

1 **Differential protein metabolism and regeneration in hypertrophic diaphragm and atrophic**
2 **gastrocnemius muscles in hibernating Daurian ground squirrels**

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4 Xia Yan ^{1,2}, Xuli Gao^{1,2}, Xin Peng^{1,2}, Jie Zhang^{1,2}, Xiufeng Ma^{1,2}, Yanhong Wei^{1,2,3}, Huiping
5 Wang^{1,2}, Yunfang Gao^{1,2,*}, Hui Chang ^{1,2,*}

6

7 ¹ Shaanxi Key Laboratory for Animal Conservation, Northwest University, Xi'an, 710069, P.R.
8 China.

9 ² Key Laboratory of Resource Biology and Biotechnology in Western China (College of Life
10 Sciences, Northwest University), Ministry of Education, Xi'an, 710069, P.R. China.

11 ³ School of Basic Medical Sciences, Ningxia Medical University, Yinchuan, 750004, China

12 # Equal contributors

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16 **All the co-authors' email addresses**

17 Xia Yan: 2364348698@qq.com

18 Xuli Gao 672622062@qq.com

19 Xin Peng: 1084875064@qq.com

20 Jie Zhang: 270685828@qq.com

21 Xiufeng Ma: 1639084401@qq.com

22 Yanhong Wei: lovely_yhwei@126.com

23 Huiping Wang: wanghp@nwu.edu.cn

24

25 *** Corresponding author:**

26 Dr. Yunfang Gao

27 College of Life Sciences, Northwest University,

28 229# North Taibai Road

29 Xi'an, 710069 China.

30 Tel.: +86 29 88303935.

31 gaoyunf@nwu.edu.cn

32

33 Dr. Hui Chang

34 College of Life Sciences, Northwest University,

35 229# North Taibai Road

36 Xi'an, 710069 China.

37 Tel.: +86 29 88303935.

38 changhui@nwu.edu.cn

39

40

41 **Abstract**

42 Whether differences in regulation of protein metabolism and regeneration are involved in the
43 different phenotypic adaptation mechanisms of muscle hypertrophy and atrophy in hibernators?
44 Two fast-type muscles (diaphragm and gastrocnemius) in summer active and hibernating Daurian
45 ground squirrels were selected to detect changes in cross-sectional area (CSA), fiber type
46 distribution, and protein expression indicative of protein synthesis metabolism (protein expression
47 of P-Akt, P-mTORC1, P-S6K1, and P-4E-BP1), protein degradation metabolism (MuRF1, atrogin-
48 1, calpain-1, calpain-2, calpastatin, desmin, troponin T, Beclin1, and LC3-II), and muscle
49 regeneration (MyoD, myogenin, and myostatin). Results showed the CSA of the diaphragm muscle
50 increased significantly by 26.1%, whereas the CSA of the gastrocnemius muscle decreased
51 significantly by 20.4% in the hibernation group compared with the summer active group. Both
52 muscles displayed a significant fast-to-slow fiber-type transition in hibernation. Our study further
53 indicated that increased protein synthesis, decreased protein degradation, and increased muscle
54 regeneration potential contributed to diaphragm muscle hypertrophy, whereas decreased protein
55 synthesis, increased protein degradation, and decreased muscle regeneration potential contributed
56 to gastrocnemius muscle atrophy. In conclusion, the differences in muscle regeneration and
57 regulatory pattern of protein metabolism may contribute to the different adaptive changes observed
58 in the diaphragm and gastrocnemius muscles of ground squirrels.

59

60 **Key words:** hibernation, protein metabolism, regeneration, skeletal muscle, differential adaptation

61

62 **Abbreviation**

63 Akt: protein kinase B

64 mTOR: the mammalian target of rapamycin

65 mTORC1: mammalian target of rapamycin in complex 1

66 S6K1: 70 kDa ribosomal protein S6 kinase 1

67 4E-BP1: eukaryotic initiation factor 4E-binding protein 1

68 CSA: cross-sectional area

69 myoD: myogenic differentiation 1

70 Beclin1: B-cell Lymphoma 2 interacting protein 1

71 LC3: microtubule-associated protein light chain 3

72 MuRF1: Muscle RING finger 1

73 Atrogin-1/MAFbx: muscle atrophy F-box

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76 Introduction

77 Although hibernating mammals are recognized as models of disuse-resistant skeletal muscle
78 atrophy (Bodine 2013, Ivakine and Cohn 2014, Lee et al. 2008, Reilly and Franklin 2016), not all
79 types of skeletal muscle maintain constant quality during long periods of hibernation. Our and other
80 previous studies have found that different types of skeletal muscles exhibit different degrees of
81 atrophy during mammalian hibernation (Cotton 2016, Zhang et al. 2019). The diaphragm is a fast-
82 type respiratory muscle. Inactivity caused by mechanical ventilation can lead to diaphragm atrophy
83 (Powers et al. 2013). However, although breathing in hibernating mammals is considerably inhibited
84 during hibernation (Larson et al. 2014, Staples and Brown 2008), such a condition does not induce
85 diaphragm atrophy, but rather hypertrophy. For example, previous studies have reported increases
86 in diaphragm muscle weight of 31.1% and 19% in hibernating Syrian hamsters (*Mesocricetus*
87 *auratus*) (Deveci and Egginton 2002) and golden-mantled ground squirrels (*Callospermophilus*
88 *lateralis*), respectively (Reid et al. 1995, Rourke et al. 2004). However, in the fast-type
89 gastrocnemius muscle, hindlimb unloading in non-hibernating rats resulted in a 42% decrease in
90 muscle weight and 34%–46% decrease in the cross-sectional area (CSA) of slow and fast muscle
91 fibers (Hu et al. 2017). In addition, muscle weight in the gastrocnemius muscle also showed a
92 decrease in small hibernating rodents (8.1%–29.8%), but to a lesser degree and with less atrophy
93 than that found in non-hibernators (Cotton 2016).

94 Skeletal muscles, as highly plastic tissue, undergo certain adaptive changes in structure and
95 function when the environment changes (Blaauw et al. 2013). Muscle size is controlled by the
96 balance between protein synthesis and degradation. Muscle hypertrophy occurs when synthesis is
97 greater than degradation; in contrast, muscle atrophy occurs when degradation is greater than
98 synthesis (Romanello and Sandri 2016). The Akt-mTOR signaling pathway plays a key role in the
99 initiation of protein synthesis in skeletal muscle under the physiological state (Bodine et al. 2001).
100 Activated mTORC1 (mammalian target of rapamycin in complex 1) phosphorylates downstream
101 targets S6K1 (70 kDa ribosomal protein S6 kinase 1) and 4E-BP1 (eukaryotic initiation factor 4E-
102 binding protein 1), resulting in increased protein synthesis (Gordon et al. 2013, Liu et al. 2013).
103 During hibernation, however, the phosphorylation and activity of Akt and mTOR can be modified.
104 For example, both are decreased in the thigh and femoral muscles of thirteen-lined ground squirrels
105 (*Ictidomys tridecemlineatus*) during hibernation and in the pectoral muscles of greater tube-nosed
106 bats (*Murina leucogaster ognevi*) during torpor (Cai et al. 2004, Lee et al. 2010, Wu and Storey
107 2012). Furthermore, the expression of phosphorylated 4E-BP is also decreased in the thigh muscles
108 of thirteen-lined ground squirrels during hibernation (Wu and Storey 2012).

109 Protein degradation of skeletal muscles mainly includes the calpain degradation, ubiquitin-
110 proteasome, and autophagy-lysosome pathways (Scicchitano et al. 2015). Calpains are the
111 promoters of muscle protein degradation, which can release myofibrillar proteins from sarcomeres.
112 The released myofibrillar proteins can be further ubiquitinated and transported to proteasomes for
113 degradation (Bartoli and Richard 2005, Huang and Forsberg 1998). Muscle RING finger 1 (MuRF1)

114 and muscle atrophy F-box (MAFbx)/atrogen-1 are ubiquitin protein ligases and important molecular
115 markers for evaluating skeletal muscle atrophy (Foletta et al. 2011). The ubiquitin proteasome
116 system depends on multiple proteasomes, of which 26S proteasome can cleave the target protein as
117 peptides (Chen et al. 2015). 26S proteasome is composed of 20S proteasome which mediates the
118 activity of chymotrypsin and trypsin, and plays an important role in ubiquitin protease system
119 (Souza et al. 2014). We previously found that calpain-1 and calpain-2 protein expression is
120 decreased in the soleus muscle, but unchanged in the extensor digitorum longus (EDL) muscle in
121 Daurian ground squirrels during hibernation, whereas the expression of calpastatin, an endogenous
122 inhibitor of calpains, is increased in both (Chang et al. 2018b). Calpain can degrade substrates such
123 as desmin, troponin T, troponin I, titin, alpha-fodrin and alpha-actinin, (Barta et al. 2005). Desmin
124 and troponin T are more sensitive to calpain than other substrates (Li et al. 2017). Desmin is located
125 around the Z-discs and connects the adjacent Z-discs to the sarcolemma and the nucleus (Capetanaki
126 et al. 1997). Troponin T plays an important role in regulating protein system, which can bind to
127 tropomyosin to form a complex (Perry 1998). Furthermore, various stress conditions (including
128 fasting, oxidative stress, and hypoxia) can induce autophagy as an adaptive physiological response
129 to restore cell metabolism. Increased autophagy is a survival-promoting mechanism rather than a
130 death-promoting mechanism (He et al. 2012, Levine and Yuan 2005, Moresi et al. 2012), and is an
131 important pro-survival mechanism in myocardial hibernation (May et al. 2008). However, previous
132 study has indicated that autophagy is inhibited in fast muscles, including quadriceps and anterior
133 tibial muscles, of hibernating thirteen-lined ground squirrels (Andres-Mateos et al. 2013). Therefore,
134 we hypothesize that the opposite adaptabilities of skeletal muscles in hibernating Daurian ground
135 squirrels, that is, hypertrophy and atrophy, are due to changes in the balance between protein
136 synthesis and degradation.

137 Muscle regeneration includes an increase in protein synthesis (hypertrophy) and proliferation of
138 muscle satellite cells (hyperplasia) and is a repair mechanism of muscle injury (Zanou and Gailly
139 2013). Previous studies have shown that the regeneration potential of disused skeletal muscle is
140 changed (Suetta et al. 2013, Wall et al. 2014). MyoD (myogenic differentiation) and myogenin are
141 myogenic regulatory factors (MRFs). MyoD is a molecular marker of muscle satellite cells
142 activation into muscle progenitor cells (Zanou and Gailly 2013), and myogenin plays a key role in
143 the fusion of myoblasts to form myotubes (Hasty et al. 1993). Even though the number of satellite
144 cells decreases during mechanical unloading, the expression of markers of satellite cell activation
145 increases (Arentson-Lantz et al. 2016, Guitart et al. 2018). Myostatin, a transforming growth factor-
146 beta (TGF β) family member, is a negative regulator of the proliferation and differentiation of muscle
147 satellite cells. Inactivation of myostatin can lead to skeletal muscle hypertrophy, whereas
148 overexpression can lead to muscle atrophy (Langley et al. 2002, McFarlane et al. 2011, Rodriguez
149 et al. 2014). Myostatin not only regulates the growth and size of skeletal muscle, but also interacts
150 with the Akt-mTOR pathway to regulate protein synthesis (Schiaffino et al. 2013, Trendelenburg et
151 al. 2009). So far, however, contradictions still exist regarding whether skeletal muscle regeneration

152 is involved in maintaining muscle quality in hibernating small mammals. For example, previous
153 studies have reported no atrophy in muscles ablated of satellite cells in hibernating thirteen-lined
154 ground squirrels (Andres-Mateos et al. 2012), but also reported that muscle satellite cells are not
155 quiescent and actually increase during hibernation (Brooks et al. 2015). Therefore, in the current
156 study, we attempted to clarify any differences in regeneration between two types of skeletal muscle
157 with different adaptive changes, and whether regeneration plays a differential regulatory role in
158 muscle maintenance in hibernating Daurian ground squirrels.

159 In this study, we examined two fast-type muscles (diaphragm and gastrocnemius) that exhibit
160 different adaptative changes during hibernation (hypertrophic and atrophic adaptation, respectively)
161 in Daurian ground squirrels. To elucidate the differential regulation of protein metabolism and
162 muscle regeneration in the two types of skeletal muscle, we measured the CSA, fiber type
163 distribution, protein synthesis metabolism (protein expression of P-Akt, P-mTORC1, P-S6K1, and
164 P-4E-BP1), protein degradation metabolism (MuRF1, atrogin-1, calpain-1, calpain-2, calpastatin,
165 desmin, troponin T, Beclin1 and LC3-II), proteasome activity, and muscle regeneration (MyoD,
166 myogenin and myostatin) in the diaphragm and gastrocnemius muscles of summer active (SA) and
167 hibernating (HIB) Daurian ground squirrels.

168 **Methods**

169 **Acquisition and use of animals**

170 The animals' acquisition and use were approved by the Northwest University Ethics Committee.
171 As described by our laboratory previously (Chang et al. 2018a, Chang et al. 2018b), sixteen Daurian
172 ground squirrels of both sexes were captured from the Weinan plain in the Shaanxi province of
173 China and fed with water and rat chow *ad libitum*. The ground squirrels were moved to a cold room
174 at 4-6°C when they entered torpor in November with 1 individual per cage. The ground squirrels
175 used in this experiment were in a natural hibernation state. The time of entering torpor was judged
176 by putting sawdust on the back of each individual and reducing a body temperature (T_b) below 9°C.
177 T_b was measured by thermal imaging using a visual thermometer (Fluke VT04 Visual IR
178 Thermometer, USA). According to our observations, the ground squirrels did not eat and drink after
179 entering torpor state. Moreover, most ground squirrels recovered to hibernation state after 1-2 days
180 of interbout arousals. The ground squirrels were divided into 2 groups randomly ($n = 8$, with 5
181 females and 3 males in each group): (1) summer active (SA): active ground squirrels in July with a
182 T_b of 36-38°C; (2) hibernation (HIB): ground squirrels experiencing two months of hibernation with
183 T_b maintained at 5-8°C and were sampled in torpor state.

184 **Muscle collection**

185 After the body weight was recorded, the ground squirrels were anesthetized with 90 mg/kg
186 sodium pentobarbital intraperitoneally. Then the diaphragm and gastrocnemius muscles from both
187 legs were separated and removed. Subsequently, the muscle samples were put into liquid nitrogen

188 and stored for the follow-up experiments. The animals were sacrificed by an overdose injection of
189 sodium pentobarbital while finishing surgical intervention.

190 **Immunofluorescent analysis**

191 The muscle fiber cross-sectional area (CSA) and fiber type composition were measured by
192 immunofluorescent analysis as described by our laboratory previously (Chang et al. 2018b). Briefly,
193 5 mm of the mid-belly of lateral gastrocnemius muscle was cut into 10- μ m thick frozen muscle
194 cross-sections at -20°C with a cryostat (Leica, Wetzlar, CM1850, Germany). Because of the uneven
195 thickness of the diaphragm, the fixed geometric position of the muscle strips was cut for slicing (see
196 the yellow box in **Figure 1A**). Then the slides with sections were fixed in 4% paraformaldehyde for
197 30 min, and subsequently permeabilized in 0.1% Triton X-100 (dissolve in PBS) for 30 min. The
198 slides were then blocked with 1% bovine serum albumin (BSA) in PBS for 60 min at room
199 temperature, and immediately incubated at 4°C overnight with the anti-laminin rabbit polyclonal
200 antibody (1:200, Boster, BA1761-1) to visualize the myofiber interstitial tissue and the anti-skeletal
201 slow myosin mouse monoclonal antibody (1:200, Boster, BM1533) to visualize the type I MHC in
202 both muscles. The slides were rinsed twice in PBS and incubated with Alexa Fluor 647-labeled IgG
203 secondary antibody (1:200; Thermo Fisher Scientific, #A21245) and FITC-labeled IgG secondary
204 antibody (1:200; Sigma, F1010) for 60 min. The staining method of anti-MYH1 (IIx) mouse
205 antibody (1:400, Abcam, ab127539) was the same as that of anti-skeletal slow myosin mouse
206 monoclonal antibody, only the first antibodies were different, with anti-MYH1 (IIx) mouse antibody
207 followed by FITC-labeled IgG secondary antibody. Anti-MYH2 (IIa) rabbit antibody and anti-
208 laminin rabbit polyclonal antibody need to be stained separately. First, anti-MYH2 (IIa) rabbit
209 antibody (1:200, Abcam, ab124937) was incubated overnight at 4°C and followed by Alexa Fluor
210 488-labeled anti-rabbit antibody (Thermo Fisher Scientific, A-21235). Next, anti-laminin rabbit
211 polyclonal antibody was incubated overnight at 4°C and followed by Alexa Fluor 647-labeled anti-
212 rabbit antibody. The staining method of anti-MYH4 (IIb) rabbit antibody (1:100, Santa Cruz
213 Biotechnology, #34820) was the same as that of anti-MYH2 (IIa) rabbit antibody, only the first
214 antibodies were different, with anti-MYH4 (IIb) rabbit antibody followed by Alexa Fluor 488-
215 labeled anti-rabbit antibody. Photographs were acquired by using confocal microscopy (Olympus,
216 Osaka, Japan) at an objective magnification of 40 \times . Image-Pro Plus 6.0 software was used to
217 measure the CSA of at least 10 different visual fields of each sample.

218 **Proteasome activity**

219 The chymotrypsin and trypsin activities of diaphragm and gastrocnemius muscles were
220 determined by ultraviolet spectrophotometry according to the instructions of chymotrypsin assay
221 kit (Nanjing Jiancheng Bioengineering Institute, A080-3-1) and trypsin assay kit (Nanjing
222 Jiancheng Bioengineering Institute, A080-2-2).

223 **Western blots**

224 As described previously by our lab (Chang et al. 2016, Chang et al. 2018b), the total protein was
225 extracted from the frozen diaphragm and gastrocnemius muscles of ground squirrels by
226 homogenization and put into a sample buffer (pH 6.8, 100 mM Tris, 4% SDS, 5% glycerol, 5% 2-
227 β -mercaptoethanol, and bromophenol blue). Then the muscle protein extracts were resolved by
228 SDS-PAGE using Laemmli gels (10%) with the 1% 2,2,2-Trichloroethanol (TCE) (aladdin,
229 J1522028, China). After electrophoresis, the total proteins bands are visualized by putting the gel on
230 the UV transilluminator and irradiating the gel for 2 min, and Syngene G:BOX system (Syngene,
231 Frederick, MD) was used to take photographs of the gel. Then the protein gel was transferred
232 electrically to PVDF membranes (0.45 μ m) using a Bio-Rad semi-dry transfer apparatus. The
233 blotted PVDF membranes were incubated with 1% BSA in TBS (Tris-buffered saline; 50 mM Tris-
234 HCl, 150 mM NaCl, pH 7.5) and anti-skeletal slow myosin mouse monoclonal antibody (1:500,
235 Boster, BM1533), anti-MYH2 (IIa) rabbit antibody (1:1000, Abcam, ab124937), anti-MYH4 (IIb)
236 rabbit antibody (1:1000, Santa Cruz Biotechnology, #34820), anti-MYH1 (IIx) mouse antibody
237 (1:1000, Abcam, ab127539), P-Akt (Ser473) (1:1,000, abcam, 81283), P-mTORC1
238 (Ser2448)(1:1,000, sigma, 4504476), P-S6K1 (Thr389) (1:1,000, Cell Signaling Technology (CST),
239 9205S), P-4E-BP1 (Thr37/46)(1:1,000, CST, 2855S), calpain-1 (1:1,000, CST, 2556S), calpain-2
240 (1:1,000, CST, 2539S), calpastatin (1:1,000, CST, 4146S), desmin (1:1,000, CST, 4024S), troponin
241 T (1:1,000, Sigma, T6277), MuRF1 (1:1000, Abcam, ab172479), atrogin-1 (1:1,000, Proteintech,
242 12866-1-AP), Beclin1 (1:1000, CST, 3738), LC3 (1:1000, abcam, ab48394), MyoD (1:1,000,
243 proteintech, 18943-1-AP), myogenin (1:1,000, abcam, 124800) and myostatin (1:1,000, proteintech,
244 19142-1-AP) antibodies, respectively, in TBS containing 0.1% BSA at 4°C overnight. Then the
245 membrane was washed with TBST for 4 times (10 minutes/time) and incubated with HRP-
246 conjugated anti-mouse secondary antibody (1:10000, Thermo Fisher Scientific, A28177) or HRP-
247 conjugated anti-rabbit secondary antibody (1:5000, Thermo Fisher Scientific, A27036) for 2 h at
248 room temperature. Then the PVDF membrane was washed for 3 times (10 min/time). The
249 fluorescent band were visualized using enhanced chemiluminescence reagents (Thermo Fisher
250 Scientific, NCI5079). The NIH Image J software was used to carry out quantification analysis. The
251 density of immunoblot band in each individual lane was standardized by the summed densities from
252 a group of total protein bands in the same lane. This method of standardizing by total protein has
253 been proved to be more accurate and appropriate in comparison with standardizing by housekeeping
254 proteins such as GAPDH, actin and tubulin (Vigelso et al. 2015, Zhang et al. 2016b).

255 **Statistical analyses**

256 All data were analyzed using SPSS 19.0 and expressed as means \pm SEM. An independent-samples
257 *t*-test was used to determine the significant differences between SA and HIB ground squirrels. A
258 value of $P < 0.05$ was considered to be statistically significant.

259 **Results**

260 **Body weight and muscle wet weight**

261 As shown in **Table 1**, the body weight of HIB group was significantly reduced by 11% ($P < 0.05$)
262 as compared with SA group at experiment time.

263 Compared with SA group, the muscle weight of the gastrocnemius muscle in the HIB group was
264 significantly reduced by 18% ($P < 0.05$), while the muscle weight of the diaphragm muscle was
265 significantly increased by 14% ($P < 0.05$) (**Figure 1B**).

266 **Fiber CSA and fiber type distribution**

267 The CSA and fiber type distribution of the diaphragm and gastrocnemius (lateral) muscle fibers
268 were measured by immunofluorescent staining. Compared with the SA group, the CSA of the
269 diaphragm muscle increased significantly (26.1%, $P < 0.05$), whereas that of the gastrocnemius
270 muscle decreased significantly (20.4%, $P < 0.05$) in the HIB group (**Figure 1C and 1D**).

271 As shown in **Figure 2A**, results showed that both the MHCI and MHC II fiber isoforms were
272 expressed in the diaphragm and gastrocnemius muscles. The percentage of type I fibers in the
273 diaphragm and gastrocnemius muscles was significantly increased (33% and 36%, respectively, P
274 < 0.05) in the HIB group compared with that in the SA group (**Figure 2B and 2C**). The proportion
275 of MHC IIa fiber in the HIB group was significantly reduced by 6% ($P < 0.05$) in the diaphragm
276 muscle, while it was significantly increased in the gastrocnemius muscle by 9% ($P < 0.05$) as
277 compared with SA group (**Figure 2B and 2C**). In contrast, the proportion of MHC IIb fiber was
278 significantly increased by 21% ($P < 0.05$) in the diaphragm muscle, while it was significantly
279 decreased by 15% ($P < 0.05$) in the gastrocnemius muscle of the HIB group as compared with that
280 in the SA group (**Figure 2B and 2C**). As compared with SA group, the proportion of MHC IIx fiber
281 in the diaphragm and gastrocnemius muscles in the HIB group was significantly increased by 7%
282 ($P < 0.05$) and 16% ($P < 0.05$), respectively (**Figure 2B and 2C**).

283 Besides, the protein expression levels of MHC I, MHC IIa, MHC IIb and MHC IIx in the
284 diaphragm and gastrocnemius muscle were analyzed by western blots. As compared with SA group,
285 MHC I protein expression level in the HIB group was significantly increased by 1.41-fold ($P < 0.05$)
286 and 2.07-fold ($P < 0.05$) in the diaphragm and gastrocnemius muscles, respectively (**Figure 3A and**
287 **3B**). In the diaphragm muscle, the protein expression level of MHC IIa was decreased significantly
288 in the HIB group compared with that in the SA group (28%, $P < 0.05$). However, the MHC IIa
289 expression was significantly increased by 1.34-fold ($P < 0.05$) in the gastrocnemius muscle of the
290 HIB group as compared with SA group (**Figure 3A and 3C**). The protein expression level of MHC
291 IIb was significantly increased by 1.36-fold ($P < 0.05$) in the diaphragm muscle, while it was
292 significantly decreased by 34% ($P < 0.05$) in the gastrocnemius muscle in the HIB group compared
293 with that in the SA group (**Figure 3A and 3D**). The protein expression level of MHC IIx in the
294 diaphragm and gastrocnemius muscles in the HIB group was 1.48-fold ($P < 0.05$) and 1.3-fold ($P <$
295 0.05) higher than that in the SA group, respectively (**Figure 3A and 3E**).

296 **Protein expression levels of MuRF1, atrogin-1, Beclin1 and LC3-II indicative of protein** 297 **degradation metabolism,**

298 Compared with that in the SA group, MuRF1 protein expression significantly decreased in the
299 diaphragm muscle (16.0%, $P < 0.05$), but significantly increased in the gastrocnemius muscle (1.3-
300 fold, $P < 0.05$) in the HIB group (**Figure 4A and 4B**). The expression level of atrogin-1 was
301 significantly decreased by 17% ($P < 0.05$) in the diaphragm muscle, while it was significantly
302 increased by 1.3-fold ($P < 0.05$) in the gastrocnemius muscle in the HIB group compared with that
303 in the SA group (**Figure 4A and 4C**). In addition, autophagy-related proteins Beclin1 and LC3-II
304 both showed significant increases (1.2-fold and 1.5-fold, respectively, $P < 0.05$) in the diaphragm
305 muscle of the HIB group compared with that in the SA group. In contrast, both were significantly
306 decreased in the gastrocnemius muscle (32.6% and 31.9%, respectively, $P < 0.05$) of the HIB group
307 compared with that of the SA group (**Figure 4A, 4D and 4E**).

308 **Proteasome activity**

309 Compared with SA group, chymotrypsin and trypsin activities in HIB group were significantly
310 decreased by 60.5% and 52.8% ($P < 0.05$), respectively, in diaphragm muscle, but were significantly
311 increased by 32.7% and 79.9% ($P < 0.05$), respectively, in gastrocnemius muscle (**Figure 5A and**
312 **5B**).

313 **Protein expression levels of calpain-1, calpain-2, calpastatin, desmin and troponin T indicative** 314 **of protein degradation metabolism**

315 The protein expression level of calpain-1 and calpain-2 both showed a significant decrease (30%
316 and 46.3%, respectively, $P < 0.05$) in the diaphragm muscle of the HIB group compared with levels
317 in the SA group. In contrast, calpain-1 and calpain-2 protein expression levels were significantly
318 increased in the gastrocnemius muscle (1.9-fold and 1.5-fold, respectively, $P < 0.05$) in the HIB
319 group compared with levels in the SA group (**Figure 6A, 6B and 6C**). Furthermore, contrary to
320 calpain-1 and calpain-2, calpastatin protein expression showed a significant 1.6-fold ($P < 0.05$)
321 increase in the diaphragm muscle, but a significant 32.6% ($P < 0.05$) decrease in the gastrocnemius
322 muscle of the HIB group compared with that in the SA group (**Figure 6A and 6D**). The protein
323 expression level of desmin was significantly increased by 1.51-fold ($P < 0.05$) in the diaphragm
324 muscle, while it was significantly decreased by 23% ($P < 0.05$) in the gastrocnemius muscle in the
325 HIB group compared with that in the SA group (**Figure 6A and 6E**). However, the protein
326 expression level of troponin T in both diaphragm and gastrocnemius muscles showed no significant
327 difference between the HIB and SA groups (**Figure 6A and 6F**).

328 **Protein expression levels of P-Akt, P-mTORC1, P-S6K1 and P-4E-BP1 indicative of protein** 329 **synthesis metabolism**

330 Western blots analysis was used to detect the protein expression levels of P-Akt, P-mTORC1, P-
331 S6K1, and P-4E-BP1 in the diaphragm and gastrocnemius muscles. As shown in **Figure 7**, P-Akt
332 protein expression significantly increased by 1.2-fold ($P < 0.05$) in the diaphragm muscle, but
333 significantly decreased by 55.3% ($P < 0.05$) in the gastrocnemius muscle in the HIB group versus

334 the SA group (**Figure 7A and 7B**). Similarly, P-mTORC1 protein expression showed a significant
335 1.4-fold ($P < 0.05$) increase in the diaphragm muscle, but a significant 30.9% ($P < 0.05$) decrease
336 in the gastrocnemius muscle in the HIB group compared with that in the SA group (**Figure 7A and**
337 **7C**). Moreover, the P-S6K1 and P-4E-BP1 protein expression levels in the diaphragm muscle
338 increased significantly by 1.4-fold ($P < 0.05$) and 1.3-fold ($P < 0.05$), respectively, in the HIB group
339 compared with that in the SA group. In contrast, the P-S6K1 and P-4E-BP1 protein expression levels
340 in the gastrocnemius muscle decreased significantly by 30.9% ($P < 0.05$) and 22.7% ($P < 0.05$),
341 respectively, in the HIB group compared with levels in the SA group (**Figure 7A, 7D and 7E**).

342 **Protein expression levels of MyoD, myogenin and myostatin indicative of muscle regeneration**

343 MyoD and myogenin protein expression levels showed a significant 1.3-fold ($P < 0.05$) and 1.4-
344 fold ($P < 0.05$) increase, respectively, in the diaphragm muscle, but a significant 26.7% ($P < 0.05$)
345 and 12.2% ($P < 0.05$) decrease, respectively, in the gastrocnemius muscle of the HIB group
346 compared with that of the SA group (**Figure 8A, 8B and 8C**). In contrast, the myostatin protein
347 expression level decreased by 38.2% ($P < 0.05$) in the diaphragm muscle but increased by 2.3-fold
348 ($P < 0.05$) in the gastrocnemius muscle in the HIB group compared with the SA group (**Figure 8A**
349 **and 8D**).

350 **Discussion**

351 In the present study, changes in key signals of protein synthesis, protein degradation, and muscle
352 regeneration were detected to determine the mechanism(s) related to the differential adaptability of
353 the diaphragm and gastrocnemius muscles in hibernating Daurian ground squirrels. The wet weight
354 of the diaphragm muscle was significantly increased, while it was significantly decreased in
355 gastrocnemius muscle (**Figure 1B**). Due to its importance as a respiratory muscle, the CSA of the
356 diaphragm muscle fibers showed significant hypertrophy (26.1% increase) (**Figure 1C and 1D**)
357 during hibernation. However, the CSA of the gastrocnemius muscle was not completely preserved,
358 instead showing significant atrophy (20.4% decrease) (**Figure 1C and 1D**). Consistent with our
359 findings, previous studies have also shown significant muscle wet weight loss (14%) in the
360 gastrocnemius muscle of hibernating golden-mantled ground squirrels (Wickler et al. 1991), but
361 significant muscle weight gain (40% and 19%) in the diaphragm muscle of hibernating Syrian
362 hamsters (Deveci and Egginton 2002) and golden-mantled ground squirrels, respectively (Reid et
363 al. 1995). In addition, the results of both immunofluorescent analysis and western blots showed that
364 the expressions of MHC I and MHC IIx in the HIB group were significantly increased in the
365 gastrocnemius and diaphragm muscles, the expression of MHC IIa was significantly increased in
366 the gastrocnemius muscle, while it was significantly decreased in the diaphragm muscle, besides,
367 MHC IIb expression was significantly reduced in the gastrocnemius muscle while it showed a
368 significant increase in the diaphragm muscle compared with the SA group. Furthermore, both the
369 diaphragm and gastrocnemius muscles displayed a significant fast-to-slow fiber type transition
370 (**Figure 2**). Consistent with our recent study, the gastrocnemius muscle showed a fast-to-slow fiber

371 type transition during hibernation in Daurian ground squirrels (Ma et al. 2019), in contrast, the fiber
372 type in the gastrocnemius muscle of the hindlimb unloading rat showed a significant slow-to-fast
373 fiber type shift (Jones et al. 2003). Both type I and type II fibers of the diaphragm were significantly
374 atrophied in the mechanically ventilated rats (Ichinoseki-Sekine et al. 2014). Therefore, our study
375 again demonstrates that there is a fast-to-slow fiber type transition in different skeletal muscles in
376 hibernating ground squirrels. In this study, we investigated the mechanism(s) related to the
377 differences in the physiological adaptations of the diaphragm and gastrocnemius muscles in
378 hibernating Daurian ground squirrels from three aspects: i.e., protein synthesis, protein degradation,
379 and muscle regeneration.

380 MuRF1 and atrogin-1 are considered as molecular markers of muscular atrophy. Earlier studies
381 have shown that MuRF1 protein expression is significantly increased in the gastrocnemius muscle
382 of hindlimb-unloaded rats, which subsequently induces overexpression of ubiquitin protein and
383 muscle atrophy (Su et al. 2014). Moreover, the expression level of atrogin-1 mRNA is significantly
384 increased by 2-fold in the gastrocnemius muscle of hindlimb unloading mice (Al-Nassan et al. 2012).
385 Furthermore, both the protein expression levels of MuRF1 and atrogin-1 were significantly
386 increased in the diaphragm of mechanically ventilated rats (Maes et al. 2014). Previous studies have
387 shown that chymotrypsin and trypsin activities were transiently increased in the gastrocnemius
388 muscle after 5 days of hindlimb-unloaded rats (Magne et al. 2011). Earlier studies have reported
389 significant increases in both chymotrypsin and trypsin activity in the diaphragm muscle of
390 mechanically ventilated rats (McClung et al. 2008). Our results showed that MuRF1, atrogin-1
391 protein expression, chymotrypsin and trypsin activities were all significantly increased in the
392 gastrocnemius muscle of hibernating squirrels compared with the summer active group (**Figure 4B**
393 **and 4C**), which is consistent with our recent study (Ma et al. 2019, Wei et al. 2018) and further
394 indicating that high MuRF1 and atrogin-1 protein expression may be involved in protein degradation
395 and gastrocnemius muscle atrophy. In contrast, we found that MuRF1, atrogin-1 protein expression,
396 chymotrypsin and trypsin activities were significantly decreased in the diaphragm muscle, which
397 may be an anti-atrophy mechanism of this muscle in hibernating Daurian ground squirrels.

398 The calpain system plays an essential role in muscle protein degradation and is a likely component
399 of the targets of disuse atrophy, especially in relation to myofibrillar disassembly (Jackman and
400 Kandarian 2004). Previous studies have demonstrated that calpain-induced myofibrillar protein
401 degradation (Smuder et al. 2010) as well as calpain activity (e.g., by 95%) (Bruells et al. 2016) are
402 both increased in the diaphragm of rats under mechanical ventilation. Our results showed that
403 protein expression of calpain-1 and calpain-2 increased by 94.6% and 47.2%, respectively, whereas
404 that of calpastatin (an endogenous inhibitor of calpains) decreased by 42.4% in the gastrocnemius
405 muscle of the hibernating group compared with that of the summer active group (**Figure 6B, 6C**
406 **and 6D**), suggesting that the up-regulation of calpain signals may contribute to gastrocnemius
407 muscle atrophy. However, consistent with our previous studies in the soleus and extensor digitorum
408 longus muscles (both showing no significant atrophy in hibernation) (Chang et al. 2018b, Yang et

409 al. 2014), the protein expression levels of calpain-1 and calpain-2 decreased by 30% and 46.6%,
410 respectively, whereas that of calpastatin increased by 60% in the diaphragm muscle of hibernating
411 ground squirrels compared with the summer active group (**Figure 6B, 6C and 6D**). Higher calpain-
412 1 (1.44-fold) and calpain-2 (2.38-fold) activity has also been observed in the longissimus dorsi and
413 soleus muscles of hibernating long-tailed ground squirrels (*Spermophilus undulatus*) compared with
414 summer active squirrels (Popova et al. 2017). Calpain can hydrolyze substrates such as desmin and
415 troponin T (Barta et al. 2005). Our study showed that desmin was significantly decreased in the
416 gastrocnemius muscle of the HIB group and significantly increased in the diaphragm muscle
417 compared with the SA group, however, troponin T showed no significant changes between the
418 gastrocnemius and diaphragm muscles (**Figure 6**), which indicated that different substrates have
419 different sensitivity to the calpain system. Our previous study showed desmin expression was
420 unchanged in soleus muscle and extensor digitorum longus muscle of Daurian ground squirrels
421 during hibernation, but was significantly reduced by 39-51% in hindlimb unloading rats (Chang et
422 al. 2018b). Our recent study also showed that the protein expression of desmin in gastrocnemius
423 muscle was significantly decreased, while troponin T was unchanged during hibernation in Daurian
424 ground squirrels (Ma et al. 2019). Therefore, our data suggest that the muscle-specific activation of
425 the calpain system and degradation of different substrates may be involved in the different
426 adaptabilities of the diaphragm and gastrocnemius muscles in Daurian ground squirrels during
427 hibernation.

428 Beclin1 (B-cell Lymphoma 2 interacting protein 1) and LC3 (microtubule-associated protein light
429 chain 3) are two molecular markers of autophagy. Beclin1 can form complexes that induce proteins
430 to be located on the autophagic membrane (Kihara et al. 2001). Furthermore, LC3 is involved in the
431 formation of the autophagic membrane, whereby LC3-I converts into LC3-II for the formation of
432 autophagosomes (Tanida et al. 2005, Tanida et al. 2004). Earlier studies have reported significant
433 increases in the mRNA and protein expression levels of Beclin1 (1.91-fold and 30%, respectively)
434 and LC3 (1.82-fold and 30%, respectively) in the diaphragm muscles of mechanically ventilated
435 rats (Smuder et al. 2018). Furthermore, hindlimb unloading in mice reportedly results in the up-
436 regulation of Beclin1 mRNA and induction of autophagy in soleus muscle atrophy (Cannavino et
437 al. 2014). In the current study, the protein expression levels of Beclin1 and LC3-II in the
438 gastrocnemius muscle of hibernating ground squirrels were significantly lower (Beclin1, -31.9%,
439 LC3-II, -32.6%, $P < 0.05$) than those in the summer active group, whereas the expression levels of
440 Beclin1 and LC3-II in the diaphragm muscle were significantly higher (Beclin1, 46%, LC3-II,
441 22.2%, $P < 0.05$). Our results showed that autophagy was suppressed in the gastrocnemius muscle
442 but was promoted in the diaphragm muscle of the hibernating ground squirrels. Consistent with our
443 gastrocnemius muscle results, earlier research demonstrated a decrease in the LC3-II/LC3-I ratio in
444 the quadriceps and tibialis anterior muscles of thirteen-lined ground squirrels during hibernation,
445 thus indicating suppression of autophagy (Andres-Mateos et al. 2013). Our data suggest that protein
446 degradation causing gastrocnemius muscle atrophy occurred primarily through the ubiquitin

447 pathway rather than the autophagy-lysosome pathway. The elevated level of autophagy in the
448 diaphragm muscle may correspond to the elevated level of diaphragm muscle protein synthesis,
449 both of which promoted protein turnover and diaphragm hypertrophy.

450 As key molecules mediating the Akt-mTOR signaling pathway in protein synthesis, the protein
451 expression levels of Akt and mTOR are significantly decreased in the diaphragm after mechanical
452 ventilation, as is the protein expression of downstream target 4E-BP1 (Hudson et al. 2015, Yu et al.
453 2018). Moreover, gastrocnemius myofibrillar protein content and synthesis (mg/day) are shown to
454 decrease significantly (by 26% and 64%, respectively) in rats undergoing tail suspension
455 (Linderman et al. 1994). In the present study, four protein synthesis markers, i.e., P-Akt, P-mTORC1,
456 P-S6K1, and P-4E-BP1, were significantly increased by 17%, 37%, 40%, and 31% ($P < 0.05$),
457 respectively, in the diaphragm muscle, but were significantly decreased by 55%, 31%, 42% and 23%
458 ($P < 0.05$), respectively, in the gastrocnemius muscle during hibernation compared with levels
459 during summer activity (**Figure 7**). Similar to our findings in the gastrocnemius muscle, Akt activity
460 and phosphorylated Akt (Ser 473) are reported to decrease (by 60% and 40%, respectively) in
461 skeletal muscle during hibernation in Richardson's ground squirrels (*Spermophilus richardsonii*)
462 compared with euthermic controls, which may contribute to the coordinated suppression of energy-
463 expensive anabolism during winter torpor (Abnous et al. 2008). Moreover, research has shown that
464 Akt/PKB activity exhibits seasonal peaks in the gastrocnemius muscle of yellow-bellied marmots
465 (*Marmota flaviventris*) during their annual cycle, thereby demonstrating tissue-specific seasonal
466 activation (Hoehn et al. 2004). Thus, our results suggest that the up-regulation of protein synthesis
467 contributes to the diaphragm muscle hypertrophy, whereas the down-regulation of protein synthesis
468 contributes to the gastrocnemius muscle atrophy found in hibernating Daurian ground squirrels.

469 Whether muscle regeneration potential in different skeletal muscles is altered in response to
470 hibernation has remained unexplored. Here, we determined the protein expression levels of key
471 markers, such as MyoD, myogenin, and myostatin, in satellite cell regulatory pathways. The
472 expression level of MyoD showed a significant 1.3-fold ($P < 0.05$) increase in the diaphragm muscle,
473 but a significant 26.7% ($P < 0.05$) decrease in the gastrocnemius muscle of hibernating squirrels
474 compared with the active group (**Figure 8A and 8B**). Mechanical ventilation is known to induce a
475 decrease in MyoD mRNA and protein expression in the diaphragm muscle of rats (Maes et al. 2008,
476 Racz et al. 2003), suggesting the inactivation of quiescent satellite cells. Furthermore, muscle disuse
477 can induce a decline in satellite cells together with an up-regulation in MyoD, suggesting that
478 activation of satellite cells and fusion to existing myofibers may take place during hindlimb
479 immobilization (Guitart et al. 2018). Unlike our results, however, earlier research found no changes
480 in MyoD protein levels, but a decrease in mRNA transcript levels in several hindlimb thigh muscles
481 of thirteen-lined ground squirrels during hibernation (Tessier and Storey 2010). Therefore, our data
482 suggest that the differential regulation of MyoD protein expression in muscle regeneration may be
483 involved in the different adaptabilities of the diaphragm and gastrocnemius muscles in ground
484 squirrels.

485 Previous studies have found that myogenin protein content is severely decreased (e.g., by 63%)
486 in the diaphragm muscle after mechanical ventilation (Maes et al. 2008). Furthermore, although
487 myogenin mRNA expression showed no change in 7-d immobilized mice (Guitart et al. 2018),
488 levels were found to double ($P < 0.05$) following two weeks of immobilization in healthy young
489 men (Wall et al. 2014). In the current study, the expression level of myogenin showed a significant
490 1.4-fold ($P < 0.05$) increase in the diaphragm muscle, but a significant 12.2% ($P < 0.05$) decrease
491 in the gastrocnemius muscle of the hibernating squirrels compared with the summer active squirrels
492 (**Figure 8A and 8C**). Consistent with our diaphragm muscle results, myogenin is reported to be up-
493 regulated (2.4-fold) in the cardiomyocytes of thirteen-lined ground squirrels during late torpor,
494 indicating a propensity for hypertrophy (Zhang et al. 2016a). Furthermore, in accordance with our
495 gastrocnemius muscle results, myogenin expression is significantly decreased (by 52%) in the
496 hindlimb thigh muscles, including oxidative and glycolytic fiber types, of thirteen-lined ground
497 squirrels during late torpor relative to the euthermic state (Zhang et al. 2016b). Therefore, we
498 speculate that high myogenin expression contributes to diaphragm hypertrophy, whereas low
499 expression contributes to gastrocnemius atrophy in hibernating Daurian ground squirrels.

500 Myostatin is a potent negative regulator of skeletal muscle growth. Moreover, myostatin
501 negatively regulates the activity of the Akt pathway, which promotes protein synthesis and increases
502 activity of the ubiquitin-proteasome system to induce atrophy (Rodriguez et al. 2014). Up-regulation
503 of myostatin can be triggered by mechanical ventilation (Liang et al. 2018). Furthermore, myostatin
504 knockout-induced hypertrophy involves little or no input from satellite cells (Amthor et al. 2009).
505 However, the role of myostatin in disuse muscle atrophy remains controversial. For example,
506 increased myostatin mRNA and protein levels have been reported in mice following 11-d of
507 spaceflight (Allen et al. 2009) and in humans after chronic disuse (Reardon et al. 2001); in contrast,
508 decreased myostatin protein levels have been observed after 14 d of immobilization in healthy
509 young men (Wall et al. 2014). In the current study, the protein expression level of myostatin
510 decreased by 38.2% ($P < 0.05$) in the hypertrophic diaphragm muscle but increased by 2.3-fold (P
511 < 0.05) in the atrophic gastrocnemius muscle (**Figure 8A and 8D**). Research thus far has indicated
512 that myostatin protein levels are maintained in the hindlimb thigh muscles of thirteen-lined ground
513 squirrels during early hibernation and torpor (Brooks et al. 2011). Inconsistent with our findings,
514 thirteen-lined ground squirrels show low levels of myostatin in the gastrocnemius muscle over
515 prolonged hibernation, indicating possible slow regeneration in response to injury and possible
516 protection against the formation of fibrotic tissue (Andres-Mateos et al. 2012). Other research has
517 also shown unaltered myostatin expression in atrophied left ventricles of grizzly bears (*Ursus*
518 *arctos horribilis*), who tolerate extended periods of extremely low heart rate during hibernation
519 (Barrows et al. 2011). Therefore, our results suggest different regulation mechanisms of muscle
520 regeneration in the diaphragm and gastrocnemius muscles of hibernating animals, whereby the
521 muscle regeneration potential of the diaphragm is enhanced and that of the gastrocnemius muscle
522 is weakened. Variations in muscle regeneration ability may participate in the different adaptive

523 mechanisms of muscles in hibernators. A major novelty in the current study was our use of two
524 different types of skeletal muscle to clarify muscle regeneration potential in hibernation.

525 In conclusion, different patterns of protein synthesis, protein degradation, and muscle
526 regeneration were demonstrated in gastrocnemius muscle atrophy and diaphragm muscle
527 hypertrophy during hibernation. Specifically, in the gastrocnemius muscle, protein synthesis,
528 autophagy, and muscle regeneration were suppressed, and protein degradation was promoted, which
529 likely contributed to muscle atrophy. In contrast, in the diaphragm muscle, protein synthesis,
530 autophagy, and muscle regeneration were promoted, and protein degradation was inhibited, which
531 likely contributed to muscle hypertrophy. Thus, the changes in protein synthesis and degradation
532 displayed muscle specificity during hibernation. Collectively, the differences in muscle regeneration
533 potential and regulatory patterns of protein metabolism may contribute to the different adaptabilities
534 of the diaphragm and gastrocnemius muscles in Daurian ground squirrels during hibernation.

535

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539

540 **Competing interests**

541 The authors declare that they have no competing interests.

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543 **References**

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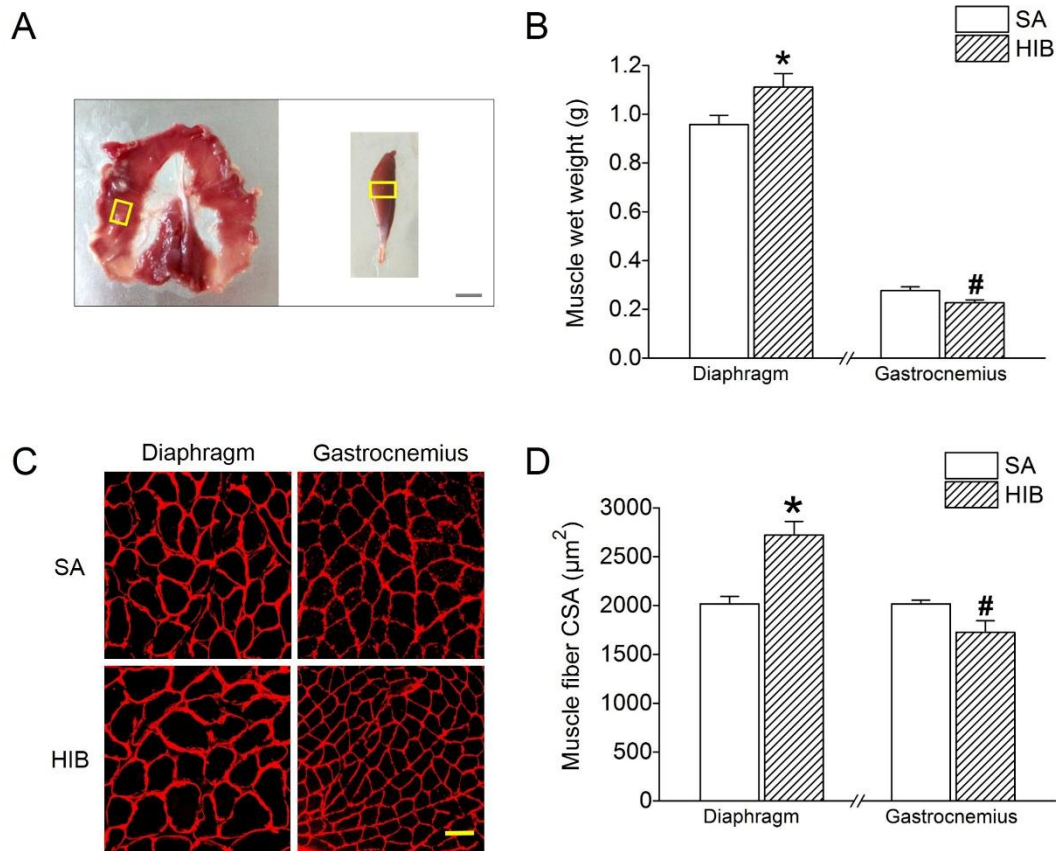
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914 **Figure legend**

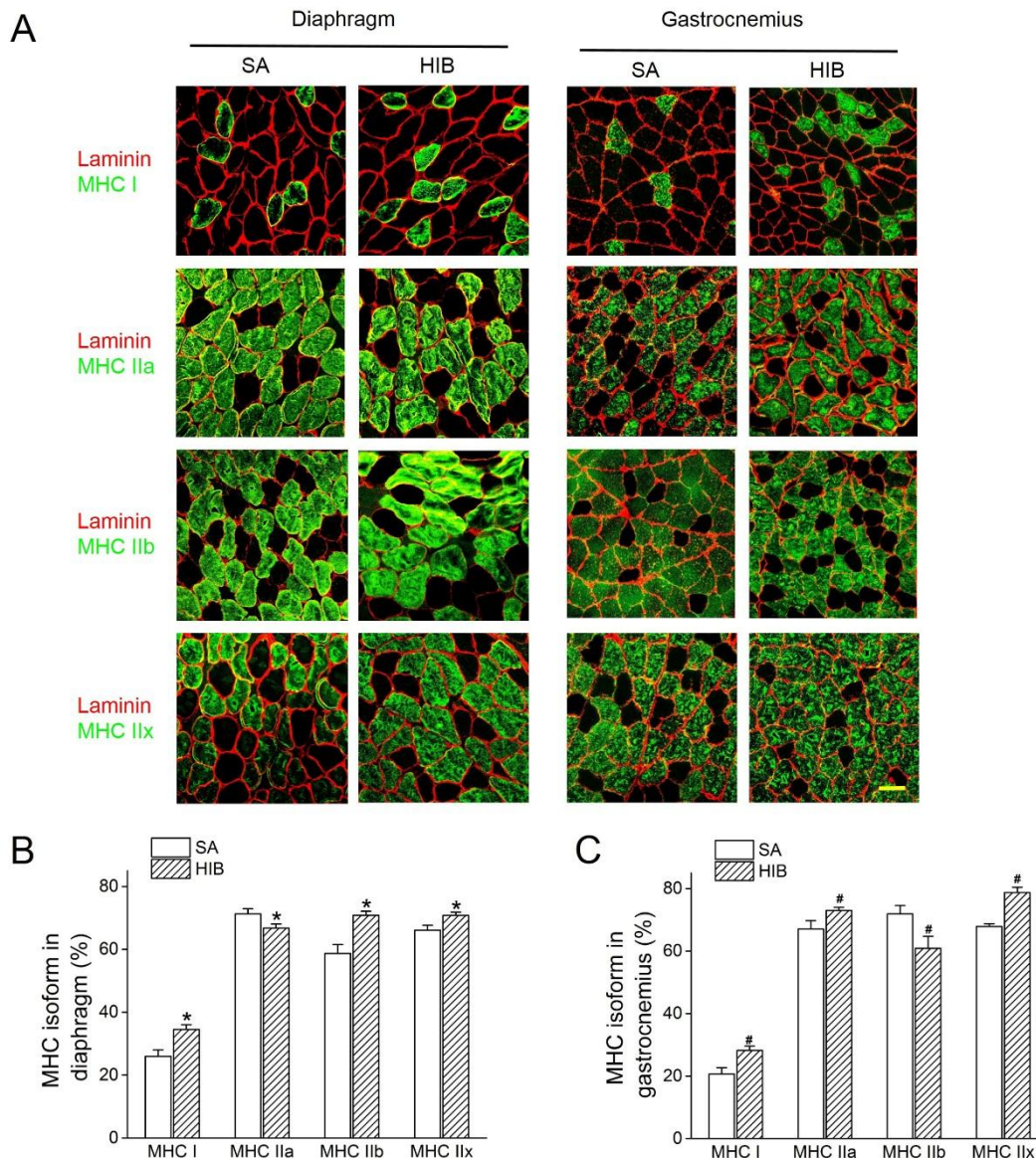
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917 **Figure 1.** Muscle wet weight and fiber cross-sectional area (CSA) in diaphragm and gastrocnemius
918 muscles.

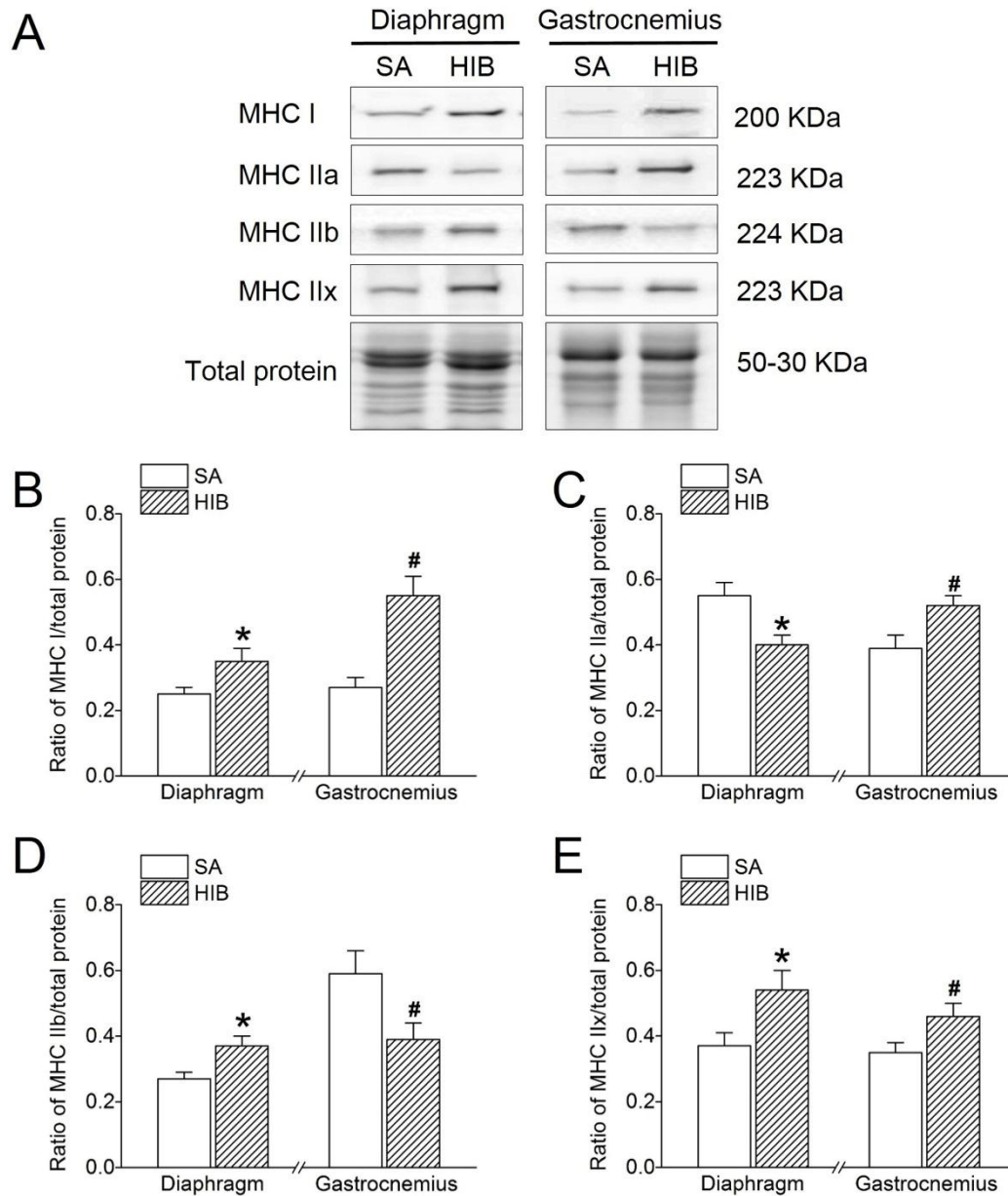
919 **(A)** Photos of diaphragm (left) and gastrocnemius (right) muscles. Scale bar = 4 mm. The yellow
920 box shows the fixed geometric position for frozen section. **(B)** Muscle wet weight (g) in different
921 groups. **(C)** Representative images showing cross-sections in diaphragm and gastrocnemius muscles.
922 Red represents laminin stain of myofiber interstitial tissue. Scale bar = 50 μm. **(D)** Bar graph
923 showing the changes of muscle fiber CSA. SA: summer active ground squirrels, HIB: hibernating
924 ground squirrels. Data represents mean ± SEM, $n = 8$. * $P < 0.05$, compared with SA in diaphragm
925 muscle. # $P < 0.05$, compared with SA in gastrocnemius muscle.



926

927 **Figure 2.** Fiber-type distribution in diaphragm and gastrocnemius muscles.

928 (A) Representative immunofluorescent images showing MHC I, MHC IIa, MHC IIb, and MHC IIx
 929 fibers with green staining in diaphragm and gastrocnemius muscles. Red represents laminin stain of
 930 myofiber interstitial tissue. Scale bar = 50 μ m. (B) Bar graph showing the changes of fiber-type
 931 distribution in diaphragm muscle. (C) Bar graph showing the changes of fiber-type distribution in
 932 gastrocnemius muscle. SA: summer active ground squirrels, HIB: hibernating ground squirrels.
 933 Data represents mean \pm SEM, $n = 8$. * $P < 0.05$, compared with SA in diaphragm muscle. # $P < 0.05$,
 934 compared with SA in gastrocnemius muscle.



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936 **Figure 3.** Protein expression levels of MHC I, MHC IIa, MHC IIb, and MHC IIx.

937 (A) Representative immunoblots of MHC I, MHC IIa, MHC IIb, and MHC IIx in each group. (B)

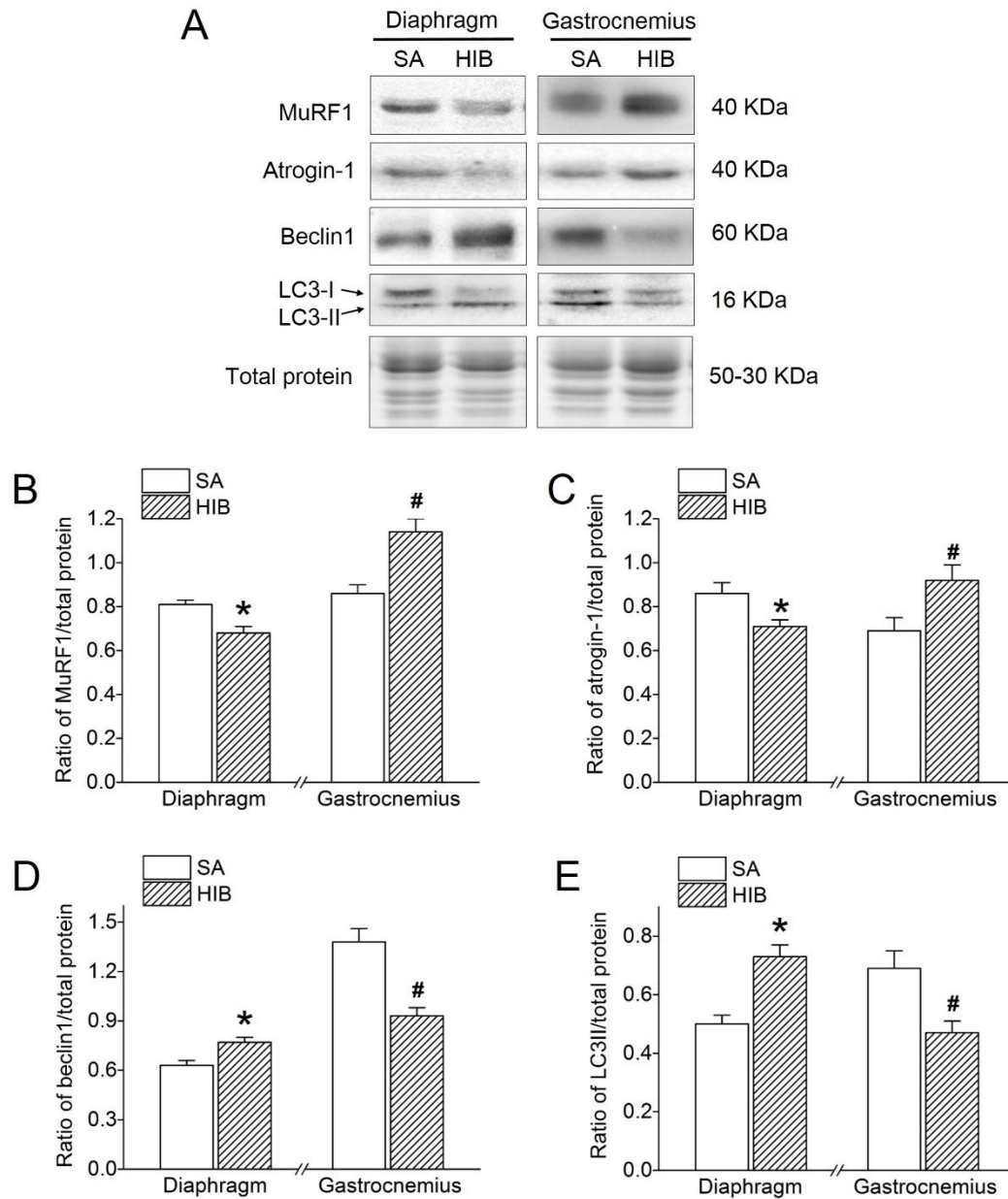
938 Changes of the ratio of MHC I to total protein. (C) Changes of the ratio of MHC IIa to total protein.

939 (D) Changes of the ratio of MHC IIb to total protein. (E) Changes of the ratio of MHC IIx to total

940 protein. SA: summer active ground squirrels, HIB: hibernating ground squirrels. Data represent

941 mean \pm SEM, $n = 8$. * $P < 0.05$, compared with SA in diaphragm muscle. # $P < 0.05$, compared with

942 SA in gastrocnemius muscle.



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Figure 4. Protein expression levels of MuRF1, atrogin-1, Beclin1 and LC3-II.

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(A) Representative immunoblots of MuRF1, atrogin-1, Beclin1 and LC3-II in each group. (B)

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Changes of the ratio of MuRF1 to total protein. (C) Changes of the ratio of atrogin-1 to total protein.

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(D) Changes of the ratio of Beclin1 to total protein. (E) Changes of the ratio of LC3-II to total

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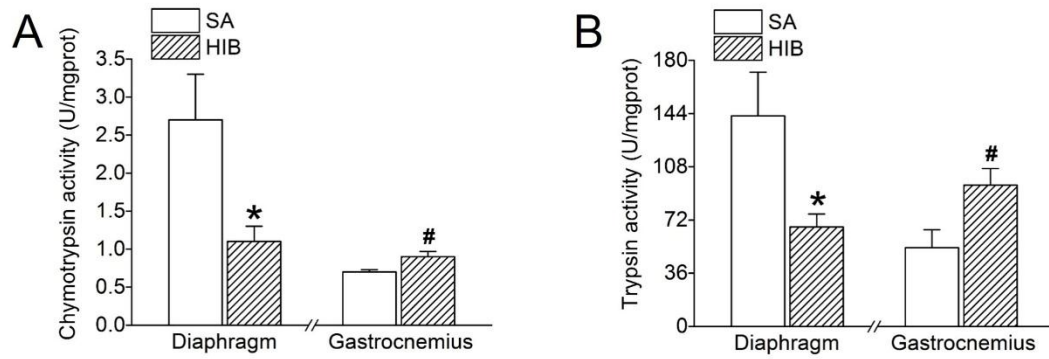
protein. SA: summer active ground squirrels, HIB: hibernating ground squirrels. Data represent

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mean \pm SEM, $n = 8$. * $P < 0.05$, compared with SA in diaphragm muscle. # $P < 0.05$, compared with

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SA in gastrocnemius muscle.



951

952 **Figure 5. Proteasome activity.**

953 **(A) Chymotrypsin proteasome activity. (B) Trypsin proteasome activity.** SA: summer active
954 ground squirrels, HIB: hibernating ground squirrels. Data represent mean \pm SEM, $n = 8$. * $P <$
955 0.05, compared with SA in diaphragm muscle. # $P <$ 0.05, compared with SA in gastrocnemius
956 muscle.

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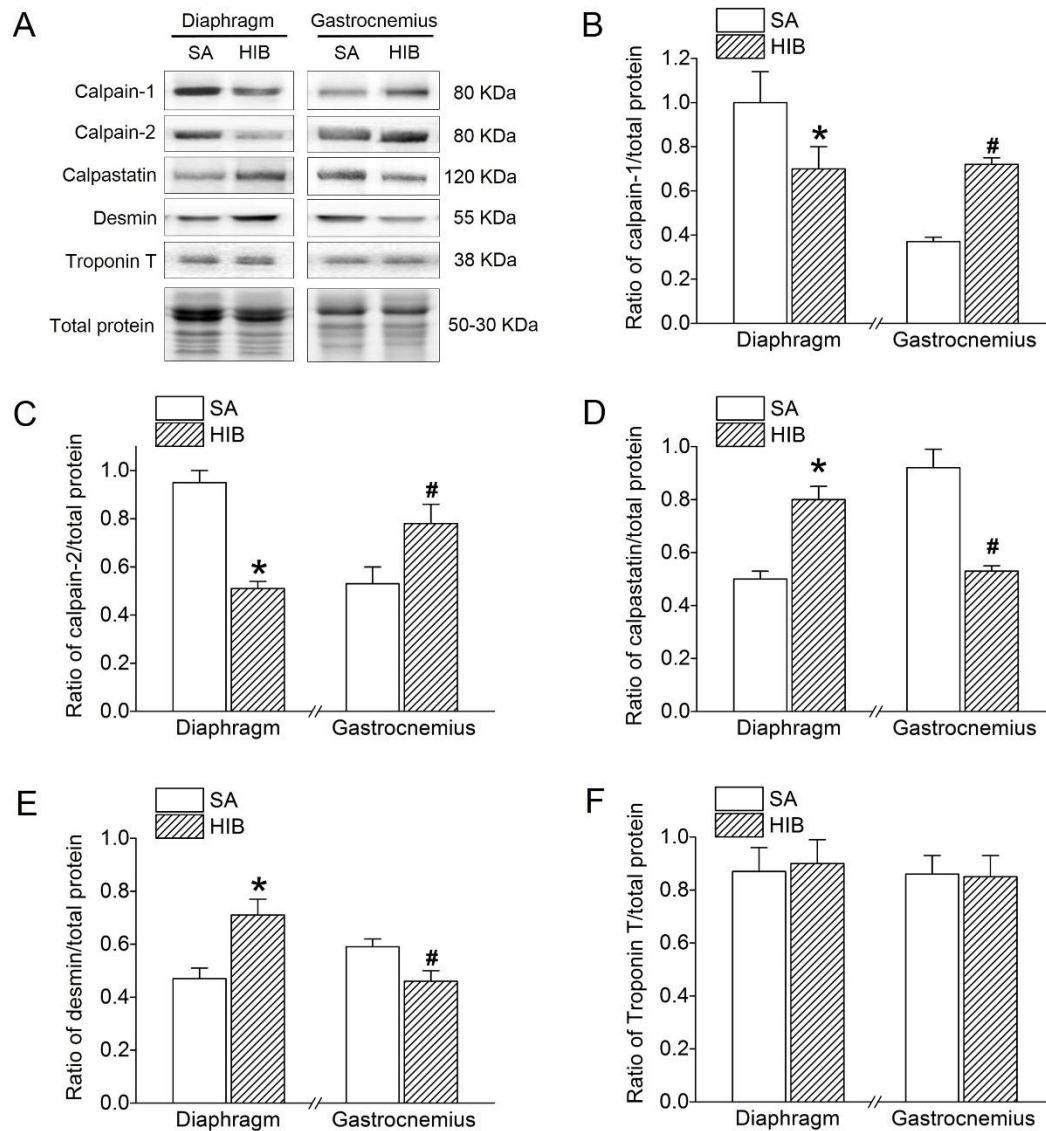
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966 **Figure 6.** Protein expression levels of calpain-1, calpain-2, calpastatin, desmin and troponin T.

967 (A) Representative immunoblots of calpain-1, calpain-2, calpastatin, desmin and troponin T in each

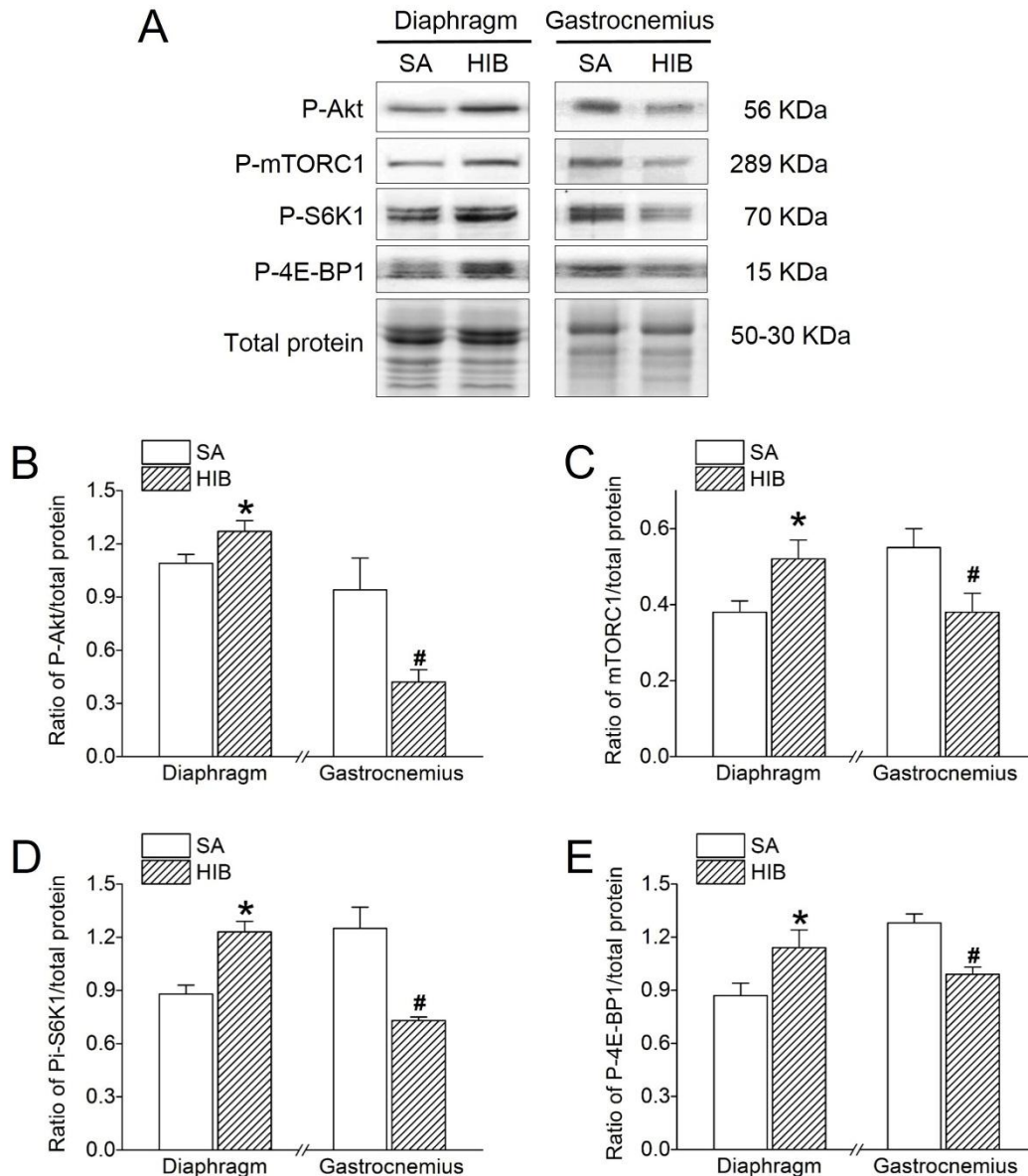
968 group. (B) Changes of the ratio of calpain-1 to total protein. (C) Changes of the ratio of calpain-2

969 to total protein. (D) Changes of the ratio of calpastatin to total protein. (E) Changes of the ratio of

970 desmin to total protein. (F) Changes of the ratio of troponin T to total protein. SA: summer active

971 ground squirrels, HIB: hibernating ground squirrels. Data represent mean \pm SEM, $n = 8$. * $P < 0.05$,

972 compared with SA in diaphragm muscle. # $P < 0.05$, compared with SA in gastrocnemius muscle.



973

974 **Figure 7.** Protein expression levels of P-Akt, P-mTORC1, P-S6K1 and P-4E-BP1.

975 (A) Representative immunoblots of P-Akt, P-mTORC1, P-S6K1 and P-4E-BP1 in each group. (B)

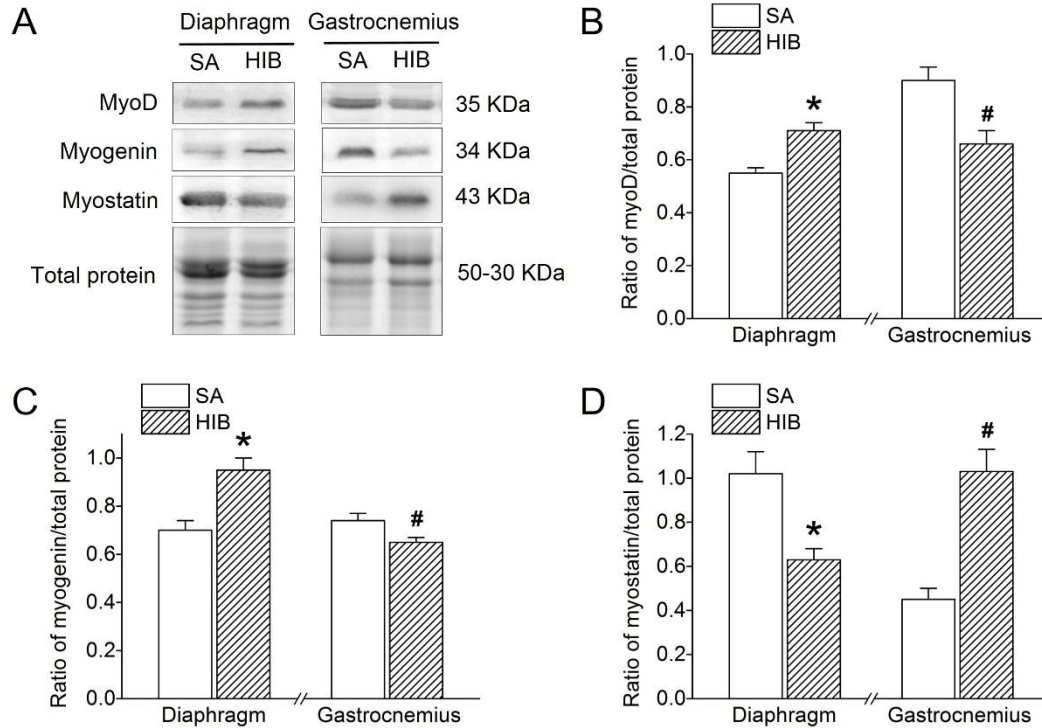
976 Changes of the ratio of P-Akt to total protein. (C) Changes of the ratio of P-mTORC1 to total protein.

977 (D) Changes of the ratio of P-S6K1 to total protein. (E) Changes of the ratio of P-4E-BP1 to total

978 protein. SA: summer active ground squirrels, HIB: hibernating ground squirrels. Data represent

979 mean \pm SEM, $n = 8$. * $P < 0.05$, compared with SA in diaphragm muscle. # $P < 0.05$, compared with

980 SA in gastrocnemius muscle.



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982 **Figure 8.** Protein expression levels of MyoD, myogenin and myostatin.

983 (A) Representative immunoblots of MyoD, myogenin and myostatin in each group. (B) Changes of
 984 the ratio of MyoD to total protein. (C) Changes of the ratio of myogenin to total protein. (D) Changes
 985 of the ratio of myostatin to total protein. SA: summer active ground squirrels, HIB: hibernating
 986 ground squirrels. Data represent mean \pm SEM, $n = 8$. * $P < 0.05$, compared with SA in diaphragm
 987 muscle. # $P < 0.05$, compared with SA in gastrocnemius muscle.

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1005 **Table 1.** Body weight (BW) for all the groups.

	BW before hibernation (g)	BW at experiment time (g)
1007 SA	288.3 ± 7.9	277.0 ± 16.2
1008 HIB	277.0 ± 16.2	247.8 ± 21.6*

1009 SA: summer active ground squirrels, HIB: hibernating ground squirrels. Data represent mean ± SEM,
1010 $n = 8$. * $P < 0.05$ compared with SA group.

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1012