**Sample Collection of Pressure Ulcer Biopsies**

Chronic wound samples were collected as described previously [1]. Briefly, pressure ulcer biopsies were collected from four patients presenting to the Johns Hopkins Wound Center. Chronicity was defined as wounds lasting greater than 30 days [2]. Biopsy samples were flash frozen in liquid nitrogen, shipped via dry ice, and stored at -800C prior to taxonomy and metabolomics analysis.

**NMR Compound Identification and Quantification**

**Metabolite Extraction**

Small molecule metabolites were extracted as described previously [5] with some modifications. Biopsy samples were resuspended in ice-cold 60% aqueous methanol and homogenized using a tissue homogenizer (Tissue Tearor™ Model 985370-395, Biospec Products Inc., Bartlesville, OK) set to 2-minute intervals of 10 seconds on and 5 seconds off. Tissues were transferred to glass tubes and lysed by sonication prior to addition of 1:1 aqueous chloroform and vortexing. Aqueous layers were collected by centrifugation and transferred to clean tubes prior to lyophilization for 4 hours with low heat. Lyophilized samples were resuspended in 550 μL of NMR buffer (10mM NaH2PO4/ Na2HPO4 containing 0.5 mM 4,4-dimethyl-4-silapentane-1-sulfonic acid (DSS) in 100% D2O, pH 7), assayed for pH, and transferred to 5mm NMR tubes (Bruker) prior to analysis.

**NMR Analysis**

1D 1H NMR spectra was acquired as described previously [5]. NMR spectra were acquired on a Bruker 600-MHz (1H Larmor frequency) AVANCE III solution NMR spectrometer equipped with a SampleJet™ automatic sample loading system, a 5 mm triple resonance (1H, 15N, 13C) liquid helium-cooled TCI probe (cryoprobeTM), and Topspin™ software (Bruker version 3). One-dimensional NMR spectra were acquired using the Bruker supplied noesypr1d pulse sequence with 256 scans, using a spectral width of 9600 Hz at 298K (25 °C). Free induction decays were collected into 32K data points, with a dwell time interval of 52 μsec amounting to an acquisition time of ~ 1.7 sec, using a 2 second relaxation recovery delay between acquisitions, and a NOESY mixing time period of 50 msec. Spectral processing and analysis was performed using the Chenomx NMR software (version 6.0) (Chenomx Inc., Edmonton, AB, Canada) according to recommended protocols and previous metabolomics analyses [5-7]. For each sample, NMR spectra were manually phased, baseline corrected, a line broadening function of 0.5 Hz applied, and calibrated to DSS at δ = 0.0 ppm. For metabolite identification, the Chenomx small molecule library for 600-MHz (1H Larmor frequency) magnetic field strength NMR was used, and NMR spectral patterns were fitted for each sample independently. The internal DSS standard was used for quantitation of identified metabolites.

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