A Small Volatile Bacterial Molecule Triggers Mitochondrial Dysfunction in Murine Skeletal Muscle

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Abstract

Mitochondria integrate distinct signals that reflect specific threats to the host, including infection, tissue damage, and metabolic dysfunction; and play a key role in insulin resistance. We have found that the *Pseudomonas aeruginosa* quorum sensing infochemical, 2-amino acetophenone (2-AA), produced during acute and chronic infection in human tissues, including in the lungs of cystic fibrosis (CF) patients, acts as an interkingdom immunomodulatory signal that facilitates pathogen persistence, and host tolerance to infection. Transcriptome results have led to the hypothesis that 2-AA causes further harm to the host by triggering mitochondrial dysfunction in skeletal muscle. As normal skeletal muscle function is essential to survival, and is compromised in many chronic illnesses, including infections and CF-associated muscle wasting, we here determine the global effects of 2-AA on skeletal muscle using high-resolution magic-angle-spinning (HRMAS), proton (\(^1\)H) nuclear magnetic resonance (NMR) metabolomics, *in vivo* \(^31\)P NMR, whole-genome expression analysis and functional studies. Our results show that 2-AA when injected into mice, induced a biological signature of insulin resistance as determined by \(^1\)H NMR analysis, and dramatically altered insulin signaling, glucose transport, and mitochondrial function. Genes including Glut4, IRS1, PPAR-\(\gamma\), PGC1 and Sirt1 were downregulated, whereas uncoupling protein UCP3 was up-regulated, in accordance with mitochondrial dysfunction. Although 2-AA did not alter high-energy phosphates or pH by *in vivo* \(^31\)P NMR analysis, it significantly reduced the rate of ATP synthesis. This effect was corroborated by results demonstrating down-regulation of the expression of genes involved in energy production and muscle function, and was further validated by muscle function studies. Together, these results further demonstrate that 2-AA, acts as a mediator of interkingdom modulation, and likely affects insulin resistance associated with a molecular signature of mitochondrial dysfunction in skeletal muscle. Reduced energy production and mitochondrial dysfunctional may further favor infection, and be an important step in the establishment of chronic and persistent infections.

Introduction

Pathogens modulate host cell functions to promote their own survival within the host dynamic environment, to evade the host immune system by hijacking functions of cell organelles, including plasma rafts [1], golgi [2], and mitochondria [3]. Mitochondria act as signaling platforms in diverse biological processes, including apoptosis [3], metabolism, and innate immune signaling [4]. Bacterial small molecules can alter mitochondrial function [5], [6], with bacterial effector proteins and toxins primarily affecting mitochondrial programmed apoptosis [3]; and bacterial membrane constituents, such as lipopolysaccharide (LPS) and peptidoglycan (PGN) triggering metabolic diseases, including insulin resistance [7].

Environmental stimuli can alter mitochondrial function via coordinated changes in gene expression [8]. For instance, specific members of the peroxisomal proliferator activator receptor (PPAR)-\(\gamma\) and proliferator activator receptor (PPAR)-\(\gamma\) coactivator (PGC1) gene families respond to physiological stimuli to regulate genes that control mitochondrial biogenesis [9], nuclear and mitochondrial oxidative metabolism, tricarboxylic acid (TCA) cycle enzymes, whole body glucose homeostasis, and lipid oxidation and electron transport complexes [10]. Also, cellular stress and infection are sensed by the innate immune system by pattern recognition receptors, which upon activation, initiate defense and repair pathways [11], [12]. It is possible that, similarly to viruses, bacteria may activate the inflammasome via altered cell metabolism and mitochondrial activity [13–16].

Metabolic responses begin promptly upon the initiation of infection, and progress as a series of coordinated events [17]. Mitochondria may play a key role in the development of insulin
resistance [18]. For example, glucose stimulated insulin secretion from pancreatic β cells requires intact mitochondrial function [19]; modifications in mitochondrial oxidative activity and mitochondrial adenine triphosphate synthesis is linked to insulin resistance [19], and these changes involve the up-regulation of mitochondrial uncoupling proteins (UCPs) [20]; altered mitochondrial fatty acid oxidation, together with the accumulation of intracellular fatty acid metabolites (acyl-CoA and diacylglycerol), disrupts insulin signaling, a phenomenon exacerbated by free fatty acids (FFA) [21]; and genes involved in mitochondria biogenesis such as the PPAR-γ and PGC-1 (α and β) are down-regulated in patients with insulin resistance [22], [23] and possibly also down-regulated in insulin resistant cystic fibrosis (CF) patients [24], [25].

CF patients are particularly susceptible to highly problematic Pseudomonas aeruginosa infections. This pathogen, which causes chronic infections that are often intractable to traditional antibiotic therapy [26],[27], employs cell-to-cell communication systems, termed quorum sensing (QS). QS regulates collective behaviors, that favor chronic infections, and potentially compromise host suffering.

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Materials and Methods

**Experimental animals**

6-wk-old male CD1 mice weighing approximately 20–25 g were purchased from Charles River Laboratory (Boston, MA). The animals were maintained on a regular light-dark cycle (lights on from 8:00 h to 20:00 h) at an ambient temperature of 22±1°C, with free access to food and water. Mice were injected intraperitoneally (IP) with 100 μl of 2-AA (6.75 mg /kg mice), and mouse skeletal muscle was analyzed 4 days post 2-AA treatment. In vivo 31P NMR spectroscopy was performed on intact mice, and ex vivo 1H NMR spectroscopy was performed on intact gastrocnemius muscle samples.

**Ethics Statement**

This study was carried out in strict accordance with the recommendations of the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health. The protocol was approved by the Committee on the Ethics of Animal Experiments at Massachusetts General Hospital (Permit Number: 2006N000993/2). All procedures were performed under sodium pentobarbital anesthesia, and every effort was made to minimize suffering.

### 31P NMR spectroscopy

**Data acquisition.** The theoretical basis of saturation transfer experiments and calculations were as described by Forsen and Hoffman [36], [38]. Animals were analyzed using in vivo 31P NMR spectroscopy 4 days post 2-AA treatment. Mice were transiently anesthetized with isoflurane (3.0%) plus O2 (2.0 l/min) delivered through a nose cone, and then placed in a customized restraining tube. Each animal’s right hind limb was placed into a solenoid coil (four turns; length, 2 cm; diameter, 1 cm) tuned to 31P frequency (162.1 MHz). During MR imaging, mice were continuously anesthetized with isoflurane (1.5%) plus O2 (1.0 l/min). The rectal body temperature was maintained at 37±1°C using heated water blankets. All in vivo 31P NMR experiments were performed in a horizontal bore magnet (proton frequency at 400 MHz, 21 cm diameter, Magnex Scientific, Varian, Palo Alto, CA, USA) using a Bruker Advance console. Field homogeneity was adjusted using the H1 signal of tissue water. A 90° pulse was optimized for detection of phosphorus spectra (repetition time 2 s, 400 averages, 4,096 data points). Saturation 90° selective pulse trains (duration, 36.533 ms; bandwidth, 75 Hz) followed by crushing gradients were used to saturate the γ-ATP peak. The same saturation pulse train was also applied downfield of the inorganic phosphate (Pi) resonance, symmetrically to the γ-ATP resonance. T1 relaxation times of Pi and phosphocreatine (PCr) were measured using an inversion recovery pulse sequence in the presence of γ-ATP saturation. An adiabatic pulse (400 scans; sweep width, 10 kHz, 4,000 data points) was used to invert Pi and PCr, with an inversion time between 132 and 7,651 ms.

**Data analysis.** 31P NMR spectra were analyzed using the MestReNova NMR software package (Mestrelab Research S.L., v. 6.2.1 NMR solutions, Website: www.mestrec.com). Free induction decays were zero-filled to 8,192 points and apodized with exponential multiplicative (30 Hz) before Fourier transformation. The spectra were then manually phased and corrected for baseline broad features using the Whittaker smoother algorithm [39]. The Levenberg-Marquardt algorithm was used to least-square-fit a model of mixed Gaussian/Lorentzian functions to the data. Similarly, the T1,relaxation time for Pi and PCr was calculated by fitting the function $y = A1 \left(1 - 2e^{-\frac{t}{T1,rel}}\right)$ to the inversion recovery data, where $y$ is the z magnetization, and $t$ is the inversion time.

**Calculation of intramyocellular pH.** The formula pH $= 6.75 + \log\left([s-3.27]/(5.69 - s)\right)$, where $s$ is the chemical shift difference (in ppm) between the Pi and the PCr peaks [40] was used to calculate intramyocellular pH.

**Calculation of ATP concentration.** ATP concentration was measured using the Bioluminescence Assay Kit CLS II, Cat# 1699695 (Roche Diagnostics Corporation, Indianapolis, IN 46250–0414, USA).

**Calculation of ATP synthesis rate.** 31P-NMR spectra data, and the ATP concentration, were used to calculate the ATP synthesis rate, as described by Forsen and Hoffman [39]. In brief, the chemical reaction between Pi and ATP is:

$$Pi \rightarrow ATP + Pi \quad \text{at} \quad k_r$$

Where $k_f$ and $k_r$ are reaction rate constants in each direction. The influence of the chemical exchange between Pi and ATP on the longitudinal magnetization $M_{(Pi)}$ of Pi is described by:
\[
\frac{dM(P)}{dt} = \frac{M_0(P) - M(P)}{T_1(P)} - k_f M(P) + k_s M(ATP)
\]  
(2)

At equilibrium \(\frac{dM(P)}{dt} = 0\), so at saturated ATP, \(M(ATP) = 0\)
the equation (2) becomes

\[
\frac{M(P)}{M_0(P)} = \frac{1}{1 + k_f T_1(P)}.
\]  
(3)

The spin lattice relaxation time \(T_{1\text{app}}\), measured using the
inversion recovery pulse sequence in the presence of the ATP
saturation, is related to the intrinsic \(T_{1\text{pp}}\) by:

\[
\frac{1}{T_{1\text{app}}} = \frac{1}{T_{1\text{pp}}} + k_f
\]  
(4)

Combining (3) and (4) gives:

\[
k_f = \frac{1}{T_{1\text{app}}} \times \frac{\Delta M(P)}{M_0(P)}
\]  
(5)

where \(\Delta M(P)/M_0(P)\) is the fractional change of the longitudinal
magnetization \(M(P)\) of Pi. All the quantities on the right side of
(5) can be calculated from the NMR data. Finally the unidirectional
ATP synthesis flux can be calculated as

\[
\left(\frac{dATP}{dt}\right)_{\text{synth}} = k_f [P_i]
\]  
(6)

where \(P_i\) is the concentration of \(P_i\) extrapolated from the baseline
NMR spectrum by comparing the peak integrals from \(P_i\) and \(\gamma\-
ATP\), with respect to ATP concentration.

**Extraction of RNA Samples**

The left gastrocnemius muscle was harvested at 4 days post 2-
AA treatment (n = 3, for each time point), to determine changes
in whole muscle gene expression. Mice were anesthetized by IP
injection of 40 mg/kg pentobarbital, and the muscle specimens
were excised and immediately immersed in 1 ml Trizol
(GibcoBRL, Invitrogen, Carlsbad, CA) for RNA extraction. All
mice were then administered a lethal dose of pentobarbital
(200 mg/kg) by IP injection. Each muscle specimen was homog-
enized for 60 s with a Brinkman Polytron 3000 before total RNA
were excised and immediately immersed in 1 ml Trizol
injection of 40 mg/kg pentobarbital, and the muscle specimens
whole muscle gene expression. Mice were anesthetized by IP
AA treatment (n = 3, for each time point), to determine changes in

**High-Resolution Magic Angle Spinning (HRMAS) \(^1\text{H} NMR
spectroscopy of intact skeletal muscle tissue**

At 4 days post 2-AA treatment, three experimental and three
untreated control animals were analyzed with HRMAS \(^1\text{H} NMR.
The skeletal muscle tissue underlying the hind limb burn site was
harvested, immediately frozen in liquid nitrogen, and stored at
\(-80^\circ\text{C}\). HRMAS \(^1\text{H} NMR spectroscopy of muscle tissue was
performed on a Bruker BioSpin Avance NMR spectrometer
(proton frequency at 600.13 MHz, 89 mm Vertical Bore) using a
4-mm triple resonance (\(^1\text{H}, ^{13}\text{C}, ^{1}\text{H}\) HRMAS probe (Bruker,
Billerica, Massachusetts). The temperature was maintained at 4
°C with a BTO-2000 thermocouple unit in combination with a magic
angle spinning (MAS) pneumatic unit (Bruker). The MAS speed
was stabilized at 4.0 ± 0.001 kHz with a MAS speed controller. \(^1\text{H}
NMR spectra were acquired using a Carr-Purcell-Meiboom-Gill
(CPMG) spin echo pulse sequence, (90°-\(\tau\)-180°-\(\tau\_w\)-acquisition),
with an inter-pulse delay (\(\tau\)) of 250 µs. Hard 90° (8 µs) and 180°
(16 µs) pulse trains were employed. The relaxation delay was set to
2 s, and spectra were collected both with and without water
suppression. The transverse relaxation time (\(T_2\)) was measured
using the same CPMG pulse sequence by varying n from 0 to 520.
Free induction decay (FID) signals were acquired with 8 k points,
600 ms acquisition time, 8 dummy scans, and 128 scans.

HRMAS \(^1\text{H} NMR spectra were analyzed using the MestRe-C
NMR software package (Mestrelab Research, Santiago de
Compostela, Spain, www.mestrec.com). FIDs were zero-filled to
16 k points, and apodized with exponential multiplication (1 Hz)
before Fourier transformation. The spectra were then manually
phased and corrected for baseline broadening (Whittaker smoother,
smooth factor 10,000). The Levenberg-Marquardt algorithm was
used to least-squares-fit a model of mixed Gaussian/
Lorentzian functions to the data.

The (CH\(_2\))\(_{n-2}\) peak at 1.32 ppm was selected for quantification of
intramyocellular lipids (IMCL). Because the sample was spun at magic
angle, and the sample volume was much smaller (25 µl) and
more homogeneous (reduced bulk magnetic susceptibility effects)
than the typical voxel size (1 ml) of \(in vivo\) \(^1\text{H} MRS, no chemical
shift difference was observed between IMCL and extramyocellular
lipids (EMCL). The small size of the muscle biopsies, and the fact that
the samples were collected from the most myocellular part of the
muscle, suggest that the main contribution to the (CH\(_2\))\(_{n-2}\) peak was
from IMCL lipids.

**Absolute quantification of metabolites from 1-D CPMG
spectra**

Resonance intensities were measured for -CH\(_3\) protons of
trimethylsilyl- propionic-2,2,3,3-d\(_4\) acid (TSP), and compared to
the resonance intensities measured for metabolite. The peak
intensities of most of the metabolites, as well as of TSP, were
calculated from the intensity of the respective resonance (X)
measured from the T2-filtered HRMAS \(^1\text{H} MR spectrum. The calculated peak intensities were then corrected for T2 relaxation,
using Ic(X) = Ir(X) * exp(T_{CPMG}/T2(X))/n, where Ir(X) is the
measured intensity, T_{CPMG} is the CPMG echo time, and n is the
number of protons in the functional group, and corresponds to
the resonance of the metabolite. In accordance with the “external standard” technique [41], metabolite concentrations were quanti-
fied relative to the absolute concentration (µmol) of the respective
metabolite (M) = Ic(M)/Ic(TSP) * wt, where wt is the weight of the
sample in grams.
Figure 1. NMR spectra of in vivo $^{31}$P NMR saturation-transfer on mouse hind limb skeletal muscle. Representative summed $^{31}$P-NMR spectra acquired from control and 2-AA treated mice at day 4, before (A) and after (B) saturation of the γ-ATP resonance, with the difference spectrum between the two shown below (A–B). The arrow on 2 (A) and after (B) saturation of the spectra acquired from control and 2-AA treated mice at day 4, before measurements was performed in each group with t-test Criterion for significance was $p < 0.0125$. All analysis was performed using SPSS v12, SPSS Inc.).

Microarray hybridization

Biotinylated cRNA was generated with 10 μg of total cellular RNA according to the protocol outlined by Affymetrix Inc. (Santa Clara, CA, USA). The cRNA was hybridized onto MOE430A oligonucleotide arrays (Affymetrix, CA, USA), stained, washed, and scanned according to the Affymetrix protocol.

Genomic data analysis

Data files of the scanned image files hybridized with probes from RNA extracted from the gastrocnemius muscle isolated at the specified times from experimental and control mice (n = 3) were converted to cell intensity files (.CEL files) with the Microarray suite 5.0 (MAS, Affymetrix, CA, USA). The data were scaled to a target intensity of 500, and all possible pairwise array comparisons of the replicates to normal control mice were performed for each time point (i.e., four combinations when two arrays from each time point were compared to the two arrays hybridized to RNA from control mice) using a MAS 5.0 change call algorithm. Probe sets that had a signal value difference greater than 100 and for which one of the two samples being compared was not called “absent”, were scored as differentially modulated when 1) the number of change calls in the same direction were at least 3, 4, and 6, when the number of comparisons were 4, 6, and 9, respectively; and 2) the other comparisons were unchanged. Based on the ratios of 100 genes determined to be invariant in most conditions tested (Affymetrix, CA), an additional constraint of a minimum ratio of 1.65 was applied to control for the known false positives at 5%. The Microarray data is available in http://www.ncbi.nlm.nih.gov/geo/info/linking.html and the accession number is GSE43779. GO analysis has been performed using the Gene-Spring GX software (version 11) by Agilent Technologies.

Cell culture

The C2C12 murine skeletal muscle cell line (American type culture collection, Bethesda, MD) was maintained in Dulbecco’s modified Eagle’s medium (DMEM, Gibco) supplemented with 10% fetal bovine serum (Gibco) containing penicillin/streptomycin and gentamycin (Gibco) in the presence of 5% CO$_2$ at 37°C. The cells were seeded in T-75 tissue culture flasks (Falcon, USA) and used between passages 2 and 3.

2-AA cell treatment

C2C12 cells were plated at a density of 10$^5$/ml in 6-well plates and grown overnight at 37°C in 5% CO$_2$. Cells in the treatment groups were treated with 0.8 mM 2-AA for 24, 36 and 48 h, and then 2-AA treated or non-treated cells were washed with PBS.

Western blot analysis

Cellular extracts were prepared in RIPA buffer (Cell Signaling Technology). Twenty five micrograms of total protein were added to Laemmli buffer, boiled for 5 min, resolved by 7.5% or 10% polyacrylamide gel electrophoresis (PAGE) in Tris/glycine/SDS buffer (25 mM Tris, 250 mM glycine, 0.1% SDS), and transferred to PVDF membranes (Bio-Rad, Hercules, CA). The membranes were blocked for 2 h in TBS-T (20 mM Tris-HCL, 150 mM NaCl, 0.1% Tween20) containing 5% non-fat milk. The membranes were then washed three times in TBS-T and probed overnight with rabbit antibodies specific for goat PPAR-γ, rabbit SIRT-1, mouse monoclonal PGC-1β (Santa Cruz Biotechnology, Inc., Santa Cruz, CA) at a dilution of 1:1,000, and mouse α-tubulin (Santa Cruz Biotechnology, Inc) at a dilution of 1:2,000.

<table>
<thead>
<tr>
<th>Table 1. In vivo $^{31}$P-NMR saturation transfer analysis of limb skeletal muscle from control and 2-AA treated mice.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Control</strong></td>
</tr>
<tr>
<td><strong>ATP synthesis flux (reaction $\text{Pi} \rightarrow \gamma$-ATP)</strong></td>
</tr>
<tr>
<td>$\Delta M/M_0$</td>
</tr>
<tr>
<td>$T_{\text{obs}}$ (s)</td>
</tr>
<tr>
<td>$K_r$ (s$^{-1}$)</td>
</tr>
<tr>
<td>ATP (μmol/g)</td>
</tr>
<tr>
<td>Pi (μmol/g)</td>
</tr>
<tr>
<td>ATP synthesis rate (μmol/g/s)</td>
</tr>
<tr>
<td><strong>ATP synthesis flux (reaction $\gamma$-ATP→PCr)</strong></td>
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<td>$\Delta M/M_0$</td>
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<td>ATP synthesis rate (μmol/g/s)</td>
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</tbody>
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Values are means ± SEM. $\Delta M/M_0$ is the fractional change in $\text{Pi}$ or PCr magnetization as a result of saturation transfer; $T_{\text{obs}}$ is the observed spin lattice relaxation time of $\text{Pi}$ or PCr during γ-ATP saturation in seconds; $K_r$ is the rate constant for the reactions $\gamma$-ATP and PCr→γ-ATP, calculated as $(1/T_{\text{obs}})$ × $(\Delta M/M_0)$. ATP synthesis is calculated as $P_i$ or PCr × $K_r$; NS: not significant. Unpaired one-tailed Student’s t-test was used for the comparisons. doi:10.1371/journal.pone.0074528.g001
Following three washes in TBS-T, the membranes were incubated with secondary horse-radish peroxidase (HRP)-conjugated rabbit anti goat IgG, goat anti-rabbit IgG (Santa Cruz Biotechnology, Inc) or goat anti-mouse IgG secondary antibodies (Promega, Madison, WI), respectively for 1 h, and then washed three times in TBS-T. The blots were visualized with SuperSignal West Pico

Figure 2. 2-AA treatment differentially modulates the genes involved in energy production and intermediate metabolism in skeletal muscle. Differentially expressed genes involved in energy production (A) and intermediate metabolism (B) in response to 2-AA treatment. Grey boxes represent up-regulation, and black boxes represent down-regulation, of the respective gene in muscle from 2-AA treated versus control mice. The negative log10 of p-values represented by gray triangles are shown in the right vertical axis. The expression of certain key genes is down-regulated, consistent with the in vivo 31P-NMR data (Figure 1 and Table 2).

doi:10.1371/journal.pone.0074528.g002

Table 2. 1H NMR HRMAS analysis on gastrocnemius muscle from 2-AA treated and control mice.

<table>
<thead>
<tr>
<th>Chemical Shift PPM</th>
<th>Chemical group</th>
<th>Control</th>
<th>4 days Post 2-AA</th>
<th>Percent Change</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.30</td>
<td>(CH3)n</td>
<td>0.14±0.01*</td>
<td>0.08±0.02</td>
<td>+118.9</td>
<td>0.029b</td>
</tr>
</tbody>
</table>

Footnote: * values (µmol/g muscle) are means ± standard errors from 8 samples per group; b p value for comparisons between 2-AA treated and control mice obtained with the Student’s t-test; + indicates increase.

doi:10.1371/journal.pone.0074528.t002
Chemiluminescent Substrate (Thermo Scientific, Rockford, IL), according to the manufacturer’s instructions.

MTT assay for cell cytotoxicity

The cytotoxicity of cells treated with 0.8 mM 2-AA was measured by MTT assay as previously described [31].

Plasma FFA assay

Blood was drawn by heart puncture at the time of sacrifice, and the plasma FFA level was measured via the calorimetric FFA assay kit that uses acylation of coenzyme A (NEFA C; Wako Chemicals USA, Inc., Richmond, VA).

Neuromuscular Function Studies

Functional neuromuscular studies were performed to determine the tensions developed after perturbation with the bacterial molecule and test the integrity of neurotransmission at 4 days post 2-AA treatment. Mice were anesthetized with pentobarbital (60–70 mg/kg, IP), with adequate depth of anesthesia confirmed by the absence of the withdrawal response to toe clamping. Anesthesia was maintained with supplemental intermittent doses of pentobarbital (10–20 mg/kg, IP), every 15–20 minutes. The body temperature was monitored using a rectal thermistor and maintained at 35.5–37°C with a heat lamp. Neuromuscular transmission was monitored by evoked mechanomyography using a peripheral nerve stimulator (NS252, Fisher & Paykel Health Care, Irvine, CA) along with a Grass Force transducer and corresponding software (Grass Instruments, Quincy, MA). With the mice in dorsal recumbency, the tendon of insertion of the tibialis muscle was surgically exposed on each side, and individually attached to separate grass FT03 force displacement transducers. The sciatic nerve was exposed at its exit from the lumbosacral plexus at the thigh and tied with ligatures for indirect nerve stimulation of the muscles. Distal to the ligatures, stimulation electrodes were attached for nerve-mediated stimulation of the tibialis muscle. The knee was rigidly stabilized with a clamp to prevent limb movement during nerve stimulation. Baseline tensions of 10 grams, which yielded optimal evoked tensions, were applied on the immobilized and sham-immobilized tibialis muscles. The sciatic-nerve-evoked tensions of the respective tibialis muscles that were calibrated in grams of force were recorded via a Grass P122 amplifier and displayed using the Grass Polyview Software (Grass Instruments, Quincy, MA). Supramaximal electrical stimuli of 0.2 msec duration were applied to the sciatic nerve at 2 Hz for 2 sec (train-of-four pattern, TOF), every 20 sec, using a Grass S88 stimulator and SIU5 stimulus isolation unit (Grass Instruments, Quincy, MA). The evoked muscle tension developed during TOF stimulation was recorded at the end of 15-min. This was followed by tetanic stimulation at 50 Hz for 5 s to assess the maximal tetanic muscle tension, and the muscle fade associated with stimulus. All values are expressed as mean ± S.E.M. (standard errors of mean). Differences between the two sides of the 2-AA group and control mice were compared using two-way ANOVA test and Bonferroni’s multiple comparison tests as a Post hoc testing (GraphPad Prism version 5.00 for Windows, GraphPad Software, San Diego California USA, www.graphpad.com). Differences of p value <0.05 were designated as significant.

Results

2-AA reduces ATP synthesis rate and energy production gene expression in skeletal muscle without significantly altering high-energy phosphates or pH

In vivo and ex vivo NMR magnetic spectroscopy allows measurements of physiological and metabolic biomarkers in intact systems [35], [36]. We used in vivo 31P NMR to assess the rate of

![Figure 3. NMR spectra from 1H-NMR HRMAS analysis of gastrocnemius skeletal muscle from 2-AA treated versus control mice. The spectra were acquired from 2-AA treated mice at 4 d versus control mice, and scaled to the phosphocreatine plus creatine peak (3.02 ppm). Resonance signals of lipids correspond to: 1) terminal methyl CH₃ protons (0.9 ppm); 2) acyl chain methylene protons (CH₂)n of intramyocellular lipids (IMCLs) (1.3 ppm); 3) methylene protons CH₂C=O (1.6 ppm); 4) allicy methylene protons C=C=CH₂-C of monounsaturated fatty acyl moieties (MUFA) (2.05 ppm); 5) α methylene protons CH₂CO (2.25 ppm); 6) diallyllic methylene protons =C=CH₂C= of polyunsaturated fatty acyl moieties (PUFAs); and 7) N-methyl protons of phosphocreatine and creatine (3.0 ppm), respectively. The NMR spectra demonstrate increased biomarkers of insulin resistance IMCLs. doi:10.1371/journal.pone.0074528.g003

Bacterial QS Affects Skeletal Muscle Function

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ATP synthesis, and whether 2-AA alters muscle concentrations of high-energy phosphates as a function of perturbed mitochondrial function.

The levels of phosphomonoesters and inorganic phosphate and the ratio Pi/PCr were decreased in the 2-AA treated mice versus the control mice, whereas the levels of PCR were somewhat higher in the 2-AA versus the controls, but not significantly. The intramyocellular pH was not significantly different in the experimental versus control animals (7.26 ± 0.06 and 7.30 ± 0.05, respectively (p = 0.60)).

$^{31}$P NMR spectra were acquired from control and 2-AA treated mice at day 4, before and after saturation of the γ-ATP resonance. Figure 1 shows the summed spectra (non-saturated (A)), upon saturation of the γ-ATP peak (B) with the difference spectrum (A-B) from the 6 control and the 6 2-AA-treated mice, with the mean results presented in Table 1. The synthesis rates were derived from the NMR data and the ATP concentration assays, with both analyses demonstrating significantly decreased ATP levels in the 2-AA versus the control mice. The fractional change, $\Delta M/M_0$, and the observed spin lattice relaxation time, $T_{1\text{app}}$, were used to calculate the $k_f$ rate constant using the equation $k_f = \frac{1}{T_{1\text{app}}} \times \frac{dM_{(Pi)}}{dM_{(Pi)}}$ for the Pi → γ-ATP reaction or $k_f = \frac{1}{T_{1\text{app}}} \times \frac{dM_{(PCr)}}{dM_{(PCr)}}$ for the PCr → γ-ATP reaction. The ATP synthesis rate was obtained as the product of $k_f$ and P$_i$ concentration. The NMR-measured fractional change for the Pi → γ-ATP reaction $\Delta M/M_0$ decreased by 30.6% in the 2-AA mice versus the controls (percent change in $\Delta M/M_0$ Table 1). The ATP concentration was lower in 2-AA mice versus controls by approximately 81% ($p<0.001$ in the unidirectional (one-tailed) t-test (Table 1). Likewise, the ATP synthesis rate was reduced by 90% in the 2-AA versus control mice ($p<0.001$ unidirectional (one-tailed) t-test). Accordingly, the unidirectional ATP synthesis rate for the PCR → γ-ATP reaction was significantly decreased by 82% in the 2-AA versus control mice (one-tailed t-test, $p<0.001$).

Figure 1 presents the transcriptionome results for the expression of energy production (Fig. 2A) and intermediate metabolism (Fig. 2B) genes, and demonstrates their expression was lower in the skeletal muscle of the 2-AA versus control mice. Several components of the mitochondrial respiratory (proton transport and/or electron transport) chain were down-regulated, including subunits of NADH dehydrogenases and ATP synthase (F$\delta$F$_0$ ATPase or complex V). Also genes involved in oxidative phosphorylation and genes for acetyl-coA biosynthesis from pyruvate (Fig. 2B) were significantly down-regulated. Moreover, the downstream TCA cycle genes, including pyruvate dehydrogenase (lipoamide) beta, succinate dehydrogenase subunits, and citrate synthase were down-regulated. These results strongly suggest that 2-AA leads to metabolic dysfunction in skeletal muscle.

2-AA increases insulin resistance biomarker IMCLs and reprograms the expression of key metabolic genes

IMCL levels [42], [43] can serve as useful indices of insulin resistance/metabolic abnormalities in non-vertebrates [44], and vertebrates [45–47], including obese and/or type 2 diabetic patients, where increased IMCL levels are due to impaired insulin-stimulated glucose uptake [37], [48], [49]. Figure 3 shows representative $^1$H-NMR spectra from control and 2-AA mice. These results demonstrate a notable rise in IMCLs after 2-AA treatment. Quantitative results of these data (Table 2) demonstrate a significant rise in ICML 4 days post 2-AA treatment. Correspondingly, the expression of genes involved in insulin signaling (i.e., IRS1) and glucose transport (i.e., GLUT4) were down-

### Table 3. Differential expression of key metabolic genes in skeletal muscle from 2-AA treated mice versus untreated control mice.

<table>
<thead>
<tr>
<th>Gene Bank Accession No.</th>
<th>Name of Gene</th>
<th>Gene Symbol</th>
<th>GO Biological Process</th>
<th>Fold Change</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>NM_133249</td>
<td>peroxisome proliferative activated receptor, gamma, coactivator 1 beta</td>
<td>Ppargc1b (PGC-1β)</td>
<td>Lipid metabolism</td>
<td>−2.904</td>
<td>0.00823</td>
</tr>
<tr>
<td>NM_011146</td>
<td>peroxisome proliferator activated receptor gamma</td>
<td>Pparg (PPAR-γ)</td>
<td>Lipid metabolism</td>
<td>−18.38</td>
<td>0.00256</td>
</tr>
<tr>
<td>AI645527</td>
<td>uncoupling protein 3 (mitochondrial, proton carrier)</td>
<td>Ucp3</td>
<td>Mitochondrial uncoupling: proton leackage</td>
<td>+5.291</td>
<td>0.00213</td>
</tr>
<tr>
<td>AW108044</td>
<td>uncoupling protein 2 (mitochondrial, proton carrier)</td>
<td>Ucp2</td>
<td>Mitochondrial uncoupling: proton leackage</td>
<td>−2.3</td>
<td>0.00274</td>
</tr>
<tr>
<td>NM_019812</td>
<td>sirtuin 1 (silent mating type information regulation 2, homolog) 1 (S. cerevisiae)</td>
<td>Sirt1</td>
<td>muscle development</td>
<td>−2.3</td>
<td>0.043</td>
</tr>
</tbody>
</table>

Values are the relative expression intensity of the 2-AA treated versus control mice after 4 d. Gene annotations for biological functions are from the Gene Ontology Consortium and the Ingenuity database.

(+) Upregulation of genes compared with control untreated muscle.

(−) Downregulation of genes compared with control untreated muscle.

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Bacterial QS Affects Skeletal Muscle Function
regulated (Table 3). Table 3 also lists genes whose altered expression in skeletal muscle post 2-AA treatment could lead to metabolic dysfunction, including down-regulation of the PGC-1β, PPAR-γ lipid metabolism genes, the UCP2 mitochondrial uncoupling: proton leak gene, and Sirt1, which has been proposed to lie at the center of a loop regulating the actions of PGC and PPARs [50]; and up-regulation of the UCP3 mitochondrial uncoupling: proton leak gene. Furthermore, the protein expression level of PGC-1β, PPAR-γ and Sirt1 was significantly dampened in mouse skeletal muscle cell line C2C12 (Fig. 4) following 2-AA treatment, corroborating with our mouse transcriptome data. This dampening effect was not due to 2-AA cytotoxicity (Fig. 5).

Table 4 and Figure 2B show that 2-AA also alters fatty acid oxidation. Several genes involved in lipid metabolism were down-regulated (Fig. 2B). Eleven fatty acid oxidation genes were differentially expressed post 2-AA treatment, with most being down-regulated (Table 4). These genes encode proteins that increase the non-esterified fatty acids cytosolic pool, and function in fatty acid β-oxidation. Their reduced expression could contribute to muscle lipid accumulation and the lipid metabolism dysfunction produced by 2-AA. Plasma FFAs were not altered by 2-AA treatment.

In addition to this, the transcriptome data shows that stress activated protein kinase (SAPK) pathway genes are significantly down-regulated (Table 5) in mouse skeletal muscle at 4 days 2-AA treatment. Therefore, it confirms the specific action of 2-AA in skeletal muscle.

![Figure 4. 2-AA treatment dampens key metabolic protein levels in mouse skeletal muscle cells.](image)

Figure 4. 2-AA treatment dampens key metabolic protein levels in mouse skeletal muscle cells. Western blotting of cellular extracts with specific antibodies of PGC-1b, PPAR-γ and Sirt1 in 2-AA treated cells at the indicated time points. One representative experiment (out of three) is shown. Loading was normalized relative to mouse α-tubulin. Densitometric data are the average of three replicate experiments and are expressed as mean ± SD (vertical bars). *p<0.05 vs. naive. DU, densitometric units.

doi:10.1371/journal.pone.0074528.g004

2-AA affects skeletal muscle function

Since 2-AA reduces ATP synthesis rate and energy production gene expression in skeletal muscle while reprograms the expression of key metabolic genes as presented above, we carried out further analysis and physiological studies to directly examine whether the 2-AA effects on metabolic gene expression and ATP synthesis impact muscle function. Our results show that the expression of all muscle contraction-related genes is significantly down regulated (Table 6 and Fig. 6) as well as muscle development–related genes (Fig. 6) indicating thus muscle dysfunction 4 days after 2AA treatment. In addition, Table 7 shows that at 4 days post 2-AA treatment, the absolute twitch tension of tibialis muscle was significantly reduced in the 2-AA versus the control mice. The evoked first single twitch tensions of tibialis muscle during TOF stimulation in the 2-AA mice were reduced to 72% on the left side and 80% on the right side, compared to the control mice (p<0.05). The maximum response of tetanic stimulation (Tmax) also was significantly different on the left side of 2-AA mice decreased 75% versus the controls.

Discussion

We show here that 2-AA, a diagnostically important bacterial interkingdom infochemical, leads to skeletal muscle dysfunction, and induces a biological signature of mitochondrial dysregulation and insulin resistance. Our results demonstrate that 2-AA down-regulates genes, including PPAR-γ, PGC-1β and Sirt1 that function in mitochondrial biogenesis, oxidative phosphorylation, and metabolic pathways, including insulin signaling, glucose transport, energy production, fatty acid oxidation, and skeletal muscle function. PPARs, in conjunction with PGC-1 and Sirt1, activate oxidative metabolism genes, and mediate insulin sensitivity in skeletal muscle; and their dysregulation could underlie metabolic dysfunction [50]. Such down-regulation may be mediated via an upstream regulatory pathway involving mitochondrial uncoupling, and ultimately lead to the skeletal muscle dysfunction observed here, and in burned skeletal muscle [33], [36], [51]. To our knowledge, 2-AA is the first QS molecule seen to promote these effects.

The 2-AA mediated suppression of PPAR-γ correlates with the reduced rate of ATP synthesis in the skeletal muscle of 2-AA treated mice (Fig. 1 and Table 1), as well as the downregulation of glucose transporter and insulin signaling genes (Table 3). The transcription factor PPAR-γ plays a pivotal role in maintaining oxidative phosphorylation, insulin-mediated signaling, and glucose homeostasis, along with other co-activators like PGC-1 and Sirt1.
As such, our results suggest that PPAR-γ suppression could affect energy homeostasis and insulin-induced glucose metabolism in skeletal muscle, which could then cause mitochondrial dysfunction and insulin resistance [55], [56]. Indeed, PPAR-γ downregulation in CF deficient cells leads to chronic inflammation [24], [57]. Also, PPAR-γ overexpression can rescue mitochondrial dysfunction in chronic mitochondrial disease [58].

That 2-AA down-regulates PGC-1β and upregulates UCP3 (Table 3) is consistent with its reduction of ATP synthesis rate and down-regulation of PPAR-γ. The PGC-1β protein plays a major role in mitochondrial metabolism, as it increases mitochondrial biogenesis and muscle cell respiration [8]; and is hypothesized to have a central role in regulating energy homeostasis and metabolism [23], [35], [36]. As such, PGC-1β down-regulation could lead to the down-regulation of oxidative phosphorylation genes (OXPHOS) [35], [36], as their expression is down-regulated by 2-AA (Fig. 2A). Consequently, these changes could lead to mitochondrial uncoupling, as suggested by the up-regulation of UCP3 (Table 3). To this end, our data suggest that 2-AA dysregulates components of mitochondrial metabolism at the transcriptional level, to result in skeletal muscle dysfunction (Table 6–7). Interestingly, PPAR-γ was suggested to act as the N-acyl-homoserine lactone (AHL) signaling molecule N-3-oxo-decanoyl homoserine lactone (3-oxo-C12-HSL) mammalian receptor and it is shown to function as an antagonist of PPAR-γ transcriptional activity and inhibit the DNA binding ability of PPAR-γ [59].

Cells overexpressing PGC-1β exhibit increased activity of ATP consuming reactions [8]. Here downregulation of PGC-1β coincides with reduced ATP synthesis rate. That 2-AA also reduces IRS1 expression (Table 3) suggests that PGC-1β, which is downregulated here, perturbs IRS1 expression, and consequently effects insulin resistance in skeletal muscle. As such, PGC-1 may contribute to insulin resistance to then mediate inflammation and disrupt glucose homeostasis [13]. In addition, the 2-AA mediated down-regulation of Sirt1 (Table 3) is possibly associated with energy expenditure and insulin sensitivity, and likely reflects the

**Table 4.** Differential expression of genes involved in fatty acid oxidation in mouse skeletal muscle at 4 days 2-AA treatment versus control muscle.

<table>
<thead>
<tr>
<th>Gene Bank Accession No.</th>
<th>Gene Name</th>
<th>Fold Change</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>BG060909</td>
<td>stearoyl-Coenzyme A desaturase 2</td>
<td>+10.69</td>
<td>0.00507</td>
</tr>
<tr>
<td>NM_009127</td>
<td>stearoyl-Coenzyme A desaturase 1</td>
<td>−4.379</td>
<td>0.0249</td>
</tr>
<tr>
<td>NM_010726</td>
<td>phytanoyl-CoA hydroxylase</td>
<td>−4.708</td>
<td>0.000639</td>
</tr>
<tr>
<td>NM_010726</td>
<td>phytanoyl-CoA hydroxylase</td>
<td>−4.708</td>
<td>0.000639</td>
</tr>
<tr>
<td>AK017272</td>
<td>lipoprotein lipase</td>
<td>−8.606</td>
<td>0.00755</td>
</tr>
<tr>
<td>AK017272</td>
<td>lipoprotein lipase</td>
<td>−8.606</td>
<td>0.00755</td>
</tr>
<tr>
<td>AK017272</td>
<td>lipoprotein lipase</td>
<td>−8.606</td>
<td>0.00755</td>
</tr>
<tr>
<td>BB114220</td>
<td>L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain</td>
<td>−6.56</td>
<td>0.002</td>
</tr>
<tr>
<td>AV018774</td>
<td>L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain</td>
<td>−5.24</td>
<td>0.00184</td>
</tr>
<tr>
<td>NM_008121</td>
<td>L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain</td>
<td>−5.945</td>
<td>0.0167</td>
</tr>
<tr>
<td>NM_010023</td>
<td>dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)</td>
<td>−5.248</td>
<td>0.00263</td>
</tr>
<tr>
<td>AK002555</td>
<td>acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)</td>
<td>−4.842</td>
<td>0.0126</td>
</tr>
<tr>
<td>AK002555</td>
<td>acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)</td>
<td>−7.626</td>
<td>0.00187</td>
</tr>
<tr>
<td>NM_133249</td>
<td>peroxisome proliferative activated receptor, gamma, coactivator 1 beta</td>
<td>−2.904</td>
<td>0.00823</td>
</tr>
</tbody>
</table>

(+) Upregulation of genes compared with control untreated muscle.

(−) Downregulation of genes compared with control untreated muscle.

doi:10.1371/journal.pone.0074528.t004

**Table 5.** Downregulation of stress activated protein kinase (SAPK) pathway genes in mouse skeletal muscle at 4 days 2-AA treatment versus control muscle.

<table>
<thead>
<tr>
<th>Gene Bank Accession No.</th>
<th>Gene Name</th>
<th>Fold Change</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>BM119623</td>
<td>activating transcription factor 2</td>
<td>−2.160</td>
<td>0.0335</td>
</tr>
<tr>
<td>BG071068</td>
<td>guanine nucleotide binding protein (G protein), beta polypeptide 1</td>
<td>−2.770</td>
<td>0.0165</td>
</tr>
<tr>
<td>AV021455</td>
<td>guanine nucleotide binding protein (G protein), gamma 2</td>
<td>−4.480</td>
<td>0.0199</td>
</tr>
<tr>
<td>BQ175363</td>
<td>mitogen-activated protein kinase kinase kinase 9</td>
<td>−8.400</td>
<td>0.00541</td>
</tr>
<tr>
<td>NM_005852</td>
<td>mitogen-activated protein kinase kinase kinase 12</td>
<td>−2.012</td>
<td>0.0455</td>
</tr>
<tr>
<td>AF220195</td>
<td>mitogen-activated protein kinase 8 interacting protein 2</td>
<td>−62.110</td>
<td>0.0116</td>
</tr>
<tr>
<td>AF262046</td>
<td>mitogen-activated protein kinase 8 interacting protein 3</td>
<td>−3.759</td>
<td>0.0119</td>
</tr>
</tbody>
</table>

(−) Downregulation of genes compared with control untreated muscle.

doi:10.1371/journal.pone.0074528.t005
impaired mitochondrial function [60]. The pleotropic transcription factor PGC-1 functions in the regulation of differential gene expression, in conjunction with other transcription factors (e.g., PPAR, SIRT-1), in cells exhibiting high energy-demands, including skeletal muscle [8], [60], [61]. Here, 2-AA down-regulates PGC-1β, IRS1, IGFs and GLUT4 expression (Table 3), indicating a connection between PGC-1β and metabolic genes. This suggests that PGC-1β acts to regulate energy metabolism genes in skeletal muscle, and that mitochondrial dysfunction leads to the down-regulation of the insulin signaling pathway, and impaired systemic insulin activity (Fig. 7). To this end, our findings suggest a more general role for PGC-1β in skeletal muscle metabolism, and possibly in the progression of chronic infection [62], in addition to the insulin resistance seen in obese and/or type 2 diabetic patients [48], [49], [63], and CF patients with a high incidence of diabetes [25].

2-AA also downregulates genes involved in fatty acid oxidation, energy production, intermediary metabolism, and the TCA cycle (Table 4; Fig. 2b) This downregulation could in turn lead to a demand for increased muscle contractile gene expression to fulfill functional requirements; however, our results show that 2-AA reduces the expression of these genes (Fig. 6). This reduction could underlie the observed muscle function impairment (Table 7), and correspond to the impaired muscle strength in CF patients [64]. Our data suggest that this functional impairment may be due to reduced mitochondrial coupling, as both ATP synthesis and TCA flux are reduced, and the ratio of ATP synthesis and TCA flux can serve as an index of mitochondrial coupling [37].

\[\text{In vivo} \ \text{31P magnetization-transfer can non-invasively determine the unidirectional flux of } P_i \text{ to ATP ("ATP synthesis"), and has} \]

Table 6. Downregulation of muscle contraction genes in mouse skeletal muscle at 4 days 2-AA treatment versus control muscle.

<table>
<thead>
<tr>
<th>Gene Bank Accession No.</th>
<th>Gene Name</th>
<th>Fold Change</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>AK003186</td>
<td>tropomyosin 2, beta</td>
<td>−2.822</td>
<td>0.0291</td>
</tr>
<tr>
<td>NM_010867</td>
<td>myomesin 1</td>
<td>−6.41</td>
<td>0.0203</td>
</tr>
<tr>
<td>BM246564</td>
<td>phosphodiesterase 4B, cAMP specific</td>
<td>−2.161</td>
<td>0.0488</td>
</tr>
<tr>
<td>AK002271</td>
<td>tropomyosin 1, alpha</td>
<td>−3.175</td>
<td>0.021</td>
</tr>
<tr>
<td>BI248947</td>
<td>caldesmon 1</td>
<td>−5.736</td>
<td>0.0334</td>
</tr>
<tr>
<td>BC003284</td>
<td>WD repeat domain 21</td>
<td>−3</td>
<td>0.0288</td>
</tr>
<tr>
<td>BC024358</td>
<td>tropomyosin 2, beta</td>
<td>−3.439</td>
<td>0.0359</td>
</tr>
<tr>
<td>AY094172</td>
<td>calcium channel, voltage-dependent, beta 1 subunit</td>
<td>−2.317</td>
<td>0.0211</td>
</tr>
<tr>
<td>AA245637</td>
<td>ATPase, Ca++ transporting, cardiac muscle, slow twitch 2</td>
<td>−2.121</td>
<td>0.0402</td>
</tr>
<tr>
<td>X53753</td>
<td>tropomyosin 3, gamma</td>
<td>−2.399</td>
<td>0.0426</td>
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<tr>
<td>BC025840</td>
<td>titin</td>
<td>−2.281</td>
<td>0.0397</td>
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<tr>
<td>AK013026</td>
<td>annexin A6</td>
<td>−2.847</td>
<td>0.00242</td>
</tr>
<tr>
<td>AK010153</td>
<td>titin</td>
<td>−3.873</td>
<td>0.0149</td>
</tr>
<tr>
<td>AW558570</td>
<td>endothelin receptor type A</td>
<td>−4.527</td>
<td>0.0147</td>
</tr>
<tr>
<td>BB288010</td>
<td>myomesin 2</td>
<td>−14.32</td>
<td>0.0221</td>
</tr>
<tr>
<td>BB705075</td>
<td>Calponin 3, acidic (Cnn3), mRNA</td>
<td>−2.413</td>
<td>0.0044</td>
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<tr>
<td>BM122177</td>
<td>titin</td>
<td>−2.901</td>
<td>0.0328</td>
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<tr>
<td>BB478751</td>
<td>titin</td>
<td>−3.778</td>
<td>0.0137</td>
</tr>
<tr>
<td>NM_033268</td>
<td>actinin alpha 2</td>
<td>−4.234</td>
<td>0.0349</td>
</tr>
<tr>
<td>BC026142</td>
<td>myosin, heavy polypeptide 11, smooth muscle</td>
<td>−3.538</td>
<td>0.00149</td>
</tr>
<tr>
<td>NM_022314</td>
<td>tropomyosin 3, gamma</td>
<td>−2.607</td>
<td>0.0251</td>
</tr>
<tr>
<td>BB474208</td>
<td>myomesin 2</td>
<td>−8.349</td>
<td>0.039</td>
</tr>
<tr>
<td>BB633014</td>
<td>calponin 2</td>
<td>−2.342</td>
<td>0.00402</td>
</tr>
<tr>
<td>BB883102</td>
<td>calponin 3, acidic</td>
<td>−3.216</td>
<td>0.0354</td>
</tr>
<tr>
<td>AW108242</td>
<td>RIKEN cDNA 8030451F13 gene</td>
<td>−2.775</td>
<td>0.0286</td>
</tr>
<tr>
<td>BM232388</td>
<td>tropomyosin 1, alpha</td>
<td>−4.137</td>
<td>0.00079</td>
</tr>
<tr>
<td>AV241307</td>
<td>myomesin 2</td>
<td>−10.55</td>
<td>0.0258</td>
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</tbody>
</table>

(−): Downregulation of genes compared with control untreated muscle.

doi:10.1371/journal.pone.0074528.t006
been used to show that abnormal mitochondrial function occurs in obesity and diabetes [37]. This technique [65], [66] has enabled us to noninvasively measure fast enzyme reaction exchange rates, to provide an index of the net skeletal muscle rate of oxidative ATP synthesis catalyzed by mitochondrial ATPase. This is by definition proportional to the oxygen consumption rate by the P/O ratio, e.g., the ratio of the net rate of ATP synthesis by oxidative phosphorylation to the rate of oxygen consumption [67],[68]. Unidirectional ATP synthesis flux, measured by NMR, is thought to primarily reflect flux through F1F0-ATP synthase, with negligible influence of the coupled glyceraldehyde-3-phosphate dehydrogenase (G3PDH), or phosphoglycerate kinase (PGK) reactions [66]. Although the net glycolytic contribution of G3PDH and PGK to ATP production is small, versus oxidative phosphorylation, these enzymes occur at near equilibrium, allowing high unidirectional ATP production. As such, we assume the contribution of glycolytic reactions to unidirectional ATP synthesis flux is negligible.

IMCLs levels are increased in mouse gastrocnemius muscle following 2-AA treatment, as assessed by HRMAS 1H NMR spectroscopy (Table 2 and Fig 3). Although the source of these accumulated lipids is beyond this study, it has been shown that EMCLs, IMCLs, and triglycerides all contribute to cellular lipid peaks [42], [69], [70]. IMCL probably serve as energy substrates for oxidative metabolism [71], and can be mobilized and utilized with turnover rates of several hours [72]. Furthermore, the lipid peak at 1.4 ppm in Figure 3 is attributed to methylene protons of intra-myocellular triglyceride acyl chains, primarily due to IMCL [42], to suggest that the increase in NMR-visible lipids at 1.4 ppm post 2-AA treatment is primarily due to increased IMCL. This is further supported by human studies [73],[74] where IMCLs were further supported by human studies [73],[74] where IMCLs were to suggest that the increase in NMR-visible lipids at 1.4 ppm in Figure 3 is attributed to methylene protons of

Table 7. Absolute wet-weights of tibialis (TA), soleus (So) and gastrocnemius (GC) muscles, and absolute twitch tensions (ST; single twitch, Tmax; maximum response of tetanic stimulation at 50 Hz for 5 sec) of tibialis muscle, at 4 days post 2-AA treatment, versus corresponding control muscle.

<table>
<thead>
<tr>
<th>Wet weight (mg) and twitch height (g)</th>
<th>Control</th>
<th>2-AA</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Left</td>
<td>Right</td>
</tr>
<tr>
<td>TA</td>
<td>54.0±3.2</td>
<td>54.7±2.4</td>
</tr>
<tr>
<td>So</td>
<td>8.1±0.8</td>
<td>8.0±0.5</td>
</tr>
<tr>
<td>GC</td>
<td>153.0±8.3</td>
<td>152.7±6.4</td>
</tr>
<tr>
<td>ST</td>
<td>44.6±1.3$^1$</td>
<td>45.0±1.2$^1$</td>
</tr>
<tr>
<td>Tmax</td>
<td>121.0±7.0$^1$</td>
<td>118.7±5.0</td>
</tr>
<tr>
<td>N</td>
<td>6</td>
<td>6</td>
</tr>
</tbody>
</table>

Values are means ± SEM. Differences between the two sides of the 2-AA group and control group were compared using one-way ANOVA test and Bonferroni’s multiple comparison as a Post hoc testing. Differences were assumed to be significant if the p-value was <0.05. There are no significant differences in net muscle weights between the experimental and control mice (p>0.05). The twitch heights of single twitch stimulation and tetanic stimulation show significant differences between control and 2-AA mice (p<0.05).

1Significant difference of single twitch height between control and 2-AA group in left side (p = 0.043).
2Significant difference of single twitch height between control and 2-AA group in right side (p = 0.047).
3Significant difference of maximum response of tetanic stimulation between control and 2-AA group in left side (p=0.011).

Lt: Left side of muscle. Rt: Right side of muscle.

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suggested to serve as metabolic biomarkers of insulin resistance. Nevertheless, lipid accumulation may reflect increased inflammation versus mitochondrial dysfunction [13], although 2-AA immunomodulation is characterized by decreased inflammation [31]. Here, increased IMCLs were associated with altered expression of key regulators of insulin signaling and glucose metabolism (Table 3), which can lead to insulin resistance in association with mitochondrial dysfunction. To this end, 2-AA might mediate insulin resistance, as IMCLs are biomarkers of such resistance, and it down-regulates IRS1, IGFs, and GLUT4. Nevertheless we have not directly demonstrated insulin resistance by traditional methods.

Although the exact mechanism of abnormal insulin function is unknown, there is increasing evidence that plasma FFAs may act to induce insulin resistance [75]. However, intramyocellular accumulation of toxic FFA metabolites, i.e fatty acyl-coenzyme A, diacylglycerol, and ceramides, has been also shown to impair insulin signal transduction, glucose transport/phosphorylation, and glycogen synthesis [46], [75], [76]. Because fatty acid metabolism and glucose levels are closely linked, we propose that the observed accumulation of lipids or triglycerides in muscle, may lead to insulin resistance [77], although we did not observe any alteration in plasma FFA, in agreement with the unchanged FFA levels in CF patients [25]. In addition, previous studies have suggested that muscle activity of lipoprotein lipase (LPL) is related to insulin resistance [78] and that insulin may downregulate the activity of lipoprotein lipase in skeletal muscle [79]. This is in accordance with the decreased expression of the LPL gene in the skeletal muscle of the 2-AA treated mice (Table 4).

CF patients often develop skeletal muscle wasting [80], and insulin resistance [25], [81]. 2-AA mediated downregulation of muscle gene functions is associated with tissue loss and low ATP synthesis rate in skeletal muscle. Our results suggest that 2-AA may act as an important contributor of host metabolic alterations in disease states characterized by chronic infection. CF is one such syndrome, where the associated pathophysiology stems as much from the underlying gene mutation as from the colonization and
adaptation of particular flora in the mucosal pulmonary milieu [92]. In acute infections, metabolic alterations are short-lived and reverse quickly [83], [94], whereas in chronic infections the protracted metabolic response leads to muscle wasting [85], [96]. P. aeruginosa and 2-AA in chronically infected CF lungs is considered pathognomonic [32], [33], [87], [88]. As such, further investigation into the potential clinical significance of 2-AA is warranted, 2-AA modulates immune responses to promote host tolerance and chronic infection [31]. To this end, it is possible that the 2-AA mediated changes of the host metabolome may further contribute to host tolerance and chronic P. aeruginosa infection. Indeed, inhibition of PPAR-γ reduces the phagocytic activity of macrophages [89], which may serve to evade the host defense mechanism, and possibly favor infection and allow long term bacterial presence promoted by 2-AA [31]. Our results are consistent with other chronic infections, including HIV [90], tuberculosis [91], chronic Escherichia coli in skeletal muscle [92], and chronically infected CF patients [93].

Conclusion

Based on our multidisciplinary results, Figure 7 proposes a novel mechanism for the bacterial pathogen infochemical, 2-AA, to mediate host metabolic dysregulation that results in mitochondrial dysfunction, and potentially insulin resistance, in skeletal muscle. The metabolic changes promoted by 2-AA may be clinically relevant in molecular medicine in general, and CF in particular, as: a) ATP synthesis rate and IMCLs can be measured clinically using non-invasive and non-irradiating metabolic assays; b) PGC-1β activity may be induced; and c) PGC-1β agonists may alleviate insulin resistance and prevent damage in organs remote from the infection site. In addition, our results provide further insights into the molecular and metabolic processes mediated by 2-AA that accompany infections caused by 2-AA producing pathogens, including Pseudomonas aeruginosa and Burkholderia species [32], [33], as well as 2-AA-related molecules produced by other pathogens.

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Author Contributions

Conceived and designed the experiments: AAT LGK. Performed the experiments: CC AB NP SL MM. Analyzed the data: AAT CC AB LGK. Contributed reagents/materials/analysis tools: AAT JAVM RGT LGR. Wrote the paper: AAT AB LGK.

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