1	Action of Neurotensin, CRH, and RFRP-3 in E2-induced Negative Feedback
2	Control: Studies Using a Mouse ARC Hypothalamic Cell Model
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1 Abstract

The recently established immortalized hypothalamic cell model mHypoA-55 $\mathbf{2}$ possesses characteristics similar to those of Kiss-1 neurons in the arcuate nucleus 3 (ARC) region of the hypothalamus. Here, we show that Kiss-1 gene expression in these 4 cells was downregulated by 17*β*-estradiol (E2) under certain conditions. Both $\mathbf{5}$ 6 neurotensin (NT) and corticotropin-releasing hormone (CRH) were expressed in these 7 cells and upregulated by E2. Stimulation of mHypoA-55 cells with NT and CRH significantly decreased mRNA 8 Kiss-1 expression. А mammalian 9 gonadotropin-inhibitory hormone homolog, RFamide-related peptide-3 (RFRP-3), was also found to be expressed in mHypoA-55 cells, and RFRP-3 expression in these cells 10 was increased by exogenous melatonin stimulation. E2 stimulation also upregulated 11 12RFRP-3 expression in these cells. Stimulation of mHypoA-55 cells with RFRP-3 significantly increased the expression of NT and CRH. Furthermore, melatonin 1314 stimulation resulted in the increase of both NT and CRH mRNA expression in 15mHypoA-55 cells. On the other hand, in experiments using mHypoA-50 cells, which were originally derived from hypothalamic neurons in the anteroventral periventricular 16 nucleus, Kiss-1 gene expression was upregulated by both NT and CRH, although E2 17increased both NT and CRH expression, similarly to the mHypoA-55 cells. 18

Our observations using the hypothalamic ARC cell model mHypoA-55 suggest that NT and CRH have inhibitory effects on Kiss-1 gene expression under the influence of E2 in association with RFRP-3 expression. Thus, these neuropeptides might be involved in E2-induced negative feedback mechanisms.

23

1 Introduction

 $\mathbf{2}$ Neurons in the hypothalamus, especially those that secrete gonadotropin-releasing hormone (GnRH), serve as the final pathway by which the brain 3 regulates gonadotropin secretion [1]. After the discovery of inactivating mutations in the 4 $\mathbf{5}$ kisspeptin receptor (Kiss1R) in families of patients with hypogonadotropic 6 hypogonadism [2, 3], it is generally agreed that hypothalamic Kiss-1 neurons, which 7project to GnRH neurons, control GnRH release through Kiss1R expressed by the GnRH neurons. Therefore, Kiss-1 neurons in the hypothalamus have been defined as 8 9 being positioned at the highest level in the control of the 10 hypothalamic-pituitary-gonadal (HPG) axis. These neurons have been shown to be 11 located in two different regions of the hypothalamus: the arcuate nucleus (ARC) and the anteroventral periventricular (AVPV) region in mammals [4]. Although studies have 12demonstrated a bimodal effect of 17β-estradiol (E2) on the hypothalamus, having both 1314 positive and negative feedback effects on GnRH neurons that do not express estrogen receptor α (ER α) [5], it is now postulated that Kiss-1 neurons within the ARC are the 15center for negative feedback by E2, whereas those in the AVPV are defined as the center 16 of positive feedback. These conclusions are based on the observations that Kiss-1 17expression in the ARC is inhibited by E2, whereas AVPV Kiss-1 expression is 18 stimulated by E2 [6]. 19

Kiss-1 neurons might also play a role as a GnRH pulse generator. Previous studies recorded multiunit activity that correlates with pulsatile secretion of pituitary luteinizing hormone (LH) in a variety of animals [7, 8]. A neuronal population within the ARC, referred to as KNDy neurons, express Kiss-1, neurokinin B (NKB), and dynorphin (Dyn). Kiss-1–expressing KNDy neurons have been shown to generate synchronized oscillatory patterns of activity by receiving autosynaptic excitatory and
inhibitory input from NKB and Dyn [9, 10].

Although Kiss-1 neurons in the ARC and AVPV express and release kisspeptin, 3 these two populations possess distinct characteristics. Owing to the heterogeneous 4 $\mathbf{5}$ nature and complexity of the hypothalamus, investigation into the molecular events 6 involved in E2-induced feedback control in unique neuronal cell populations has been 7 difficult. Recently, a hypothalamic cell model, mHypoA-55, was established from microdissected ARC primary cultures of female-adult-derived murine hypothalamus, 8 which exhibits endogenous Kiss-1 expression as well as ERa and ERB. mHypoA-55 9 10 cells also express NKB and Dyn, suggesting that they represent ARC kisspeptin neurons 11 [11]. On the other hand, mHypoA-50 cells, which were established from microdissected AVPV primary cultures, are also known as a Kiss-1-expressing cell model that 12possesses ER α and ER β . However, although mHypoA-50 cells express tyrosine 1314 hydroxylase, they do not express NKB and Dyn, supporting their identity as putative 15AVPV kisspeptin neurons [11]. Notably, these cell models exhibit different responses to E2 in the regulation of Kiss-1 gene expression. E2 induces an increase in Kiss-1 mRNA 16expression in mHypoA-50 cells, but it downregulates Kiss-1 mRNA expression in 17mHypoA-55 cells under certain experimental conditions [11]. Therefore, the molecular 18events involved in differential E2-mediated regulation, which supposedly occurs in the 1920AVPV and/or ARC region of the hypothalamus, could be examined using these cell 21models.

In this study, we aimed to examine E2-induced negative feedback mechanisms using ARC hypothalamic mHypoA-55 cells. We focused on the action of neurotensin (NT) and corticotropin-releasing hormone (CRH). NT was first isolated from bovine

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hypothalamus in recognition of its potent vascular effects [12]. In mammals, NT is 1 $\mathbf{2}$ abundantly expressed in the central nervous system, with particularly high expression in the hypothalamus, including the AVPV and ARC regions [13, 14], and has been 3 implicated in regulating a diverse repertoire of physiological functions and motivated 4 behaviors including feeding, locomotor activity, social behavior, and reproduction $\mathbf{5}$ 6 [15-17]. CRH is a most important physiological ACTH-releasing factor and is involved 7in the stress response. CRH is mainly produced within the paraventricular nucleus of the hypothalamus and is released at the median eminence from the neurosecretory terminals 8 of these neurons [18]. In addition, CRH neurons are found in many other regions in the 9 brain, including the olfactory bulb, medial preoptic nucleus, and middle hypothalamus 10 11 [19].

We found that NT and CRH might participate in the E2-induced negative feedback regulation of the HPG axis in association with RFamide-related peptide-3 (RFRP-3), a mammalian gonadotropin-inhibitory hormone (GnIH) homolog.

1 Materials and Methods

2 Materials

The following chemicals and reagents were obtained from the indicated sources: GIBCO fetal bovine serum (FBS) (Invitrogen, Carlsbad, CA); Dulbecco's modified Eagle's medium (DMEM), water-soluble E2, penicillin-streptomycin, and melatonin (Sigma-Aldrich Co., St. Louis, MO); and NT and CRH (Life Technologies Japan., Ltd., Tokyo, Japan). RFRP-3 was synthesized with an automated solid-phase peptide synthesizer (PSSM-8; Shimadzu, Kyoto, Japan) and purified by reversed phase high-performance liquid chromatography.

10

11 Cell culture

mHypoA-50 and mHypoA-55 cells were purchased from CEDARLANE 12(Ontario, Canada). The embryonic rat hypothalamic cell line R8 (rHypoE-8) was 13purchased from COSMO BIO CO., LTD. (Tokyo, Japan). Cells were plated in 35-mm 14 15tissue culture dishes and incubated with high-glucose DMEM containing 10% 16 heat-inactivated FBS and 1% penicillin-streptomycin at 37°C under a humidified atmosphere of 5% CO₂ in air. After 24 h, cells were used for each experiment. When 17cells were stimulated by E2, cells were cultured with E2 in phenol red-free DMEM 18 19supplemented with 1% charcoal-stripped FBS (Gemini Bio-Products, West Sacramento, 20 CA). When stimulated with the indicated neuropeptides, cells were incubated without (control) or with the test reagents in high-glucose DMEM containing 1% 2122heat-inactivated FBS and 1% penicillin-streptomycin for the indicated time periods.

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24 Western blot analysis

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Cell extracts were lysed on ice with RIPA buffer (phosphate-buffered saline

[PBS], 1% NP-40, 0.5% sodium deoxycholate, 0.1% sodium dodecyl sulfate) containing 1 0.1 mg/mL phenylmethylsulfonyl fluoride, 30 mg/mL aprotinin, and 1 mM sodium $\mathbf{2}$ orthovanadate, scraped for 20 s, and centrifuged at $14,000 \times g$ for 10 min at 4°C. 3 Protein concentration in the cell lysates was measured using the Bradford method. 4 $\mathbf{5}$ Denatured protein (10 µg per well) was resolved in a 10% sodium dodecyl sulfate 6 polyacrylamide gel electrophoresis (SDS-PAGE) gel according to standard protocols. $\overline{7}$ Protein was transferred onto polyvinylidene difluoride membranes (Hybond-P PVDF, Amersham Biosciences, Little Chalfont, UK), which were blocked for 2 h at room 8 9 temperature in Blotto (5% milk in Tris-buffered saline). Membranes were incubated with anti-kisspeptin antibody (1:500 dilution; Abcam, Cambridge, UK), anti-NT 10 11 antibody (1:200 dilution; Santa Cruz Biotechnology, Inc., Dallas, TX), or anti-CRH antibody (1:200 dilution; Santa Cruz Biotechnology, Inc.) in Blotto overnight at 4°C 1213and washed 3 times for 10 min per wash with Tris-buffered saline/1% Tween. 14 Subsequent incubation with horseradish peroxidase (HRP)-conjugated antibodies was 15performed for 1 h at room temperature in Blotto, and additional washes were performed 16 appropriately. Following enhanced chemiluminescence detection (Amersham Biosciences), membranes were exposed to X-ray film (Fujifilm, Tokyo, Japan). Fetal rat 17brain tissue was used as positive control, and this experimental protocol was approved 18by the animal care and use committee of the Experimental Animal Center for Integrated 1920Research at Shimane University (IZ27-82).

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RNA preparation, reverse transcription, PCR, and quantitative real-time PCR

Total RNA from stimulated cells was extracted using TRIzol-LS (Invitrogen) 23according to the manufacturer's instructions. To obtain cDNA, 1.0 µg total RNA was 24

reverse transcribed using an oligo-dT primer (Promega, Madison, WI) and prepared 1 $\mathbf{2}$ using a First-Strand cDNA Synthesis Kit (Invitrogen) in reverse transcription (RT) buffer. The preparation was supplemented with 10 mM dithiothreitol, 1 mM of each 3 dNTP, and 200 U RNase inhibitor/human placenta ribonuclease inhibitor (Code No. 4 $\mathbf{5}$ 2310; Takara, Tokyo, Japan) in a final volume of 10 µL. The reaction was incubated at 6 37°C for 60 min. For the detection of Kiss-1, NT, and CRH mRNAs, after PCR amplification for Kiss-1 7using primers rat (forward: 5'-ATGATCTCGCTGGCTTCTTGG-3' 8 and reverse: 5'-GGTTCACCACAGGTGCCATTTT-3'), NT (forward: 9 5'-GTGTGGACCTGCTTGTCAGA-3' 10 and reverse: 11 5'-TCATGCATGTCTCCTGCTTC-3'), CRH (forward: 5'-ATCCGCATGGGTGAAGAATACT-3' 12and reverse: 5'-TGGAAGGTGAGATCCAGAGAGA-3') RFRP-3 13and (forward:

14 5'-CAGGGACCAGGAGCCATTTC and reverse: 5'-CTCCTCTCCTCGTTCGCTTTC-3'), 15amplicons were electrophoresed in agarose gels and visualized with ethidium bromide staining. Quantification of Kiss-1, NT, and CRH mRNA was obtained through 16quantitative real-time PCR (ABI Prism 7000; Perkin-Elmer Applied Biosystems, Foster 17City, CA) following the manufacturer's protocol (User Bulletin No. 2) and utilizing 18Universal ProbeLibrary Probes and FastStart Master Mix (Roche Diagnostics, 1920Mannheim, Germany). Using specific primers for rat Kiss-1, NT, CRH, and RFRP-3, the simultaneous measurement of mRNA and GAPDH permitted normalization of the 21amount of cDNA added per sample. For each set of primers, a no-template control was 22included. Thermal cycling conditions were as follows: 10 min denaturation at 95°C, 23followed by 40 cycles of 95°C for 15 s and 60°C for 1 min. Reactions were followed by 24

melting curve analysis (55-95°C). To determine PCR efficiency, a 10-fold serial 1 dilution of cDNA was performed as previously described [20]. PCR conditions were $\mathbf{2}$ optimized to generate >95% PCR efficiency and only those reactions with between 95% 3 and 105% efficiency were included in subsequent analyses. Relative differences in 4 $\mathbf{5}$ cDNA concentration between baseline and experimental conditions were then calculated 6 using the comparative threshold cycle (Ct) method [21]. Briefly, for each sample, a Δ Ct 7was calculated to normalize to the internal control using the following equation: $\Delta Ct =$ $\Delta Ct(gene) - Ct(GAPDH)$. To obtain differences between experimental and control 8 9 conditions, $\Delta\Delta$ Ct was calculated as Δ Ct(sample) – Δ Ct(control). Relative mRMA levels were then calculated using the following equation: fold difference = $2^{\Delta\Delta Ct}$. 10

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12 Statistical analysis

All experiments were repeated independently at least three times. Each experiment in each experimental group was performed using duplicate samples. When we determined the mRNA expression, two samples were assayed in duplicate. Six averages from three independent experiments were statistically analyzed. Data are expressed as mean \pm SEM values. Statistical analysis was performed using Student's *t* test or one-way analysis of variance (ANOVA) with Bonferroni's post hoc test, as appropriate. *P* < 0.05 was considered statistically significant.

1 Results

mHypoA-55 cells possess characteristics similar to those of kisspeptin neurons in the ARC region

We used the recently established cell line mHypoA-55 as a model of 4 hypothalamic Kiss-1-expressing cells in the ARC region. As previously demonstrated, $\mathbf{5}$ 6 mHypoA-55 cells express both Kiss-1 mRNA and the kisspeptin protein. mHypoA-50 7 cells, which are derived from Kiss-1–expressing cells in the AVPV region, also express both Kiss-1 mRNA and kisspeptin. Although both cell models express kisspeptin, these 8 9 cells are distinct. mHypoA-55 cells express both Tac2 (which encodes NKB) and Dyn genes, but mHypoA-50 cells do not express these genes (Fig. 1A). The responses to E2 10 11 in these cell models were also distinct. A previous study demonstrated that Kiss-1 gene expression was increased by E2 at 24 h in mHypoA-50 cells, whereas it was reduced by 12E2 at 4 h in mHypoA-55 cells [11]. Similar to the previous results, Kiss-1 mRNA 1314 expression in mHypoA-55 cells was not increased by E2; rather, it was significantly reduced at 4 h after the addition of E2 and returned to the control level at 24 h (F(2,6) =1520.38, P = 0.0021) (Fig. 1B). In contrast, E2 treatment significantly increased Kiss-1 16mRNA expression up to 3.03 ± 0.54 -fold at 24 h in the mHypoA-50 AVPV cell model 17(F(2,15) = 7.025, P = 0.0070) (Fig. 1C). 18

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20 Effect of NT on Kiss-1 mRNA expression in mHypoA-55 cells

The hypothalamic model mHypoA-55 cells exhibit a heterogeneous character; these cells express NT mRNA and its protein product in addition to Kiss-1, NKB, and Dyn. NT expression was also observed in mHypoA-50 cells (Fig. 2A). NT expression within mHypoA-55 cells was upregulated in the presence of E2. When mHypoA-55 cells were stimulated with E2 for 24 h, NT expression within these cells was significantly increased 1.71 ± 0.19 -fold (F(2,6) = 8.16, P = 0.019). A significant increase in NT mRNA expression was not observed by stimulation with E2 for 4 h (the time at which Kiss-1 mRNA expression was significantly reduced by E2 treatment in mHypoA-55 cells) (Fig. 2B). When mHypoA-55 cells were stimulated by NT, Kiss-1 mRNA expression was significantly reduced (F (3,8) = 9.92, P = 0.0045). At 10 nM NT, Kiss-1 mRNA expression was reduced to almost half that of untreated cells (Fig. 2C).

8

9 Effect of E2 on CRH expression in mHypoA-55 cells

CRH 10 is а hypothalamic neuropeptide that controls the 11 hypothalamic-pituitary-adrenal axis. Accumulating evidence suggests the importance of this peptide in reproductive function [22, 23]. CRH mRNA was detected by RT-PCR 12from the extracts of mHypoA-55 ARC and mHypoA-50 AVPV cells. CRH protein was 1314 also expressed in these cells (Fig. 3A). Next, we examined the role of CRH in 15mHypoA-55 cells. As observed in NT experiments, CRH expression in mHypoA-55 was also influenced by E2. By 24 h, but not 4 h of incubation with E2, CRH mRNA 16levels in mHypo-A55 cells were significantly increased by 5.89 ± 1.87 -fold (F(2,6) = 175.93, P = 0.038) (Fig. 3B). When mHypoA-55 cells were stimulated by CRH, Kiss-1 18 mRNA expression in these cells was significantly reduced to 0.62 ± 0.17 -fold at 100 nM 1920versus the untreated control cells (F(3,8) = 8.64, P = 0.0069) (Fig. 3C), which was similar to the effect of NT. 21

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23 **RFRP-3 expression in mHypoA-55 cells and the effect of melatonin**

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The avian homolog of RFRP-3, GnIH, was first identified as neuropeptide that

1	inhibits gonadotropin release in birds [24]. We found that the RFRP-3 gene is expressed
2	in mHypoA-55 cells (Fig. 4A). Similar to the phenomenon observed in birds [25], 10
3	μM melatonin stimulation increased RFRP-3 mRNA expression 1.93 \pm 0.39-fold in
4	mHypoA-55 cells ($F(3,12) = 4.69$, $P = 0.022$) (Fig. 4B). In addition, RFRP-3 expression
5	in mHypoA-55 cells was slightly but significantly upregulated by E2 stimulation: 1.55 \pm
6	0.19-fold compared with unstimulated cells (t(1.94) = 2.74, $P = 0.017$) (Fig. 4C).

7

8 Effect of RFRP-3 stimulation on the expression of NT and CRH in mHypoA-55 9 cells

Next, we examined how RFRP-3 affects the expression of NT and CRH genes 10 11 in mHypoA-55 cells. mHypoA-55 cells were simulated with increasing concentrations 12of RFRP-3 and cultured for 24 h, and then NT and CRH mRNA expression was examined. NT mRNA expression was significantly increased by RFRP-3 1.94 \pm 13140.24-fold at 100 nM (F(6,12) = 6.35, P = 0.0080) (Fig. 5A). CRH mRNA expression 15was also stimulated by RFRP-3. At all tested concentrations (10 nM, 100 nM, and 1 μ M), RFRP-3 significantly increased CRH mRNA expression (F(3,12) = 3.93, P = 160.036), and was increased 2.39 ± 0.72 -fold at 10 nM (Fig. 5B). Furthermore, we found 17that melatonin, which had the ability to stimulate RFRP-3 expression, increased the NT 18 and CRH gene expression by 1.55 ± 0.21 -fold and 2.96 ± 0.54 -fold, respectively, both 1920of which were statistically significant (NT: t(2.13) = 3.96, P = 0.0083; CRH: t(2.13) =3.63, P = 0.011) (Fig. 6A and B). 21

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Effect of NT and CRH on the expression of the Kiss-1 gene in the AVPV cell model,
 mHypoA-50

1	As shown above, similar to the mHypoA-55 ARC Kiss-1-expressing cell
2	model, AVPV model mHypoA-50 cells also express NT and CRH. Lastly, we examined
3	how these neuropeptides affect Kiss-1 gene expression in mHypoA-50 cells. When
4	mHypoA-50 cells were stimulated with E2, NT expression within these cells was
5	significantly increased 1.71 \pm 0.19-fold at 24 h (F(2,6) = 12.87, P = 0.0068) (Fig. 7A).
6	This observation was similar to those observed in ARC model mHypoA-55 cells.
7	However, in contrast with NT's inhibition of Kiss-1 gene expression in mHypoA-55
8	cells, compared with the unstimulated control, 10 nM NT increased Kiss-1 mRNA
9	expression 3.63 ± 1.45 -fold in mHypoA-50 cells (t(2.13) = 2.19, $P = 0.047$) (Fig. 7B).
10	Similarly, CRH mRNA expression in mHypoA-50 cells was increased by E2 stimulation,
11	as was observed in mHypoA-55 cells. By incubation with E2, CRH mRNA levels in
12	mHypo-A50 were significantly increased by 3.2 \pm 0.38-fold at 4 h and 3.74 \pm 0.93-fold
13	at 24 h_(F(2,6) = 6.22, $P = 0.035$)_(Fig. 7C). In mHypo-A50 cells, Kiss-1 mRNA
14	expression was significantly increased by stimulating the cells with CRH (1.75 \pm
15	0.29-fold) (t(1.86) = 2.61, $P = 0.016$) (Fig. 7D). This CRH effect in mHypoA-50 cells
16	was completely the opposite of that observed in mHypoA-55 cells.

1 **Discussion**

 $\mathbf{2}$ Studies on the cellular mechanisms involving the E2-induced positive and negative feedback mechanisms are somewhat difficult because the hypothalamus 3 consists of a complex, heterogeneous array of neuronal phenotypes. Development of the 4 $\mathbf{5}$ hypothalamic Kiss-1-expressing cell models mHypoA-55 and mHypo-A50 has enabled 6 the examination of the local mechanisms of E2-induced feedback control that occur in 7 specific regions of the hypothalamus in rodents. At present, accumulating evidence supports the concept that the hypothalamic Kiss-1 neurons in the ARC region generate a 8 9 pulsatile mode of GnRH secretion and mediate the negative feedback action of sex steroids [6, 26]. Conversely, Kiss-1 neurons in the AVPV region of the hypothalamus 10 11 are considered to control the surge mode of GnRH secretion evoked by the positive 12feedback action of E2 [27, 28]. These conclusions are based on the observations that Kiss-1 expression in the ARC is inhibited by E2, whereas AVPV Kiss-1 expression is 1314 stimulated by E2 [6].

15In this study, we mainly utilized mHypo-A55 cells as a model for the ARC region of the hypothalamus and examined the possible mechanisms of the E2-induced 16 negative feedback control. As reported previously [11], mHypoA-55 cells have 17characteristics similar to those of Kiss-1 neurons in the ARC region. These cells 18 19 coexpress NKB and Dyn, and significant repression of Kiss-1 expression was observed 20under certain conditions (4 h after E2 stimulation) [11]. Similar to the phenomenon observed in the previous study, Kiss-1 expression was not increased by E2; rather, 21significant repression of Kiss-1 was observed at 4 h in our mHypoA-55 cells. In contrast, 22E2 significantly increased Kiss-1 expression in AVPV model mHypoA-50 cells. 23Therefore, we used mHypoA-55 cells as a model to study the E2-induced negative 24

1 feedback mechanisms.

 $\mathbf{2}$

NT and CRH have been reported to have some influence on the HPG axis. 3 Several lines of evidence implicate NT-producing cells as a target for the action of E2 to 4 $\mathbf{5}$ trigger the GnRH/LH surge. E2 induces the expression of the NT gene in AVPV lesions 6 in rats [29, 30]. In addition, it was reported that administration of NT directly into the 7 rat medial preoptic area evoked LH secretion, whereas antiserum directed against NT delivered into this region blocked the LH surge [31, 32]. These observations suggest NT 8 9 has some effect on E2-induced positive feedback mechanisms. On the other hand, a number of studies suggest CRH as a prime candidate for stress-induced suppression of 10 11 the GnRH pulse generator [23, 33], although CRH can stimulate LH secretion and 12increases GnRH pulse amplitude in sheep [34, 35]. CRH expression in the hypothalamus has also been reported to be increased after administration of E2 in 1314ovariectomized monkeys [36].

15In the hypothalamic ARC cell model, mHypoA-55, we confirmed that NT and 16CRH mRNA expression was upregulated by E2, and these observations were consistent with previous reports that E2 could positively control the expression of these 17neuropeptides. Interestingly, NT significantly reduced Kiss-1 gene expression in the 18 19 mHypoA-55 cells. Furthermore, similar to the effect of NT, exogenous CRH 20administration reduced Kiss-1 gene expression in mHypoA-55 cells. This is quite 21similar to the phenomenon observed in a previous in vivo study, which showed that CRH could decrease Kiss-1 expression in the medial preoptic area and ARC in rats [37]. 22Our observation that NT and CRH expression was upregulated by E2 implies that NT 23and CRH could be involved in E2-induced negative feedback regulation of the pulsatile 24

GnRH release in the hypothalamus. In contrast, exogenous NT and CRH administration 1 $\mathbf{2}$ differently affected the AVPV cell model mHypoA-50; both NT and CRH increased Kiss-1 gene expression in mHypoA-50 cells, although these peptides were upregulated 3 by E2 in mHypoA-50 cells. These observations suggest that NT and CRH have a 4 completely different role in Kiss-1 neurons in the AVPV region. In addition, these 5 6 results reconfirm that the Kiss-1-expressing cells exhibit different characteristics in 7 each cell model. These results concerning the distinct action of NT and CRH in mHypoA-55 and mHypoA-50 imply that the E2-mediated increase in NT and CRH 8 9 expression stimulates the production of Kiss-1 in the AVPV region, ultimately initiating the surge in GnRH secretion from GnRH neurons, as previous studies have suggested. 10 Indeed, a previous study reported that close apposition of NT- and Kiss-1-expressing 11 cells was observed, although NT and Kiss-1 mRNAs were not coexpressed in the mouse 12AVPV neurons [38]. In addition, it was reported that kisspeptin neurons in both the 1314ARC and AVPV express the GnRH receptor and close apposition of GnRH 15immunoreactive fibers was observed on some Kiss-1 neurons in both regions [39]. Our current observations imply that NT and CRH are involved in the E2-induced positive 16and negative feedback mechanism by differentially changing the Kiss-1 gene expression 17in the AVPV and ARC regions of the hypothalamus. However, we should note that our 1819 observations do not completely support this hypothesis because an increasing effect of 20E2 on NT and CRH mRNA expression was not observed at 4 h of E2 treatment, the time at which Kiss-1 mRNA expression was significantly reduced by E2 treatment in 21mHypoA-55 cells. Hypothetically, if E2-induced NT or CRH expression was involved 22in the reduction of Kiss-1 gene expression in mHypoA-55 cells, E2-induced reduction 23of Kiss-1 gene expression should have occurred at 24 h after stimulation. Our present 24

1 data do not directly address the mechanism(s) underlying the time lag of the 2 E2-stimulated increase in NT and CRH mRNA expression or the E2-mediated reduction 3 of Kiss-1 gene expression in mHypoA-55 cells, both of which will likely be 4 investigated in future studies.

In this study, we observed that mHypoA-55 cells express RFRP-3, a $\mathbf{5}$ 6 mammalian homolog of GnIH. In mice, cell bodies of GnIH neurons are located in the 7 dorsomedial hypothalamic nucleus [40], and its neuronal fibers are in close proximity to GnRH and kisspeptin neurons that express the GnIH receptor [41]. Because 8 mHypoA-55 cells express the RFRP-3 gene, it is plausible that mHypoA-55 cells are 9 derived from GnIH-expressing neurons in the ARC region of hypothalamus. RFRP-3 10 11 mRNA expression within mHypoA-55 cells was upregulated by melatonin stimulation 12and this observation was similar to that observed in GnIH neurons in birds [25], suggesting that RFRP-3-expressing mHypoA-55 cells have characteristics similar to 1314 those of GnIH neurons in birds. Interestingly, RFRP-3 has the ability to stimulate the 15expression of NT and CRH, both of which could repress Kiss-1 gene expression. These observations imply that NT and CRH as well as RFRP-3 might participate in the 16negative feedback control, supposedly by repressing Kiss-1 gene expression. GnIH 17neurons have been shown to express ER α and respond to E2 [40]. Because we observed 18 19 that RFRP-3 expression in mHypoA-55 cells was upregulated by E2, we can speculate on the possible role of RFRP-3 in E2-induced negative feedback mechanisms. There are 20several published reports that indicate the possible involvement of GnIH in the 21mechanism of E2-induced positive feedback control based on the observation that E2 22suppresses GnIH gene expression [41-43]. RFRP-3 might be the gatekeeper of the 23E2-induced negative feedback control, but we speculate that RFRP-3-associated 24

E2-independent mechanisms might be involved in the suppression of the Kiss-1 gene 1 $\mathbf{2}$ through NT and CRH. It has been shown that environmental stress can increase the expression of GnIH and suppress reproduction in vertebrates [44]. Furthermore, 3 glucocorticoids can directly control GnIH expression [45]. Because melatonin could 4 regulate the expression of RFRP-3, the photoperiodic milieu or eye activity may be 5 6 involved in the reduction of Kiss-1 gene expression by increasing NT or CRH. Our 7 results showing that melatonin stimulation increased the expression of NT and CRH mRNAs support this hypothesis. However, we should keep in mind that the effect of 8 9 RFRP-3 or melatonin differs depending on the type of experimental model. GnIH and RFRP-3 have been shown to inhibit GnRH neuron activity and gonadotropin release in 10 11 several seasonal animals (sheep, hamster, and quail) and non-seasonal species such as 12rat and mouse. In contrast, no evidence of RFRP-3 directly modulating LH secretion was observed in ewes [46, 47]. Furthermore, recent studies using male Syrian and 1314 Siberian hamsters demonstrated the stimulatory effects of RFRP-3 on the reproductive 15axis [48, 49]. In the female Syrian hamster, RFRP-3 works alongside Kiss-1 neurons to maintain proper synchronization of reproductive activity with the time of day, the stage 16 of the estrous cycle, and the seasonal changes in photoperiods [50]. RFRP-3 controls 17seasonal reproduction [51] and also controls feeding and reproductive behaviors [52]. 1819 Using a Kiss-1-expressing cell model for the ARC region of the hypothalamus, we 20propose the possible involvement of E2-induced or RFRP-3-associated NT and CRH expression in the regulation of Kiss-1 gene expression in the ARC hypothalamic region 21that governs negative feedback mechanisms in the HPG axis. We used immortalized 22hypothalamic cell models, and it should be noted that clonal cell lines come with 23

connections and architecture. It is still unclear whether the phenomenon observed in this 1 study occurs in vivo. NT, CRH, and RFRP-3 are expressed in the hypothalamus and $\mathbf{2}$ their neuronal fibers indeed exist in the ARC region in each experimental model [39, 53, 3 54]. However, coexpression of these peptides in ARC Kiss-1 neurons is uncertain. 4 $\mathbf{5}$ Nevertheless, we were able to dissect the molecular signaling events controlling 6 Kiss-1/NT/CRH and RFRP-3 neurons using this cell model. Furthermore, these models may allow for the investigation of paracrine and autocrine regulation of these 7 neuropeptides. 8

We summarized our current results in Figure 8. In this study, we used an ARC 9 hypothalamic cell model in which Kiss-1 gene expression was repressed by E2 under 10 11 certain conditions (4 h after E2 stimulation). CRH and NT expression was upregulated by E2 and we found that NT and CRH negatively regulated Kiss-1 gene expression in 12these cells. Because RFRP-3, which was regulated by melatonin or E2, could induce the 1314 expression of NT and CRH in these cells, RFRP-3 might be involved in the suppression 15of Kiss-1 gene expression in the ARC region of the hypothalamus. Although NT and CRH were similarly increased by E2, these two peptides increased the Kiss-1 gene 16 expression in an AVPV hypothalamic cell model. Our findings might provide clues 17regarding the feedback mechanism of E2 in the hypothalamus. 18

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32

1 Figure Legends

 $\mathbf{2}$

3 Figure 1

4 Hypothalamic mHypoA-55 and mHypoA-50 cell characteristics and the effect of E2 on
5 Kiss-1 mRNA expression.

(A) Cell lysates (10 µg) from mHypoA-55 cells and mHypoA-50 cells were analyzed by 6 7SDS-PAGE followed by immunoblotting and incubation with antibodies against kisspeptin. The bands were visualized using HRP-conjugated secondary antibody. (B) 8 9 RT-PCR analysis of Kiss-1, NKB (Tac2), and Dyn gene expression in mHypoA-55 and mHypoA-50 cells. Total RNA was prepared and RT-PCR was carried out for 40 cycles 10 11 using NKB- (Tac2) and Dyn-specific primers. PCR products were resolved in a 1.5% 12agarose gel and visualized with ethidium bromide staining. mHypoA-55 cells (B) and mHypoA-50 cells (C) were stimulated with 100 nM E2 for 4 and 24 h, after which 1314 mRNA was extracted and reverse transcribed. Kiss-1 mRNA levels were measured by 15quantitative real-time PCR. Results are expressed as the fold induction over unstimulated cells and presented as mean ± SEM values of three independent 16 experiments, each performed with duplicate samples. **P < 0.01 vs. control. Statistical 17significance was determined by one-way ANOVA with Bonferroni's post hoc test. 18

19

20 **Figure 2**

Effect of E2 on NT mRNA expression and the effect of NT on Kiss-1 mRNA expression
in mHypoA-55 cells.

(A) NT mRNA and its protein product were expressed in mHypoA-55 cells. Total RNA
 from mHypoA-55 and mHypoA-50 cells was prepared and RT-PCR was carried out for

40 cycles using an NT-specific primer. PCR products were resolved in a 1.5% agarose 1 gel and visualized with ethidium bromide staining. Cell lysates (10 µg) from $\mathbf{2}$ mHypoA-55 cells and mHypoA-50 cells were analyzed by SDS-PAGE followed by 3 immunoblotting and incubation with antibodies against NT. The bands were visualized 4 $\mathbf{5}$ using HRP-conjugated secondary antibody. (B) mHypoA-55 cells were stimulated with 6 100 nM E2 for 4 and 24 h, after which mRNA was extracted and reverse transcribed. 7 NT mRNA levels were measured by quantitative real-time PCR. (C) mHypoA-55 cells were stimulated with indicated concentrations of NT for 24 h, after which mRNA was 8 9 extracted and reverse transcribed. Kiss-1 mRNA levels were measured by quantitative real-time PCR. Results are expressed as the fold induction over unstimulated cells and 10 11 presented as mean ± SEM values of three independent experiments, each performed with duplicate samples. **P < 0.01, *P < 0.05 vs. control. Statistical significance was 12determined by one-way ANOVA with Bonferroni's post hoc test. 13

14

15

16 Figure 3

Effect of E2 on CRH mRNA expression and the effect of CRH on Kiss-1 mRNA
expression in mHypoA-55 cells.

(A) Total RNA from mHypoA-55 and mHypoA-50 cells was prepared and RT-PCR
was carried out for 40 cycles using a CRH-specific primer. PCR products were resolved
in a 1.5% agarose gel and visualized with ethidium bromide staining. Cell lysates (10
µg) from mHypoA-55 cells and mHypoA-50 cells were analyzed by SDS-PAGE
followed by immunoblotting and incubation with antibodies against CRH. The bands
were visualized using HRP-conjugated secondary antibody. (B) mHypoA-55 cells were

stimulated with 100 nM E2 for 4 and 24 h, after which mRNA was extracted and 1 $\mathbf{2}$ reverse transcribed. CRH mRNA levels were measured by quantitative real-time PCR. (C) mHypoA-55 cells were stimulated with indicated concentrations of CRH for 24 h, 3 after which mRNA was extracted and reverse transcribed. Kiss-1 mRNA levels were 4 $\mathbf{5}$ measured by quantitative real-time PCR. Results are expressed as the fold induction 6 over unstimulated cells and presented as mean ± SEM values of three independent experiments, each performed with duplicate samples. **P < 0.01, *P < 0.05 vs. control. 7 Statistical significance was determined by one-way ANOVA with Bonferroni's post hoc 8 9 test.

10

11 Figure 4

RFRP-3 expression and the effect of melatonin or E2 on its gene expression in
 mHypoA-55 cells.

14 (A) Total RNA from mHypoA-55 cells was prepared and RT-PCR was carried out for 1540 cycles using an RFRP-3-specific primer. PCR products were resolved in a 1.5% agarose gel and visualized with ethidium bromide staining. (B) mHypoA-50 cells were 16 stimulated with indicated concentrations of melatonin for 24 h, after which mRNA was 17extracted and reverse transcribed. RFRP-3 mRNA levels were measured by quantitative 18 real-time PCR. (C) mHypoA-55 cells were stimulated with 100 nM E2 for 24 h, after 1920which mRNA was extracted and reverse transcribed. RFRP-3 mRNA levels were measured by quantitative real-time PCR. Results are expressed as the fold induction 21over unstimulated cells and presented as mean ± SEM values of three independent 22experiments, each performed with duplicate samples. *P < 0.05 vs. control. Statistical 23significance was determined by Student's t test or one-way ANOVA with Bonferroni's 24

1 post hoc test.

- 2
- 3

4 Figure 5

5 Effect of RFRP-3 on the expression of NT and CRH mRNAs in mHypoA-55 cells.

6 mHypoA-50 cells were stimulated with indicated concentrations of RFRP-3 for 24 h, 7 after which mRNA was extracted and reverse transcribed. NT (A) and CRH (B) mRNA 8 levels were measured by quantitative real-time PCR. Results are expressed as the fold 9 induction over unstimulated cells and presented as mean \pm SEM values of three 10 independent experiments, each performed with duplicate samples. ***P* < 0.01, **P* < 11 0.05 vs. control. Statistical significance was determined by one-way ANOVA with 12 Bonferroni's post hoc test.

13

14 Figure 6

15 Effect of melatonin on the expression of NT and CRH mRNAs in mHypoA-55 cells.

16 mHypoA-50 cells were stimulated with 10 nM melatonin for 24 h, after which mRNA 17 was extracted and reverse transcribed. NT (A) and CRH (B) mRNA levels were 18 measured by quantitative real-time PCR. Results are expressed as the fold induction 19 over unstimulated cells and presented as mean \pm SEM values of three independent 20 experiments, each performed with duplicate samples. **P < 0.01, *P < 0.05 vs. control. 21 Statistical significance was determined by Student's *t* test.

22

23 Figure 7

24 Effect of E2 on NT and CRH mRNA expression and the effect of these peptides on

1 Kiss-1 mRNA expression in the AVPV model mHypoA-50 cells.

 $\mathbf{2}$ The AVPV hypothalamic cell model mHypoA-50 was stimulated with 100 nM E2 for 4 and 24 h, after which mRNA was extracted and reverse transcribed. NT (A) and CRH 3 (C) mRNA levels were measured by quantitative real-time PCR. mHypoA-50 cells were 4 $\mathbf{5}$ stimulated with 10 nM NT (B) and 100 nM CRH (D) for 24 h, after which mRNA was 6 extracted and reverse transcribed. Kiss-1 mRNA levels were measured by quantitative 7real-time PCR. Results are expressed as the fold induction over unstimulated cells and presented as mean ± SEM values of three independent experiments, each performed 8 with duplicate samples. **P < 0.01, *P < 0.05 vs. control. Statistical significance was 9 determined by Student's t test or one-way ANOVA with Bonferroni's post hoc test. 10 11

12

13 **Figure 8**

Schematic summary of the possible involvement of NT and CRH in the negativefeedback regulation by E2.

In mHypoA-55 AVPV Kiss-1–expressing cells, CRH and NT expression was increased
by E2, and these peptides in turn negatively regulated Kiss-1 gene expression.
Melatonin and E2 increased the expression of RFRP-3 in these cells, and RFRP-3
increased the expression of NT and CRH.