

27 **Abstract**

28 Resolution of inflammation is now known to be an active process which in part is
29 instigated and controlled by specialised pro-resolving lipid mediators (SPM's) derived
30 from dietary omega-3 fatty acids. Resolvin E1 (R_vE₁) is one of these SPM's derived
31 from the omega-3 fatty acid eicosapentaenoic acid. Using both molecular and
32 phenotypic functional measures we report that in a model of Lipopolysaccharide
33 (LPS) induced inflammation, R_vE₁ attenuated mRNA gene expression levels of both
34 interleukin-6 and monocyte chemoattractant protein-1 whilst having no effect on
35 tumour necrosis factor- α or Interleukin-1 β in C2C12 skeletal muscle myotubes.
36 Findings at the molecular level were transferred into similar changes in extracellular
37 protein levels of the corresponding genes with the greatest attenuation being noted
38 in IL-6 protein concentrations. R_vE₁ instigated beneficial morphological changes
39 through the prevention of endotoxin induced skeletal muscle atrophy, thus resulting
40 in a rescue of endotoxin force losses in tissue engineered skeletal muscle. These
41 findings demonstrate, in our model of endotoxin induced inflammation in skeletal
42 muscle, that R_vE₁ has pro-resolving properties in this cell type. Our data provides
43 rationale for further investigation into the mechanistic action of R_vE₁ in skeletal
44 muscle, with the vision of having potential benefits for the prevention/resolution of *in-*
45 *vivo* skeletal muscle atrophy.

46 **Introduction**

47 A loss of skeletal muscle size (wasting) is common in a number of disease states as
48 well as being prevalent in the 'healthy' ageing process (Romanick, Thompson &
49 Brown-Borg, 2013). In turn skeletal muscle wasting impairs functional capacity,
50 which is associated with impaired quality of life and increased mortality (Ruiz et al.,
51 2008; Roshanravan et al., 2017). Systemic and local inflammation is often prevalent
52 in elderly individuals (Argilés et al. 2005) and cachexic diseases (Saini et al., 2006;
53 Candore et al., 2010) and is therefore thought to play a major role in mediating the
54 loss of skeletal muscle size. Direct evidence for this has come from *in-vitro* studies,
55 where incubation of myotubes with pro-inflammatory cytokines causes atrophy and
56 up regulation of catabolic signalling pathways (Li et al., 1998; Girven et al., 2016;
57 Alvarez et al., 2002). There is therefore a need to further develop intervention
58 strategies aimed at dampening or resolving inflammation in order to prevent skeletal
59 muscle wasting and offset subsequent decline in muscle function.

60 Omega-3 polyunsaturated fatty acids (ω -3) are bioactive lipids found in a variety of
61 foods including fish oils. Nuts and seeds. The most common PUFA's are
62 Eicosapentaenoic acid (EPA) and Docosahexaenoic acid (DHA), which have shown
63 to elicit a variety of potential health benefits in both clinical and laboratory based
64 studies (Chagas et al., 2017; Calder et al., 2017; Poudyal et al., 2011). Though the
65 beneficial effects of omega-3's is now widely accepted in specific disease states
66 such as Cardiovascular disease (Tavazzi et al., 2008), the mechanisms of action are
67 still poorly described. Research investigated the role of membrane make up both in
68 terms of lipid raft formation and the ratio of omega-3:omega-6 in the lipid bilayer

69 structure (Calder, 2011). Though these factors may contribute to the anti-
70 inflammatory role of omega-3 fatty acids, cellular based research proposed a novel
71 set of naturally occurring ω -3 derived mediators termed Specialised Pro-Resolving
72 Mediators (SPM's) which have been identified as having pro-resolving effects in
73 several cell types, and may be critical in defining the health benefits of ω -3 (Serhan
74 et al., 2000; Liu et al., 2017; Norling et al., 2016; Jeromson et al., 2015).

75 The 'E-series' resolvins are biosynthesised from the omega-3 fatty acid
76 Eicosapentaenoic acid (EPA). In particular 5S,12R,18R-trihydroxy-
77 6Z,8E,10E,14Z,16E-eicosapentaenoic acid (R_vE_1) is synthesised during the
78 metabolism of EPA by either acetylated cyclooxygenase-2 (COX-2) or the mono-
79 hydroxylase PY450 (Serhan et al., 2000; Serhan, 2004). Indeed, the detection of
80 R_vE_1 at nanogram concentrations has been reported *in-vivo* (Ohira et al., 2010) and
81 at these concentrations R_vE_1 has been shown to elicit pro-resolving actions *in-vitro*
82 in an acute inflammatory model of leukocyte infiltration (Schwab et al., 2007). Further
83 investigations have shown that R_vE_1 is able to attenuate Lipopolysaccharide (LPS)
84 induced pro-inflammatory cytokine transcription in pancreatic islets (Lund et al.,
85 2010) and can reduce circulating levels of Interleukin-1 β (IL-1 β) and Interleukin-6
86 (IL-6) in animal (murine) models (Hasturk et al., 2007; Campbell et al., 2010; Seki et
87 al., 2010). Importantly, Lund and colleagues found that inflammatory markers such
88 as Tumour Necrosis Factor-alpha (TNF- α) and Monocyte chemoattractant protein 1
89 (CCL-2) were reduced to the largest extent when R_vE_1 was co-incubated with LPS
90 treated human pancreatic islets *in vitro*, which is of particular interest in skeletal
91 muscle physiology as both play roles in the initiation and infiltration phases of the
92 inflammatory process in skeletal muscle (Lund et al., 2010) highlighting the potential
93 for advantageous properties of R_vE_1 in the resolution of skeletal muscle
94 inflammation. Moreover, cyclic production of IL-6 through IL-1 β signalling may further
95 exacerbate atrophy in skeletal muscle (Haddad et al., 2005; Luo et al., 2003), thus
96 highlighting the importance of attenuating levels of these cytokines. It is therefore
97 plausible that R_vE_1 may have efficacy as a therapeutic intervention for the resolution
98 of inflammatory signalling and prevent subsequent atrophy in skeletal muscle.

99 The aim of the current study was to investigate the preventative effects of R_vE_1 on
100 LPS induced inflammation in C2C12 *in-vitro* muscle cultures to provide a first
101 indication of its role skeletal muscle inflammation. Initially we explored the time
102 course of TNF α , IL-6, IL-1 β and CCL-2 induction following incubation of myotubes
103 with LPS, and thereafter sought to determine if the elevations in pro-inflammatory
104 cytokine production could be prevented by the addition of R_vE_1 to the cultures.
105 Thereafter we investigated if R_vE_1 could prevent inflammation induced myotube
106 atrophy and whether this would translate in to improvements in muscle function
107 utilising '3D'-skeletal muscle tissue engineering techniques.

109 **Methods**

110 *Cell Culture*

111 The C2C12 murine myoblast cell line (C2C12) was used for all experiments.
112 C2C12's were cultured at 37°C and 5% CO₂ (HeraCell, Thermo Scientific, UK) in
113 growth medium (GM) composed of: Dulbecco's modified Eagle's medium (DMEM)
114 (Fisher Scientific, UK) plus 20% FBS (PAN Biotech, Germany), and 1% penicillin–
115 streptomycin (PS) solution (Invitrogen, Paisley, UK), until 80-95% confluency was
116 attained. Cells were then enzymatically dissociated using Trypsin-EDTA (Sigma
117 Aldrich, UK) and counted using the trypan blue exclusion method and subsequently
118 seeded into 12 well plates (Thermo-Scientific) at a density of 12.5×10^3 cells/cm² in
119 standard GM. Cells were grown to confluency (approximately 3 days), at which point
120 medium was changed to differentiation media (DM) composed of DMEM (Fisher
121 Scientific, UK) plus 2% Horse Serum (HS) (Fisher Scientific, UK), and 1% penicillin–
122 streptomycin (PS) solution (Invitrogen, Paisley, UK) to initiate differentiation.
123 Following three days of differentiation, myotubes were exposed to one of 3
124 conditions: i) Vehicle Control (CON): DM + 0.1 µl/ml EtOH; ii) LPS (LPS): DM + 100
125 ng/ml LPS (Sigma Aldrich, UK); iii) Resolvin E1 (R_vE₁): DM + 100 ng/ml LPS + 100
126 nM R_vE₁ (Bertin Pharma, France) and subsequently analysed for mRNA expression,
127 myotube size and myokine release. Specifically, RNA was extracted at 0.5, 1.5, 3
128 and 6 h of experimental treatment. Based on the initial mRNA induction, following 3
129 hours of treatment, medias were removed and replaced with standard DM for a
130 further 72 h, at which point cells were fixed for immunocytochemistry analysis and
131 conditioned mediums harvested for further analysis. Furthermore, initial mRNA
132 screening of the basal effect of R_vE₁ showed no effect on the genes of interest
133 (Figure S4), thus authors deemed the condition unnecessary for subsequent
134 experimentation.

135 To determine if the inflammatory stimulus could impact on muscle force production
136 and the effects of R_vE₁, a tissue engineering approach was employed. Fibrin based
137 hydrogels were fabricated as previously described (Martin, Aguilar-Agon, et al.
138 2017). Briefly, two 6mm sutures were pinned into PDMS (Sylgard 184 Elastomer,
139 Dow Corning, UK) coated 35mm plates 12mm apart using 0.15mm minuten pins
140 (Entomoravia, Czech Republic). Plates were sterilised using Ultraviolet light and
141 washing with 70% ethanol and subsequently left to dry for 1 hour. Each plate then
142 received 500µl of GM containing 10U/ml thrombin (Sigma-Aldrich) and 80µg/ml
143 aprotinin (Sigma-Aldrich) which was spread evenly over the surface of the plate
144 ensuring that the sutures were covered. 200µl of 20mg/ml stock fibrinogen (Sigma-
145 Aldrich) solution was then added to the plate, and was agitated gently to ensure
146 even distribution and then left to incubate for 10 minutes at room temperature before
147 being transferred to the incubator (37°C) for one hour for polymerisation. Post
148 incubation, 100,000 C2C12's seeded on the surface of each hydrogel in GM + 0.25
149 mg/ml of 6-Aminocaproic acid (AA). Once cells reached confluency (approximately 3

150 days) medium was changed to DM + 0.5 mg/ml AA for 2 days. Post differentiation,
151 cells were maintained in maintenance medium consisting of DMEM, 7% FBS, 1%PS
152 and 0.5 mg/ml AA (MM) for the remainder of the 14-day culture period. 72 h before
153 the end of the 14-day culture period experimental hydrogels were changed into one
154 of 3 conditions: i) CON; ii) LPS; iii) R_vE₁ as described above. After 3 h of incubation
155 in the experimental medias, medias were removed and replaced with MM for the
156 remainder of the culture period. All experiments were conducted with cells between
157 passages 4 and 8 (n=9, across 3 biological repeats for each analysis method).

158

159 *RNA Extraction*

160 Cells isolated for mRNA analysis were lysed in 400 µl of TRI Reagent and frozen at -
161 80°C prior to further analysis. RNA extraction was performed as per the
162 manufacturer's instructions. In brief, chloroform was added to ensure dissociation of
163 nucleotide complexes (0.2 ml per 1 ml of TRI reagent), and samples were agitated
164 and left to stand for 5 mins before being centrifuged at 12,000 g for 15 min. The
165 aqueous phase was removed and 2-propanol (0.5 ml per 1 ml of TRI reagent) was
166 added to the aqueous phase and mixed by inversion. Following 10 minutes'
167 incubation at room temperature samples were centrifuged at 12,000 g for 10mins to
168 pellet RNA. RNA pellets were washed in 75% ethanol, centrifuged for a further 5mins
169 at 7,500 g, and air dried for 5-10 mins. Once isolated, RNA was suspended in 50 µl
170 RNA storage solution (Ambion, Life Technologies) and stored in RNase free tubes
171 for mRNA analysis.

172

173 *RT-qPCR*

174 One step quantitative RT-qPCR was used to determine expression of target mRNA's
175 in C2C12 cultures. Primer sequences (Table 1) were checked for specificity and
176 assay efficiency by performing standard curve analysis with a top standard of 200 ng
177 of RNA. Output was analysed using ViiA 7 RUO Software where melt curve analysis
178 was used to check for specificity of primers. Optimisation of standard curves was
179 assumed with efficiencies of 100 ± 10%.

180 Reactions were made up in 384 well RNase free plates (Applied Biosystems, UK)
181 and consisted of 20 ng (4 ng/µl) of RNA, 0.1 µl of both forward and reverse primers
182 (Life Technologies) (Table 1), 0.1 µl of Quantifast Reverse Transcriptase kit (Qiagen)
183 and 4.7 µl of SYBR green mix (Qiagen) to create 10 µl reactions. Once prepared,
184 plates were transferred to the ViiA 7™ Real Time PCR thermal cycler (Applied
185 Biosystems, Life Technologies) which was programmed to perform the following
186 steps: 10 min hold at 50°C (reverse transcription), followed by a 5 min hold at 95 °C
187 (activation of 'hot start' Taq polymerase), and cycling between 95 °C for 10s
188 (denaturation) and 60 °C for 30 s (annealing and extension). Fluorescence was
189 detected after every cycle and data was analysed using RPIIβ as the housekeeping
190 gene. Data was made relative using the comparative Ct method (Livak and

191 Schmittgen 2001) with any changes in target genes being in comparison to that of
192 the vehicle control condition for each experimental repeat.

193

194 *Extracellular cytokine analysis*

195 Cell supernatants were collected from culture wells for analysis of extracellular
196 protein concentrations. Protein concentrations for IL-6, TNF- α , IL-1 β and CcL-2 were
197 measured using 'sandwich' based ABTS ELISA kits (PeproTech, US). In brief, 1.0
198 $\mu\text{g}/\text{mL}$ of anti-murine capture antibody was added to an ELISA microplate (NUNC
199 maxiSorp, Fisher, UK). Following overnight incubation at room temperature, the plate
200 was washed 4 times with wash buffer (0.05% Tween-20 PBS) before being blocked
201 (1% BSA in PBS) for 1 hour. The plate was washed 4 times and 100 μL of serially
202 diluted standards or supernatant sample were added and incubated at room
203 temperature for 3 hours with moderate agitation (500 rpm). The plate was again
204 washed 4 times before being incubated with detection antibody for 2 hours at room
205 temperature with agitation as above. Following 4 washes, 100 μL of ABTS liquid
206 substrate (Sigma-Aldrich, Dorset, UK) was added to each well and the plate was
207 loaded into a VarioskanTM Flash Multimode Reader (ThermoFisher). Colour
208 development was monitored every 10 minutes for 1 hour at 405 nm with a
209 wavelength correction of 650 nm.

210

211 *Fluorescent staining*

212 Cells grown on 13 mm coverslips in 12 well plates were fixed with 3.7%
213 formaldehyde solution made up in PBS for 30 min. Fixed cells were then washed in
214 TBS twice and cells were permeabilised using a 0.2% Triton X-100 (Sigma) solution
215 made up in TBS for 1 hour. Following a further two washes cells were stained with
216 Phalloidin (1:200 in TBS) to visualise the F-actin filaments in myotubes and DAPI
217 (1:1000) to counter stain nuclei. After an hour of incubation, cells were washed 3 x
218 with TBS and subsequently mounted onto microscope slides with FlouromountTM
219 aqueous mounting medium (Sigma Aldrich). Images were captured using a Leica
220 DM2500 fluorescent microscope (Leica, UK) at 20x magnification and 7 images were
221 obtained per coverslip, equating to 21 images per condition, per biological repeat.
222 Analysis of myotube width and number were conducted using Image J software
223 (NIH, Bethesda, MD). Myotubes were identified as elongated structures containing 3
224 or more nuclei and expressing high levels of F-actin. Myotube number was counted
225 per image and an average of 3 measures of each myotube was obtained to calculate
226 myotube width.

227

228 *Assessment of tissue engineered skeletal muscle function*

229 Prior to functional tests, hydrogels were washed once in a Krebs Ringer HEPES
230 buffer (KRH; 10mM HEPES, 138 mM NaCl, 4.7mM KCl, 1.25 mM CaCl₂, 1.25 mM
231 MgSO₄, 5 mM Glucose, 0.05% Bovine Serum Albumin in dH₂O) and attached to a

232 model 403A Aurora force transducer (Aurora Scientific, UK). Following the addition
233 of 4 ml of KRH buffer, wire electrodes were positioned either side of the hydrogel in
234 order to allow for electric field stimulation. Maximal twitch force was determined
235 using a single 3.6 v/mm, 1.2 ms impulse and maximal tetanic force was measured
236 using a 1 second pulse train at 100Hz and 3.6 v/mm, generated using labVIEW 2012
237 software (National Instruments, UK). Data was acquired using Powerlab (ver. 8/35)
238 and associated software (Labchart 8, AD Instruments, UK).

239

240 *Statistical Analysis*

241 Data are presented as means \pm SEM unless otherwise stated (n=9). Statistical
242 analyses were performed using SPSS v.23 (SPSS Inc., Chicago, IL, US). Data were
243 tested for normal distribution and homogeneity of variance. A one-way analysis of
244 variance (ANOVA), or non-parametric equivalent, for a between-between design was
245 used to analyse the differences between conditions at a single time point. For
246 comparisons across time points, a one-way analysis of variance (ANOVA), or non-
247 parametric equivalent, for a between-between design was used to analyse the
248 differences between both time and condition and any interaction effect between the
249 two. Where significance was reported, Bonferroni post-hoc tests or a series of non-
250 parametric equivalents were used to identify where any significance lay between
251 conditions and time points. Statistical significance was assumed if $p \leq 0.05$. Further
252 analysis of effect sizes (r) were used to calculate the magnitude of effect: Trivial
253 < 0.02 ; Small 0.2-0.5; Moderate 0.5-0.8; Large > 0.8 (Cohen, 1992).

254

255 **Results**

256 *LPS induces elevations in mRNA of pro-inflammatory markers in skeletal muscle* 257 *myotubes*

258 To quantify the induction of pro-inflammatory markers, RT-qPCR was used to
259 measure the mRNA expression of selected pro-inflammatory markers across a six-
260 hour time course in response to LPS exposure. A pre-defined dose of 100 ng/ml of
261 LPS was seen to induce significant increases across all four selected markers at
262 differing time points in comparison to CON (See Figure S1). Significant increases in
263 TNF- α were seen at 0.5 hrs (4.97 vs. 0.97) whereas the greatest induction of IL-6
264 (21.66 vs. 2.12) and CcL-2 (67.38 vs. 1.27) was observed at 3 hrs and IL-1 β mRNA
265 levels were significantly elevated at 6 hrs (4.00 vs. 1.98).

266

267 *Resolvin E1 attenuates LPS induced mRNA induction of pro-inflammatory markers* 268 *and related extracellular protein release*

269 Utilising the time points optimised for maximal LPS induced mRNA expression in the
270 initial experiments, the effects of an optimised dose of R ν E $_1$ (100 nM; See Figure S2)
271 were investigated. Selected doses during preliminary experiments were based on

272 previous literature identifying RvE₁ at nano-molar concentrations in-vivo (Ohira et al.,
273 2010). Cultures were simultaneously exposed to RvE₁ along with LPS had reduced
274 levels of both IL-6 (23.44 vs. 14.92, p<0.05) and CcL-2 (45.10 vs. 32.68, p<0.05) in
275 comparison to LPS alone (Figure 1). However, no changes were noted in TNF- α
276 (3.56 vs. 3.89, p>0.05) or IL-1 β mRNA expression (2.96 vs. 2.98, p>0.05).
277 Subsequently, extracellular protein levels of all markers were measured in the
278 conditioned media to investigate if myokine release reflected the transcriptional
279 changes. Twenty-four hours post LPS exposure all proteins measured showed
280 significant increases in the LPS condition compared to that of the CON (Figure 2).
281 However, with the addition of RvE₁, significant reductions were only noted in IL-6
282 (3900 \pm 157 pg/m vs. 2500 \pm 729 pg/ml, p<0.05, r=1.92). Reduced levels of both
283 CcL-2 (20006 \pm 4441 pg/m vs. 16014 \pm 4884 pg/ml, p>0.05, r=0.82) and IL-1 β (11340
284 \pm 3354 pg/m vs. 9223 \pm 3580 pg/ml, p>0.05, r=0.59) were observed, although these
285 changes did not reach statistical significance. No differences were noted in TNF- α
286 extracellular protein following RvE₁ addition in comparison with LPS alone (127.2 \pm
287 35.8 pg/m vs. 124.8 \pm 45.4 pg/ml, p>0.05, r=0.05).

288

289 *RvE1 attenuates LPS induced atrophy*

290 Myotubes incubated acutely with LPS for 3 hours displayed significant atrophy at
291 later time points, with the most severe level of morphological atrophy noted at 72 hrs
292 post LPS exposure displaying a 53.56 % reduction compared with 24 hrs and 48 hrs
293 (24 % and 32 % reductions, respectively: See Figure S3). When RvE₁ was added to
294 myotubes acutely along with LPS, the resulting atrophy was resolved by 31.83 %
295 compared to the LPS condition (9.71 \pm 0.59 μ m vs. 15.45 \pm 1.21 μ m, p<0.05). No
296 difference was seen in myotube number across all three conditions confirming the
297 phenotypic change was atrophic in nature as opposed to being hyperplastic (Figure
298 3).

299

300 *Functional resolution of LPS induced force losses in tissue engineered skeletal* 301 *muscle*

302 A tissue engineering approach was adopted to investigate if LPS induced atrophy in
303 skeletal muscle myotubes led to a decrement of its functional capacity in terms of
304 force generation. LPS exposure was used as previously described as well as the 72
305 hrs post exposure time point where myotube atrophy was maximal. After LPS
306 exposure, peak tetanic force (μ N) of tissue engineered skeletal muscle was
307 significantly reduced in comparison to that of the control (93.48 \pm 3.27 % vs. 59.34 \pm
308 7.07 %, p<0.05, r= 1.80). Furthermore, with the addition of RvE₁ combined with LPS,
309 force decrements were resolved by 13.35%, which although did not reach statistical
310 significance, did represent a large effect (59.34 \pm 7.07 % vs. 72.69 \pm 5.15 %, p>0.05,
311 r=1.00) (Figure 4).

313 Discussion

314 The resolution of inflammation is defined as an active process and one which has
315 been shown to be in part mediated by lipid derived SPM's (Ohira et al., 2010). In the
316 present investigation we sought to determine if the novel SPM, R_vE₁ can resolve
317 inflammation in cultured C2C12 myotubes and thus act as a potential therapeutic for
318 muscle wasting. This data is the first to show the pro-resolving action of R_vE₁ in
319 skeletal muscle during endotoxin induced inflammation, resulting in the attenuation
320 of muscle loss and attenuated loss of muscle function in a '3D' tissue engineered
321 skeletal muscle model.

322 Diseases in which muscle wasting is noted are associated with elevated levels of
323 circulating pro-inflammatory cytokines. In the present investigation, LPS (100ng)
324 exposure resulted in elevations in mRNA levels of TNF- α , IL-6, CcL-2 and IL-1 β
325 across a 6-hour time course. These data are in agreement with Frost et al., (2002)
326 who also found time dependent responses of these pro-inflammatory cytokines in
327 response to a similar dose of LPS exposure in single cell myoblasts. Similar
328 responses have also been identified in fused myotubes further supporting the
329 findings of the current investigation (Boyd et al., 2006). Comparable findings have
330 also been reported utilising cytokine exposure such as TNF- α to induce IL-6 mRNA
331 gene expression (Alvarez et al., 2002). Moreover, in the present study conditioned
332 medium samples from myotube cultures 24 hours after an acute 3 hour LPS
333 exposure showed elevations in myokine levels of IL-6, TNF- α , IL-1 β and CcL-2
334 which also mirrors responses previously reported in the *in-vitro* literature (McCoin et
335 al., 2015; Podbregar et al., 2013; Peake et al., 2015) as well as displaying similar
336 trends to *in-vivo* investigations (Lang et al., 2003). Therefore, exposure of C2C12
337 myotubes to 100ng LPS over a 3-hour time course provided an ideal model to
338 explore the effect of R_vE₁.

339 Addition of R_vE₁ to the culture medium alongside LPS resulted in substantial
340 attenuation of the mRNA induction of pro-inflammatory cytokines, and whilst these
341 were not directly mirrored in the secreted extracellular levels of corresponding
342 proteins, there was clear evidence of attenuated levels. Similar trend reductions
343 have been seen in CcL-2 in regards to the effects of R_vE₁ (Lund et al., 2010), though
344 the current work showed contradictory effects on TNF- α . This suggests that R_vE₁ has
345 tissue-specific effects however dampening of LPS induced myotube inflammation in
346 our model highlights the efficacy of the use of R_vE₁ in this cell type/tissue indicating
347 that it may be an important nutritional therapeutic for reducing inflammation in
348 skeletal muscle.

349 Elevations in pro-inflammatory cytokines have previously been shown to induce an
350 atrophic response in muscle cells *in vitro* (Magee, Pearson & Allen 2008; Romanick,
351 Thompson & Brown-Borg, 2013) suggesting that the inflammation observed in

352 human diseases may be a major driver of the associated muscle wasting. In the
353 present study, 3 hours of incubation with LPS resulted in 46% myotube atrophy 72
354 hours later, similar to that observed by both Yi-Ping *et al*, (2000) and Magee *et al.*,
355 (2016) in response to TNF- α exposure. However, when LPS was co-incubated with
356 R_vE₁ myotube size was preserved, with only a small (~14%) reduction compared to
357 control cells. Interestingly, the current data set suggests that the attenuation of an
358 atrophic phenotype utilising R_vE₁ is via an attenuation of IL-6 with no effect seen on
359 TNF- α . This is contradictory to previous research identifying TNF- α as a key
360 mediator of cachexia, thus future research should look to investigate these signalling
361 differences across tissue type and based upon specific interventions. Furthermore,
362 this ~14% reduction equated to a greater preservation of myotube size than that
363 seen in response to EPA incubation in a pro-inflammatory state (Magee, Pearson &
364 Allen 2008). Though the time course and inflammatory stimulus differed to the
365 current investigation, our data provides initial evidence that R_vE₁ may have greater
366 pro-resolving properties in skeletal muscle.

367 Tissue engineered muscle models have been shown to closely replicate the
368 physiology and function of native tissue, with more recent studies utilising them to
369 closely replicate muscle from diseases with associated changes in muscle
370 phenotype (Martin *et al.*, 2017; Martin *et al.*, 2017). Further to this, work in tissue
371 engineered constructs has defined the linear relationship between myotube
372 phenotype in tissue engineered constructs and force output (Martin *et al.*, 2013), as
373 well as its ability to produce classic muscle mechanics closely replicative of native
374 tissue (Huang *et al.*, 2005). Thus, the use of this model as an assay of force
375 production allowed us to contextualise our molecular and morphological findings,
376 depicting that R_vE₁ prevents decrements in maximal force production associated with
377 LPS exposure. This data suggests that R_vE₁ associated attenuation of inflammation
378 is capable of having positive effects on muscle phenotype (size and function).

379 The proposed mechanism of action by which R_vE₁ impacts the inflammatory
380 resolution process has been shown to differ between cell types. Two cell surface
381 receptors have been identified for R_vE₁; Leukotriene B4 receptor 1 (BLTR1) and the
382 G-protein coupled receptor Chemerin Receptor 23 (ChemR23) (Arita *et al.*, 2007;
383 Norling & Perretti, 2013; Cash, Norling & Perretti, 2014); the latter of which has
384 previously been reported to be expressed on the sarcolemma of skeletal muscle
385 (Sell *et al.*, 2009). R_vE₁ has been shown to display specific binding to ChemR23 with
386 a K_d of 11.3 nM, resulting in the attenuation of TNF- α mediated NF κ B activation (Arita
387 *et al.*, 2005; Ohira *et al.*, 2010). With the current findings providing the initial
388 evidence for the pro-resolving capacity of R_vE₁ in skeletal muscle, future work needs
389 to seek to understand whether beneficial effects of R_vE₁ are receptor dependent, and
390 if so, provide an insight into the identity to direct future investigations for therapeutic
391 strategies in cachexic disease states.

392 In conclusion, the current work has systematically developed an *in-vitro* method of
393 LPS induced inflammatory atrophy in skeletal muscle myotubes for the screening of

394 anti-Inflammatory/pro-resolving compounds. The process used both mono-layer *in-*
395 *vitro* approaches as well as recently defined '3D' tissue engineered skeletal muscle
396 culture, to enable the quantification of the effect of inflammatory atrophy on
397 functional output in a controlled culture setting. Using these methodologies, we have
398 shown potential application of R_vE₁ in this cell type. Future work should be directed
399 towards investigating the specific binding potential of R_vE₁ in skeletal muscle, to
400 identify its mechanism of action, furthering our understanding of its potential role as a
401 naturally occurring pro-resolving mediator in diseases states with associated
402 cachexia as well as in ageing populations.

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605 **Additional Information**

606 *Competing financial interests*

607 The authors declare no competing financial interests.

608 **Table Legends**

609 *Table 1.* Primer sequences used for RT-qPCR measurements of pro-inflammatory
610 cytokine mRNA expression in the present study.

611 **Figure Legends**

612 *Figure 1:* Pro-inflammatory cytokine mRNA expression in response to 100 ng/ml LPS
613 or LPS + RvE₁ 100 nM in comparison with an unstimulated control (CON). RvE₁
614 attenuated the elevations in IL-6 and CcL-2 mRNA levels whilst having no impact on
615 TNF- α and IL-1 β . Time points were selected from previous experiments (Figure S1)
616 Data displayed as mean \pm SEM. * denoting $p < 0.05$ between the condition and CON;
617 # denoting $p < 0.05$ between LPS and LPS+ RvE₁.

618 *Figure 2:* Pro-inflammatory cytokine extracellular protein concentrations in response
619 to 100 ng/ml LPS or LPS + RvE₁ 100 nM in comparison with an unstimulated control
620 (CON) 24h post stimulation. RvE₁ attenuated the elevation in IL-6 in the cell culture

621 medium following LPS stimulation, whilst having little effect on TNF- α , CcL-2 and IL-
622 1 β . Data displayed as mean \pm SEM, * denoting $p < 0.05$ between the condition and
623 CON. # denoting $p < 0.05$ between LPS and LPS+ RvE1.

624 *Figure 3:* Myotube morphology 72 hrs following acute (3 hrs) exposure to 100 ng/ml
625 LPS. The presence of LPS alone or in combination with RvE1 has no effect on
626 myotube number (a). In comparison, myotube atrophy occurs (b) following LPS
627 exposure which is prevented by co-incubation with RvE1. Data are expressed as
628 mean \pm SEM. * denoting $p < 0.05$ between the condition and CON. # denoting $p < 0.05$
629 between LPS and LPS+RvE1.

630 *Figure 4:* Maximal contractile force from engineered muscles cultured for 72 hrs
631 following acute (3 hrs) incubation with 100 ng/ml LPS or LPS + RvE1 100 nM.
632 Incubation of engineered muscle with LPS resulted in impaired muscle function
633 which was partially prevented by co-incubation with RvE1. All conditions were
634 compared to CON controls within individual experiments to calculate relative force.
635 Data are expressed as mean \pm SEM * denoting $p < 0.05$ between the condition and
636 CON.

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