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Acute restraint stress does not alter corticosteroid receptor or 11-Hydroxysteroid dehydrogenase gene expression at Hypothalamic-Pituitary-Adrenal axis regulatory sites in captive male white-crowned sparrows (*Zonotrichia leucophrys gambelii*)

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1 **Acute restraint stress does not alter corticosteroid receptors or 11 β -**
2 **hydroxysteroid dehydrogenase gene expression at hypothalamic-pituitary-**
3 **adrenal axis regulatory sites in captive male white-crowned sparrows**
4 **(*Zonotrichia leucophrys gambelii*)**

5 **Jesse S. Krause^{1,2}, Jonathan H. Pérez^{2,4,5}, Angus M.A. Reid^{5,6}, Jeffrey Cheah¹, Valerie**
6 **Bishop⁵, John C. Wingfield², and Simone L. Meddle⁵**

7

8 **¹Department of Biology, University of Nevada, Reno, 1664 N. Virginia Street, Reno, NV**
9 **89557, USA**

10 **²Department of Neurobiology, Physiology and Behavior, University of California Davis,**
11 **One Shields Avenue, Davis, CA 95616, USA**

12 **³Department of Biology, University of South Alabama, 5871 USA Dr. N. Room 124, Mobile,**
13 **AL 36688, USA**

14 **⁴Institute of Biodiversity, Animal Health & Comparative Medicine, University of Glasgow,**
15 **Glasgow G12 8QQ, Scotland, UK.**

16 **⁵The Roslin Institute, The Royal (Dick) School of Veterinary Studies, University of**
17 **Edinburgh, Easter Bush, Midlothian, EH25 9RG, Scotland, UK**

18 **⁶MRC Human Genetics Unit, Institute of Genetics & Molecular Medicine, University of**
19 **Edinburgh, EH4 2XU, Scotland, UK**

20 **Running Title: Effects of acute restraint on gene expression**

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22 **Corresponding author: Jesse S. Krause**

23 **Email: jskrause@unr.edu**

24

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26 **corticosteroid, bird, corticosterone binding globulin (CBG), gonadotropin inhibitory**
27 **hormone (GnIH), 11 β Hydroxysteroid dehydrogenase (11 β HSD1, 11 β HSD2),**
28 **glucocorticoid receptor, mineralocorticoid receptor**

29

30 **Abstract**

31 Capture-restraint is often used to investigate the acute hypothalamic-pituitary-adrenal axis (HPA)
32 response to stress in wild and captive animals through production of glucocorticoids. Although
33 this approach is useful for understanding changes in glucocorticoids, it overlooks potential
34 changes in the complex regulatory systems associated with the glucocorticoid response,
35 including genomic receptors, steroid metabolizing enzymes, carrier proteins, and downstream
36 target proteins (e.g. gonadotropin-inhibitory hormone; GnIH). The present study in captive male
37 white-crowned sparrows (*Zonotrichia leucophrys*) tests the hypothesis that corticosteroid
38 receptors (mineralocorticoid - MR and glucocorticoid - GR), 11 β -hydroxysteroid dehydrogenase
39 1 (11 β HSD1) and 2 (11 β HSD2), corticosteroid binding globulin (CBG), and GnIH undergo rapid
40 changes in expression to mediate the glucocorticoid response to acute stress. To determine
41 dynamic changes in gene mRNA expression in the hippocampus, hypothalamus, pituitary gland,
42 and liver, birds were sampled within 3 minutes of entering the room and after 10, 30, and 60
43 minutes of capture restraint stress in a cloth bag. Restraint stress handling increased CBG and
44 decreased GnIH mRNA expression in the liver and hypothalamus, respectively. MR, GR,
45 11 β HSD1, and 11 β HSD2 mRNA expression in the brain, pituitary gland and liver did not
46 change. No correlations were found between gene expression and baseline or stress-induced
47 plasma corticosterone levels. No rapid changes of MR, GR, 11 β HSD1, and 11 β HSD2 mRNA
48 expression during a standardized acute restraint protocol suggests that tissue level sensitivity
49 may remain constant during acute stressors. However, the observed rise in CBG mRNA
50 expression could act to facilitate transport to target tissues or buffer the rise in circulating
51 glucocorticoids. Further studies on tissue specific sensitivity are warranted.

53

54 **Introduction**

55 In vertebrates the hypothalamic-pituitary-adrenal (HPA) axis regulates the production of
56 glucocorticoid hormones, cortisol or corticosterone, that circulate through the blood stream
57 bound to corticosteroid binding globulin (CBG) which is produced by the liver (Schoech,
58 Romero et al. 2013). In response to a challenge or stressor, the activity of the HPA axis is
59 modulated, resulting in increased glucocorticoid production, which can be several orders of
60 magnitude higher than initial capture or baseline levels (de Kloet 2014). The actions of
61 glucocorticoids are mediated through two separate classes of receptors: the high affinity
62 mineralocorticoid receptor (MR) and the low affinity glucocorticoid receptor (GR) (de Kloet
63 2014). The difference in receptor affinity allows for primary activation of the MR at low levels
64 of glucocorticoids, often referred to as ‘baseline’. GR is activated as glucocorticoid levels elevate
65 above baseline in response to a challenge or stressor, which results in behavioral and
66 physiological adjustments (Joëls, Karst et al. 2008, de Kloet 2014). The cellular levels of
67 glucocorticoids are further affected by the enzymes 11 β -hydroxysteroid dehydrogenase 1
68 (11 β HSD1) and 2 (11 β HSD2). 11 β HSD2 deactivates corticosterone by metabolizing it to a less
69 biologically active glucocorticoid, while this process is reversed by 11 β HSD1 (Seckl and
70 Chapman 1997). Thus, these enzymes act antagonistically to one another to regulate intracellular
71 corticosterone levels which has direct effects on receptor activation. In addition, there is
72 evidence that CBG can mediate glucocorticoid signaling by either facilitating the delivery of
73 steroids to their target tissues, reducing the bioavailability by binding steroids at the target tissue,
74 or controlling the amount of steroid that is free in the plasma (Hammond, Smith et al. 1991,
75 Grasa, Cabot et al. 2001, Breuner and Orchinik 2002, Schoech, Romero et al. 2013, Sivukhina

76 and Jirikowski 2014, Gulfo, Ledda et al. 2016, Gulfo, Castel et al. 2019). Ultimately, all these
77 factors combine to determine the rate at which MR and/or GR are activated, thus affecting stress
78 physiology.

79 The hippocampus, the paraventricular nucleus (PVN) of the hypothalamus and the
80 anterior pituitary gland are the major control sites for HPA axis function in mammals (Dallman,
81 Akana et al. 1992, Joëls and Kloet 2017) and birds (Bouillé and Baylé 1975, Bouillé and Baylé
82 1976, Hodgson, Meddle et al. 2007, Dickens, Romero et al. 2009, Krause, McGuigan et al. 2015,
83 Smulders 2017, Cornelius, Perreau et al. 2018). Through the interactions of MR and GR, the
84 hippocampus controls the amplitude and timing of circadian rhythms for baseline glucocorticoids
85 (Dallman, Akana et al. 1992, Sapolsky, Romero et al. 2000, Smulders 2017). Stress-induced
86 levels of glucocorticoids are thought to provide negative feedback at the level of the PVN and
87 anterior pituitary gland primarily through GR (Sapolsky, Romero et al. 2000, Landys,
88 Ramenofsky et al. 2006). Pharmacological or genetic manipulations of MR, GR, 11 β HSD1 and
89 11 β HSD2 at each or all levels of the HPA axis can affect baseline and/or stress-induced plasma
90 glucocorticoids, which suggests a complex and coordinated signaling cascade (Harris,
91 Kotelevtsev et al. 2001, Kolber, Wiczorek et al. 2008, Schmidt, Sterlemann et al. 2009, Harris,
92 Holmes et al. 2013, Pérez, Swanson et al. 2020).

93 Field biologists often assess acute HPA axis function by using a standard capture restraint
94 protocol for up to 60 minutes and taking serial blood samples to measure circulating
95 glucocorticoids. However, it remains unknown if the corticosteroid receptors or glucocorticoid
96 metabolizing enzymes also change within this standard 60-minute restraint stress protocol. We
97 hypothesized that the regulatory components of the HPA axis undergo rapid changes in
98 expression in order to potentiate glucocorticoid signaling. In order to determine the rapidity at

99 which gene expression of the regulatory elements of the HPA axis may change, tissues from
100 male captive white-crowned sparrows were sampled within three minutes of entering the room
101 and after 10, 30, and 60 minutes of restraint stress. We predicted that gene expression for MR,
102 GR, and 11 β HSD1 would be upregulated and 11 β HSD2 downregulated in response to stress in
103 the hippocampus, hypothalamus, pituitary gland, and liver. In addition, we quantified gene
104 expression of two known downstream targets of glucocorticoids; CBG and gonadotropin
105 inhibitory hormone (GnIH) (Calisi, Rizzo et al. 2008, Kirby, Geraghty et al. 2009). We predicted
106 that hepatic CBG expression would be upregulated to buffer the increase in plasma
107 glucocorticoids induced by restraint stress. We also predicted upregulation of gonadotropin-
108 inhibitory hormone (GnIH), because it is elevated by increased GR activation and plays a role in
109 suppressing reproductive pathways (Kirby, Geraghty et al. 2009, Calisi, Díaz-Muñoz et al. 2011,
110 Ernst, Lynn et al. 2016).

111 **Methods**

112 *Birds*

113 A total of 35 male Gambel's white-crowned sparrows, (*Zonotrichia leucophrys*
114 *gambelii*), were caught using mist nets and baited potter traps in late October through early
115 November 2015 in the vicinity of Davis, California (38.5449° N, 121.7405° W). Birds were
116 housed in individual cages (35 cm (w) x 40 cm (l) x 45 cm (h)) in three separate indoor aviaries at
117 20 \pm 2°C. A diet of 60% Mazuri maintenance chow and 40% wild bird seed and water were
118 provided *ad libitum*. Birds were exposed to naturally changing photoperiod for Davis, CA, USA
119 (38.55° N, -121.74° E) during the acclimation and experimentation period. Increasing natural
120 photoperiod results in the activation of physiological cascades for migration and breeding
121 (Farner and Follett 1966). Increasing photoperiod in captive Gambel's white-crowned sparrows

122 does not significantly affect HPA axis activity as they do not undergo the seasonal changes in
123 baseline and stress-induced corticosterone observed in free-living individuals (Romero and
124 Wingfield 1999, Ramenofsky, Campion et al. 2017).

125

126 *Blood and Tissue collection*

127 The effect of restraint stress on plasma levels of glucocorticoids was determined on a
128 mid-March photoperiod 12L:12D (lights on: 07:00 and off 19:00) on separate days from tissue
129 collection. Approximately 60 μ L of blood was collected following venipuncture of the alar vein
130 with a 26-gauge needle and collected into a heparinized glass microcapillary tubes (VWR:
131 15401-56). Samples were collected within 3 minutes of entering the room and 30 minutes post
132 restraint in an opaque cloth bag. Birds were bled at 09:00 over two consecutive days. Blood was
133 centrifuged at 15,000 *g* for 5 minutes to separate plasma from red blood cells. The plasma was
134 aspirated with a Hamilton syringe, transferred into a labeled microcentrifuge tube, and stored at -
135 30°C until radioimmunoassay for corticosterone.

136 Birds were euthanized in early July when the photoperiod was 14L:10D (lights on: 07:00
137 and off 21:00) to ensure they were in a fully reproductive state which was confirmed by
138 assessment of an enlarged cloacal protuberance and large testes size. As determined at the time
139 of euthanasia, the testes had an average length of 6.96 ± 1.28 mm and width of 5.2 ± 1.12 mm
140 ($n=35$; mean \pm S.D.) and there was no evidence of body or wing feather molt. Birds were
141 sampled between the hours of 09:00 and 11:00 over two consecutive days and were randomly
142 assigned to four groups on each day; a baseline sampled in under 3 minutes ($n=8$), and three
143 other groups in which the bird was placed into a cloth bag for 10 ($n=8$), 30 ($n=9$) or 60 ($n=9$)
144 minutes. The time points were chosen as they represent the standardized capture restraint time

145 intervals at which blood samples are collected in stress physiology studies. Birds were
146 euthanized by sedation with isoflurane followed by rapid decapitation. Birds were dissected and
147 tissues were quickly collected and fresh frozen on powdered dry ice, wrapped in aluminum foil
148 and placed in labeled plastic bags and stored at -80°C. In the case of the liver, the left lobe was
149 collected. Samples were later shipped on dry ice to the Roslin Institute, University of Edinburgh
150 where they were stored at -80°C until cDNA preparation. All work was approved by University
151 of California, Davis - Institutional Animal Care and Use Committee (IACUC) under protocol
152 19758, United States Fish and Wildlife Service permits - Federal MB90026B-0, and California
153 State SC13449.

154 *Preparation of cDNA*

155 Whole frozen brains were warmed to -18°C in a cryostat and the hippocampus (~30mg)
156 and hypothalamus (~80-100mg) were dissected in standardized blocks for isolation of RNA. The
157 hippocampus from both hemispheres was isolated from the dorsal aspect of the telencephalon.
158 Hypothalamic blocks were created by placing the brain into a brain matrix and landmarks were
159 used according to Stokes, Leonard et al. (1974) to make a coronal cut just caudal to the Tractus
160 septomesencephalicus (TrSM) and a rostral coronal cut at the start of the cerebellum. Tissues
161 were homogenized using an Ultra Turrax homogenizer (IKA-Werke GmbH & Co. KG) in
162 conjunction with 1000µL of trizol (Sigma-Aldrich T9424), except for the pituitary gland in
163 which 300µL was used due to the small mass (<3mg). Total RNA was extracted from 250µL of
164 tissue homogenate using Zymo Research Direct-zol 96 well plates (R2057) including the DNA
165 digestion step per the manufacturer's instructions. Total RNA for hippocampus, hypothalamus,
166 pituitary gland, and liver were assessed using a Nanodrop 1000 (Thermo Scientific) and found to
167 have an average yield of 261±112, 254±126, 26 ±10, and 219±89 ng/µL (mean±SD) with an

168 average 260/280 ratio of 2.05 ± 0.05 , 2.02 ± 0.02 , 2.06 ± 0.16 , and 2.08 ± 0.02 (mean \pm SD),
169 respectively. cDNA was produced by reverse transcribing 250 ng of RNA per sample using the
170 High Capacity Reverse Transcription Kit (Applied Biosystems) according to the manufacturer's
171 guidelines and the final volume was adjusted to 110 μ L per sample using ultra-pure (Milli-Q)
172 water.

173 *Quantitative polymerase chain reaction (qPCR)*

174 All assays used Brilliant 111 Ultra-fast SYBR Green qPCR Master mix (Agilent
175 Technologies 60083) which was read on an Agilent Mx3005p qPCR system and processed with
176 MxPro software (Agilent Technologies) as previously described (Reid, Wilson et al. 2017). In
177 brief, a 20 μ L total reaction volume per sample was generated by combining 10 μ L SYBR Green,
178 8 μ L cDNA, 0.4 μ L 20 μ M forward primer, 0.4 μ L 20 μ M reverse primer, 0.3 μ L 1/500 dilution of
179 ROX reference dye solution, and 0.9 μ L Milli-Q H₂O. Each assay used the following thermal
180 conditions: 50°C; 120s, 95°C; 120s, (40 cycles of 95°C; 15s, 60°C; 30s), then 95°C; 60s, 60°C;
181 30s, 95°C; 15s. Apparent reaction efficiencies were determined by analyses of the standard
182 curves and ranged between 92.4 - 96.8%. The R² for standard curves ranged between 0.984-
183 1.000.

184 Primers were designed using the relevant white-throated sparrow coding sequence (cds)
185 unless white-crowned sparrow cds were available (CBG and GnIH). CBG was recently identified
186 in *Taeniopygia guttata* after nearly 40 years of research. Primers were designed against the
187 published because few genome sequences have been updated (Vashchenko, Das et al. 2016).
188 Multiple primer combinations were tested for each gene using the previously mentioned thermal
189 conditions for SYBR reactions and with FastStart PCR (Roche) using a standard PCR thermal
190 conditions [95°C; 240s, (40 cycles of 95°C; 30s, 58°C; 30s, 72°C; 30s), then 72°C; 420s].

191 Products from both PCR and qPCR reactions were visualized using 2% agarose gel
192 electrophoresis. The primer combination for each gene was selected on the amplicons that
193 yielded highest amplifying reaction that lacked visible primer dimers or infidelity signals (Table
194 1). Once primers were selected, FastStart amplicons were isolated from the agarose gel using a
195 QIAquick Gel Extraction Kit (Qiagen 28704). Amplicons were sent for sequencing and GR, MR,
196 11 β HSD1, 11 β HSD2, YWHAZ were found to have sequence homologies with the published
197 white-throated sparrow (*Zonotrichia albicolis*) genome of 98, 95, 100, 99.72, and 98.82%
198 respectively. The CBG amplicon shared 90% identity with *Taeniopygia guttata* CBG, and the
199 GnIH amplicon shared 98% identity with the published *Zonotrichia leucophrys gambelii* GnIH
200 amplicon. Stock amplicons were serially diluted to produce standard curves for qPCR. For each
201 gene assay per tissue, duplicate samples from each bird were all run on a single plate. The
202 purified cDNA was used to generate standard curves by quantification on a Nanodrop and then a
203 serial dilution was conducted from an aliquot of the stock amplicon solution. For each gene assay
204 per tissue, duplicate samples from each bird were all run on a single plate. All genes were
205 normalized to the reference gene YWHAZ due to its reliability in previous avian studies (Olias,
206 Adam et al. 2014, Reid, Wilson et al. 2017).

207 MxPro software compares Ct values of unknown samples to those of standards with
208 known target concentration to determine an absolute measure of the number of target cDNA
209 copies in each reaction volume, which represented a constant proportion of total RNA. Absolute
210 expression values for each gene of interest were then divided by the corresponding YWHAZ
211 absolute expression value to give a normalized relative measure of expression, with arbitrary
212 units, for each sample. This controlled for any inconsistency in total RNA representation (e.g.
213 difference in total RNA reverse-transcribed per sample), as well as any disproportional

214 representation caused by large differences in unassessed transcripts (e.g. ribosomal RNAs or
215 tissue-specific genes under certain seasonal conditions) compared to YWHAZ basal expression.
216 Additional retrospective assessment of YWHAZ for reference suitability found expression to be
217 consistent across all samples for each tissue type (see results).

218

219 *Quantification of plasma corticosterone*

220 Corticosterone concentrations were determined using a previously validated
221 radioimmunoassay for corticosterone (Krause, Pérez et al. 2017). In brief, 15 μ L from baseline
222 plasma samples and 10 μ L from the 30-minute samples were combined with 2000CPM of
223 tritiated corticosterone (Perkin Elmer NET399250UC). 4mL of freshly distilled dichloromethane
224 was used to extract corticosterone from the plasma samples. Aspirated dichloromethane was
225 placed into a water bath at 35°C and was dried using nitrogen gas. Dried extracts were
226 reconstituted in 550 μ L of phosphate buffer saline with gelatin (PBSG). 100 μ L of reconstituted
227 extract was added to a scintillation vial and combined with 3mL of scintillation fluid (Perkin
228 Elmer Ultima Gold: 6013329) to determine extraction recovery percentages. Next, 200 μ L of
229 reconstituted extracts were added to duplicate RIA assay tubes with 100 μ L of tritiated
230 corticosterone (Perkin Elmer NET399250UC) and 100 μ L of antiserum (MP Biomedical 07–
231 120016, lot 3R3-PB-20E antibody). Unbound steroid was separated from bound steroid using
232 500 μ L of dextran coated charcoal solution. Samples were then placed in a centrifuge for 10
233 minutes at 4°C at 3000 g to separate bound from free steroids in solution. The supernatant
234 containing bound steroids was decanted into scintillation vials and 3.5mL of scintillation fluid
235 were added. Mean recovery was 85.25 \pm 4.2% (mean \pm SD) and intra- (calculated using C.V.
236 between duplicates) and inter-assay variations were 5.05 and 6.14%, respectively.

237

238 **Statistical Analyses**

239 Statistical analyses of the data were performed in R Statistical Analysis software with R
240 studio version 3.6.3 (R Core Development Team 2018). Gene expression data were analyzed
241 using an analysis of variance (ANOVA) with the main effect of sampling time points. The
242 residuals were checked for normal distribution using Shapiro-Wilks and normality using
243 Levene's test. If the assumptions were not met, the data were log transformed. All post hoc tests
244 were performed using the emmeans package (Lenth, Singmann et al. 2018) to perform Tukey's
245 Honestly Significant Difference (HSD) tests and generate effects size estimates based on
246 Cohen's D. Pearson's correlations were used to investigate the relationship between either
247 baseline or stress-induced corticosterone and gene expression in each of the measured tissues.

248 **Results**

249 *Effects of restraint handling stress on gene expression*

250 MR, GR, 11 β HSD1 and 11 β HSD2 mRNA expressions were not affected by restraint handling in
251 any of the tissues measured (Figs. 1&2; Table 2). However, restraint handling resulted in
252 changes in mRNA expression of GnIH in the hypothalamus and CBG in the liver (Fig. 3; Table
253 2). Hypothalamic GnIH expression was higher at the 3-minute compared to 10-minute sampling
254 points ($t=4.26$, $P=0.002$, $df=21$, Cohen's $d=2.39$) and 30 ($t=2.82$, $P=0.04$, $df=21$, Cohen's
255 $d=1.38$; Fig. 2A). CBG in the liver was higher at the 60-minute sampling point compared to the
256 3-minute ($t=3.04$, $P=0.02$, $df=23$, Cohen's $d=1.57$) and 10 minute ($t=2.82$, $P=0.045$; Fig. 2B,
257 $df=23$, Cohen's $d=1.50$) sampling points.

258 YWHAZ gene expression was not affected by restraint handling in the hippocampus ($F_{3,22}=0.25$,
259 $P=0.85$), hypothalamus ($F_{3,24}=0.007$, $P=0.99$), pituitary gland ($F_{3,19}=0.04$, $P=0.98$), or liver
260 ($F_{3,23}=2.21$, $P=0.11$).

261 *Relationships between gene expression and circulating corticosterone*

262 No correlations were found between circulating baseline or stress-induced glucocorticoids and
263 any of the genes measured (Table 2).

264

265 **Discussion**

266 We tested whether regulatory elements downstream of plasma levels of corticosterone
267 respond rapidly to the stress of a standardized restraint handling protocol. There were no changes
268 in MR, GR, 11 β HSD1, or 11 β HSD2 mRNA expression, suggesting that with respect to
269 standardized restraint stress protocols lasting 1 hour or less, quantification of plasma
270 corticosteroid levels may be sufficient to characterize HPA axis activity in white-crowned
271 sparrows.. In rock doves, *Columba livia*, transcriptomic analysis showed no changes in MR, GR,
272 11 β HSD1, or 11 β HSD2 mRNA expression in the hypothalamus nor pituitary gland following 30
273 minutes of restraint stress (Calisi, Austin et al. 2017). Our findings along with Calisi et al. 2017,
274 may be explained by the fact that changes in gene expression, particularly for genomic receptors,
275 may occur on a longer time scale and were likely missed in the present study given the maximum
276 observation window of one hour. For instance, in rats, 120 minutes, but not 15, 30, or 60
277 minutes, of acute stress decreased hippocampal GR expression but not MR (Paskitti, McCreary
278 et al. 2000), upregulated hypothalamic GR expression but not MR, and decreased pituitary GR
279 expression but not MR (Karandrea, Kittas et al. 2000). In birds, MR and GR mRNA expression

280 vary over longer time periods, for example in response to seasonal changes (Liebl, Shimizu et al.
281 2013, Krause, McGuigan et al. 2015, Li, Davis et al. 2020), social stress (Cornelius, Perreau et
282 al. 2018), early life stress (Zimmer and Spencer 2014), chronic stress (Dickens, Romero et al.
283 2009), selection for high HPA axis activity (Hodgson, Meddle et al. 2007), and range expansion
284 (Liebl and Martin 2013).

285 Another possible mechanism for rapidly modulating tissue level availability of
286 corticosterone is through glucocorticoid regulatory enzymes. 11 β -hydroxysteroid dehydrogenase
287 1 (11 β HSD1) catalyzes the reactivation of corticosterone from inactive metabolites, and 11 β -
288 hydroxysteroid dehydrogenase 2 (11 β HSD2) catalyzes the deactivation corticosterone to inactive
289 metabolites. In the current study, we did not detect any rapid effects of stress on the expression
290 of 11 β HSD1 or 11 β HSD2. A study in rodents found upregulation of 11 β HSD1 mRNA in the
291 hippocampus at 1 and 2 hours post physiological stressor, but no other brain regions involved
292 with HPA axis signaling were investigated (Spiers, Chen et al. 2016). 11 β HSD2 is not highly
293 expressed in the brain of mammals (unlike in birds) thus no comparative studies could be found
294 investigating the effects of stress (Chapman, Holmes et al. 2013). In white-crowned sparrows,
295 pharmacological blockade of 11 β HSD1 and 11 β HSD2 enzyme function during both systemic
296 administration and infusion into the third ventricle of the brain (11 β HSD2, only) altered levels of
297 plasma corticosteroids over the course of a standardized restraint stressor (Pérez, Swanson et al.
298 2020). The central administration of pharmacological antagonists to the third ventricle suggested
299 that 11 β HSD2 was involved in regulating negative feedback control at PVN of the
300 hypothalamus. While, systemic injections targeted the liver, kidneys, and pituitary gland
301 suggested that 11 β HSD2 and 11 β HSD1 are important for balancing net deactivation of
302 corticosterone by the kidney and net reactivation by the liver and/or possible negative feedback

303 at the pituitary gland (Pérez, Swanson et al. 2020). However, regulation of gene expression is not
304 the only way to modulate enzyme kinetics. Both enzymes are dependent upon cofactors, NAD⁺
305 and NADPH, for proper functioning and thus these could potentially regulate their activity.
306 Studies on 3 β -hydroxysteroid dehydrogenase (3 β HSD) have been shown to undergo rapid
307 modulation, by changes of NAD⁺ cofactors, in songbirds (Pradhan, Newman et al. 2010). Our
308 data suggest that rapid regulation of expression is not occurring, but further studies will need to
309 elucidate if either 11 β HSD1 or 2 undergoes a rapid response to cofactors.

310 Binding assays in birds have verified the presence of both MR and GR in the liver
311 (Lattin, Waldron-Francis et al. 2012), but we found no effect on liver GR or MR mRNA
312 expression in response to restraint handling stress. We have not found any published studies to
313 date that have investigated the effects of short-term acute stress on corticosteroid receptor gene
314 expression in the liver of any species. This represents a serious gap in our knowledge for how the
315 liver responds to acute stress. In house sparrows, *Passer domesticus*, a chronic stress paradigm
316 also had no effect on MR or GR in the liver when analyzed using receptor binding assays (Lattin
317 and Romero 2014). However in fish and rodents, treatment of hepatocytes or whole animals with
318 glucocorticoids increased GR mRNA expression after 24 h of exposure but not at 1, 4, or 8h post
319 treatment (Sathiyaa and Vijayan 2003, Liu, Nakagawa et al. 2005). In addition, 6 h of chronic
320 immobilization for 1 day in rodents resulted in upregulation of 11 β HSD1 and down regulation of
321 11 β HSD2 (Chen 2020). Thus, changes in gene expression associated with glucocorticoid
322 signaling appear to be context and duration dependent.

323 Rapid changes in the expression of downstream targets of corticosteroid were observed
324 following restraint stress. CBG expression in the liver increased in as little as 30 minutes in
325 response to acute restraint stress. The current literature shows mixed results for the effects of

326 restraint handling on circulating plasma CBG in birds; some species show a decline while others
327 are unaffected (Breuner, Lynn et al. 2006). Gambel's white-crowned sparrows do not show a
328 decline in circulating CBG after 1 hour of restraint (Breuner, Lynn et al. 2006). The binding
329 capacity of CBG in songbirds has been reported to be relatively high, allowing binding of
330 additional steroids or potentially buffering the loss of cleaved CBG (Charlier, Underhill et al.
331 2009, Li, Sun et al. 2017) so that a substantial increase in circulating CBG may not be necessary
332 to regulate HPA axis activity. Based on our data, a longer time course than that used previously
333 by Breuner et al., (2006) may be required to detect a corresponding change in circulating CBG.
334 Alternatively, increased CBG transcript production may be keeping pace with increased CBG
335 cleavage and clearance during a stressor. Long-term stressors, such as food removal or restriction
336 studies, have shown that plasma CBG levels decline in white-crowned sparrows within 22 hours
337 (Lynn, Breuner et al. 2003).

338 GnIH is important for reducing the activity of the hypothalamic-pituitary-gonadal (HPG)
339 axis, but contrary to our predictions, GnIH expression was markedly reduced after 10 and 30
340 minutes of restraint stress. Hypothalamic GnIH peptide and mRNA typically increase with stress,
341 and glucocorticoid receptors colocalize with GnIH neurons (Calisi, Rizzo et al. 2008, Kirby,
342 Geraghty et al. 2009, Gojska and Belsham 2014). Nonetheless studies in captive breeding zebra
343 finches have shown GnIH immunoreactive cells to decrease in response to restraint stress and
344 food removal (Ernst, Lynn et al. 2016, Wilsterman, Alonge et al. 2020). Studies in European
345 starlings and rats have shown that GnIH levels in both sexes peak following clutch completion,
346 which may serve to suppress HPG axis function in the event that the clutch is lost the
347 reproductive system can reactivate (Calisi, Geraghty et al. 2016). Thus, it is difficult to determine
348 the functional significance of the observed decline in GnIH, given its transient occurrence

349 (Kirby, Geraghty et al. 2009, Calisi, Díaz-Muñoz et al. 2011). Based on our existing knowledge
350 of GnIH the decrease in expression may play a functional role in altering either HPG axis
351 activity or sexual behavior in response to acute environmental stressors.

352 **Conclusion**

353 This is the first study in birds to test whether or not rapid changes in corticosteroid receptors or
354 the 11 β Hydroxysteroid dehydrogenase system occur at multiple levels within the HPA axis and
355 at target tissues during a standardized restraint handling sampling period. Our findings suggest
356 that neither the expression of corticosteroid receptors nor the 11 β -hydroxysteroid dehydrogenase
357 system change over the course of a standardized restraint handling protocol at any regulatory
358 point within HPA axis. However, hepatic mRNA expression of CBG was rapidly upregulated
359 which may serve to buffer circulating levels of glucocorticoids and may also be important for
360 delivering corticosterone to target tissues. Thus, genes that are regulated by glucocorticoid
361 signaling - GnIH and CBG, undergo rapid changes. Our data suggest that tissue level sensitivity
362 for glucocorticoids as accessed by corticosteroid receptors and 11 β HSD enzymes suggests that
363 these elements are stable on the acute time scale. Long-term stress studies are required to
364 understand if these regulatory elements change over longer time periods.

365

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376

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558 **Table and Figure Legends**

559 **Table 1.**

560 Primers that were utilized in this study.

Gene	Accession Number	Primer	Primer Seq
Corticosteron Binding Globulin (CBG)	KU180443.1	F	GCAGATCTCTGGCATCAC
		R	GAGGAAGGGATGGCTGAATC
Glucocorticoid Receptor (GR)	XM_002192952.3	F	TGAAGAGCCAGTCCCTGTTGAG
		R	CAACCACATCATGCATAGAGTCCAGCA
Mineralocorticoid Receptor (MR)	NM_001076690.1	F	AAGAGTCGGCCAAACATCCTTGTCT
		R	AAGAAACGGGTGGTCCTAAAATCCCAG
Gonadotropin Inhibitory Hormone (GnIH)	AB128164.1	F	CTGCCTCGAGACATTGAGGA
		R	GACCACCACTGAAGCAAAT
11 β -Hydroxysteroid dehydrogenase 1 (11 β HSD1)	XM_005492865.1	F	GCTCATCCTCAACCACATCG
		R	CCATCTAGGGCGAACTTGGT
11 β -Hydroxysteroid dehydrogenase 2 (11 β HSD2)	XM_005490743.3	F	ATATCCAGGCCACACCAAC
		R	CACGTTGTCCCTGTTTTGTAGT
Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta (YWHAZ)	NM_001031343.1	F	GTGGAGCAATCACAACAGGC
		R	GCGTGCGTCTTTGTATGACTC

561

562 **Table 2.**

563 Analyses of variance results investigating the effects of acute capture restraint stress on gene expression
 564 and Pearson's correlations between baseline and stress-induced corticosterone and gene expression of
 565 glucocorticoid receptor (GR), mineralocorticoid receptor (MR), 11 β -hydroxysteroid dehydrogenase 1
 566 (11 β HSD1), 11 β -hydroxysteroid dehydrogenase 2 (11 β HSD2), corticosterone binding globulin

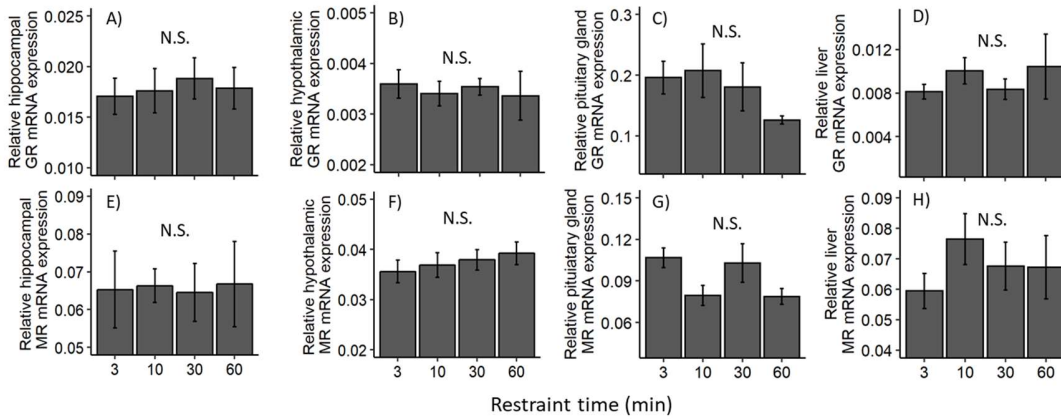
567 (CBG) and gonadotropin inhibitory hormone (GnIH) mRNA in tissues including the hippocampus,
 568 hypothalamus, pituitary gland, and liver of male white crowned sparrows.

	Gene expression			Baseline CORT Correlation			Stress-induced CORT Correlation		
	DF	F	P	DF	r	P	DF	r	P
Mineralocorticoid receptor (MR)									
Hippocampus	3,22	0.01	0.98	24	0.28	0.10	24	0.22	0.26
Hypothalamus	3,24	0.73	0.54	2	0.24	0.21	26	0.13	0.48
Pituitary gland	3,14	3.13	0.06	16	0.05	0.81	16	0.02	0.92
Liver	3,22	0.86	0.48	24	0.27	0.17	24	0.14	0.46
Glucocorticoid receptor (GR)									
Hippocampus	3,22	0.13	0.94	24	0.22	0.27	24	0.13	0.51
Hypothalamus	3,24	0.12	0.94	26	0.06	0.73	26	0.28	0.15
Pituitary gland	3,14	1.20	0.34	15	0.11	0.66	15	0.17	0.49
Liver	3,22	0.45	0.71	24	0.02	0.88	24	0.28	0.16
11β-Hydroxysteroid dehydrogenase 1 (11βHSD1)									
Hippocampus	3,21	1.24	0.31	23	-0.05	0.8	23	0.08	0.68
Hypothalamus	3,23	0.23	0.87	25	-0.01	0.92	25	0.03	0.87
Pituitary gland	3,16	0.39	0.76	18	0.43	0.06	18	0.26	0.25
Liver	3,22	0.77	0.51	25	0.33	0.63	25	0.22	0.26
11β-Hydroxysteroid dehydrogenase 2 (11βHSD2)									
Hippocampus	3,21	1.95	0.15	23	0.01	0.93	23	-0.07	0.71
Hypothalamus	3,22	1.84	0.16	24	-0.27	0.16	24	-0.04	0.81
Pituitary gland	3,16	0.13	0.93	18	0.52	0.01	18	0.16	0.5
Liver	3,22	0.77	0.52	24	0.21	0.29	24	0.35	0.07
Corticosterone binding globulin (CBG)									
Liver	3,23	22.85	0.02	25	0.06	0.75	25	0.16	0.41
Gonadotropin-inhibitory hormone									
Hypothalamus	3,21	8.76	<0.0001	23	0.03	0.88	23	0.16	0.56

569

570 **Figure 1.**

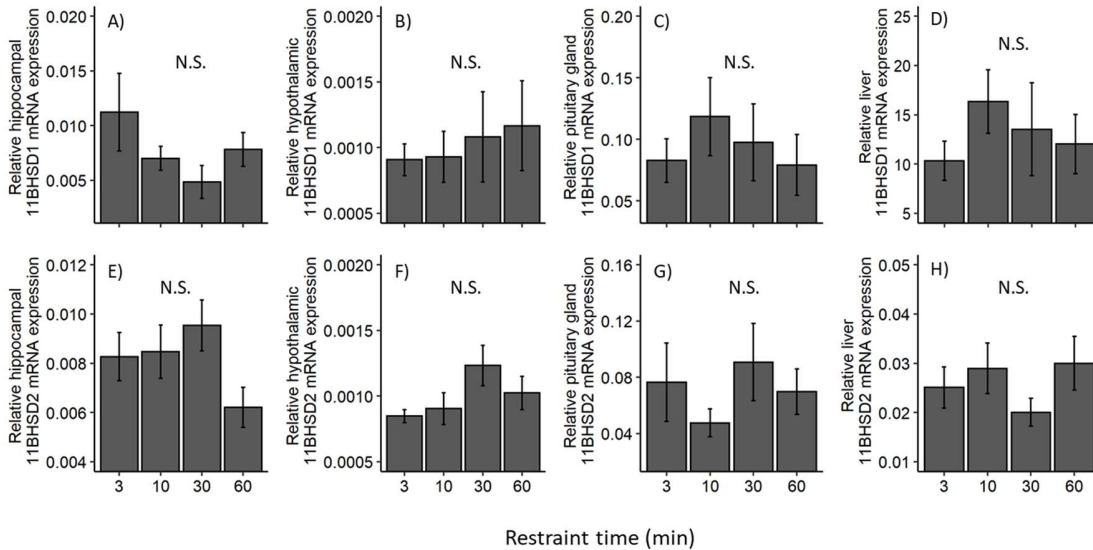
571 Effects of capture restraint stress on the expression of glucocorticoid (GR; A, B, C, D) and
 572 mineralocorticoid (MR; E, F, G, H) receptor mRNA in the hippocampus, hypothalamus, pituitary gland,
 573 and liver from time of capture in male white-crowned sparrows. Data were normalized relative to the
 574 house keeping gene YWHAZ. Letters that are different from one another indicate a significant difference
 575 using contrasts with a Tukey's correction. Values represent means \pm SEM.



576

577 **Figure 2.**

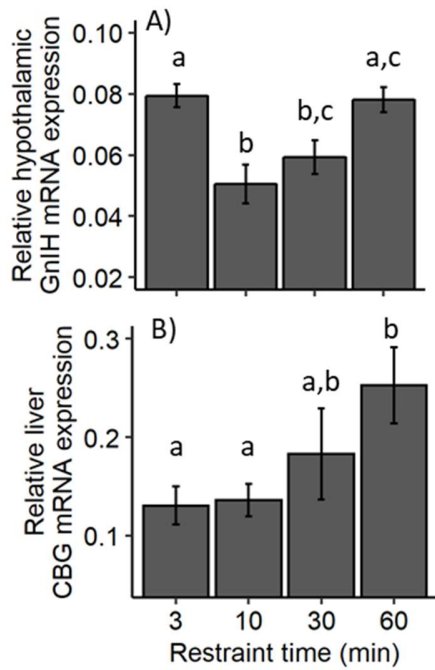
578 Effects of capture restraint stress on the expression of 11 β -hydroxysteroid dehydrogenase 1 (11 β HSD1;
 579 A, B, C, D) and 11 β -hydroxysteroid dehydrogenase 2 (11 β HSD2; E, F, G, H) mRNA in the hippocampus,
 580 hypothalamus, pituitary gland, and liver from time of capture in male white-crowned sparrows. Data were
 581 normalized relative to the house keeping gene YWHAZ. Letters that are different from one another
 582 indicate a significant difference using contrasts with a Tukey's correction. Values represent means \pm SEM.



583

584 **Figure 3.**

585 Effects of restraint stress on the expression of (A) hypothalamic gonadotropin inhibitory hormone (GnIH)
586 and (B) liver corticosteroid binding globulin (CBG) mRNA. Data were normalized relative to the house
587 keeping gene YWHAZ. Letters that are different from one another indicate a significant difference using
588 contrasts with a Tukey's correction. Values represent means \pm SEM.



589

590 Supplemental Figure 1. YWHAZ reference gene expression in hippocampus, hypothalamus, pituitary
591 gland and liver of white crowned sparrows exposed to restraint handling.

