Integrin-associated ILK and PINCH1 protein content are reduced in skeletal muscle of maintenance haemodialysis patients

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Key points

- Patients with renal failure undergoing maintenance haemodialysis are associated with insulin resistance and protein metabolism dysfunction.
- Novel research suggests that disruption to the transmembrane protein linkage between the cytoskeleton and the extracellular matrix in skeletal muscle may contribute to reduced amino acid metabolism and insulin resistance in haemodialysis.
- ILK, PINCH1 and pFAKTyr397 were significantly decreased in haemodialysis compared to controls, whereas Rac1 and Akt2 showed no different between groups.
- Rac1 deletion in the Rac1 knockout model did not alter the expression of integrin-associated proteins.
- Phenylalanine kinetics were reduced in the haemodialysis group at 30 and 60 min post meal ingestion compared to controls; both groups showed similar levels of insulin sensitivity and β-cell function.
- Key proteins in the integrin–cytoskeleton linkage are reduced in haemodialysis patients, suggesting for the first time that integrin-associated proteins dysfunction may contribute to reduced phenylalanine flux without affecting insulin resistance in haemodialysis patients.

Dr Draicchio has a background in Biotechnology before moving into the research theme of Human Metabolism and metabolic disorders of type 2 diabetes and chronic kidney disease in the Laboratory of Dr Richard Mackenzie in collaboration with Dr Nick Burd. Her research suggests that disruption to the transmembrane protein linkage between the cytoskeleton and the extracellular matrix in skeletal muscle may contribute to reduced amino acid metabolism and insulin resistance in hemodialysis. Richard W.A. Mackenzie is a Reader in Insulin Resistance and Metabolism at the University of Roehampton (London). With over 10 years’ experience in investigating the mechanisms that govern contraction- and insulin-stimulated glucose transport in skeletal muscle, he has a particular interest in the role of inositol hexakisphosphate (IP6) kinase 1 (IP6K1) in the inhibition Akt/PKB and reduced insulin signalling in skeletal muscle. His research focus requires molecular and whole-body approaches to investigate the disease processes in human metabolism and type 2 diabetes.
Abstract  Muscle atrophy, insulin resistance and reduced muscle phosphoinositide 3-kinase-Akt signalling are common characteristics of patients undergoing maintenance haemodialysis (MHD). Disruption to the transmembrane protein linkage between the cytoskeleton and the extracellular matrix in skeletal muscle may contribute to reduced amino acid metabolism and insulin resistance in MHD patients. Eight MHD patients (age: 56 ± 5 years; body mass index: 32 ± 2 kg m⁻²) and non-diseased controls (age: 50 ± 2 years; body mass index: 31 ± 1 kg m⁻²) received primed continuous L-[ring-²H₅]phenylalanine before consuming a mixed meal. Phenylalanine metabolism was determined using two-compartment modelling. Muscle biopsies were collected prior to the meal and at 300 min postprandially. In a separate experiment, skeletal muscle tissue from muscle-specific Rac1 knockout (Rac1 mKO) was harvested to investigate whether Rac1 depletion disrupted the cytoskeleton-integrin linkage, allowing for cross-model examination of proteins of interest. ILK, PINCH1 and pFAK(Tyr397) were significantly lower in MHD (P < 0.01). Rac1 and Akt showed no difference between groups for the human trial. Rac1 deletion in the Rac1 mKO model did not alter the expression of integrin-associated proteins. Phenylalanine rates of appearance and disappearance, as well as metabolic clearance rates, were lower in the MHD group at 30 and 60 min post meal ingestion compared to controls (P < 0.05). Both groups showed similar levels of insulin sensitivity and β-cell function. Key proteins in the integrin–cytoskeleton linkage are reduced in MHD patients, suggesting for the first time that integrin–associated proteins dysfunction may contribute to reduced phenylalanine flux without affecting insulin resistance in haemodialysis patients.

Introduction

Patients with renal failure undergoing maintenance haemodialysis (MHD) demonstrate several metabolic and phenotypic alterations including muscle wasting (Workeneh & Mitch, 2010; van Vliet et al. 2018) as a result of increased degradation of muscle proteins through activation of the ubiquitin–proteasome system (Workeneh & Mitch, 2010). Decreased muscle mass results in decreased motor function and glucose storage capacity (Johansen et al. 2003). Using the ‘gold standard’ euglycaemic-hyperinsulinaemic clamp, DeFronzo et al. (1981) showed that patients with renal failure demonstrated insulin resistance, a finding that is supported elsewhere (Kobayashi et al. 2005; Bailey et al. 2006; Semenovich, 2006; Turcotte & Fisher, 2008; Thomas et al. 2015).

Glucose transport into skeletal muscle is known to occur via two distinct pathways: (i) insulin-mediated GLUT4 translocation, partly requiring functional IRS-1-Akt/AS160 signalling (Deshmukh, 2016), and (ii) contraction-stimulated GLUT4 movement via Ca²⁺-dependent AMPK/AS160 signalling (Wright et al. 2005; Kramer et al. 2006; Mackenzie & Elliott, 2014; Sylow et al. 2017). Of note, it is widely accepted that it is the first pathway that is defective in insulin resistant skeletal muscle. More recently, a third pathway that facilitates glucose transport has been identified, termed the tension-mediated pathway (Chambers et al. 2009; Jensen et al. 2014; Sylow et al. 2015). It is hypothesized that this latter pathway requires a structurally stable linkage between the extracellular matrix and the actin–cytoskeleton to encourage normal nutrient uptake.

The dystroglycan complex and integrins are major surface receptors of the extracellular matrix (ECM) in skeletal muscles ( Von der Mark et al. 1991; Hynes, 2002; Postel et al. 2008; Williams et al. 2015). Integrins are transmembrane proteins formed by α and β subunits, which mediate interactions between the ECM and the cytoplasmic integrin cytoskeleton (Postel et al. 2008), and they are responsible for transducing signals across the membrane to the intracellular integrin-binding proteins (Williams et al. 2015; Kang et al. 2016). Although the role of integrins in ECM and muscle cell integrity has been extensively characterized (Legate & Fässler, 2009; Wickström et al. 2010), little is known about the function of the integrin-binding intracellular complexes in both mechanical stability (Postel et al. 2008; Wickström et al. 2010) and normal nutrient metabolism in skeletal muscle. Once activated, the integrin complex stimulates downstream targets implicated in both insulin-like growth factor and insulin receptor substrate signalling, including integrin-linked kinase (ILK), focal adhesion kinase (FAK), serine/threonine-specific protein kinase (Akt), Rho GTPase Rac1 and glycogen synthase kinase 3β.
(GSK-3β) (Williams et al. 2015). Thus, integrin and its associated target kinases appear to be implicated in muscle protein synthesis (Byun et al. 2012; Clemente et al. 2012), insulin-mediated glucose uptake (Huang et al. 2006; Bisht et al. 2007; Bisht & Dey, 2008) and cytoskeletal stabilization (Williams et al. 2015).

Muscle atrophy, a recognized characteristic of MHD (van Vliet et al. 2018), has been linked with reduced muscle integrin-associated protein content (Pattison et al. 2004; Postel et al. 2008; Wang et al. 2008; Peter et al. 2011). In addition, reduced integrin-associated protein expression is also noted in insulin resistance with decreased Akt phosphorylation, a candidate for reduced insulin-mediated glucose (Urso et al. 2006). Given that kidney failure patients display signs of muscle atrophy (Workeneh & Mitch, 2010; van Vliet et al. 2018), we hypothesized that MHD patients would demonstrate reduced integrin-associated protein content in skeletal muscle compared to non-MHD individuals. We further hypothesized that the structural and signalling disruption might lead to impaired regulation of protein metabolism and nutrient flux. The present study used two compartment whole-body measures of phenylalanine kinetics and surrogate measures of insulin resistance to partly test this hypothesis.

Rac1 is a well characterized member of Rho GTPase family and is implicated in cytoskeletal reorganization, transcriptional regulation, cell migration and nutrient uptake (Burridge & Wennerberg, 2004; Ueda et al. 2008). Rac1 is known to promote GLUT4 translocation and glucose uptake via mechanisms requiring actin remodelling in skeletal muscle (Torok et al. 2004; JeBailey et al. 2007; Sylow et al. 2013b). Thus, proteins involved in vesicle trafficking may only operate fully in the presence of a functional cytoskeleton (Ueda et al. 2008). The ILK PINCH parvin (IPP) complex functions at one of the early steps of the integrin signalling cascade (Wu, 1999; Stanchi et al. 2009). The pseudokinase integrin-linked kinase ILK recruits downstream targets implicated in insulin-mediated glucose uptake and links integrins to the actin cytoskeleton (Gheyara et al. 2007); among its downstream targets, there are PDK1 and GSK-3β (through PINCH1), as well as α-actinin and Rac1 (through parvin) (Williams et al. 2015). ILK directly interacts with the β-integrin subunits and is stimulated by both integrin activation and growth factors and appears to act as an upstream regulator of Akt (Wu & Dedhar, 2001; Tang et al. 2007). Therefore, this integrin signalling pathway is suggested to facilitate glucose uptake via both insulin-dependent and independent mechanisms in a cross-sarcolemma fashion.

Accordingly, in the present study, we probed skeletal muscle from insulin resistant, but otherwise healthy controls, and made comparisons with MHD patients in both a fasted and postprandial state for integrin-associated protein signalling. Using an established muscle-specific Rac1 knockout rodent model (Sylow et al. 2013a; Raun et al. 2018), a secondary aim was to investigate the potential linkage between actin cytoskeleton and integrin-associated signalling.

**Methods**

**Ethical approval**

Ethics for human experiments was approved by the local Ethics Board (University of Illinois at Urbana-Champaign) and met all conditions outlined in the seventh revision of the Declaration of Helsinki for use of human volunteers (Clinical Trial Registration Number: NCT03478722).

All experiments regarding the mouse models were approved by the Danish Animal Experimental Inspectorate (License: 2016-15-0201-0 1043).

**Human experiment**

Eight MHD patients [mean ± SEM age 56 ± 5 years, male sex = 6 (75%), body mass index = 32 ± 2 kg m⁻², body fat = 31 ± 3%, homeostatic model assessment of insulin resistance (HOMA IR) = 3.9 ± 0.9 and HOMA β-cell = 4.3 ± 1.24] and eight matched insulin resistant controls [age 50 ± 2 years, male sex = 6 (75%), body mass index = 31 ± 1 kg m⁻², body fat = 29 ± 2%, HOMA IR = 4.0 ± 0.6 and HOMA β-cell = 4.8 ± 0.65] were recruited for the study. These participants were part of a larger investigation being conducted in our laboratory. [HOMAIR; fasting insulin (μU mL⁻¹) × fasting glucose (mmol L⁻¹)/22.5] and HOMA of β-cell function [HOMA β-Cell; 20 × fasting insulin (μU mL⁻¹)/fasting glucose – 3.5 (mmol L⁻¹)] were calculated using validated equations (Uwaifo et al. 2002). Volunteers received written and verbal details on the experimental design, the study aims and potential risks before providing their written consent. For MHD patients, we requested physician clearance from their nephrologist to further that ensure it was safe for the patient to participate in the study.

A full description of the pre-screening and experimental procedures is provided elsewhere (van Vliet et al. 2018). The MHD patients analysed in the present study have been in dialysis treatment for ~5 years and their current nutritional status comprised ingestion of protein-rich meals to achieve the recommended protein intakes (set at 1.2 g kg⁻¹ body weight day⁻¹) to limit muscle protein losses observed in end-stage kidney disease.

MHD patients were studied ~24 h after a dialysis treatment session (i.e. non-dialysis day). Volunteers ingested an identical meal (320 kcal; 22 g of protein, 43 g of carbohydrates, 7 g of fat) at least 12 h prior to trials and arrived in a fasted state to the laboratory...
at 07:00 h. An 18-gauge cannula was positioned into a dorsal hand vein to allow frequent sampling of arterialized blood (every 30–60 min) with a thermoregulated hot box (−65°C). A second 18-gauge cannula was placed into an antecubital vein for the primed constant infusion of L-[ring-2H5]phenylalanine (prime; 2.0 μmol kg−1 free fat mass, infusion rate; 0.05 μmol kg−1 free fat mass min−1). A baseline blood sample was collected at t = −180 min immediately prior to the start of the infusion protocol. Muscle biopsies were collected at t = −120 and −0 min of the infusion, reflecting a post-absorptive state.

Subsequently, volunteer ingested a mixed meal (546 kcal; 20 g of protein, 59 g of carbohydrates, 26 g of fat), the completion of which marked the start of the postprandial phase (t = 0 min). An additional muscle biopsy was collected at 300 min. Biopsies were sampled from the middle region of the vastus lateralis (15 cm above the patella) with a Bergström needle modified for suction under local anaesthesia (2% lidocaine) (van Vliet et al. 2018). The post-absorptive muscle biopsies were sampled from the same incision with the needle pointed in the distal and proximal directions, respectively (van Vliet et al. 2018). Muscle samples were immediately frozen in liquid nitrogen and stored at −80°C until subsequent analysis. Blood samples were centrifuged at 3000 g for 10 min at 4°C and plasma was stored at −80°C for subsequent analysis.

**Mouse models**

Considering the importance of an intact cytoskeleton for normal glucose uptake in skeletal muscles, we aimed to investigate the potential role of the major actin regulators, Rac1, in the integrin signalling pathway. Thus, nine muscle specific tetracycline-inducible knockout (mKO) mice and seven control mice were analysed in the present study. A full description of the Rac1 muscle-specific tetracycline-inducible knockout (mKO) mouse model used in this experiment is provided elsewhere (Sylow et al. 2013b, 2013a). Skeletal muscle from Rac1 mKO mice were analysed when the mice were 31–33 weeks of age. Rac1 mKO was induced at 12–16 weeks of age by adding doxycycline (a tetracycline analogue) in the drinking water (1 g L−1; Sigma Aldrich, Copenhagen, Denmark) for 3 weeks to deplete Rac1 specifically in skeletal muscle (PMID: 29 749 029). This treatment was repeated at week 10 of the intervention period to ensure continuous Rac1 knockout throughout the entire intervention period. An 18-week diet intervention was started at 14–18 weeks of age and mice received either a standard rodent chow diet (Altromin no. 1324; Brogaarden, Horsholm, Denmark) or a 60% high-fat diet (HFD) (no. D12492; Brogaarden) and water ad lib. Body weight was assessed every week. In the present study, we investigated skeletal muscles of chow-fed mice. All animals were maintained under a 12:12 h light/dark photocycle, and group housed at 20–21°C. For muscle tissue sampling, mice were fasted for 3–5 h from 07:00 h and anaesthetized (I.P. injection of 7.5/9.5 mg (chow/HFD) pentobarbital sodium 100 g−1 body weight). After 25 min, skeletal muscle was excised and quickly frozen in liquid nitrogen and stored at −80°C until processing.

**Immunoblotting**

Relative total muscle protein content and phosphorylation levels of relevant proteins were determined by standard immunoblotting techniques loading equal amounts of protein. The primary antibodies used were anti-Integrin linked ILK antibody (ab227154; Abcam, Cambridge, MA, USA), anti-PINCH1 antibody [EP1943Y] (ab76112; Abcam), α-parvin (D7F9) XP Rabbit mAb (8190S; Cell Signaling Technology, Beverly, MA, USA) (37), pFAK tyr397 (D20B1) Rabbit mAb (8556S; Cell Signaling Technology) (Tuguzbaeva et al. 2019), anti-total FAK (ab40794; Abcam) (Bian et al. 2019), anti-Rac1 (ARC03; Cytoskeleton Inc., Denver, CO, USA) (Raun et al. 2018), anti-total Akt2 (no. 3063; Cell Signaling Technology) (Raun et al. 2018), pAkt Tyr377 (no. 9271; Cell Signaling Technology) (Karushueva et al. 2019), pAkt Thr308 (no. 9275; Cell Signaling Technology) (Raun et al. 2018), anti-IP6K1 antibody (ab129595; Abcam) and anti-dystrophin (ab15277; Abcam) (Jelinkova et al. 2019).

Polivinyldened difluoride membranes (Immobilon TransferMembrane; Millipore, Burlington, MA, USA) were blocked in Tris-buffered saline-Tween 20 containing 2% skimmed milk or 5% BSA protein for 30–60 min at room temperature. Membranes were incubated with primary antibodies overnight at 4°C, followed by incubation with rabbit or mouse peroxidase-conjugated secondary antibody for 30 min at room temperature. Coomassie brilliant blue staining was used as a loading control (Welinder & Ekblad, 2011). Bands were visualized using the ChemiDoc MP Imaging System (Bio-Rad, Hercules, CA, USA). Raw data for all the above protein analyses are openly available via figshare: https://doi.org/10.6084/m9.figshare.12886943.

**Blood analysis**

Blood metabolites were determined using a point-of-care chemistry analyser (Piccolo Xpress Chemistry Analyzer; Abaxis, Union City, CA, USA). Plasma insulin concentrations were determined using a commercially available enzyme-linked immunosorbent assays (Alpcob Diagnostics, Salem, NH, USA). Plasma phenylalanine concentrations (unlabelled) and phenylalanine enrichments (labelled) were determined by gas chromatography-mass spectrometry analysis (Agilent 7890A GC/5975C; MSD, Little Falls, DE, USA).
as described previously (van Vliet et al. 2016). Briefly, plasma samples were prepared for amino acid analysis using a mixture of isopropanol:acetoni-trile:water (3:3:2, v/v) and centrifuged at 20 000 g for 10 min at 4°C. Subsequently, the supernatant was dried, and the amino acids converted into tert-butylidemethylsilyl derivatives prior to gas chromatography-mass spectrometry analysis. L-[ring-2H5]phenylalanine, m/z 336 (m+0) and 341 (m+5) were monitored for unlabelled and labelled phenylalanine, respectively.

Data modelling
Plasma insulin and endogenous glucose concentrations were used to model the measures of insulin sensitivity (ISI) (Matsuda index) (Matsuda & DeFronzo, 1999; acute insulin response to glucose (AIRg), second phase insulin response (ΔI_{G60–120}/ΔG_{60–120}) (Lorenzo et al. 2013) and disposition index (DI = S_I × AIRg) (Utzschneider et al. 2009).

Whole body phenylalanine rate of disappearance (R_d), rate of appearance (R_a) and metabolic clearance rates (MCR values) were calculated as described previously (Bergman et al. 1989; Gastaldelli et al. 1999; Barclay et al. 2020). Raw data for insulin and phenylalanine metabolism are openly available via figshare: https://doi.org/10.6084/m9.figshare.12886943.

Statistical analysis
R software (R Foundation for Statistical Computing, Viena, Austria) and the Lme4 package (Bates et al. 2015) were used to perform linear mixed effects analyses of the relationship between insulin, phenylalanine or protein values, and time and condition (controls and MHD). Condition interacting with time was entered as a fixed effect into the model, whereas the main effects of subjects and time were considered as the random effects. If the null hypothesis was rejected, post hoc tests were performed to determine which groups differed from each other. P < 0.05 was considered statistically significant.

Results
ISI
HOMAIR and HOMA_{β-Cell} (P > 0.05) were comparable between groups, suggesting no difference metabolic dysfunction between MHD and non-MHD individuals (data not shown). Estimations of ISI and β-cell function based on the 59 g of oral carbohydrate load are shown in Fig. 1. These data show that there were no significant differences for ISI (P = 0.3948) (Fig. 1A). β-cell function was also similar between groups with AIRg (P = 0.2006) (Fig. 1B), second phase insulin response to oral glucose (P = 0.8286) (Fig. 1C) or DI (P = 0.5605) (Fig. 1D), showing no difference at 2 h after feeding.

Whole-body protein metabolism was estimated using L-[ring-2H5]phenylalanine to allow for the calculations of phenylalanine R_d, R_a and MCR (Fig. 2) from time 0 to 300 min of the postprandial period. The MHD group showed a significant decrease in R_d, (P = 0.0451 at 30 min; P = 0.0131 at 60 min; P = 0.0002 at 90 min and P = 0.0015 at 300 min) (Fig. 2A and B), R_a (P = 0.0007 at 30 min; P = 0.0022 at 60 min; P = 0.0003 at 90 min and P = 0.00141 at 300 min) (Fig. 2C and D) and MCR (P = 0.0021 at 30 min; P = 0.0025 at 60 min; P = 0.0001 at 90 min and P = 0.0003 at 300 min) (Fig. 2E and F) in the 300 min after feeding that, overall, was not apparent for the control group. In the controls, R_d, (P = 0.9664 at 30 min; P = 0.9933 at 60 min; P = 0.1129 at 90 min and P = 0.2512 at 300) (Fig. 2A and B) and R_a (P = 0.6071 at 30 min; P = 0.3175 at 60 min; P = 0.1523 at 90 min and P = 0.903 at 300 min) (Fig. 2C and D) did not show relevant changes after feeding, whereas MCR (Fig. 2E and F) only showed a decrease at 90 min (P = 0.0247) and 300 min (P = 0.0252), but not at 30 min (P = 0.7865) or 60 min (P = 0.6762). There were significantly differences at 30 min for R_d (P = 0.0476) and MCR (P = 0.0345), but not for R_a (P = 0.1595), between groups.

Both R_d (P = 0.0501) and R_a (P = 0.0402) were significantly different at 60 min, whereas MCR expressed a tendency to be different (P = 0.0695). Similar trends between groups were observed at 90 min (R_d, P = 0.2539; R_a, P = 0.4363; MCR, P = 0.1637) and 300 min (R_d, P = 0.2977; R_a, P = 0.415; MCR, P = 0.4043).

Human skeletal muscle analysis
We investigated total and phosphorylated states of proteins implicated in the integrin signalling cascade, as well as those involved in the insulin-dependent pathway in eight MHD patients and eight controls. From the western blot analyses, ILK (Fig. 3A) and PINCH1 protein content (Fig. 3B), proxy indicators of integrin signalling activity, were significantly reduced in the MHD patients compared to the controls in both the fasted (P = 0.0133 and P = 0.0001, respectively) and postprandial (P = 0.0001 and P = 0.0001, respectively) state. pFAK_Tyr397/total FAK (Fig. 3D) was also reduced in MHD; however, statistical analyses revealed a significant decrease in the fasted state (P = 0.0026), but not in the postprandial (P = 0.1164) state. The actin cytoskeleton regulating protein Rac1 was not different in MHD compared to control (P = 0.5783 and P = 0.3024 in the fasted and postprandial states, respectively) (Fig. 3E). Representative blots are shown in Fig. 3H. No difference was noted for either Akt2 (P = 0.8552 and P = 0.2496 in the fasted and postprandial...
states, respectively) (Fig. 4A) or IP6K1 ($P = 0.4544$ and $P = 0.2759$ in the fasted and postprandial states, respectively) (Fig. 4B) between groups. Representative blots are shown in Fig. 4C. Parvin ($P = 0.6778$ fasted and $P = 0.2886$ postprandially) (Fig. 4C), total FAK ($P = 0.3963$ fasted and $P = 0.6549$ postprandially) (Fig. 4E) and dystrophin ($P = 0.3091$ fasted and $P = 0.437$ postprandially) (Fig. 4G) were similar between groups. No bands were detected for phosphorylation targets at AktS473 or AktT308 in control or in MHD skeletal muscles (data not shown). No significant differences were observed in protein content between fasted and postprandial state for ILK ($P = 0.1742$ for MHD and $P = 0.5391$ for controls) (Fig. 3A), PINCH1 ($P = 0.5384$ for MHD and $P = 0.2276$ for controls) (Fig. 3B), parvin ($P = 0.6804$ for MHD and $P = 0.4003$ for controls) (Fig. 3C), pFAKTyr397 ($P = 0.9352$ for MHD and $P = 0.2554$ for controls) (Fig. 3D), dystrophin ($P = 0.1533$ for MHD and $P = 0.1324$ for controls, Fig. 3G) or IP6K1 ($P = 0.7282$ for MHD and $P = 0.0783$ for controls) (Fig. 4B), except for total FAK and Rac1, which resulted significantly decrease post meal ingestion in controls ($P = 0.0342$ (Fig. 3E) and $P = 0.033$ (Fig. 3F), respectively), but not in the MHD ($P = 0.0551$ and $P = 0.052$, respectively) and total Akt2 that resulted reduced post meal in the MHD group ($P = 0.0051$) (Fig. 4A), but not in the controls ($P = 0.0693$).

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**Rac1 mKO mouse muscle analysis**

In a separate experiment, skeletal muscle from nine muscle-specific Rac1 knockout (Rac1 mKO) and seven wild-types was analysed. Rac1 is a well-known regulator of the actin cytoskeleton (JeBailey et al. 2007), although it is unknown whether Rac1 regulates the protein expression of the integrin nexus and actin cytoskeleton proteins. Rac1 deletion did not alter the expression of integrin-associated proteins compared to the wild-type in skeletal muscle [ILK, $P = 0.774$ (Fig. 5A); PINCH1, $P = 0.0589$ (Fig. 5B); parvin, $P = 0.0696$ (Fig. 5C); pFAKTyr397, $P = 0.9984$ insulin-stimulated and $P = 0.9116$ not insulin-stimulated, (Fig. 5D); total FAK, $P = 0.9784$ (Fig. 5E)] confirming the results obtained in the MHD human samples, where Rac1 protein expression was unaltered. Also, pAktS473 ($P = 0.2496$ insulin-stimulated and $P = 0.9974$ not insulin-stimulated) (Fig. 5G), pAktT308 ($P = 0.8119$ insulin-stimulated and $P = 0.9986$ not insulin-stimulated) (Fig. 5H) and total Akt2 ($P = 0.857$, Fig. 5I) levels were not altered by the lack of Rac1 as also reported previously (Raun et al. 2018). The activity of both pAktS473 and pAktT308 increased under insulin stimulation within the Rac1 mKO ($P = 0.0551$ and $P = 0.0509$, respectively, Figure 5G and H) as well as within the wild type ($P = 0.0022$ and $P = 0.0247$, respectively, Figure 5G and H) compared with saline. pFAKTyr397 activity was unaltered.
by insulin stimulation within both groups (Rac1 mKO; \( P = 0.4904 \) and \( P = 9127; \) WT, Figure 5D), confirming the results observed in the MHD models, where a decrease in pFAK\(^{Tyr397} \), together with ILK or PINCH1 did not alter insulin sensitivity's levels in MHD compared to controls. Furthermore, IP6K1 (\( P = 0.3278 \) ) (Fig. 5F) and dystrophin (\( P = 0.2054 \) ) (Fig. 5I) expression was similar in both Rac1 mKO and wild-type. Blots in Fig. 5M and N were cropped from the same membrane.

**Discussion**

The present study investigated integrin-associated protein signalling in skeletal muscle of MHD patients. In addition, using a Rac1 KO insulin resistant rodent model, we also examined the potential role that this important actin–cytoskeleton regulatory protein would play in upstream integrin-associated signalling in skeletal muscle. We hypothesized that integrin-associated protein expression would be reduced in both MHD patients

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**Figure 2. Whole-body phenylalanine kinetics**

Whole-body phenylalanine kinetics at baseline and postprandial for both MHD and controls (MHD, \( n = 8 \) and controls, \( n = 8 \)). Phenylalanine \( R_d \) (A and B), phenylalanine \( R_d \) (C and D) and phenylalanine MCR (E and F) at baseline, as well as 30, 60, 90 and 300 min post meal ingestion. A, C, and E, phenylalanine trend over time of each individual. B, D, and F, individual data points, quartiles and means. *Significant difference between MHD and non-MHD (\( P < 0.05 \)). †Significant differences from time 0. \( P < 0.05 \), \( P < 0.01 \), \( P < 0.001 \). \( \dagger P < 0.05 \), \( \dagger \dagger P < 0.01 \), \( \dagger \dagger \dagger P < 0.001 \).
Evidence suggests that the over development of the ECM structure is linked to increased insulin resistance in mouse models (Kang et al. 2011, 2013, 2014; Williams et al. 2015) as a result of a proposed increase in the physical barrier to hormonal and nutrient transport across the sarcolemma (Jansson, 2007; Williams et al. 2015). In support of this, Williams et al. (2015) suggested that ECM protein accumulation within the interstitial space impedes substrate transport as a result of increased diffusion distance. Located directly downstream of the ECM structure,
cytoplasmic integrin-associated proteins appear to have an important role as effectors in integrins signalling in skeletal muscle, providing an essential linkage between the ECM, the sarcolemma and the actin–cytoskeleton (Gheyara et al. 2007), therefore contributing to ECM structure stability. Integrin-deficient mice show progressive muscle dystrophy after birth (Mayer et al. 1997) as a result of a decreased function of the myotendinous junction (MTJ), which gives structural stability between ECM and the associated myofibrils and their non-contractile structural proteins (Postel et al. 2008). The central component of the IPP complex, ILK, is recruited to the MTJ, which requires the presence of the ECM protein laminin, as well as integrin-α7 in the sarcolemma (Postel et al. 2008), suggesting the involvement of ILK in ECM stability. In line with our hypothesis, our data showed a reduction in integrin-associated ILK and PINCH1, suggesting that MHD patients may present with reduced stability in the extracellular matrix as a result of dysregulation of integrin-associated protein signalling.

Yet the influence of a reduced integrin-associate protein nexus on nutrient uptake is unclear. The research suggests that the over development of the ECM and its transmembrane associated structures are linked to insulin resistance in mouse models (Kang et al. 2011, 2013, 2014; Williams et al. 2015). In support of this Williams et al. (2015) have shown that ECM protein accumulation within the interstitial space impedes substrate transport. Conversely, Kang et al. (2013) demonstrated that a reduction of ECM-associated glycosaminoglycan hyaluronan induced by i.v. injection of PEGylated recombinant hyaluronidase PH-20 led to a dose-dependent increase in glucose infusion rates and glucose clearance in mouse skeletal muscle during a hyperinsulinemic–euglycaemic clamp. Taken together, these data may suggest that an increase in protein content within both the interstitial space and ECM is linked to insulin resistance and reduced nutrient transport, whereas a reduction in the protein content within these compartments may increase nutrient uptake as a result of a reduction in the physical barrier between the ECM and the intracellular compartments. Therefore, we further postulated that a reduction in the integrin-associated nexus and a reduction in ECM structural protein content may result in increased phenylalanine flux and improved glucose handling in MHD patients during the post-absorptive state (Williams et al. 2015).

Total phenylalanine rate of appearance (Rₐ) is a measure of the appearance of dietary protein-derived phenylalanine and that from whole body protein breakdown into circulation (van Vliet et al. 2018), whereas phenylalanine Rₐ and MCR reflect whole-body amino acid clearance and its subsequent utilization and storage to the different tissue compartments within the body (Matthews, 2007; Barclay et al. 2020).

In the present study, we show that one-compartment models of the Matsuda index (ISI) and disposition index (DI) were similar between groups, whereas phenylalanine Rₐ, Rₐ and MCR rates decreased immediately after time 0 in MHD but not in controls, who maintained a more constant trend over time, suggesting that the haemodialysis group may suffer from decreased skeletal muscle amino acid uptake and utilization in the post-absorptive state. Moreover, phenylalanine Rₐ, Rₐ and MCR were also significantly lower in the period immediately after feeding (30 and 60 min) in the MHD group. Taken together, these results suggest that disruptions to the integrin-associate protein nexus may contribute to dysregulation in amino acid metabolism but not ISI (Fig. 1).

![Figure 4. Skeletal muscle protein content for Akt2 and IP6K1](image)

Skeletal muscle protein content for Akt2 (A) and IP6K1 (B) in the fasted state and post meal ingestion (MHD, n = 8 and controls, n = 8). Representative western blots of the proteins of interest including the corresponding Coomassie brilliant blue staining, except for IP6K1 (C). No significant difference was noted (P > 0.05). †Significant differences between fasted and post meal within the same group. †P < 0.05, ††P < 0.01, †††P < 0.001. Quartiles, means and individual data points are shown.
Figure 5. Skeletal muscle protein content of targets of interest in TA muscles
Skeletal muscle protein content of targets of interest in TA muscles of chow-fed WT (n = 7) and Rac1 mKO mice (n = 9). Insulin-stimulated and not insulin-stimulated (saline) samples were considered as separated groups for the phosphorylated proteins. Content of ILK (A), PINCH1 (B), parvin (C), pFAK Tyr397/total FAK (D), total FAK (E), IP6K1 (F), pAkt S473/total Akt2 (G), pAkt T308/total Akt2 (H), total Akt2 (I) and dystrophin (J). Representative western blots of Rac1 including the corresponding Coomassie brilliant blue staining, confirming the effectiveness of knockout (K). Representative blots including the corresponding Coomassie brilliant blue staining (L). Analogous results were obtained in gastrocnemius mouse muscles. No significant difference was noted (P > 0.05). † Denotes significant differences between saline and insulin stimulation within the same group. † P < 0.05, †† P < 0.01, ††† P < 0.001. Quartiles, means and individual data points are shown.

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We have previously shown that MHD patients demonstrated an anabolic resistance of muscle protein synthesis rates after mixed meal ingestion, supporting the notion that MHD patients may present with dysregulation in amino acid flux and metabolism (van Vliet et al. 2018). The findings from the present study suggest that this dysregulation in amino acid metabolism may be partly attributed to disruptions to the integrin-associate protein nexus in skeletal muscle. A decrease in the integrin-associated proteins may be explained by a separate finding that MHD patients display both increased basal myofibrillar protein synthesis and muscle caspase-3 protein content (van Vliet et al. 2018). This evidence, together with increased basal muscle protein synthesis and degradation rates, may indicate that MHD muscle is over-stimulated and remains in a state of constant flux (van Vliet et al. 2018). However, it is not clear why phenylalanine flux is reduced in MHD patients given that amino acid requirements are probably increased, given the raised muscle protein synthesis and breakdown rates in this population. However, this raised turnover may be linked to an up-regulation in the genes regulating the ubiquitin proteasome pathway (Hasselgren, 1999; Lecker et al. 1999; Mitch et al. 1999; Bodine et al. 2001; Ikemoto et al. 2001; St-Amand et al. 2001; Bey et al. 2003; Stevenson et al. 2003; Urso et al. 2006). In addition, the reduction in phenylalanine flux post meal, and thus the proposed availability to cell demands, may partly explain why this population group presents with both reduced muscle mass (van Vliet et al. 2018) and muscle atrophy (Johansen et al. 2003). Interestingly, van Vliet et al. (2018) also showed that both basal and fed-state muscle LAT1 protein content are decreased in MHD patients. LAT1 is an amino acid transporter found in proximity of capillaries (Hodson et al. 2018; van Vliet et al. 2018). Blood flow and capillary recruitment play a fundamental role in nutrient and hormonal delivery to muscle (Mitch et al. 1999; Williams et al. 2015). Therefore, a decrease in this protein in MHD could be a result of capillary rarefaction in MHD skeletal muscles, which is linked to insulin resistance and poor nutrients perfusion (Mitch et al. 1999; Solomon et al. 2011; Bonner et al. 2013; Williams et al. 2015), a finding that may also have contributed to the reduced phenylalanine flux observed in our MHD sample.

Several studies suggest a role of the IPP complex in muscle degeneration (Gheyara et al. 2007; Postel et al. 2008). Postel et al. (2008) showed that zebrafish unable to express ILK developed mechanical instability in skeletal muscle. In addition, ILK-KO mice displayed progressive muscular dystrophy, with ILK mutants showing displacement of FAK, dystrophin and α7β1D-integrin subunits (Gheyara et al. 2007). These results are similar to those observed in mice and humans lacking α7-integrin subunit, suggesting that ILK may act as a cytoplasmic effector of α7β1-integrin in the pathogenesis of muscle degeneration (Gheyara et al. 2007; Postel et al. 2008). The adapter protein PINCH1 is known to bind with ILK and locates to integrin-mediated adhesion sites (Li et al. 2005; Stanchi et al. 2009; Karaköse et al. 2015). Several studies suggest a crucial role of PINCH1 in promoting cell adhesion, ECM assembly, muscle attachment and Akt activity (Wu, 1999; Eke et al. 2010; Vakaloglou & Zervas, 2012). Genetic ablation of PINCH1 in skeletal muscle results in cell death at the embryonic stage in mice (Sakai et al. 2003; Li et al. 2005; Wickström et al. 2010). Moreover, the interaction between ILK and PINCH1 is necessary to prevent degradation of IPP complex (Fukuda et al. 2003; Li et al. 2005), suggesting that defects in one of these proteins lead to impairment of the associated kinases of the IPP complex, partly supported by our finding that showed significant reductions in the protein content of ILK and PINCH1 in MHD skeletal muscle.

The inositol hexakisphosphate (IP6) kinase1 (IP6K1) produces the diphosphoinositol pentakisphosphate, which competes with phosphatidylinositol (3,4,5)-trisphosphate with respect to binding the pleckstrin homology domain of Akt, preventing Akt translocation to the cell membrane and its phosphorylation by PDK1, leading to decreased muscle ISI (Naufahu et al. 2018). IP6K1 can therefore represent a negative feedback mechanism in the insulin-dependent Akt pathway, which has been shown to be increased in insulin resistant models, whereas Akt is reduced (Chakraborty et al. 2010; Naufahu et al. 2018).

We further hypothesized that disruptions to the integrin-actin cytoskeleton linkage, largely as a result of impairments in the Rho GTPase Rac1, would result in upstream dysregulation of integrin-associated protein and Akt signalling in skeletal muscle, showing a decrease in Akt activity and an increase in IP6K1 protein, which may then contribute to the reduced nutrient handling in MHD patients. By contrast, our results showed that Rac1, as well as Akt2 and IP6K1, were similar in MHD muscle compared to insulin resistant matched controls despite differences in ILK and PINCH1.

These finding give rise to two notions (i) Rac1 and Akt2 probably do not play a major role in the development of insulin resistance in MHD muscle, given that MHD and controls present with similar levels of insulin resistance and muscle protein content of Rac1 and Akt2 and (ii) Rac1 is not essential for upstream integrin-associated protein regulation. In a separate experiment, we used a Rac1 KO rodent model to further investigate the role of this molecule on the integrin-associated protein signalling. These experiments revealed that there was no difference in the IPP complex protein content in Rac1 mKO compared to wild-type rodents. Both Rac1 and Akt are important regulators of insulin-stimulated glucose transport (JeBailey et al. 2007; Ueda et al. 2010; Sylow et al. 2013a, 2014; Moller et al. 2019). Several
studies suggest that Akt2 and Rac1 bifurcate downstream of phosphoinositide 3-kinase (Nozaki et al. 2012; Satoh, 2014; Takenaka et al. 2015) into two distinct parallel pathways, both promoting GLUT4 trafficking and muscle glucose uptake in an insulin-dependent manner (JeBailey et al. 2007; Ueda et al. 2008, 2010; Sylow et al. 2014; Raun et al. 2018; Moller et al. 2019), which is regulated via actin cytoskeleton organisation (Jaffe & Hall, 2005; Chiu et al. 2011; Sit & Manser, 2011; Spiering & Hodgson, 2011; Moller et al. 2019). Our data show that Rac1 is not different between MHD and non-MHD individuals and that both display similar degrees of ISI. In addition, our KO Rac1 mouse model showed no difference in integrin-associated proteins compared to the wild-type. Taken together, these data suggest that Rac1 may not be required for effective actin-integrin structural stability/remodelling or nutrient flux in MHD skeletal muscle. However, we cannot completely rule out a contribution of Rac1 in these processes. We recognize that whole-body phenylalanine kinetics and ISI are not direct measures of local amino acid turnover or insulin action in skeletal muscle, yet it has been recognized that skeletal muscle is a major disposal site for amino acids (Chang & Goldberg, 1978) and glucose (Thiebaud et al. 1982) in the postprandial state. We do acknowledge the limitations of our measurement and admit that the inclusion of multiple amino acid tracers and two-compartment models of glucose metabolism and ISI would offer a more accurate measures nutrient kinetics in this population. We also acknowledge that we analysed small sample size groups; therefore, further research involving more participants is required to give more robustness to our findings.

Conclusions

In conclusion, our results suggest that neither ISI, nor DI appear to be different between MHD patients and controls in the postprandial state. This finding may be explained by the similar levels of Rac1 and Atk2, two protein kinases implicated in insulin-dependent glucose uptake. Phenylalanine metabolism was lower within the MHD group, which may be linked to disruptions to the ILK-PINCH1 nexus and LAT1 (van Vliet MHD group, which may be linked to disruptions to the protein kinases implicated in insulin-dependent glucose metabolism). Hence, the similar levels of Rac1 and Atk2, two controls in the postprandial state. This finding may be different between MHD patients and non-MHD individuals, therefore, further research involving more participants is needed. We also acknowledge that we analysed small sample size groups; measures nutrient kinetics in this population. We also recognize that Rac1 is not different between MHD and non-MHD patients. Taken together, these data suggest that Rac1 may not be required for effective actin-integrin structural stability/remodelling or nutrient flux in MHD skeletal muscle. However, we cannot completely rule out a contribution of Rac1 in these processes. We recognize that whole-body phenylalanine kinetics and ISI are not direct measures of local amino acid turnover or insulin action in skeletal muscle, yet it has been recognized that skeletal muscle is a major disposal site for amino acids (Chang & Goldberg, 1978) and glucose (Thiebaud et al. 1982) in the postprandial state. We do acknowledge the limitations of our measurement and admit that the inclusion of multiple amino acid tracers and two-compartment models of glucose metabolism and ISI would offer a more accurate measures nutrient kinetics in this population. We also acknowledge that we analysed small sample size groups; therefore, further research involving more participants is required to give more robustness to our findings.

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Additional information

**Data availability statement**

The data that support the findings of this study are openly available in figshare at: https://doi.org/10.6084/m9.figshare.12886943.

**Competing interests**

The authors declare that they have no competing interests.

**Author contributions**

FD, RM and LS contributed to the conception and design of the experiment. FD and RM contributed to the analysis and...
interpretation of data. RM, OA, KRW, SVV, PW, DR and NAB contributed to drafting the article or revising it with respect to intellectual content. FD and RM had primary responsibility for the final content. Each author contributed important intellectual content during the drafting or revision of the article, accepts personal accountability for the author’s own contributions, and agrees to ensure that questions pertaining to the accuracy or integrity of any portion of the work are appropriately investigated and resolved.

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**Keywords**

cytoskeleton, haemodialysis, ILK, insulin, integrins, metabolism, phenylalanine, PINCH, Rac1

**Supporting information**

Additional supporting information may be found online in the Supporting Information section at the end of the article.

**Statistical Summary Document**