have successfully translated to human clinical trials (22). Before the promise of this therapeutic approach in IPF may be realized, however, the preclinical efficacy and molecular mechanisms-of-action of lactate transport inhibitors must be demonstrated experimentally.

In this work, we evaluated the contribution of lactate transporters to experimental pulmonary fibrosis. We found increased expression of the lactate transporters MCT1 and MCT4 IPF patient lungs, consistent with increased glycolysis previously observed. Inhibition of these transporters attenuated bleomycin-induced lung fibrosis *in vivo* and TGFβ-induced myofibroblast differentiation *in vitro*, where MCT4 inhibition demonstrated increased therapeutic efficacy. Using metabolomics, stable isotope tracing, and high-resolution spatial metabolomic imaging, we find that lactate transport inhibition promotes glucose oxidation. These metabolic changes signal, in part, through increased protein lactylation and decreased intracellular reactive oxygen species (ROS) production. Based on these findings, we report a novel MCT4 inhibitor suitable for human clinical studies. Together, these data illuminate a novel approach to disrupt the metabolic program fueling the exuberant fibrosis at the core of IPF and provide proof-of-concept to target lactate transporters in the treatment of this deadly disease.

# Results

## MCT expression increases in human pulmonary fibrosis and experimental models

Of the four lactate transporters, MCT1 and MCT4 are the most highly expressed in the lung (23). Based on this observation, we characterized MCT1 and MCT4 expression in human IPF lung explants obtained at the time of transplantation. Consistent with a pathologic role for MCT1 and MCT4 in IPF, we found significantly increased expression of these proteins in human IPF lung compared to non-fibrotic control samples (**Figure 1A-B**). These findings were recapitulated in experimental pulmonary fibrosis where intratracheal bleomycin increased both MCT1 and MCT4 expression (**Figure 1C-D**).

A defining feature of IPF is the activation of tissue myofibroblasts, which are characterized by the *de novo* expression of smooth muscle α-actin (α-SMA); stress fiber formation; and increased migration, contraction, and extracellular matrix production (7, 9, 24). TGFβ is the most potent inducer of myofibroblast activation *in vitro* and *in vivo*. TGFβ-dependent α-SMA expression is a well-accepted and widely utilized model of myofibroblast activation relevant to pulmonary fibrosis (10, 25–27). Consistent with our findings in human IPF lungs, we observed increased expression of MCT1 and MCT4 in normal human lung fibroblasts following TGFβ treatment (**Figure 1E-F**). These findings are consistent with increased expression of other glycolytic enzymes and the associated metabolic changes that have been previously observed in these cells (9). Together, these data demonstrate that pulmonary fibrosis is associated with increased expression of lactate transporters in the lung generally and in myofibroblasts specifically.

## Myofibroblast differentiation *in vitro* requires lactate transport

Using RNA interference and pharmacologic approaches, we next tested whether MCT expression and activity were required for myofibroblast differentiation *in vitro*. Lung fibroblasts were transfected with siRNA targeting MCT1 and MCT4 separately and together. After 24 h, the cells were treated with TGFβ for 48 h to induce myofibroblast differentiation. The siRNAs reduced lactate transporter protein levels > 80% (**Figure 2A-B**). Decreasing MCT1 or MCT4 expression caused a marked reduction in TGFβ-stimulated α-SMA expression. Notably, siMCT1 also decreased MCT4 expression. Interestingly, the mRNA sequence homology of these transporters is low and the MCT1 siRNA sequences do not match the MCT4 mRNA sequence, perhaps suggesting a post-translational explanation for this phenomenon. No adverse effects of lactate transporter knockdown on cell viability were observed, and siMCT1 significantly increased cell count in both control and TGFβ-treated cells (**Supplemental Figure 2A**).

Given the reduction of MCT4 expression following siMCT1 treatment, we next evaluated the effects of pharmacologic MCT inhibitors on myofibroblast differentiation. AZD3965 is a high-affinity (*Ki* 1.6 nM) inhibitor of MCT1 (28). VB124 is a recently developed high-affinity (IC50 19 nM) inhibitor of MCT4 (21). IPF lung fibroblasts were differentiated with TGFβ in the presence of these MCT inhibitors (**Figure 2C-D**). MCT4 inhibition by VB124 alone, or in combination with AZD3965, decreased Col1a1 and α-SMA expression. These effects were also observed in normal lung fibroblasts where AZD3965 as well as VB124, separately or together, decreased α-SMA expression (**Figure 2E-F**). AR-C155858, which is a high-affinity(*Ki* 2 nM) inhibitor of both MCT1 and MCT2 (29), also decreased α-SMA expression alone and in combination with VB124 (**Supplemental Figure 2B-C**). Pharmacologic MCT inhibition did not affect cell counts over 48 h of treatment (**Supplemental Figure 2D-E**). As anticipated, decreased Col1a1 and α-SMA expression was associated with decreased myofibroblast contractility as assessed by gel contraction assay (**Figure 2G-H**). Together, these data indicate that MCT expression and activity are required for myofibroblast differentiation *in vitro*.

## MCT inhibition reprograms myofibroblast metabolism

MCTs are critical regulators of cellular lactate homeostasis. MCT1 is considered to be the main lactate importer in cells that use lactate to fuel oxidative phosphorylation or gluconeogenesis and is ubiquitously expressed. MCT1 also mediates lactate export in glycolytic cells (30, 31). MCT4 is considered to be the main lactate exporter in glycolytic cells and is up-regulated by hypoxia-inducible transcription factors (30, 32). MCT4 can also function as a lactate importer with a KM ~1 mM (33).

To evaluate the metabolic consequences of lactate transporter inhibition, we measured extracellular lactate in the conditioned medium from cells treated with MCT siRNA or pharmacologic inhibitors (**Figure 3A-B**). Silencing MCT1 and MCT4, separately or together, decreased TGFβ-stimulated lactate efflux in lung fibroblasts (**Figure 3A**). Silencing both transporters was required to block TGFβ-stimulated lactate efflux completely. By contrast, pharmacologic inhibition of either MCT1 or MCT4 did not decrease TGFβ-stimulated lactate efflux (**Figure 3B**), and inhibition of both transporters was required to decrease extracellular lactate. Similarly, inhibition of MCT1, MCT2, and MCT4 with the combination of AR-C155858 and VB124 was required to prevent increases in lactate efflux (**Supplemental Figure 3A**). Compared to lactate production, the effect of MCT inhibitors on extracellular glucose was less pronounced, although we did observe a trend toward decreased glucose consumption by cells treated with both AZD3965 and VB124 (**Supplemental Figure 3B**). These findings are consistent with prior studies suggesting compensatory roles for MCT1 and MCT4 in lactate export (34). Moreover, these data also suggest that inhibition of glycolysis is not the mechanism by which lactate transport inhibition attenuates myofibroblast differentiation.

To further interrogate the metabolic consequences of lactate transport inhibition, we next measured proton efflux (PER) and oxygen consumption (OCR) rates of lung fibroblasts treated with TGFβ in combination with MCT inhibitors (**Figure 3C, Supplemental Figure 3C**). Since MCTs co-transport protons with lactate, PER correlates with lactate efflux. Consistent with prior reports (8–10, 16, 35), we observed increases in both PER CR following TGFβ stimulation for 48 h, indicating increases in both glycolysis and oxidative phosphorylation. Similar to our direct measurements of extracellular lactate and glucose, simultaneous treatment with AZD3965 and VB124 was required to reduce PER. As anticipated, this decrease in PER was associated with a commensurate increase in OCR as myofibroblasts shifted their metabolism from glycolysis to oxidative phosphorylation. Unexpectedly, an increase in OCR was observed with AZD3965 and VB124 when administered individually. Indeed, the primary consequence of MCT1 or MCT4 inhibition alone was an increase in cellular ATP production rates driven by an increase in oxidative phosphorylation (**Figure 3D-E**). MCT inhibition decreased spare respiratory capacity, indicating that the basal respiratory rate of treated cells was closer to their maximal oxidative capacity (**Supplemental Figure 3D**). No significant differences in glycolytic capacity or electron transport chain coupling efficiency were observed (**Supplemental Figure 3D**). Together, these data suggest that the primary metabolic consequence of MCT inhibition is the activation of oxidative phosphorylation rather than inhibition of glycolysis.

To develop additional support for this hypothesis, we performed liquid chromatography-mass spectrometry-based profiling of extracellular and intracellular metabolites from cells treated with AZD3965 and VB124. As suggested by the Seahorse analysis, inhibiting a single lactate transporter had modest effects on extracellular metabolite levels (**Figure 4A-D, Supplemental Figure 4**). This analysis confirmed the results of extracellular lactate measurements by enzyme assay, which showed dual inhibition was required to decrease lactate efflux (**Figure 4B**). In addition to lactate, dual lactate transporter inhibition also had broader impacts on amino acid fluxes (**Figure 4C-D**). Several metabolites were differentially regulated by TGFβ treatment (**Supplemental Figure 4A**) and dual lactate transport inhibition, including leucine, alanine, ornithine, and ketoleucine.

Similar effects on intracellular metabolites were observed. Principal components (PC) analysis demonstrated excellent clustering of treatment groups with the drug effect corresponding to PC1 and the TGFβ treatment effect corresponding to PC2. Similar to the extracellular flux results, the magnitude of drug-induced perturbations were increased from MCT1 to MCT4 to combined inhibition (**Figure 4E**), as demonstrated by intracellular lactate levels (**Figure 4F**). As expected from measures of extracellular lactate following MCT inhibition, intracellular lactate accumulation increases modestly with MCT4 inhibition and markedly with MCT1/4 inhibition. TGFβ treatment was associated with diverse changes in the intracellular metabolomic profile of treated fibroblasts (**Supplemental Figure 4C-D**). The effect of AZD3965 alone on intracellular metabolite levels was modest (**Supplemental Figure 4G-H**). By contrast, MCT4 inhibition by VB124 alone (**Supplemental Figure 4K-L**) or combined with AZD3965 (**Figure 4G-H**) caused substantial perturbations to intracellular metabolism. Specifically, we observed enrichment of the glycolysis and tricarboxylic acid (TCA) cycle metabolite sets with MCT4 inhibition. Together, these data indicate that inhibition of lactate export leads to accumulation of upstream glycolytic intermediates that are rerouted to mitochondrial oxidative metabolic pathways.

To test this hypothesis, we next labeled lung fibroblasts with [U-13C6]-glucose (8 mM) in medium containing lactate (2 mM), glutamine (1 mM), and pyruvate (1 mM) during TGFβ stimulation and treatment with MCT inhibitors (**Figure 4I**). TGFβ increases 13C incorporation from glucose into pyruvate, lactate, citrate, succinate (SUC), and malate (MAL), consistent with increased flux from glucose into the TCA cycle. While AZD3965 had little impact on these labeling patterns, MCT4 inhibition significantly increased the fractions of these metabolites labeled by glucose, providing direct evidence for a proportional increase in glucose oxidation following MCT4 inhibition, consistent with the bioenergetic and steady-state metabolomics experiments described above.

Increased metabolite labeling by glucose must by offset by decreased labeling from other substrates. Since recent data suggest that lactate is a major oxidative fuel source in the lung (36–38), we reasoned that MCT inhibition would decrease oxidation of exogenous lactate. To test this, lung fibroblasts were cultured with [U-13C3]-lactate (2 mM) in medium containing naturally labeled glucose, glutamine, and pyruvate (**Figure 4J**). Extracellular [U-13C3]-lactate labeled ~ 50% of intracellular pyruvate and lactate at baseline with significant downstream incorporation into TCA metabolites. This labeling was decreased following TGFβ treatment, mirroring increased fractional labeling from glucose. MCT inhibition had no impact on fractional labeling of TCA intermediates by [U-13C]-glutamine (**Supplemental Figure 4M**). Interestingly, MCT4 inhibition alone or with AZD3965 decreased 13C labeling of intracellular metabolites by lactate, emphasizing the importance of bi-directional lactate transport mediated by MCTs. Similar to our measurements of extracellular lactate, the effects of MCT inhibition were more pronounced when both inhibitors were used simultaneously, again demonstrating some functional redundancy of MCT1 and MCT4 in lung fibroblasts.

## MCT inhibition attenuates pro-fibrotic transcriptional programs

To identify anti-fibrotic transcriptional programs mediated by MCT inhibition, we performed RNA-seq on lung fibroblasts treated with TGFβ in combination with AZD3965 or VB124 (**Figure 5**). Principal components analysis (PCA) of the transcriptional changes mirrored the metabolomic findings. The first principal component corresponded to TGFβ treatment, accounting for 71% of the overall variance, while MCT4 inhibition, either alone or in combination with MCT1 inhibition aligned with the second principal component (**Figure 5A**). Samples treated with the MCT1 inhibitor AZD3965 were similar to vehicle-treated controls. Differential expression analysis of TGFβ-treated cells identified the expected increased expression of extracellular matrix proteins (**Supplemental Figure 5A**) and enrichment of the epithelial-to-mesenchymal (EMT) gene set, among others (**Figure 5B**). Consistent with the PCA results, only GRIK4 and BRI3 were differentially expressed following AZD3965 (**Supplemental Figure 5B**). By contrast, VB124, alone (**Supplemental Figure 5C**) or in combination with AZD3965 (**Figure 5C**), demonstrated more substantial reprogramming of myofibroblast transcription with 443 of 24,902 genes (2%) differentially expressed at an FDR < 0.05.

Co-administration of either AZD3965 or VB124 reversed TGFβ-dependent enrichment of the EMT gene set, which is the Hallmark gene set containing genes related to fibrosis (**Figure 5B**). Leading edge analysis of the EMT gene set identified seven genes shared among all three comparisons (*i.e.*, genes increased by TGFβ and decreased by both AZD3965 and VB124) (**Figure 5D**). These genes include: biglycan (BGN), COL6A3, Frizzled 8 (FZD8), matrix Gla protein (MGP), Prostate Transmembrane Protein, Androgen Induced 1 (PMEPA1), TIMP metallopeptidase inhibitor 1 (TIMP1), and tenascin-C (TNC). Many of these genes contribute to the pathobiology of pulmonary fibrosis or serve as biomarkers of disease or treatment response (39–43). Together, these data suggest lactate transport inhibitors attenuate the pro-fibrotic transcriptional program in TGFβ-treated LFs.

## Lactate transport inhibition may signal through histone lactylation

We next sought to identify the signaling mechanism(s) linking lactate transport inhibition to anti-fibrotic transcriptional programs. Since increasing intracellular lactate was associated with more potent inhibition of α-SMA expression, we first treated cells with TGFβ in combination with extracellular lactate (10 mM). A prior study demonstrated that extracellular lactate modestly increased α-SMA expression in the absence of TGFβ (13). We found that extracellular lactate did not impact α-SMA expression in TGFβ-treated LFs (**Figure 6A-B**), suggesting that accumulation of intracellular lactate alone does not mediate the anti-fibrotic effects of MCT inhibition.

Prior work has also linked inhibition of glycolysis and lactate production to hypoxia-inducible factor 1α activation (HIF-1α), which contributes to myofibroblast differentiation (10, 13). We found maximal HIF-1α activation 6 h following TGFβ stimulation. At this time point, HIF-1α protein levels were similar across vehicle-, AZD3965-, and VB124-treated cells (**Figure 6C-D**). In LFs treated with dual inhibitors, HIF-1α protein was increased compared to vehicle, consistent with enrichment of the “Hypoxia” gene set in our RNA-seq data (**Figure 5B**). These findings, in light of prior studies, indicate that lactate transport inhibition acts downstream of HIF-1α-dependent transcriptional programs to inhibit myofibroblast differentiation.

Next, we examined TGFβ-dependent signaling. TGFβ activates both SMAD and non-SMAD signaling pathways through a cascade of protein phosphorylation events. MCT inhibitors did not decrease Smad3 or ERK phosphorylation after 48 h of TGFβ stimulation (**Figure 6E-H**).

Post-translational protein modification of histone lysine residues by lactylation has been identified as a novel mechanism of metabolic regulation of gene expression (44). Given the increase in intracellular lactate following MCT4 inhibition, we measured H3 histone lactylation by immunoblot (**Figure 6I-J**). We found that inhibition of both MCT1 and MCT4 increased histone lactylation and may account for some of the transcriptional changes observed following these treatments.

## Lactate transport inhibition contributes to antioxidant defense

Lactate metabolism is closely coupled to cellular redox homeostasis through its metabolism by lactate dehydrogenases, which transfer electrons from lactate to NADH. Since prior studies have suggested that reactive oxygen species (ROS) are important for TGFβ-mediated gene expression (45, 46), we next examined the impact of lactate transport inhibition on cellular redox homeostasis. Consistent with an increase in intracellular lactate with MCT4 inhibition, we observed a concomitant increase in intracellular NADH/NAD+ (**Figure 7A**), which was associated with a reduction in total ROS as measured by the CellROX fluorescent probe (**Figure 7B**). AZD3965, but not VB124, also decreased mitochondrial superoxide production (**Supplemental Figure 7B**). By contrast, the NADPH/NADP+ was unchanged by either TGFβ or MCT inhibitors (**Supplemental Figure 7A**). Notably, we did not observe TGFβ-dependent increases in total ROS production in our model system.

Proline biosynthesis has been previously suggested as a mechanism by which NIH-3T3 fibroblasts prevent excessive ROS accumulation following TGFβ stimulation (46). In this model, proline synthesis from glutamine consumes reducing equivalents from NADPH and NADH, thereby ameliorating reductive stress and decreasing ROS production. Compared to this prior study, we did not find that TGFβ increased proline in primary lung fibroblasts (**Supplemental Figure 7C**). Overall, the fractional labeling of proline from [U-13C5]-glutamine was modest at 10% compared to the 40% previously reported (**Supplemental Figure 7D**). While we observed trends toward increased proline production from glutamine with MCT4 inhibition, this mechanism seems unlikely to account for the effects of MCT inhibitors on ROS generation.

## MCT inhibition decreases experimental pulmonary fibrosis

Based on our *in vitro* data suggesting an anti-fibrotic effect of lactate transporter inhibition, we next tested the efficacy of MCT inhibitors in the bleomycin-induced mouse model of pulmonary fibrosis. Mice received 1.2 U/kg bleomycin by intratracheal administration. After seven days, the animals began treatment with AZD3965 (100 mg/kg twice daily) or VB124 (30 mg/kg once daily) or vehicle by oral gavage (**Figure 8A**). We anticipated that dual inhibition would likely be toxic *in vivo* and did not assess the combination of inhibitors. Compared to vehicle, mice treated with VB124 had increased weight recovery 21 days after bleomycin administration (**Supplemental Figure 8**). Lung mechanics were improved by ~ 50% of baseline compared to vehicle controls following 14 days of MCT inhibitor treatment (**Figure 8B-C**). Consistent with improved elastance and compliance measures, histologic fibrosis severity assessed by Ashcroft scoring (47) also improved.

## MCT inhibition reprograms lung metabolism *in vivo*

To investigate metabolic perturbations following lactate transporter inhibition *in vivo*, we next performed metabolomic profiling of lung and plasma from mice treated with bleomycin and MCT inhibitors (**Supplemental Figure 9.1**). While bleomycin treatment substantially altered the lung metabolic profile, treatment with AZD3965 or VB124 had little additional impact on total metabolite levels. Unlike bleomycin alone or following AZD3965 treatment, VB124 treatment was associated with significant changes in several circulating metabolites (**Supplemental Figure 9.1I**). Among these, VB124 significantly increased circulating lactate, while AZD3965 was associated with decreased circulating lactate (**Figure 9A**). This pattern was also reflected in the lung, where only modest changes were observed following bleomycin, contrary to prior reports (13). Given the impact of our treatments on circulating lactate, we calculated the ratio of lung-to-plasma lactate. This analysis demonstrated the expected increase in lactate in fibrotic lungs with levels returning to baseline following the addition of VB124 (**Figure 9A**).

We were surprised to observe a relative paucity of metabolic changes in whole lung lysates following MCT inhibition compared to our *in vitro* studies. We hypothesized that this might be a consequence of measuring steady-state metabolite levels that do not account for differences in metabolic flux. To examine this hypothesis, we performed multi-isotope imaging mass spectrometry (MIMS) of mouse lungs following administration of 15N-proline and 2H-glucose or 13C-glucose. MIMS enables the quantification of stable isotope tracer flux into tissue biomass with subcellular spatial resolution (48, 49). For three days prior to tissue collection, mice received twice daily intraperitoneal injections of 5 mg 15N-proline as a fibrosis tracer and 50 mg 2H-glucose or 13C-glucose as a metabolic tracer. Lung tissue sections were subsequently imaged by nanoscale secondary ion mass spectrometry to quantify spatially resolved isotope tracer uptake (**Figure 9B-C**). This labeling strategy was quite effective, demonstrating ~1.5-fold 15N, ~4.6-fold for 2H, and ~2.4-fold for 13C enrichment above natural isotope abundance. Pulmonary fibrosis was associated with a significant increase in 15N labeling from proline, consistent with increased collagen synthesis and deposition during the labeling period. Similar to the lung function and histological analyses, less 15N incorporation per tissue area was observed in drug-treated animals. Glucose labeling followed a similar pattern where lactate transporter inhibition caused a decrease in glucose incorporation into tissue biomass. Importantly, these findings are not merely a consequence of decreased tissue fibrosis as we chose more fibrotic areas to image (**Figure 9B**) and the enrichment values are normalized to tissue area.

## Novel MCT4 inhibitor mitigates experimental pulmonary fibrosis

Our preclinical data suggest that MCT4 inhibition, as a single target therapy, is more potently antifibrotic than MCT1 inhibition, both in terms of inhibiting myofibroblast differentiation *in vitro* and decreasing bleomycin-induced fibrosis. VB253 is a novel inhibitor of MCT4 with similar selectivity, but ~10-fold increased potency, for MCT4 inhibition. Like VB124, VB253 dose-dependently decreases **TGFβ-stimulated?** α-SMA in human IPF lung fibroblasts *ex vivo* (**Figure 10A**). Given the robust effect of MCT4 inhibition on myofibroblast differentiation, we compared VB253 to nintedanib, an anti-fibrotic medication clinically indicated for pulmonary fibrosis (**Figure 10A-B**). Nintedanib inhibits TGFβ-mediated fibroblast to myofibroblast differentiation and decreases Col1a1 expression *in vitro* and *in vivo* (50). While both drugs potently attenuated α-SMA expression, nintedanib demonstrated a moderate cytotoxic effect that was not observed with VB253 (**Figure 10B**). Nintedanib prevents myofibroblast differentiation, in part, through inhibition of TGFβ receptor phosphorylation and activation of Smad-dependent signaling pathways (51). Consistent with these findings, nintedanib dose-dependently attenuates TGFβ-mediated Smad3 phosphorylation, while VB253 and VB124 have no impact on this signaling pathway (**Figure 6**, **Supplemental Figure 10**).

We next assessed the ability of VB253 to inhibit bleomycin-induced pulmonary fibrosis. In experiments conducted independently from those reported above, VB253 was administered to young mice (8-10 weeks) beginning on day 7 following bleomycin (**Figure 10C**). Mice treated with nintedanib or pirfenidone provided comparisons to currently available therapies for pulmonary fibrosis. Three weeks after bleomycin administration, whole-body plethysmography was performed to assess breathing patterns in unrestrained mice. Enhanced pause (Penh) is a dimensionless index describing airflow during tidal breathing found to increase significantly in bleomycin-treated mice (52). VB253 restored Penh to baseline levels, suggesting normalization of respiratory patterens in bleomycin-treated mice (**Figure 10D**). This was associated with decreased pulmonary fibrosis by histologic assessment (**Figure 10E**) and α-SMA expression (**Figure 10F-G**). Morevover, the effects of VB253 compared favorably to the antifibrotic effects of nintedanib and pirfenidone.

Compared to young mice, bleomycin-induced fibrosis in aged mice is more severe and does not resolve spontaneously (53). Given that IPF incidence increases with age, some studies have suggested such aged mouse models may be more clinically relevant. Thus, we examined the antifibrotic effects of VB253 in aged (60+ weeks) mice. Similar to young mice, VB253 decreased fibrosis severity as quantified by Ashcroft score and α-SMA expression (**Figure 10H-J**). The magnitude of improvement was similar to that observed with nintedanib and pirfenidone. As anticipated, VB253 decreased total lung lactate similar to VB124 (**Figure 9A**). Taken together, these data provide compelling preclinical data for the development of lactate transporter inhibition as a therapeutic strategy for fibrotic lung disease.

# Discussion

Our findings demonstrate that lactate transport is an essential component of the metabolic reprogramming associated with myofibroblast differentiation *in vitro* and *in vivo*. We observed increased expression of the lactate transporters MCT1 and MCT4 in IPF lung explants and experimental model systems. Inhibition of these transporters decreased TGFβ-stimulated myofibroblast differentiation and the severity of bleomcyin-induced pulmonary fibrosis. Metabolically, MCT antagonists promoted glucose oxidation and decreased glucose carbon incorporation into fibrotic lung regions, which were associated with decreased oxidative stress. Beyond metabolic reprogramming, we observed changes in gene expression profiles consistent with antifibrotic metabolic signaling downstream of lactate transport inhibition, which may be mediated by changes in ROS production, protein lactylation, or other mechanisms. MCT4 inhibition consistently proved more potently antifibrotic than MCT1 inhibition, and we report a novel MCT4 inhibitor, VB253, with a more favorable pharmacologic profile than VB124 that is now in Phase 1 clinical trials [**REF?**]. Collectively, these data establish lactate transport as a metabolic opportunity for therapeutic intervention in pulmonary fibrosis.

Metabolic reprogramming is a hallmark of myofibroblast differentiation. Previous studies have identified alterations in carbohydrate, amino acid, and lipid metabolic pathways that support fibrogenesis (7). Of these, increased lactate production was among the earliest recognized metabolic changes associated with pulmonary fibrosis (13). Subsequent work demonstrated increased lactate production was driven by activation of glycolysis in myofibroblasts (9) and that inhibition of glycolysis prevented myofibroblast differentiation (8, 9, 14) and, in turn, experimental pulmonary fibrosis (15, 16). Consistent with increased glycolysis in myofibroblasts, we have now demonstrated increased expression of the lactate transporters MCT1 and MCT4 support this metabolic phenotype.

MCTs are proton-coupled monocarboxylate symporters with varying affinities for lactate, pyruvate, and other monocarboxylates (30). MCT1 is constitutively and ubiquitously expressed and primarily considered to be a lactate importer with a KM for lactate of 3-6 mM. By contrast, MCT4 expression is dynamically regulated, including by HIF-1α, and has primarily been considered to be a lactate exporter with a low lactate affinity (KM 30-40 mM). Recent data suggests, however, that MCT4 has a much higher affinity for lactate import than previously appreciated (KM 1 mM) (33). These data are most consistent with our findings that inhibition of both MCT1 and MCT4 was required to inhibit lactate export (**Figure 3**) and isotope incorporation from extracellular [U-13C3]-lactate import (**Figure 4J**). Previous studies of cancer cells have similarly recognized that MCT4-expressing cells are resistant to the cytotoxic effects of MCT1 inhibition (28). Interestingly, inhibition of either MCT1 or MCT4 reduced myofibroblast differentiation without affecting lactate export.

To clarify the metabolic consequences of lactate transporter inhibition, we performed a comprehensive metabolic analysis of myofibroblasts treated with MCT inhibitors, including bioenergetic measurements, metabolomic profiling, and stable isotope tracing experiments. The primary metabolic consequence of MCT inhibition is activation of oxidative phosphorylation. MCT inhibitors increased the fraction of mitochondrial ATP production, which was associated with increased levels of tricarboxylic acid cycle intermediates, and increased isotope incorporation from glucose substrates. Collectively, these data indicate that MCT inhibition reroutes carbon flow from glucose away from lactate fermentation and toward glucose oxidation. Several mechanisms may account for this phenomenon. Since the magnitude of these effects generally correlates with intracellular lactate levels, mass action may be an important driver of this metabolic phenomenon. Lactate accumulation is also closely coupled in NADH production through lactate dehydrogenase activity. Cytoplasmic NADH may be transported into the mitochondria through the malate-aspartate shuttle and oxidized by the electron transport chain. Recently, lactate itself was shown activate the mitochondrial electron transport chain independently of its metabolism (54), although the molecular mechanism for this effect is unknown.

How these metabolic effects signal to antifibrotic transcriptional programs remains unclear. We investigated several hypotheses based on previous studies. First, we did not observe significant changes in canonical (*i.e.*, Smad3) or non-canonical (*i.e.*, ERK) TGFβ signaling pathways. Second, TGFβ-dependent activation of HIF-1α seems to be required for myofibroblast differentiation (10). MCT1 and MCT4 potentiated HIF-1α stabilization following TGFβ (**Figure 6D**), indicating that MCT inhibition acts downstream of HIF signaling pathways. Third, post-translational modification of histone lysines by lactate serves as an epigenetic modification that stimulates gene expression (44). We observed increased histone lactylation following dual MCT inhibition, which may account for some of the transcriptional changes we observed. In addition to histones, protein lactylation has been increasingly identified as a critical regulator of protein function, including cytoskeletal proteins (55). Fourth, increased ROS production has been observed following TGFβ treatment (45, 46). While we were unable to replicate TGFβ-dependent increases in ROS in our cells and model system, we did observe decreased CellROX oxidation with MCT4 inhibition and decreased MitoSOX oxidation with AZD3965. Collectively, these studies identify two putative mechanisms for antifibrotic lactate signaling following MCT inhibition, protein lactylation and antioxidant activity; however, novel lactate targets are being increasingly recognized as important mediators of metabolic signaling (56, 57).

Through our detailed metabolic investigation of lactate transport inhibition, we have also generated valuable data on the metabolic and transcriptional consequences of human lung myofibroblast differentation. TGFβ stimulated marked changes in amino acid and nucleic acid metabolic pathways (**Supplemental Figure 4A-D**). Previous studies have identified important roles for glutamine, proline, and taurine (7, 58, 59), while the contributions of branched chain amino acid metabolism, for example, remain unexplored. Integrating these multi-omics data sets may identify novel molecular targets for future drug development.

In addition to metabolomic profiling, we have performed stable isotope tracing using glucose, lactate, and glutamine substrates in TGFβ-treated primary human lung fibroblasts. To our knowledge, these are the first comprehensive data on intracellular substrate metabolism in this commonly utilized model of myofibroblast differentiation. Overall, isotope labeling patterns changed little following TGFβ treatment (**Supplemental Figure 4.2**). Together with the results of our extracellular flux experiments, this finding suggests that TGFβ primarily increases the flow of metabolites through metabolic pathways without substantially altering the pathways themselves. Consistent with increased glucose uptake and accumulation of glycolytic metabolites, a greater fraction of pyruvate, lactate, alanine, and serine are labeled by [U-13C6]-glucose, which is offset by a decrease in the fractional labeling from [U-13C3]-lactate. Similar to our previous work (38), nearly 50% of tricarboxylic acid metabolites (citrate, 2-oxoglutarate, succinate, and malate) are labeled by [U-13C3]-lactate, highlighting the importance of lactate as a respiratory fuel source in these cells.

In addition to cellular bioenergetics, the contribution of fibroblast metabolic pathways to extracellular matrix production has been an intense area of investigation (7). Serine and glycine may be synthesized from the glycolytic intermediate 3-phosphoglycerate, and proline may be synthesized from glutamine. These pathways have been implicated in myofibroblast differentation and pulmonary fibrosis (11, 12, 46, 58, 60). Interestingly, our data suggest little incorporation of glucose or lactate carbon into serine and little incorporation of glutamine carbon into proline. These differences may be secondary to the cells studied (IMR-90 fetal lung fibroblasts or NIH-3T3 spontaneously immortalized mouse embryonic fibroblasts) or the culture medium utilized (Eagle’s minimum essential medium, which lacks serine, glycine, and proline). In this context, our study highlights that fibroblasts will preferentially use available amino acids rather than reroute substrates into biosynthetic pathways. Developing metabolic flux models using human physiologic medium (61) may provide a more accurate and complete characterization of substrate flow into energetic and biosynthetic pathways that more closely reflects fibroblast metabolism *in vivo*.

Even better than the use of *in vitro* model systems are approaches that enable the study of cell metabolism *in vivo*. Here, we performed metabolomic profiling of lung and plasma samples from mice treated with bleomycin and MCT inhibitors (**Supplemental Figure 9**). These studies did not reveal consistent changes in whole lung metabolite levels and demonstrate a potential limitation of using bulk metabolomics to monitor metabolic changes in heterogeneous cell populations *in vivo*. We sought to overcome this limitation with spatial metabolic imaging. Mice received stable isotope tracers of proline and glucose prior to euthanasia. Since these tracers are administered to live animals, multi-isotope imaging mass spectrometry identifies lung regions that are metabolically active over the labeling period. Since tissues are fixed and processed *ex vivo*, the isotope signals indicate substrate incorporation into fixable biomass (62, 63). Thus, using multi-isotope imaging mass spectrometry, we are directly quantifying isotope flux from glucose into fibrotic lung regions. We found that 15N-proline enrichment levels correlate with tissue fibrosis from histologic and biochemical assessments. This finding emphasizes the ability of cells to incorporate circulating proline for protein synthesis, and likely de-emphasizes the importance of *de novo* proline biosynthesis *in vivo*. The 2H-glucose signal provides some direct evidence for MCT-dependent metabolic reprogramming in mice, with less carbohydrate incorporation into matrix proteins. Owing to the financial and time costs of isotope tracing and imaging, only a few animals per group were studied. Nonetheless, metabolic imaging at high spatial resolution offers tremendous promise for correlating cell identities determined from spatial transcriptomic profiles with metabolic features. Stable isotopes may be safely administered to human patients prior lung biopsy or explant, an approach that would considerably advance our understanding of how cell metabolism contributes to pulmonary fibrosis.

MCT1 and MCT4 are expressed by many cells in the lung, particularly macrophages and dendritic cells (64). Although our *ex vivo* and *in vitro* experiments suggest that inhibiting myofibroblast differentiation is a primary antifibrotic mechanism, inhibition of lactate transporters expressed by other cell types may also play a role in their therapeutic effect. For example, MCT4 expression is increased as part of a HIF-1α gene expression signature in transitional AT2 cells that accumulate in pulmonary fibrosis and contribute to aberrant repair (65, 66). We are in the process of generating fibroblast-specific conditional knockout mice to explore the role of these transporters in fibroblasts specifically.

Pharmacologic interest in lactate transporters has been driven by the recognition of increased lactate transporter expression in a variety of cancers (67). AZD3965 was selected for this study as it has been investigated in human clinical trials for advanced solid organ malignancies (22). In this Phase 1 study, AZD3965 was generally well-tolerated with 7 of 40 patients experiencing dose-limiting toxicities including asymptomatic, reversible ocular changes; acidosis; and increased troponin. VB124 was the first selective MCT4 inhibitor developed (21) and here we report a second generation MCT4 inhibitor, VB253. A Phase 1 clinical trial of VB253 is currently enrolling [**REF?**]. MCT4 global knockout mice are viable and breed normally (68, 69), increasing optimism that VB253 will be well tolerated in humans. One of the barriers to translating metabolic therapies to humans has been the poor pharmacologic properties of the small molecule laboratory compounds that have been studied previously. The IC50 values for AZD3965 and VB253 are ~ 2 nM, compared to the next most potent inhibitor, lonidamine, with an IC50 of 7,000 nM (70). As a metabolic target downstream of glycolysis, lactate transport inhibitors may also be better tolerated by allowing glycolysis to continue to support of glucose oxidation, while upstream inhibitors of glycolysis have a more severe impact on cellular bioenergetics.

In conclusion, we have demonstrated that lactate transporters promote myofibroblast differentiation and pulmonary fibrosis. Using a comprehensive metabolic phenotyping strategy, we have identified antifibrotic mechanisms for MCT inhibition and demonstrated evidence for metabolic reprogramming in animal models. We have demonstrated the antifibrotic efficacy of currently available lactate transport inhibitors with accepted preclinical disease models. Collectively, our data advance lactate transport inhibition as a viable therapeutic strategy for patients with pulmonary fibrosis.

# Methods

# Acknowledgements

# Conflicts of Interest

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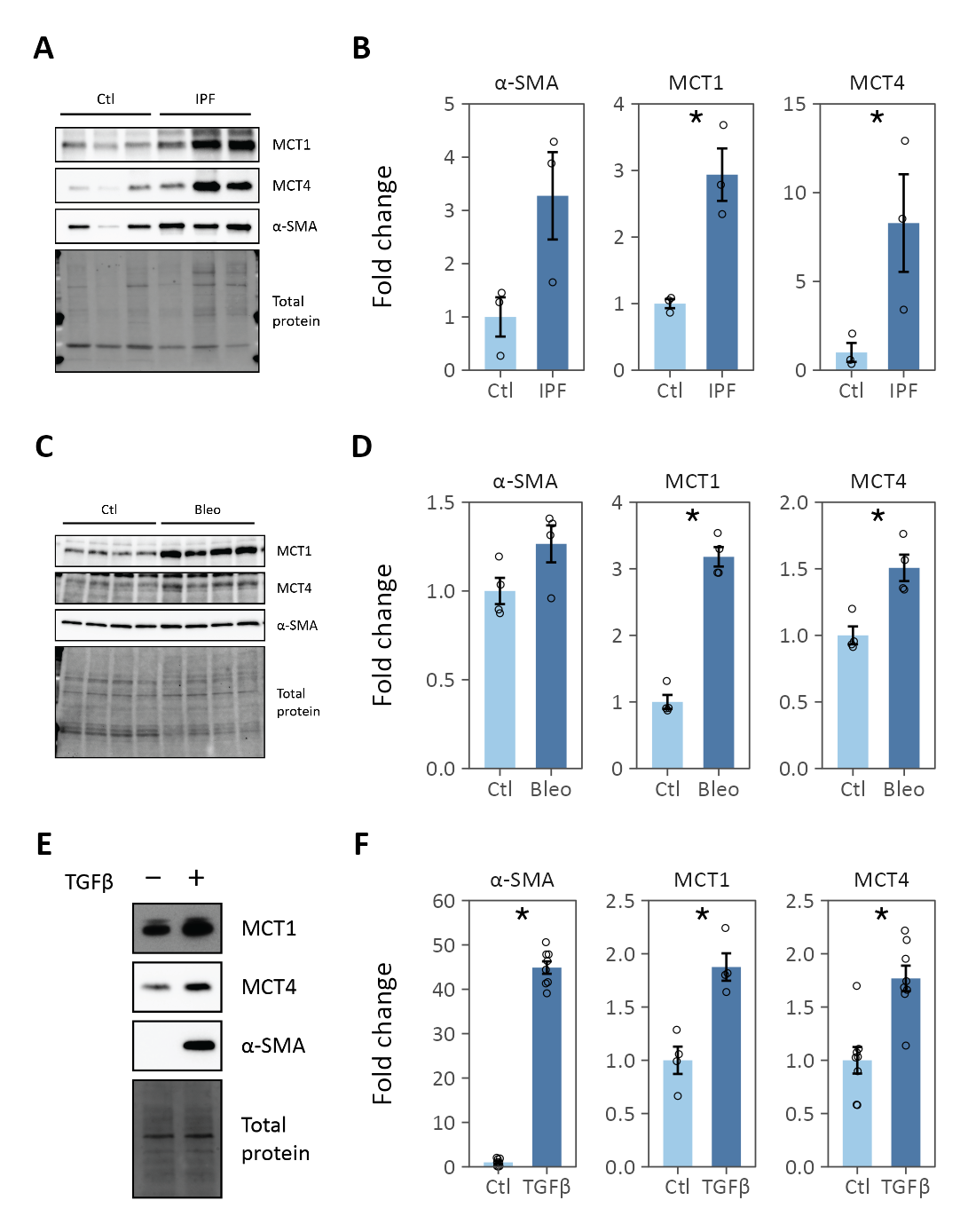
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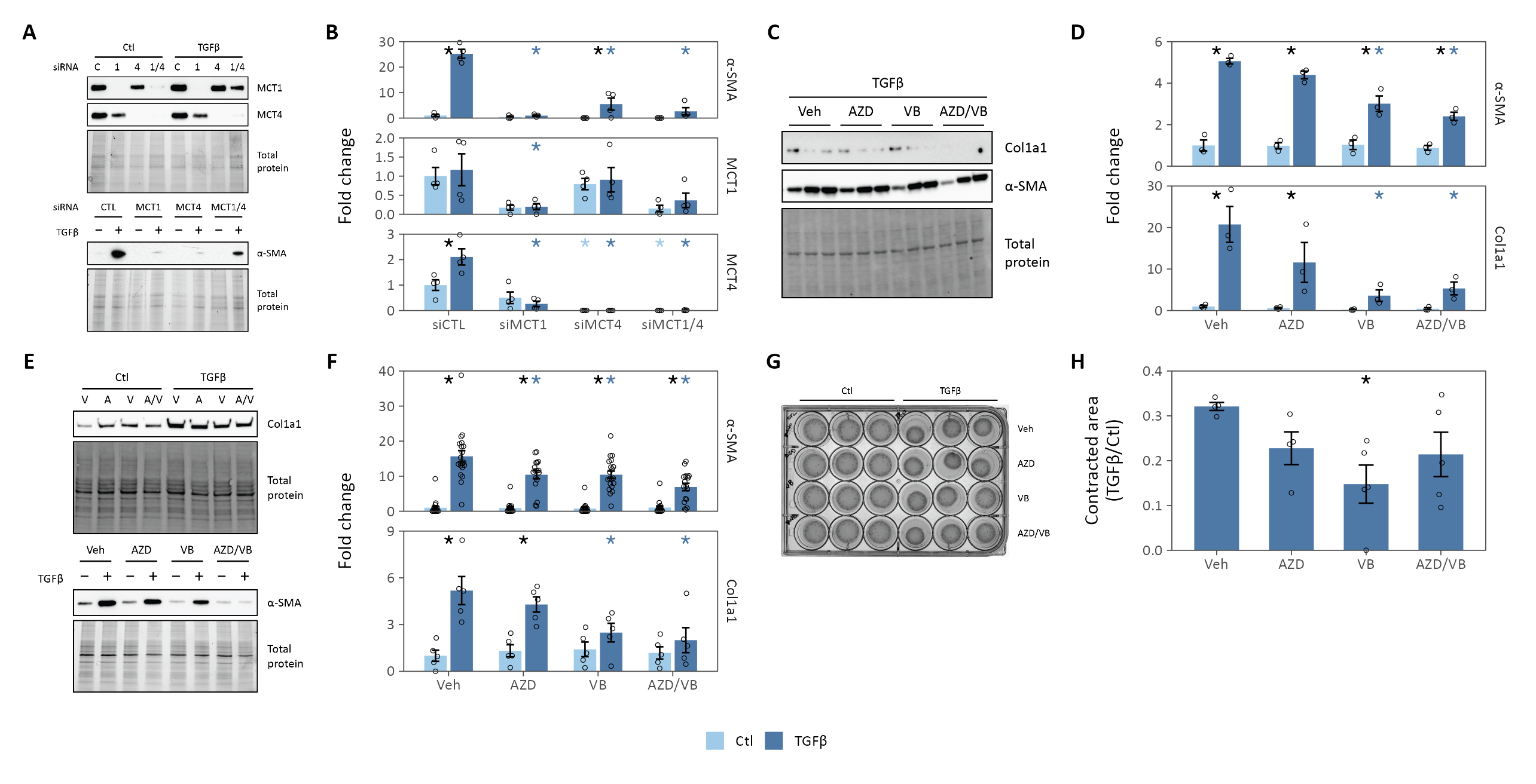
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# Figures



**Figure 1 - Lactate transporter expression increases in human IPF and experimental models.** (**A**) Immunoblot of whole lung homogenates from explanted IPF lungs and controls (Ctl). (**B**) Quantification of band densities from (A). (**C**) Immunoblot of whole lung homogenates from bleomycin (bleo)- and vehicle (Ctl)-treated mice. (**D**) Quantification of band densities from (C). (**E**) Representative immunoblot of cell lysates from normal human lung fibroblasts treated with TGFβ to induce myofibroblast differentiation. (**F**) Quantification of band densities from (E). Individual data points are biological replicates. Summary data are mean ± SEM (\* p < 0.05).



**Figure 2 - Lactate transport inhibition decreases myofibroblast differentiation *in vitro*.** (**A**) Representative immunoblot of normal lung fibroblast cell lysates after treatment with siRNA targeting MCT1 or MCT4. (**B**) Quantification of protein expression levels following MCT1 and MCT4 knockdown. (**C**) Immunoblot of IPF lung fibroblast lysates from three separate donors after treatment with TGFβ and MCT inhibitors AZD3965 (AZD) or VB124 (VB). (**D**) Quantification of band densities from (C). (**E**) Representative immunoblot of normal lung fibroblasts treated with TGFβ and MCT inhibitors. (**F**) Quantification of α-SMA expression following MCT inhibition. (**G**) Representative image of a gel contraction assay after 24 h treatment with TGFβ and MCT inhibitors. (**H**) Quantification of contracted areas. Individual data points are biological replicates. Summary data are mean ± SEM (\* p < 0.05; *black* compares TGFβ to control within a given treatment, *colored* compares the treatment effect to control for a given condition).