

1 Article

2 Effect of dietary rumen-protected L-tryptophan 3 supplementation on growth performance, blood 4 hematological and biochemical profiles, and gene 5 expression in Korean native steers under cold 6 environment

7 Wahyu Priatno ^{1†}, Jae-Sung Lee ^{1†}, Jalil G. Nejad ^{1,2}, Dong-Qiao Peng ^{1,2}, Jin-Seung Park ³, Jun-Ok
8 Moon ³, and Hong-Gu Lee ^{1,2,*}

9 ¹ Department of Animal Science and Technology, Sanghuh College of Life Sciences, Konkuk University,
10 Seoul 05029, Republic of Korea; wpriatno.wp@gmail.com; foodleeking@gmail.com

11 ² Team of an Educational Program for Specialists in Global Animal Science, Brain Korea 21 Plus Project,
12 Sanghuh College of Life Sciences, Konkuk University, Seoul 05029, Republic of Korea;
13 jalilgh@konkuk.ac.kr; pdq15689x@foxmail.com

14 ³ Institute of Integrated Technology, CJ CheilJedang, Suwon 16471, Republic of Korea; jinseung.park@cj.net;
15 junokee@cj.net;

16 * Correspondence: hglee66@konkuk.ac.kr; Tel.: +82-2-450-0523 (H.G.L.)

17 † These authors contributed equally to this work

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20 **Simple Summary:** In this study, the effect of dietary rumen-protected L-tryptophan (RPT)
21 supplement on growth performance, blood hematological and biochemical profiles, and gene
22 expression was investigated in beef steers during cold environment. We revealed that
23 supplementation of 0.1% RPT incorporated into diet was beneficial owing to enhanced growth
24 performance by increasing ADG and glucose level, decreasing feed conversion ratio, and
25 maintaining homeostasis in immune responses in beef steers during cold environment.

26 **Abstract:** We assessed the growth performance, physiological traits, and gene expressions in steers
27 fed with dietary rumen-protected L-tryptophan (RPT) under cold environment. Eight Korean native
28 steers were assigned to two dietary groups, no RPT (Control) and RPT (0.1% RPT supplementation
29 on a dry matter basis), 6 wks. Maximum and minimum temperatures throughout the experiment
30 were 6.7°C and -7.0°C, respectively. Supplementation of 0.1% RPT to a total mixed ration did not
31 increase body weight but had positive effects of elevating average daily gain (ADG) and reducing
32 the feed conversion ratio (FCR) at day 27 and 48. Metabolic parameter showed higher glucose level
33 (at day 27) in the 0.1% RPT group compared to the control group. Real-time PCR analysis showed
34 no significant differences in the expression of muscle (MYF6, MyoD, and Desmin) metabolism genes
35 between the two groups, whereas the expression of fat (PPAR γ , C/EBP α , and FABP4) metabolism
36 genes was lower in the 0.1% RPT group than in the control group. Thus, we demonstrate that long-
37 term (6 wks) dietary supplementation of 0.1% RPT was beneficial owing to enhanced growth
38 performance by increasing ADG and glucose level, decreasing FCR, and maintaining homeostasis
39 in immune responses in beef steers during cold environment.

40 **Keywords:** rumen-protected L-tryptophan; growth performance; metabolites; glucose; gene
41 expression

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43 1. Introduction

44 The climate in the Korean peninsula is becoming more polarized owing to the global climate
45 change resulting in longer colder winters and longer hotter summers [1,2]. Given this inevitable
46 phenomenon, the decline in productivity of ruminants resulting in serious economic effects due to
47 low temperature in winter is expected to accelerate [3,4]. Therefore, it is pivotal to establish a
48 nutritional strategy that helps to minimize the impaired productivity of beef cattle due to temperature
49 conditions. Cold stress causes negative effects on growth performance and immune cell population
50 by influencing metabolic and immunological activities [5,6]. Thus, hematological profiles, if
51 measured, could be a good indicator of how stressors affect immune function of the body [6,7]. The
52 thermo-neutral zone for growing Korean native beef cattle is approximately 4 to 20°C and the critical
53 temperature is approximately -10°C [1,3]. In Korea, the temperature during Nov to Feb often falls
54 below -20°C at nights and fluctuates from approximately -5°C to -15°C during daytime. Given this,
55 adaptation to cold environments in ruminants involves increasing thermal insulation, appetite, and
56 basal metabolic intensity that improve cold hardiness and reduce the risks of both acute and chronic
57 cold stress [5,6,8]. Cold stress affects beef cattle production by elevating resting heat production,
58 energy requirement for maintenance, and appetite drive, while decreasing feed digestibility. The
59 appetite stimulation may partially counteract the increased energy requirement, but it cannot fully
60 alleviate the reduced efficiency of utilization of dietary energy.

61 L-tryptophan (TRP) is known to play a pivotal role in metabolic, physiological, and organ
62 development and growth [9,10]. Lack of TRP may adversely affect feed intake and growth
63 performance. However, in most ruminants, TRP is not deficient due to ruminal fermentation [9,11].
64 In particular, TRP in ruminants has been reported to increase the secretion and activity of pancreatic
65 α -amylase, thereby increasing starch digestibility by promoting the secretion of the intestinal
66 hormone cholecystokinin (CCK) [9,12,13]. TRP is also known as a constituent of niacin, a precursor
67 of serotonin and melatonin, and to have antioxidative and stress relieving properties [9,11]. Thus,
68 TRP is proposed as an essential amino acid (AA) that can help avert the decline in animal productivity
69 due to low temperature environment under climate change. On the other hand, the amounts of
70 essential AAs such as TRP supplied by microbes are sufficient only to support maintenance and
71 normal milk and beef production and not maximal animal growth. Thus, in order to ensure the
72 highest possible productivity in ruminants, it is essential to supply more AAs, in particular TRP, to
73 meet the requirement.

74 Feeding dietary rumen-protected L-tryptophan (RPT) has been shown to not only increase
75 growth performance of lambs [14] and wool output in sheep [15] but also improve N utilization in
76 goats [9,16] and average daily gain (ADG) and N utilization in cashmere goats [11]. However, the
77 effect of RPT on performance, blood hematology, and biochemistry and related gene expression in
78 Korean native steer under cold stress conditions is yet to be investigated. Information regarding
79 ruminal bypass AA have been limited to a few essential AAs but not RPT. Therefore, we
80 hypothesized that dietary supplementation of RPT may enhance growth performance, alter blood
81 parameters, and related gene expression in Korean native steers under cold environment, which was
82 investigated in the present study.

83 2. Materials and Methods

84 2.1. Animals and feeding trial

85 The experimental procedure and methods were approved by the Animal Welfare and Ethics
86 Authority of Konkuk University, Seoul, Republic of Korea (approval no: KU18178).

87 Eight Korean native steers [249 ± 21.6 day-old; body weight (BW) = 279 ± 16.6 kg] were selected
88 and randomly assigned into one of two groups: total mixed ration (TMR) without RPT (control, n =
89 4) and TMR with 0.1% RPT (RPT, n = 4) groups. The experiment was conducted outdoors, under a
90 shed, at the experiment farm (Chungju, Chungcheongbuk-do, Republic of Korea). All animals were
91 protected from the rain by covering using a ceiling. The mean weights of the animals at the starting
92 period of experiment (at day 0) were not significantly different between the groups ($p = 0.950$). After
93 grouping by statistical analysis of individual body weights, the animals were housed in 1.0×6 m²

94 individual pens for the duration of the experiment. TMR (Nonghyup Feed Co., Ltd., Yangju-si,
 95 Korea), which did not contain antibiotics, was fed to animals as a basal diet. The animals were fed 10
 96 kg TMR/day/animal to meet nutrition requirements of the National Research Council [17]. The RPT
 97 group was fed TMR mixed with RPT (0.1% of TMR as-fed basis; CJ CheilJedang, Suwon, Republic of
 98 Korea) once a day at 0800 h. The rate of by-pass is above 95% (flowing corporation data). Water was
 99 available *ad libitum*. The chemical analysis (moisture, crude protein, crude fat, contents of 19 AAs,
 100 etc.) of the feed stored at -20°C was performed (Table 1). Body weight of animals was measured three
 101 times, at day 0, 27, and 48. The ADG of the animals was calculated by dividing the difference in
 102 weight, between the initial weight and the end weight, by the total number of days during the
 103 experiment. Feed intake (FI) was calculated by examining total daily feeding and the orts amount of
 104 individual animals every morning at 0700 prior to providing fresh feed.

105 **Table 1.** Chemical composition and amino acids of the basal diet used in this study.

	TMR ¹
Chemical composition, % on a dry matter basis	
Dry matter	86.82
Crude protein	15.05
Ether extract	2.49
Crude fiber	25.90
Crude ash	6.75
Acid detergent fiber	32.87
Neutral detergent fiber	52.26
Amino acids, % on a dry matter basis	
Tryptophan	0.09
Methionine	0.09
Niacin	0.00
Lysine	0.54
Aspartic acid	1.20
Threonine	0.48
Serine	0.57
Glutamic acid	2.04
Glycine	0.61
Alanine	0.79
Valine	0.67
Isoleucine	0.47
Leucine	0.97
Tyrosine	0.29
Phenylalanine	0.55
Histidine	0.29
Arginine	0.71
Cystine	0.12
Proline	0.91

106 ¹ TMR, total mixed ration.

107

108 2.2. Environmental qualifications and measurements

109 Temperature (°C) and relative humidity (%) were recorded during the experiment period with
 110 a portable temperature and humidity meter (MHT-381SD, Lutron Co., LTD., Taiwan) at hourly
 111 intervals (Table 2). During days 7 to 13 and 42 to 48, minimum and maximum temperatures were -
 112 7.0°C and 6.7°C, respectively. Total average temperature during the experiment period (days 7 to 48)

113 was -9.5°C and was lower than the adaptation period (days 0 to 6). The average temperature during
114 adaptation period was 1.3°C.

115 **Table 2.** Changes in the temperature and relative humidity during the experiment period.

Period, days	Temperature, °C			Relative humidity, %		
	Min	Max	AVG ¹	Min	Max	AVG
0 to 6 ²	-2.4	9.7	1.3	19.4	94.2	69.4
7 to 13	-15.7	13.4	-7.0	12.2	78.1	45.3
14 to 20	-14.0	13.5	-5.4	10.3	85.9	45.6
21 to 27	-14.6	15.8	-3.2	12.1	87.1	51.3
28 to 34	-7.3	79.8	1.9	17.9	85.3	45.9
35 to 41	-6.9	22.0	3.7	17.9	89.8	50.8
42 to 48	-5.9	23.5	6.7	15.8	89.9	61.9
7 to 48	-9.5	16.8	-0.3	15.1	87.2	52.9

116 ¹ AVG, Average of temperature and relative humidity during day and nighttime for 7 days. ² Days 0 to 6,
117 adaptation period.

118 2.3. Blood collection and analysis

119 Blood samples were collected three times at day 0, 27, and 48 of the experiment period at 1400 h
120 from jugular venipuncture into K₂ EDTA-treated vacutainers (4-mL; Becton Dickinson, Franklin
121 Lakes, NJ, USA) for measuring hematology (white blood cells, lymphocytes, monocytes,
122 granulocytes, red blood cells, hemoglobin, hematocrit, mean corpuscular hemoglobin, and
123 plateletcrit) using the VetScan HM2 analyzer (Abaxis, Union City, CA, USA). Subsequently, blood in
124 serum tubes was centrifuged at 2,500 × g for 15 min at 4°C. The serum was used for measurement of
125 biochemistry parameters (glucose, total protein, blood urea nitrogen, albumin, and triglyceride)
126 using the automated biochemical analyzer (Hitachi Automatic Analyzer model 7180, Hitachi, Tokyo,
127 Japan) according to manufacturer's instructions.

128 2.4. Tissue collection and analysis

129 Longissimus dorsi muscle sample (12 to 13 ribs) for each steer was collected by biopsy at the
130 final day of the experiment (day 48) using a spring-loaded biopsy instrument (Biotech, Nitra,
131 Republic of Slovakia). The tissue samples were washed in Diethylpyrocarbonate (D5758, Sigma
132 Aldrich, St. Louis, MO, USA) treated and autoclaved water, transferred into a 2-mL tube, and then
133 incubated in a liquid nitrogen gas locker until analysis. The tissue samples (2 g) were ground into
134 powder under freezing conditions, with liquid nitrogen, and RNA was extracted from each tissue
135 sample as previously described [18]. The concentration of RNA was determined by
136 spectrophotometric analysis (NanoDrip 1000, Thermo Scientific, Seoul, Republic of Korea). The RNA
137 integrity was estimated using an RNA Nano 6000 Assay Kit for an Agilent Bioanalyzer 2100 system
138 (Agilent Technologies, Inc., Richardson, USA). When the number of RNA integrity (RIN) was more
139 than 6, complementary DNA (cDNA) synthesis was performed. RIN in the current study was 6.5 ±
140 0.27. RNA was used for real-time PCR analysis.

141 To synthesize cDNA in the procedure of real-time PCR analysis, 1 µg of RNA was reversely
142 transcribed in a 100 µL reaction volume with an iScript™ cDNA synthesis kit (Bio-Rad Laboratories,
143 Inc., CA, USA) according to manufacturer's instructions. Quantitative real-time PCR was performed
144 on duplicate samples by using a CFX Connect™ Real-Time System (Bio-Rad Laboratories, Inc.) with
145 IQ™ SYBR Green Supermix (Bio-Rad Laboratories, Inc.) reagents. The following PCR conditions were
146 used: 95°C for 3 min and 40 cycles at 95°C for 10 s, 51°C to 65°C for 30 s and 72°C for 30 s. Specific
147 primer of genes involved in muscle (MYF6, MyoD, and Desmin) and fat (PPARγ, C/EBPα, and
148 FABP4) is shown in Table S1. Triple housekeeping genes (18S, GAPDH, and RPLP0) were used as the

149 internal controls. Primer sequences used for quantitative reverse transcription PCR assay are
150 presented in Table S1.

151 2.5. Statistical analysis

152 Data sets were analyzed using the MIXED procedure of SAS (version 9.0; SAS institute Inc., Cary,
153 NC). Whole blood for hematological analysis was collected three times (at day 0, 27, and 48). This
154 data was used for repeated measurement analysis to investigate the interaction effect (treatment ×
155 day). Growth performance including BW, ADG, and feed conversion ratio (FCR), and mRNA
156 expression were assessed using the Student's t-test by using JMP 5.0 software package (SAS Institute
157 Inc., Cary, NC, USA). The Tukey test was used to compare the differences between treatment means.
158 The normality of the data distribution was tested prior to final comparison by SAS. Statistical
159 differences were considered significant at $p < 0.05$.

160 3. Results

161 3.1. Growth performance during cold temperature

162 We investigated performance parameters of ADG, FCR, and feed intake of steers supplemented
163 with TMR containing 0.1% RPT during cold environment. As shown in Table 3, higher ADG and
164 lower FCR (both $p < 0.05$) in the RPT group compared with the control group were observed at day
165 27 of the experiment (Table 3). In addition, animals in the RPT group showed higher ($p = 0.001$) ADG
166 and lower ($p = 0.001$) FCR compared with the control group during the final day of the experiment.

167 **Table 3.** Effect of 0.1% L-tryptophan (RPT) supplementation to total mixed ration (TMR) on growth
168 performance in cattle during cold environment.

	Control ¹	RPT ²	SEM ³	P-value
Day 0				
Body weight, kg	278.5	279.7	7.69	0.950
Day 27				
Body weight, kg	285.1	301.5	8.30	0.360
ADG ⁴ , kg/day	0.224	0.753	0.130	0.030
Feed conversion ratio ⁵	44.4	13.3	13.25	0.035
Day 48				
Body weight, kg	290.9	315.7	4.72	0.194
ADG, kg/day	0.262	0.766	0.1	<0.001
Feed conversion ratio	13.03	4.82	1.18	<0.001

169 Values are expressed as means (n = 4). ¹ Control, no RPT supplementation to TMR. ² RPT, 0.1% RPT
170 supplementation to TMR. ³SEM, standard error of the mean. ⁴ADG, body weight gain against initial body
171 weight/experimental days. ⁵Feed conversion ratio, ratio of total feed intake *versus* total weight gain.

172 In the observation of feed intake (FI) in steers during cold temperature, there was no difference
173 in FI between the two groups during adaptation period (days 0 to 6); However, the FI was higher (p
174 = 0.038) in the RPT group than in the control group during the final week (Table 4). Average FI in the
175 RPT group was higher ($p = 0.005$) compared to that in the control group.

176 **Table 4.** Effect of 0.1% L-tryptophan (RPT) supplementation on feed intake in cattle during cold
177 environment.

Period, days	Control ¹	RPT ²	SEM ³	P-value
0 to 6 ⁴	8.93	8.56	0.108	0.088
7 to 13	9.24	9.21	1.647	0.948
14 to 20	9.41	9.56	1.171	0.623
21 to 27	9.60	9.68	1.200	0.791
28 to 34	9.68	10.22	1.557	0.201
35 to 41	9.15	10.02	0.743	0.063
42 to 48	9.54	10.56	0.725	0.038
7 to 48	9.43	9.86	1.533	0.011

178 Values are expressed as means (n = 4). ¹ Control, no RPT supplementation to total mixed ration. ² RPT, 0.1%
 179 RPT supplementation to TMR. ³ SEM, standard error of the mean. ⁴ Days 0 to 6, adaptation period.

180 3.2. Physiological parameters in blood during cold temperature

181 Blood hematological and biochemical parameters were measured to determine the physiological
 182 conditions of steers supplemented with TMR containing 0.1% RPT during cold environment (Table
 183 5).

184 **Table 5.** Hematological and biochemical analyses of blood in steers supplemented with TMR
 185 containing 0.1% RPT during cold environment.

Items ⁴	Control ¹			RPT ²			SEM ³	P-value		
	D 0	D 27	D 48	D 0	D 27	D 48		Treatment (T)	Days (D)	T x D
Hematological parameters										
WBC	9.28	9.44	8.92	8.66	8.70	9.34	0.335	0.6815	0.9841	0.7830
LYM	6.07	6.25	5.26	5.55	6.55	5.98	0.234	0.7329	0.5086	0.3023
MON	0.07 ^b	0.08 ^b	0.56 ^a	0.06	0.07	0.12	0.043	0.0047	0.0002	0.0019
GRA	2.98	2.94	3.44	3.01	2.09	3.29	0.214	0.4665	0.3074	0.4322
RBC	10.33	9.97	9.00	10.70	10.34	10.08	0.266	0.2118	0.2050	0.6769
HGB	13.33	13.73	12.65	13.60	14.20	13.68	0.237	0.2449	0.9520	0.4339
HCT	34.57	34.12	31.66	35.00	34.64	33.88	0.584	0.3946	0.3787	0.7956
MCH	13.03	13.85	14.10	12.83	13.80	13.70	0.248	0.6806	0.2577	0.9625
PLT	398.5	455.8	367.5	378.0	476.8	379.5	15.39	0.8862	0.0360	0.8263
Biochemical parameters										
Glucose	84.0	87.0	78.5	77.0 ^B	86.3 ^A	74.3 ^B	1.32	0.0534	0.0015	0.4345
TP	6.28	6.28	6.05	6.40	6.48	6.20	0.055	0.1524	0.1444	0.9577
BUN	15.68	19.65	15.35	15.60	18.95	16.05	0.527	0.9773	0.0036	0.8052
Albumin	3.65	3.58	3.53	3.50	3.60	3.45	0.033	0.3378	0.4384	0.5805
TG	13.3	13.3	13.0	11.8	18.8	11.3	1.09	0.7354	0.3034	0.3293

186 Values are expressed as means (n = 4). ^{a,b, A,B} indicate significant differences compared to the initial period in
 187 the control and RPT groups (p < 0.05, Turkey test). ¹ Control, no RPT TMR. ² RPT, 0.1% RPT supplementation
 188 to TMR. ³ SEM, standard error of the mean. ⁴ Abbreviations: WBC, white blood cell; LYM, lymphocyte; MON,
 189 monocyte; GRA, granulocyte; RBC, red blood cell; HGB, hemoglobin; HCT, hematocrit; MCH, mean
 190 corpuscular hemoglobin; PLT, platelet; TP, total protein; BUN, blood urea nitrogen; TG, triglyceride.

191 Our results showed that 0.1% RPT did not cause blood hematological changes except for
 192 monocytes (MON; p = 0.005). Compared to the control group during the adaptation period (day 0), a
 193 higher value of MON in the control group was observed at day 48 (p < 0.05). In contrast, animals in
 194 the 0.1% RPT group did not show any changes in the value of blood MON during whole experiment
 195 period. All values of MON in the control group and 0.1% RPT group were within the normal range.

196 All blood biochemistry parameters except glucose ($p < 0.005$) demonstrated no significant
 197 differences ($p > 0.05$) between the two groups. Lack of significant differences in serum total protein
 198 (TP), blood urea nitrogen (BUN), albumin, and triglycerides (TG) revealed that 0.1% TRP did not alter
 199 the homeostasis mechanism. Expectedly, higher ($p < 0.05$) glucose level in the RPT group, compared
 200 with the control group, was observed at day 27 of the experiment period, and the glucose level
 201 returned to the normal values at day 48 of the experiment.

202 3.3. Relative gene expression in fat and muscle loin tissues of steers during cold temperature

203 We further observed changes in gene expression related to muscle and fat metabolism in loin
 204 tissues of steers supplemented with TMR containing 0.1% RPT during cold environment (Table 6).

205 **Table 6.** Relative expression of fat (PPAR γ , C/EBP α , and FABP4) and muscle (MYF6, MyoD, and
 206 Desmin) genes in loin tissue of cattle supplemented with total mixed ration (TMR) containing 0.1%
 207 L-tryptophan (RPT) during cold environment.

	Control ¹	RPT ²	SEM ³	P-value
PPAR γ	1.000	0.274	0.2302	< 0.000
C/EBP α	1.000	0.293	0.2714	< 0.000
FABP4	1.000	0.233	0.2618	< 0.000
MYF6	1.000	0.834	0.1667	0.071
MyoD	1.000	0.857	0.1822	0.676
Desmin	1.000	0.871	0.1902	0.140

208 Values are expressed as means ($n = 4$). Loin tissue of each cattle was used to estimate expression of the fat
 209 (PPAR γ , C/EBP α , and FABP4) and muscle (MYF6, MyoD, and Desmin) genes by real-time PCR analysis. The
 210 results were normalized using GAPDH, RPLP0, and 18S as internal controls. ¹ Control, no RPT TMR. ² RPT,
 211 0.1% RPT supplementation to TMR. ³ SEM, standard error of the mean.

212 In the present study, there were no differences ($p > 0.05$) in the expression of muscle metabolism
 213 genes including MYF6, MyoD, and Desmin between the two groups. However, the expression of fat
 214 metabolism genes including PPAR γ , C/EBP α , and FABP4 was higher ($p < 0.0001$) in the RPT group
 215 compare to the control group.

216 4. Discussion

217 L-tryptophan (TRP) is reported to be a limiting AA in growing lambs [11,14] and cattle [9] during
 218 the process of non-protein N utilization. Thus, supplementation of TRP in a rumen-protected form
 219 has positive effects on growth performance. L-tryptophan metabolites can affect growth,
 220 development, and health of beef cattle [9]. It is also known as a precursor of a stress relieving
 221 neurotransmitter called serotonin [9,19]. Therefore, in the present study, we can postulate that
 222 animals in the RPT group were more tolerant to cold stress situation, and thus showing higher weight
 223 gain and lower FCR.

224 The growth hormone-releasing hormone (GHRH) somatostatin (SS) and ghrelin are known to
 225 play pivotal roles in relation to growth hormone (GH) secretion regulation and are known to be
 226 involved in the serotonin regulation in ruminants [20,21]. Despite the limitation of this study on not
 227 measuring hormones such as serotonin levels, we observed higher FI in the RPT group compared to
 228 the control group (Table 4). Ma et al. [11] supplied two dosages of rumen-protected TRP to cashmere
 229 goats and observed an increase in the final BW and ADG in the supplemented group. Higher total FI
 230 intake could also postulate the fact that the steers in the RPT group tended to consume more feed in
 231 order to receive higher amounts of RPT, enabling them to better cope with cold stress conditions
 232 during the experiment period.

233 Higher amounts of RPT [over 0.5% of TMR, dry matter (DM)] have been documented to cause
 234 decreased FI due to lower palatability [8,22,23]. However, no changes in FI was observed by
 235 supplementing RPT in Korean native steers in a previous study in our laboratory (unpublished data-
 236 under revision) under normal environmental conditions. In contrast, in the present study, higher FI

237 in the RPT group (Table 4) implies that the amount of RPT up to 0.1% did not decrease the palatability
238 of the feed. Higher FI in the RPT group may also postulate increased need of the animals to cope with
239 cold stress conditions during the experiment period.

240 Hematological parameters are important to assess the physiological status of animals and to
241 monitor stress and pathological changes [2,6,23]. Responses to a particular stress factor are
242 quantitatively related to the severity and longevity of the stress [2,6,7,23]. A study on evaluation of
243 the ruminant complete blood cell count showed that MON participate in the immune response by
244 entering the tissues from the circulation to become macrophages, capable of phagocytosis of
245 infectious organisms, particulates, and cell debris [24]. Their population is quite variable in cattle and
246 is not a sensitive indicator of disease processes, such as increases that may accompany chronic
247 inflammation, tissue necrosis, hemolysis, or a stress response [25]. Low MON numbers have been
248 associated with endotoxemia and viremia [25]. In the present study, we did not observe any
249 difference in blood hematological parameters in both groups except for the lower values of MON in
250 the 0.1% RPT group (Table 5). The higher value of MON in the control group at day 48 ($p < 0.05$) was
251 comparable to that in the control group during the adaptation period (day 0). In contrast, a constant
252 value of MON was observed in the 0.1% RTP group at day 27 and 48 under cold environment,
253 highlighting that animals supplemented with 0.1% RPT via TMR can modulate the maintenance of
254 host homeostasis under stress due to cold temperature.

255 Little is known regarding the effects of melatonin, and TRP on cattle digestive processes. In rats,
256 *in vivo* and *in vitro* studies [12,13] have shown that the stimulatory effects of melatonin or TRP on the
257 exocrine pancreas activity involves cholecystokinin secretion, which is known to be a regulator of the
258 pancreatic enzyme in cattle [26]. This effect is attributed to higher release of α -amylase, which
259 eventually increases starch digestibility in cattle [9]. As feed intake was not affected at day 27 (Table
260 4) in the present study, dietary RPT supplementation likely modulated the activity of the digestive
261 enzymes, resulting in higher glucose level in the RPT group compared to the control group at day 27.
262 Blood glucose level is one of the most common secondary stress response parameters tested, and its
263 increase is often associated to an elevation of blood cortisol in steers under stress conditions [27].
264 Similarly, a study on serum biochemical parameters of sheep under different environmental
265 temperatures showed that higher concentration of serum glucose under cold conditions (4°C)
266 compared with under optimal temperature (21°C) and heat stress (40°C) [28]. Indeed, it is known as
267 a constituent of niacin, a precursor of serotonin and melatonin, and to have antioxidative and stress
268 relieving properties [9,11]. In this study, higher blood glucose and ADG of cattle in the RPT group
269 (Tables 3 and 5) demonstrated the effects of TRP metabolites in relieving stress in these cattle.

270 In a previous study in our laboratory (unpublished data, under review) we observed that
271 relative mRNA expression levels, including MYF6, MyoG, FABP4, and LPL genes, were higher in the
272 RPT supplemented group than in the control group of Korean native steers. While the MYF6 and
273 MyoG are representative of muscle differentiation [29], FABP4 is documented to be involved in
274 intracellular transport and fatty acid metabolism [30,31]. Thus, 0.1% RPT alone may not be effective
275 to alter the expression of muscle metabolism genes including MYF6, MyoD, and Desmin. However,
276 with respect to the fat metabolism and its related genes, 0.1% RPT could decrease the expression of
277 PPAR γ , C/EBP α , and FABP4 genes. Peroxisome proliferator-activated receptors (PPARs) are ligand-
278 activated transcription factors of nuclear hormone receptor that reduces triglyceride level and is
279 involved in the regulation of energy homeostasis [32]. The C/EBP α gene provides instructions for
280 making a protein called CCAAT enhancer-binding protein alpha. This protein is a transcription
281 factor, which means that it attaches (binds) to specific regions of DNA and helps to control the activity
282 (expression) of certain genes. FABP4 encodes the fatty acid binding protein found in adipocytes [30].
283 Fatty acid binding proteins are a family of small, highly conserved, cytoplasmic proteins that bind
284 long-chain fatty acids and other hydrophobic ligands. It is thought that FABPs roles include fatty acid
285 uptake, transport, and metabolism. The decrease in gene expression of PPAR γ , C/EBP α , and FABP4
286 in the present study may be attributed to muscle tissues that utilized free fatty acid for myocyte
287 differentiation. This phenomenon could be caused by direct involvement of TRP as a blocking block
288 or by indirect involvement of metabolic components related to TRP or both. This phenomenon

289 suggests that dietary supplementation of RPT enhances muscle differentiation and intracellular
290 transportation of fatty acids by inhibiting the catabolism of fat in muscle. The intramuscular fat and
291 intramuscular fatty acid concentration are important in meat quality improvement [33,34]. It has been
292 stated that peroxisome proliferator-activated receptor γ (PPAR γ) is the pivotally important gene in
293 relation to lipid metabolism in muscle tissue [35]. Precedent studies reported the effects of different
294 dietary energy levels on intramuscular deposition and fatty-acid composition in beef cattle [36,37].
295 Most recently, Yang et al. [38] investigated the effects of diets with different energy levels on fat
296 deposition and the fatty acid profile of the *longissimus dorsi* muscle in yak and the role of genes
297 involved in lipid metabolism in changing the fatty acid composition. They concluded that the high
298 energy diets promoted the deposition and partial fatty acid content of *longissimus dorsi* muscle mainly
299 by up-regulation of mRNA expression of ACACA, SCD, FASN, SREBP-1c, PPAR γ and FABP4.
300 However, in the present study, since the energy and amino acid are adversely related, up-regulation
301 of mRNA expression of PPAR γ , C/EBP α and FABP4 could be seen in non-supplemented RPT group
302 (control) which is in line with the aforementioned study. Different energy or protein levels, herein
303 supplementation of TRP, may alter intramuscular fat deposition into muscle by regulating PPAR γ .
304 PPAR γ is in charge of some promotion including adipocyte proteins or enzymes such as such as fatty
305 acid binding protein (FABP4), fatty acid synthase (FASN) and lipoprotein lipase (LPL) [39]. Since
306 very little information is available regarding the effect of RPT on fatty acid gene expressions in
307 *longissimus dorsi* muscle, further investigations are necessary in order to confirm these results and to
308 bring more insights to the available knowledge.
309

310 5. Conclusions

311 This study indicates that long-term (6 wks) dietary supplementation of 0.1% RPT enhances
312 growth performance in Korean native steers by modulating the immune responses and elevating
313 glucose level under cold environment. In addition, 0.1% RPT reduced adipogenic gene expression,
314 which may contribute to muscle tissues that utilized free fat acid for myocyte differentiation of steers
315 during cold environment. Therefore, dietary supplementation of 0.1% RPT is beneficial in reducing
316 the decline in productivity of beef cattle during cold stress.

317 **Supplementary Materials:** Table S1: Primer sequences used for quantitative reverse transcription PCR assay.

318 **Author Contributions:** conceptualization, J.S.L. and H.G.L.; data curation, J.S.L., W.P., and D.Q.P; investigation
319 and formal analysis, W.P., J.S.L., and D.Q.P.; writing—original draft preparation, review, and editing, W.P.,
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- 420

421 **Table S1.** Primer sequences used for quantitative reverse transcription PCR assay

Gene symbol	Gene name	Annealing temperature, °C	Primers
C/EBP α	CCAAT/enhancer-binding protein alpha	60.3	F: CCGTGGACAAGAACAGCAACGA R: GGCGGTCATTGTCACTGGTCAG
FABP4	Fatty acid binding protein 4	60.0	F: GTGTGATGCATTTGTAGGT R: CTGGTGGCAGTGACACCAT
PPAR γ	Peroxisome proliferator-activated receptor gamma	61.0	F: TGGAGACCGCCCAGGTTTGC R: AGCTGGGAGGACTCGGGGTG
MyoD	Myoblast determination protein	59.6	F: AGAGTTGCTTTGCCAGAG R: CTGCCTGCCGTATAAACA
MYF6	Myogenic factor 6	60.7	F: GAAGGAGGGACAAGCATTGA R: GAGGAAATGCTGTCCACGAT
DESMIN	Desmin	61.0	F: GGACCTGCTCAATGTCAAGA R: GGAAGTTGAGGGCAGAGAAG
18S	18S ribosomal RNA	51.0	F: ACCCATTCGAACGTCTGCCCTATT R: TCCTTGGATTGTGGTAGCCGTTTCT
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	60.0	F: GGCAAGGTCATCCCTGAG R: GCAGGTCAGATCCACAACAG
RPLP0	Ribosomal protein lateral stalk subunit P0	55.0	F: CAACCCTGAAGTGCTTGACAT R: AGGCAGATGGATCAGCCA