RESEARCH

**Dysregulated healing responses in diabetic wounds occur in the early stages postinjury**

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**Abstract**

Chronic wounds are a serious and debilitating complication of diabetes. A better understanding of the dysregulated healing responses following injury will provide insight into the optimal time frame for therapeutic intervention. In this study, a direct comparison was done between the healing dynamics and the proteome of acute and obese diabetic wounds on days 2 and 7 following injury. Full thickness excisional wounds were induced on obese diabetic (B6.Cg-lepob/J, ob/ob, n = 14) (blood glucose 423.25 ± 127.92 mg/dL) and WT control (C57BL/6J, n = 14) (blood glucose 186.67 ± 24.5 mg/dL) mice. Histological analysis showed no signs of healing in obese DM wounds whereas complete wound closure/re-epithelisation, the formation of granulation tissue and signs of re-vascularisation, was evident in acute wounds on day 7. In obese DM wounds, substance P deficiency and increased MMP-9 activity on day 2 coincided with increased cytokine/chemokine levels within wound fluid. LC-MS/MS identified 906 proteins, of which 23 (Actn3, Itga6, Epb41, Sncg, Nefm, Rsp18, Rsp19, Rpl22, Macros2a1, Rpn1, Ppib, Snrnp70, Ddx5, Eif3g, Tpt1, FABPS, Cavin1, Stfa1, Stfa3, Cycs, Tkt, Mb, Chmp2a) were differentially expressed in wounded tissue on day 2 (P < 0.05; more than two-fold) and 6 (Cfd, Ptns, Hp, Hmgal, Cbx3, Syap1) (P < 0.05; more than two-fold) on day 7. A large number of dysregulated proteins on day 2 was associated with an inability to progress into the proliferative stage of healing and suggest that early intervention might be pivotal for effective healing outcomes. The proteomic approach highlighted the complexity of obese DM wounds in which the dysregulation involves multiple regulatory pathways and biological processes.

**Key Words**

- wound healing
- diabetes
- inflammation
- substance P

**Introduction**

Depending on the underlying cause, chronic wounds are subdivided into three main classes that is, leg ulcers (associated with venous disease), pressure ulcers/pressure injuries (associated with prolonged bed rest) and diabetic foot ulcers (DFUs) (associated with uncontrolled hyperglycaemia). Of these, DFUs are the most common and very difficult to treat, with standard of care involving debridement, offloading and infection control with amputation often being necessitated. It, therefore, places a socio-economic burden on the patients and enormous
financial strain on health care systems worldwide (Alexiadou & Doupis 2012, Frykberg & Banks 2015, Jones et al. 2019). In 2017, approximately 8.8% of the world's population was affected by diabetes mellitus (DM) and this percentage is projected to increase to 9.9% by the year 2045 (Cho et al. 2018). The prevalence of DFUs in DM patients is 4–10%, with a lifetime risk of 25% and due to the lack of effective treatment strategies, DFUs have a 20–80% recurrence rate (Mulder et al. 2012, Cho et al. 2018). The mortality rate amongst DFU patients (Alexiadou & Doupis 2012, Steyaert 1999, Antezana et al. 2002, Spenny et al. 2002, Leal et al. 2015). Although these and other characteristics of chronic wounds are well defined a better understanding of the complex interaction associated with dysregulation that occurs following injury is crucial for the development of more effective treatments. Using fine-tuned animal wound models to identify potential therapeutic targets can bridge the translational gap between laboratory-based and clinical studies (Sabino et al. 2018).

This study compared the healing dynamics as well as the proteome of acute wounds with that of non-healing diabetic wounds during the initial and late stages following injury. This will provide significant insight into the optimal time frame for therapeutic intervention and aid in identifying critical role players at the different stages postinjury involved in the dysfunctional healing responses.

Materials and methods

Ethics statement

This study was approved by the animal research ethics committee (SU-ACUD17-000016) at Stellenbosch University and complied with the South African Animal Protection Act (Act no. 71, 1962). In accordance with the South African National Standards 10386:2008 and the Veterinary and Para-Veterinary Professions Act, 1982, all researchers involved in handling of the animals were authorised by the South African Veterinary Council (SAVC).

Induction of full-thickness excisional wounds and sample collection

Obese DM mice (B6.Cg-lep<sup>ob</sup>/J, ob/ob, n = 14) (10–12 weeks; 46.1 ± 4.2 g) (blood glucose 23.49 ± 7.1 mmol/L or 423.25 ± 127.92 mg/dL) and healthy WT control mice (C57BL/6), n = 14) (10–12 weeks; 27.3 ± 3.1 g) (blood glucose 10.36 ± 1.36 mmol/L or 186.67 ± 24.5 mg/dL) were anaesthetised using isoflurane gas (Safeline Pharmaceuticals, Cape Town, Western Cape, South Africa). Dorsal hair was shaved, and the skin cleaned with povidone-iodine (Mundipharma, Cape Town, Western Africa). Dorsal hair was shaved, and the skin cleaned with povidone-iodine (Mundipharma, Cape Town, Western
Cape South Africa) prior to making two identical bilateral full-thickness skin excisions. The procedure included the removal of the underlying panniculus carnosus layer (Chen et al. 2013). Wounds (5 mm diameter) were located 1 cm below the base of the skull and on either side of the midline. To induce a non-healing obese DM wound, neutral endopeptidase (NEP) (1.02 mg/µL; 150 pmol/h/µg) (SRP6450, Neprylisin/CD10; Sigma-Aldrich) was injected subcutaneously around the wound edges in the ob/ob animals immediately postwounding. The expression of NEP is much greater in the ulcer margins of DFU patients (Antezana et al. 2002) than what is observed in the skin of diabetic animals (delayed healing) and healthy controls (Antezana et al. 2002, Spenny et al. 2002). Exogenous NEP administration into the wound edges of a commonly used diabetic animal model of delayed healing in this study was therefore used to induces a chronic wound that more closely mimic DFUs. Acute wounds were induced on WT control mice (saline injection) as parallel control. Additional control groups included WT control mice with NEP injection (n = 3) and streptozotocin-induced hyperglycaemic mice (intraperitoneal injection of 50 mg/kg body weight STZ, 3 days before wounding; blood glucose following STZ-injection 12.1 ± 0.6 mmol/L or 217.9 ± 10.8 mg/dL) with NEP injection (n = 3 per group). Pain management included the injection of a local anaesthetic, 7 mg/kg lignocaine (2%) (Bodene, Port Elizabeth, Eastern Cape, South Africa) immediately postwounding as well as administering 300 mg/kg local anaesthetic, 7 mg/kg lignocaine (2%) (Bodene, Port Elizabeth, Eastern Cape, South Africa) in the drinking water for a period of 3 days.

Wounds were covered by a vapour-permeable PU film (Hydro-film, Paul Hartmann AG, Heidenheim, Baden-Württemberg, Germany) and the accumulated exudate (wound fluid) harvested by needle puncture (Trengove et al. 1999, Schmohl et al. 2012) on day 2 postwounding. After recovery from the anaesthesia, mice were housed individually under standard conditions (12 h light:12h darkness cycle at a controlled temperature of 21°C) with ad libitum access to drinking water and chow (Rat and Mouse Breeder Feed, Animal Specialties, Pty, Ltd., Klapmuts, SA) and their appearance and behaviour closely monitored for signs of distress. Following cervical dislocation, wound tissue including a 5 mm margin was excised. One half of each tissue sample was snap-frozen in liquid nitrogen and stored at −80°C for protein extraction. The other half of each tissue sample was fixed in 10% buffered formalin solution and embedded in paraffin wax for histological analysis (hematoxylin & eosin; Masson’s Trichrome staining) using standardised techniques.

Assessment of macroscopic wound closure and wound fluid analysis

Wound images were taken on days 0, 2 and 7 using a Canon digital camera (EOS 600D, Canon Inc, Taiwan). The surface area (cm²) for each wound and the percentage wound closure was determined using Image J software (version 1.46, NIH.gov, USA). Wound fluid collected on day 2 was analysed using a Bio-Plex Pro Mouse Cytokine 23-plex assay (M60009RDPD, Bio-Rad) according to the manufacturer’s instructions. The cytokines assessed included Eotaxin, granulocyte colony-stimulating factor (G-CSF), granulocyte macrophage colony-stimulating factor (GM-CSF), interferon gamma (IFNγ), interleukin (IL)-1α, IL1β, IL2, IL3, IL4, IL5, IL6, IL9, IL10, IL12(p40), IL12(p70), IL13, IL17A, keratinocyte chemoattractant protein (KC), macrophage chemoattractant protein (MCP)-1, macrophage inflammatory protein (MIP)-1α, MIP-1β, RANTES and TNF alpha (TNFa). Note: due to the small volume of wound fluid collected from each animal it was necessary to pool the wound fluid from all the animals within each group prior to analysis (n = 4 per group).

MMP-9 expression in wounded tissue

The expression of MMP-9 within the wounded tissue was assessed using a sandwich ELISA kit (AB100732, Abcam) according to the manufacturer’s instructions. Snap frozen tissue samples (100 mg) were homogenised in liquid nitrogen. Assay buffer (400 µL) containing 1 mM phenylmethanesulfonyl fluoride (PMSF) (1083709100, Sigma-Aldrich) and 10 µg/mL Aprotinin (A1153-5MG, Sigma-Aldrich) was added to each sample, incubated on ice (10 min) and centrifuged at 4°C for 10 min at 12,000 g. The protein concentration within the supernatant was determined using a NanoDrop™ 2000/2000c (Thermo Fisher Scientific) (260/280 nm) and samples stored at −20°C. For each sample 6 µg of protein was used in the ELISA and the absorbance read at 450 nm using a micro-plate reader (Multiskan GO 1.00.40, Thermo-Scientific Group).

Immunohistochemistry substance P

Standard immunohistochemistry techniques were used to assess the expression of substance P antibody within the wounded area using a primary anti-substance P antibody (ab10353, Abcam) and an HRP enzyme-conjugated secondary antibody (ab6789, Abcam). Images were taken at 5× magnification using the Zeiss Axio Vision microscope (Zeiss Axio Observer 7 Inverted microscope, Zeiss).
The expression of substance P (% surface area) was determined using Image J software (version 1.46, NIH.gov, USA).

**Histology quantification of healing dynamics**

Tiles scan images of H&E and Masson’s Trichrome stained sections were taken at 10x magnification using the Zeiss Axio Vision microscope (Zeiss Axio Observer 7 Inverted microscope, Zeiss). Assessment of the histological parameters such as granulation tissue thickness (µm), epithelial thickness (µm), cellularity (nuclei within granulation tissue) (% surface area) and the number of blood vessels formed within granulation tissue was performed using Image J software (version 1.46, NIH.gov, USA). The histology index was calculated for each wound as indicated in **Table 1**.

**Protein extraction for proteomics**

Homogenised tissue samples (100 mg) were incubated in 89% ethanol containing 50 mM Tris(2-carboxyethyl)phosphine (TCEP; Fluka, Sigma-Aldrich), 1% acetic acid (Sigma-Aldrich) and 1 mg/mL caffeine (Pierce) for 1 h at 4°C. The supernatant was sonicated in methanol (Sigma-Aldrich) and 1 mg/mL caffeine (Pierce) for 1 h at 4°C. The supernatant was removed, and the pellet was sonicated (10 min at 4°C) with 600 µL of methyl tert-butylether (MTBE; Sigma-Aldrich) for 1 h at 4°C. Phase separation was induced by adding 100 mM triethylammonium bicarbonate (TEAB; Sigma-Aldrich) to each sample and centrifugation (14 min at 12,000 g). Four volumes of methanol (Sigma-Aldrich) was added to the lower phase and centrifugated at 12,000 g for 10 min. The supernatant was removed, and the pellet was sonicated (10 min at 4°C) with 200 µL 50 mM TEAB pH 7.8 containing 8 M urea (Sigma-Aldrich), 0.5% SDS and a protease inhibitor cocktail (Sigma-Aldrich). Four volumes of methanol were added, and samples centrifuged at 12,000 g for 10 min. The supernatant was removed, and protein pellet was retained for proteomic analysis. The protein samples underwent an on-bead digestion step followed by a peptide quantification assay (Bradford assay). Samples were resuspended in 50 mM triethyl ammonium bicarbonate (TEAB; Sigma-Aldrich) before reduction with 5 mM tris(carboxyethyl)phosphine (TCEP; Fluka, Sigma-Aldrich) 50 mM TEAB for 1 h at 60°C. Cystein residues were thiomethylated with 20 mM S-methyl methanethiosulfonate (Sigma-Aldrich) in 50 mM TEAB (Sigma-Aldrich) for 30 min at room temperature. After thiomethylation the samples were diluted two-fold with binding buffer (100 mM sodium acetate, 30% acetonitrile, pH 4.5). The protein solution was added to MagResyn (Resyn Biosciences, Pretoria, Gauteng, South Africa) HILIC magnetic particles prepared according to manufacturer’s instructions and incubated overnight at 4°C. After binding the supernatant was removed and the magnetic particles washed twice with washing buffer (100 mM sodium acetate, 15% acetonitrile, pH 4.5). After washing the magnetic particles were suspended in 50 mM TEAB containing trypsin (New England Biolabs, Ipswich, MA, USA) to a final ratio of 1:10. After a 6 h incubation at 37°C the peptides were extracted once with 50 µL water and once with 50% acetonitrile:water; 0.1% FA. Residual digest reagents were removed using an in-house manufactured C18 stage tip (Empore Octadecyl C18 extraction discs; Supelco). The samples were loaded onto the stage tips after activating the C18 membrane with 30 µL methanol (Sigma-Aldrich) and equilibration with 30 µL 2% acetonitrile:water; 0.05% TFA. The bound sample was washed with 30 µL 2% acetonitrile:water; 0.1% TFA before elution with 30 µL 50% acetonitrile:water; 0.05% TFA. The eluate was evaporated to dryness. The dried peptides were dissolved in 2% acetonitrile:water; 0.1% FA for LC-MS analysis. Half the contents if each vial of isobaric Tandem Mass Tag (TMT) (Thermo Fischer Scientific) were added to 14 µg of each sample. The use of 10-plex isobaric labels allowed the relative quantification of proteins by examining all the biological samples from one time point in a single run.

**Proteomics liquid chromatography and mass spectrometry**

Liquid chromatography (Dionex nano-RSLC) was performed on a Thermo Scientific Ultimate 3000 RSLC equipped with a 5 mm × 300 µm C18 trap column (Thermo Scientific). Amino acids were desalted and concentrated on a C18 extraction disc (Supelco). The samples were loaded onto the disc and washed twice with washing buffer (100 mM sodium acetate, 15% acetonitrile, pH 4.5). The protein solution was added to MagResyn (Resyn Biosciences, Pretoria, Gauteng, South Africa) HILIC magnetic particles prepared according to manufacturer’s instructions and incubated overnight at 4°C. After binding the supernatant was removed and the magnetic particles washed twice with washing buffer (100 mM sodium acetate, 15% acetonitrile, pH 4.5). After washing the magnetic particles were suspended in 50 mM TEAB containing trypsin (New England Biolabs, Ipswich, MA, USA) to a final ratio of 1:10. After a 6 h incubation at 37°C the peptides were extracted once with 50 µL water and once with 50% acetonitrile:water; 0.1% FA. Residual digest reagents were removed using an in-house manufactured C18 stage tip (Empore Octadecyl C18 extraction discs; Supelco). The samples were loaded onto the stage tips after activating the C18 membrane with 30 µL methanol (Sigma-Aldrich) and equilibration with 30 µL 2% acetonitrile:water; 0.05% TFA. The bound sample was washed with 30 µL 2% acetonitrile:water; 0.1% TFA before elution with 30 µL 50% acetonitrile:water; 0.05% TFA. The eluate was evaporated to dryness. The dried peptides were dissolved in 2% acetonitrile:water; 0.1% FA for LC-MS analysis. Half the contents if each vial of isobaric Tandem Mass Tag (TMT) (Thermo Fischer Scientific) were added to 14 µg of each sample. The use of 10-plex isobaric labels allowed the relative quantification of proteins by examining all the biological samples from one time point in a single run.

**Table 1** Histology index.

<table>
<thead>
<tr>
<th>Score</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Little epidermal and dermal organisation (epithelial thickness &lt; 30 µm); &lt;10 capillary vessels; no granulation tissue formation.</td>
</tr>
<tr>
<td>2</td>
<td>Moderate epidermal and dermal organisation (epithelial thickness &lt;100 µm), few newly formed capillary vessels evident, cellular infiltration; granulation tissue thickness (&gt;100 µm).</td>
</tr>
<tr>
<td>3</td>
<td>Complete remodelling of the epidermis and dermis, well-formed capillary vessels.</td>
</tr>
</tbody>
</table>

Scoring parameters were adapted from Galeano et al. (2001).
Scientific) and a nanoEase M/Z Peptide CSH 25 cm × 75 μm 1.7 μm particle size C_{18} column (Waters, Milford, Massachusetts, USA) analytical column. Chromatography was performed at 45°C and the outflow delivered to the mass spectrometer (Thermo Scientific Fusion, Nanospray Flex ionisation source) through a stainless-steel nano-bore emitter. MS1 scans were performed using the orbitrap detector set at 120,000 resolution over the scan range 350–1500 with AGC target at 4E5 and maximum injection time of 50 ms. MS2 acquisitions were performed using monoisotopic precursor selection for ion with charges +2→+7 with error tolerance set to ±10 ppm. Fragment ions were detected in the orbitrap mass analyser set to 50,000 resolution with the AGC target set to 5E4 and the maximum injection time to 80 ms.

**Statistical analysis**

Statistical analysis was performed using GraphPad Prism (version 8.2.0). The normal distribution of data was determined using the Shapiro–Wilks and Kolmogorov–Smirnov test. Data are presented as mean ± S.D. Two-way ANOVAs with Tukey post hoc tests were performed to determine the effect of time, group and group × time. Welch’s T-test with two-tailed P value was used for comparison of the healing dynamics and proteome between the acute and DM wounds. Level of significance was accepted at P < 0.05. P values were multiple testing corrected via the Benjamini–Hochberg FDR procedure to obtain Q-values. Functional pathway analysis and protein interactions were mapped for the differential proteins of interest (P < 0.05) (identified through biostatistical analysis of the LC-MS/MS data) using STRING (version 11.0, string-db.org).

**Results**

**Animal wellness**

All animals tolerated the procedure well with a 100% survival rate observed for a period of 7 days postwounding. Refer to Fig. 1A for representative images illustrating macroscopic wound size on days 0 and 7 in the respective groups. For both the WT saline (body weight 27.3 ± 3.1 g) and obese DM (body weight 46.1 ± 4.2 g) wounded animals, an initial drop in body weight of approximately 3 g (WT 12% decrease (P = 0.0011); obese DM 4–6% decrease), were observed during the first 2 days postwounding. The animals did, however, recovered from this initial weight loss.
(weight day 7; WT 25.2 ± 0.9 g, obese DM 45.6 ± 0.9 g) (Fig. 1B). The body weight for the WT+NEP (29.9 ± 2.4 g) and lean DM+NEP (32.2 ± 0.7 g) groups remained stable throughout the study (Fig. 1B). There were no differences evident in the wellness scores (behaviour) of animals (Fig. 1C).

Wound healing dynamics

To identify the most appropriate model representative of acute and non-healing diabetic wounds, macroscopic wound closure was compared between treatment groups. At 7 days postwounding there was no significant difference in wound closure evident between the WT saline (73.5 ± 9.7%), WT+NEP (74.9 ± 13.2%) and STZ-injected WT+NEP (74.2 ± 16.3%) groups, whereas healing was significantly delayed in obese DM wounds (43.5 ± 21.9%) (Fig. 1A and E). For all subsequent analysis, the WT saline wounds were chosen to represent acute wounds and the obese DM wounds were chosen to represent non-healing diabetic wounds. Immediately postwounding on day 0, there was no difference in wound size (WT 0.359 ± 0.021 cm², obese DM 0.424 ± 0.017 cm²) between the acute and obese DM groups (Fig. 1D). In the acute wounds, significant wound closure and re-epithelisation was evident (day 2: 29.9 ± 6.7%; day 7: 73.5 ± 3.1%) postwounding, whereas obese DM wounds remained open (day 2: 11.7 ± 3.7%; day 7: 43.5 ± 6.9%) with no epithelisation evident (P = 0.008) (Fig. 1A and E). This was confirmed using histological assessment of healing dynamics (Fig. 2A and B). On day 7 postwounding, significant granulation tissue formation (thickness 1015 ± 177 µm) was evident in acute wounds whereas none had formed in the obese DM wounds (P < 0.01) (Fig. 2A and B). Within the granulation

**Figure 2**
Histological comparison of acute and obese diabetic (DM) wounds. (A) Massons Trichrome staining. Representative images illustrating the wound area and wound edges, the formation of granulation tissue and the structural organisation within the wounded area on day 7 postwounding. Dotted line (---) indicates granulation tissue thickness. Arrows indicate capillaries. (B) Hematoxylin & eosin staining. Representative images illustrating the wound area and wound edges, the presence of cell nuclei (blue/purple) within granulation tissue and the epithelial layer. Dotted line (---) indicates the thickness of the newly formed epithelium. A full colour version of this figure is available at https://doi.org/10.1530/JME-20-0256.
tissue, cellularity was evident with nuclei representing 11.4 ± 1.1% of the surface area and newly formed capillaries were clearly visible in the acutely wounded areas (Fig. 2A and B). Quantification of the histological parameters indicated that acute wounds had an overall histological score of 2 ± 1 whereas obese DM wounds had a score of 1 ± 0 on day 7 postwounding with no signs of healing (Table 1).

Substance P and MMP-9

A significant difference was evident between groups with regards to the expression of both MMP-9 and substance P within the wounded area (Fig. 3). Despite variability in the expression of MMP-9 within the obese DM wounds, on day 2 postwounding, MMP-9 levels were four- to eight-fold higher in obese DM compared to acute wounds (P = 0.0297) and remained slightly elevated on day 7 (P = 0.05) (Fig. 3A). Immunohistochemistry illustrated a deficiency in the expression of substance P in the obese DM wounds immediately postwounding (acute 8.7 ± 3.3%; DM 1.5 ± 2.3%) (P < 0.05) as well as on day 2 (acute 19.3 ± 8.8%; DM 4.8 ± 2.6%) (P < 0.05) (Fig. 3B and C). Refer to Fig. 3C for representative images illustrating substance P expression within the wounded areas at each of the respective time points.

Cytokine profile in wound fluid

On day 2 postwounding, the level of pro-inflammatory cytokines, chemokines and anti-inflammatory cytokines within the pooled wound fluid samples were overall higher in the obese DM compared to acute wounds as illustrated in Fig. 4. All of the chemokines assessed were overexpressed with GCSF (acute 516.65 pg/mL; DM 5199.68 pg/mL), KC (acute 89.75 pg/mL; DM 1258.26 pg/mL), MCP1 (acute 166.46 pg/mL; DM 5857.79 pg/mL), MIP1α (acute 82.12 pg/mL; DM 435.79 pg/mL) and MIP1β (acute 139.19 pg/mL; DM 554.89 pg/mL) being the most prominent in obese DM wound fluid. Similarly, the pro-inflammatory cytokines IL1α (acute 28.19 pg/mL; DM 219.04 pg/mL), IL6 (acute 95.54 pg/mL; DM 873.31 pg/mL), IL12(p40) (acute 18.92 pg/mL; DM 44.71 pg/mL), IL12(p70) (acute 10.53 pg/mL; DM 96.87 pg/mL), RANTES (acute 0 pg/mL; DM 72.73 pg/mL) and TNFα (acute 8.87 pg/mL; DM 56.04 pg/mL) were prominent in obese DM wound fluid. In comparison, the expression levels of anti-inflammatory cytokines were relatively low in the obese DM wounds Fig. 4.
Proteome

A total of 906 proteins with each more than three unique peptides were identified (Fig. 5). On day 2 postwounding, 135 differentially expressed proteins ($P < 0.05$) were observed between acute and chronic wounds (Fig. 5A and B) with a prominent cluster of ribosomal protein-interactions evident. Of these 135 proteins, 20 were upregulated more than two-fold and 3 were downregulated (>two-fold) in chronic wounds (Fig. 5C and Table 2). Functional grouping indicated that the dysregulated proteins of interest on day 7 were involved in either immune modulation (Cfd, Ptms, Hp), transcriptional regulation (Hmga1, Cbx3) or neural synapses (syap1). The relative expression levels, as well as the $P$-values for the identified proteins that were either upregulated or downregulated more than two-fold in the obese DM compared to acute wounds at the respective time points, are presented in Table 2.

Discussion

Wound repair is highly complex, comprising a series of coordinated and overlapping processes. Impaired healing is one of the most serious and debilitating complications of DM, yet current treatments are far from optimal (Sen et al. 2009). A better understanding of the complex nature of chronic DM wounds and the dysregulation that occurs at specific stages postwounding is crucial for the development of more effective treatments. A direct comparison of acute and obese DM wounds in the current study clearly illustrates that extensive dysregulation in the healing responses occur within the first 2 days postinjury suggesting that early intervention might be pivotal for effective healing outcomes and to potentially limit the reoccurrence of wounds. Taken together, the data from the current study is consistent with previous observations indicating that the chronic DM wounds have an inability to progress through the normal phases of healing into the proliferative stage (Landén et al. 2016). This was evident in both macroscopic and protein level. Histological analysis showed no signs of healing within the obese DM wounds even after 7 days, whereas complete wound closure/re-epithelisation, the formation of granulation tissue and signs of re-vascularisation was evident in acute wounds. During the early stage postinjury, deficiency in substance P expression and increased protease activity (MMP-9) within the wounded tissues coincided with excessive levels of chemokines and pro-inflammatory cytokines, known to attract phagocytic immune cells, in the wound...
fluid derived from DM wounds. This is consistent with observations from (Fadini et al. 2016) indicating that phagocytic neutrophil associated NETosis is involved in delayed DFU healing. A substantially larger number of dysregulated proteins were furthermore identified in the early stage (day 2) compared to the later stage of healing (day 7) confirming the importance of the initial response in predicting outcome. The proteomic comparison at different stages postwounding furthermore enabled the novel identification of proteins potentially involved in the dysregulated healing responses. These proteins and their known roles in either wound healing-associated processes or diabetes will be discussed based on functional grouping at either the initial (2 days) or late stages (7 days) postwounding.

Initial stages structural proteins (Itga6, Epb41, Actn3)

Integrins have an important function in cell–cell and cell–matrix adhesions and have been shown to play a crucial role in angiogenesis, matrix remodelling and epithelial/fibroblast/keratinocyte migration (Chen et al. 2001, Mercurio et al. 2001, Grose et al. 2002, Desai et al. 2013). The specific α6 subunit has been identified as a candidate gene in high-fat diet-induced DM (Kobayashi et al. 2014) and its expression is altered in various DM comorbidities such as retinopathy (Robbins et al. 1994), neuropathy (Guo et al. 2015) and nephropathy (Jun et al. 1996). Of specific relevance to wound healing is the role of integrin α6 in angiogenesis and fibroblast senescence (Jun & Lau 2010, 2017).
Table 2  Dysregulated proteins of interest in chronic wounds.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Protein</th>
<th>Accession #</th>
<th>Day 2 postwounding (mean ± s.d.)</th>
<th>Day 7 postwounding (mean ± s.d.)</th>
<th>Log2 fold change</th>
<th>P-value</th>
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<tbody>
<tr>
<td>Acb1</td>
<td>Alpha-actinin-3</td>
<td>sp</td>
<td>O88990</td>
<td>ACTN3_MOUSE</td>
<td>1.73 ± 0.21</td>
<td>0.84 ± 0.11</td>
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<tr>
<td>Sip3</td>
<td>Caveolae-associated protein 1</td>
<td>sp</td>
<td>O54724</td>
<td>CAVN1_MOUSE</td>
<td>0.40 ± 0.25</td>
<td>1.08 ± 0.36</td>
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<tr>
<td>Cysc</td>
<td>Cytochrome c</td>
<td>sp</td>
<td>P62897</td>
<td>CYC_MOUSE</td>
<td>2.23 ± 0.61</td>
<td>1.07 ± 0.23</td>
</tr>
<tr>
<td>Ddx5</td>
<td>DEAD-associated protein 1-4</td>
<td>sp</td>
<td>Q66566</td>
<td>DDX5_MOUSE</td>
<td>0.37 ± 0.05</td>
<td>1.10 ± 0.39</td>
</tr>
<tr>
<td>Epfb</td>
<td>Protein 4.1</td>
<td>sp</td>
<td>P48193</td>
<td>41_MOUSE</td>
<td>0.46 ± 0.03</td>
<td>1.05 ± 0.32</td>
</tr>
<tr>
<td>Fabp5</td>
<td>Fatty acid-binding protein 5</td>
<td>sp</td>
<td>Q05816</td>
<td>FABP5_MOUSE</td>
<td>0.46 ± 0.09</td>
<td>1.08 ± 0.17</td>
</tr>
<tr>
<td>Itga6</td>
<td>Integrin alpha-6</td>
<td>sp</td>
<td>Q61739</td>
<td>ITA6_MOUSE</td>
<td>0.61 ± 0.24</td>
<td>1.08 ± 0.20</td>
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<tr>
<td>Macro2a</td>
<td>Core histone macroH2A.1</td>
<td>sp</td>
<td>Q61481</td>
<td>H2AY_MOUSE</td>
<td>0.53 ± 0.14</td>
<td>1.10 ± 0.19</td>
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<tr>
<td>Nefilm</td>
<td>Nucleolar phosphoprotein 2</td>
<td>sp</td>
<td>Q61867</td>
<td>NEF_MOUSE</td>
<td>0.48 ± 0.07</td>
<td>1.00 ± 0.10</td>
</tr>
<tr>
<td>Pppi2</td>
<td>Peptidyl-prolyl cis-trans isomerase B</td>
<td>sp</td>
<td>P24369</td>
<td>PPIB_MOUSE</td>
<td>0.46 ± 0.09</td>
<td>1.04 ± 0.18</td>
</tr>
<tr>
<td>Tpt1</td>
<td>Translationally-controlled tumor protein</td>
<td>sp</td>
<td>P63028</td>
<td>TCTP_MOUSE</td>
<td>0.43 ± 0.08</td>
<td>1.04 ± 0.27</td>
</tr>
<tr>
<td>Cdx3</td>
<td>Chromobox protein homolog 3</td>
<td>sp</td>
<td>P23198</td>
<td>CBX3_MOUSE</td>
<td>1.32 ± 0.34</td>
<td>0.62 ± 0.16</td>
</tr>
<tr>
<td>Dnajc3</td>
<td>Hsp70-Related protein 1</td>
<td>sp</td>
<td>P35173</td>
<td>DJA1_MOUSE</td>
<td>0.42 ± 0.11</td>
<td>1.14 ± 0.43</td>
</tr>
<tr>
<td>Lrp18</td>
<td>Transmembrane protein homolog 3</td>
<td>sp</td>
<td>P22730</td>
<td>LRT7_MOUSE</td>
<td>0.21 ± 0.02</td>
<td>1.07 ± 0.27</td>
</tr>
<tr>
<td>Synap-associated protein 1</td>
<td>Synap-associated protein 1</td>
<td>sp</td>
<td>P40142</td>
<td>TCK_MOUSE</td>
<td>0.36 ± 0.07</td>
<td>1.03 ± 0.36</td>
</tr>
</tbody>
</table>

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Jun and Lau (2017) demonstrated that the fibrosis associated gene, Ccn2 induce fibroblast senescence through integrin α6β1-mediated accumulation of ROS that in turn activates p53 signalling. The senescent-associated secretory phenotype (SASP) in fibroblasts, in turn, upregulates the expression of MMPs and downregulate collagen production, which restricts fibrosis in normal cutaneous wound healing (Jun & Lau 2010), but excessive signalling could hamper regeneration as was evident in the DM wounds. During angiogenesis, integrin α6 heterodimerise with the β1/4 subunit to regulate endothelial cell-matrix interactions. In functional angiogenesis, integrin α6 must be downregulated during the early stages but is essential for vessel maturation during the later stages and is therefore dynamically regulated (Desai et al. 2013). In the current study, integrin α6 was overexpressed during the initial stages postwounding and could potentially be implicated in the lack of revascularisation in DM wounds. Although cause–effect could not be established in the current study, the role of integrin α6 dysregulation in impaired healing is supported by the observations from Desai et al. (2013).

The two other structural proteins identified in this study include Protein 4.1 (Epb41) and alpha-actinin 3 (Actn3), neither of which have been studied in the context of either DM nor wound healing. Epb41 plays a role in intracellular signal transduction with very little additional data available. Actn3 mediates the interaction between cytoskeletal proteins and the sarcomeres (Z-line) within skeletal muscle (Hsu et al. 2018). It is known to affect skeletal muscle function and glycogen metabolism with deficiency linked to a loss of force generation and increased susceptibility to damage (Seto et al. 2011). This protein has been mainly studied in the context of sports performance and muscular pathologies, with only one study showing a link between Actn3 and insulin resistance (Mason et al. 2011). In chronic DM wounds (involving the underlying muscle layer), Actn3 is, therefore, most likely involved in cytoskeletal disorganisation and altered glycogen metabolism.

**Initial stages neurofilament proteins (Sncg, Nefm)**

Two proteins involved in the neurofilament network integrity and synaptic transmission, namely gamma synuclein (Sncg) and neurofilament medium polypeptide (Nefm) were differentially expressed in the acute and DM wounds in this study. Even though Sncg is considered a neuropeptide (peripheral neurons) it is also highly expressed in white adipose tissue (WAT), (Oort et al. 2008) and share functional links with leptin and fatty acid-binding protein 4 (Oort et al. 2008, Bag et al. 2015, Dunn et al. 2015). Its prominent role in lipid metabolism was confirmed in a study indicating that Sncg knockout mice are protected against high-fat diet-induced metabolic complications (Millership et al. 2012). The increased levels of Sncg detected in the DM wounds in the current study is thus likely related to the abundance of WAT within the wound edges. The overexpression of Nefm in the DM wounds is, however, consistent with observations from a streptozotocin-induced DM rat model, in which the accumulation of the Nefh and Nefm subunits in proximal axons was suggested to be contributing factors in nerve degeneration leading to DM neuropathy (Sayers et al. 2003).

**Initial stages proteins involved in ribosomal function, transcriptional translation or protein modification (Rsp18, Rsp19, Rpl22, Macroh2a1, Rpn1, Ppib, Snrnp70, Ddx5, Eif3g)**

In the DM wounds, a large cluster of ribosomal-interacting proteins were differentially expressed, of which nine proteins (Rsp18, Rsp19, Rpl22, Macroh2a1, Rpn1, Ppib, Snrnp70, Ddx5, Eif3g) were upregulated more than two-fold on day 2 postwounding. Ribosomal proteins are RNA-binding proteins that function in ribosome biogenesis and protein translation by acting as RNA chaperones, stabilising rRNA and promoting the correct folding of transcribed proteins. These proteins also have extraribosomal functions associated with apoptosis, cell cycle arrest, proliferation and migration mediated by MDM2/p53 dependent and p53-independent mechanisms (Xu et al. 2016). Ribosomal proteins furthermore play an important role in the maintenance of genomic integrity by modulating the DNA damage repair response (Xu et al. 2016). Their function has been mainly studied in the context of tumorigenesis where it has been shown that either impairment or hyperactivation of ribosomal biogenesis is associated with deregulated cell growth (Barna et al. 2008, Xu et al. 2016). Patterns of dysregulated ribosomal proteins are also thought to be predictive of disease progression in cancer and has highly specific effects on mRNA translation (Guimaraes & Zavolan 2016). To our knowledge, this is the first study to identify dysregulated ribosomal proteins in chronic DM wounds and warrants further investigation, especially since the extra-ribosomal functions (i.e. DNA damage repair, proliferation, migration) are all processes known to be impaired in DM wounds.
Initial stages proteins involved in cellular growth (Tpt1)

Consistent with the overexpression of ribosomal proteins, the growth-associated protein Tpt1 was also overexpressed more than two-fold in the DM wounds. Tpt1 is a cytoprotective protein known to promote cellular division/growth and plays a role in the oxidative stress response to either promote DNA damage repair or induce autophagy (Bommer 2017). In the context of DM, Tpt1 have been implicated in DM-associated dementia (Matsuura et al. 2018), nephropathy (Tessari et al. 2007) and the development of auto-immune DM (Yan et al. 2008), confirming its role in the pathogenesis of DM. Even though it has not been studied in the context of DM wounds, other proteomic studies have identified Tpt1 as protein of interest in burn wounds (Pollins et al. 2007) and nerve regeneration (Jiménez et al. 2005), indicating that it might have a potential role in dysregulated healing responses.

In addition to the proteins discussed previously, this study also identified differentially expressed proteins involved in metabolic regulation/lipid rafts (FABP5, Cavin1), co-factors/catalases/protease inhibitors (Stfa1, Stfa3, Cycs, Tkt) and vestibular bodies (Chmp2a) during the initial stages postwounding. The role of these proteins in wound repair is unknown. It is, however, clear from the current data, that the protein dysregulation in DM wounds evident during the early stages (day 2) postwounding is complex and involve multiple regulatory pathways and biological processes.

Late stage proteins involved in immune modulation (Cfd, Ptms, Hp), transcriptional regulation (Hmga1, Cbx3) and neural synapses (Syap1)

In the later stages postwounding (day 7), fewer proteins were differentially expressed between acute and DM wounds compared to the initial stage. On day 7 postwounding, two immune modulatory proteins namely, complement factor D (Cfd) (also known as adipsin) and parathymosin (Ptms) were downregulated in DM wounds. Cfd is thought to be one of the links between energy metabolism and the innate immune response (White et al. 1992). It has a prominent role in lipid accumulation by mediating adipogenesis within WAT and simultaneously plays a role in the cleavage of C3 in the alternative immune complement pathway to induce inflammation (White et al. 1992, Song et al. 2016, Vasilenko et al. 2017). Elevated serum Cfd levels have been detected in DM patients with retinopathy (Hase et al. 2017) and it has been implicated in age-associated deterioration of the dermal skin layer (Ezure et al. 2019). In the current study, Cfd was, however, downregulated in the DM wounds on day 7 postwounding. Similarly, Ptms known to inhibit the transcriptional activity of pro-inflammatory NfκB (Okamoto et al. 2016) was also downregulated in the DM wounds, whilst haptoglobin (Hp) which has anti-inflammatory properties (Krzyszczyk et al. 2020) was upregulated. Krzyszczyk et al. (2020) recently demonstrated that haptoglobin elicit strong anti-inflammatory effects (involving the downregulation of Hmga1 signalling) in LPS-stimulated macrophages *in vitro* and that Hp treatment of DM wounds (db/db mice) improved healing outcomes. Despite a similar profile (increased Hp and decreased Hmga1) being observed in the current study, there were no signs of healing in the DM wounds suggesting that cellular targets within the wounds might be unresponsive to signalling in this more severe wound model. The diverse regulation of different inflammatory mediators observed during the late stages of healing in this study further highlights the complexity of interactions between the underlying molecular processes in chronic wounds. In addition to these immune modulatory proteins of interest, Cbx3 and Syap1 was also diversely expressed in acute vs DM wounds on day 7, the role of these proteins in either DM or wound healing is, however, unknown.

Conclusion

This study highlighted the complex nature of obese DM wounds and suggest that early intervention immediately postinjury in high risk type 2 DM patients should be considered. It furthermore identified numerous proteins that play a potential role in the development of chronic wounds. Future studies with more in-depth investigation are, however, required to determine cause-and-effect. Validation of the proteomic findings using antibodies to target proteins of interest overtime during wound healing is required in future studies using either Western blotting or immunohistochemistry. A further limitation of the current study was not being able to distinguish between the contribution of obesity and hyperglycaemia and the results are therefore only applicable to obesity-associated type 2 diabetic patients. Given the complexity of dysregulation, therapeutic agents targeting a single pathway is unlikely to be successful (as have been evident to date with the lack of effective treatments). Biological
agents such as engineered mesenchymal stem cells or inflammatory cells (macrophages) that can ‘sense’ and restore the microenvironment through paracrine signalling and facilitate the transition into the proliferative phase of healing should be the focus of regenerative strategies.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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Data availability
http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD020134

Author contribution statement
K B performed all the experimental procedures on the animals, sample analysis and wrote the first draft of the manuscript. M V assisted with sample preparation and performed the LC-MS/MS experiments. D L T did the quality control of mass spectrometry data and performed all the bioinformatic analysis. K H M contributed to the original study design and editing of the manuscript. M v D contributed to the study design, data interpretation, statistical analysis and writing of the manuscript. All authors contributed to the editing of the final manuscript.

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