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Developmental profile and sexually dimorphic expression of Kiss1 and Kiss1r in the fetal mouse brain

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INTRODUCTION

The hypothalamic-pituitary-gonadal (HPG) axis is a complex neuroendocrine circuit responsible for controlling physiological and behavioral reproductive function. The classical description of the circuit begins with gonadotropin releasing hormone (GnRH) neurons, which reside in the basal forebrain/hypothalamus, secreting GnRH into the hypophyseal portal vasculature where it is transported to gonadotropes in the anterior pituitary (1, 2). At least one other cell type is now described as a regulatory component of this circuitry (3). Cells that express the metastasis suppressor gene Kiss1, whose protein product is commonly known as kisspeptin (KISS1), reside in and around two specific locations in the hypothalamus: the rostral periventricular portion of the pre-optic area (POA; sometimes referred to as the RP3V for the rostral periventricular area of the third ventricle), and the caudal region in and around the arcuate nucleus (ARC) (4, 5). KISS1 stimulates GnRH neuron activity and Kiss1/KISS1 expression and release is regulated by circulating gonadal hormones (6, 7). All evidence to date indicates that cells that synthesize KISS1 are functionally upstream of GnRH neurons.

Much effort has gone into characterizing the role played by Kiss1 in the HPG axis. Work with targeted disruption of the genes encoding KISS1 or its cognate receptor KISS1R has shown that KISS1/KISS1R is essential for puberty and adult reproductive competence (8–10). Two populations of kisspeptin neurons have been identified. One population of neuronal cell bodies resides in the RP3V and is responsible for mediating the pre-ovulatory GnRH/LH surge and positive feedback actions of estradiol, while the more caudal population around the ARC is responsible for controlling the oscillatory GnRH pulses and negative feedback actions of estradiol (11–13).

Data has revealed that in pre-pubertal and adult animals Kiss1 expression is regulated by estradiol and testosterone (7). Interestingly, the regulation of Kiss1 is opposite in the different regions that contain Kiss1 neurons. In the RP3V, steroid feedback is positive and up-regulates Kiss1 and in the ARC steroid feedback is...
negative and decreases Kiss1 (14). Several approaches involving genetic modifications have been used to study hormonal influences on Kiss1, including mutations that preclude GnRH synthesis (15), and those that preclude estradiol synthesis (16). The current study takes advantage of transgenic mice in which the steroidogenic factor-1 (Sf1) gene was disrupted. These Sf1 knockouts (KO) mice do not develop fetal gonads and adrenal glands, and as such there is no endogenous fetal sex-steroid production (17). This enables us to determine if Kiss1 levels are regulated by sex steroid in the fetal brain. Our hypothesis is that if gonadal steroids regulate fetal ARCl Kiss1, Sf1 disrupted (KO) XY mice (that develop as phenotypic females) should have more Kiss1 than wild-type (WT) XY, and display expression levels similar to XX mice.

The goal of the current research was to determine the expression pattern of Kiss1 during fetal development and pre-pubertally, as well as to assess Kiss1 levels in fetal gonadal mice. To accomplish this, both in situ hybridization (ISH) using digoxigenin (DIG)-labeled riboprobes and real-time PCR quantitative reverse transcription real-time PCR (QPCR) were used as complementary approaches to assess regional localization and expression levels, respectively, in brain tissue collected from embryonic day 13 (E13) to post-natal day 35 (P35). Expression of Kiss1 and KissIr was detected at E13 and maintained through puberty. Immunohistochemistry (IHC) in fetal and adult tissue revealed a Kiss1 expression pattern similar to that of Kiss1, indicating mRNA is translated into biologically active protein in early development. A sex difference in Kiss1 expression was seen at specific fetal, postnatal, and peri-pubertal ages, and levels in females always showed significantly higher mRNA levels than males. Examining Kiss1 in fetal brain tissue collected from agonadal Sf1 KO mice, revealed Kiss1 mRNA expression in XY KO mice resembled WT XX more than WT XY mice, supporting the hypothesis that the differentiated gonad regulates sexual dimorphism in Kiss1 expression even prior to birth.

MATERIALS AND METHODS

ANIMALS

GnRH-eGFP (17) and Sf1 KO (18) mice were housed in the Painter Center of Laboratory Animal Resources at Colorado State University and maintained in plastic cages with aspen bedding (autoclaved Sani Chips, Harlan Teklad, Madison, WI, USA) and environmental enrichments on a 14:10 h light-dark cycle with free access to food (#8640, Harlan Teklad, Madison, WI, USA) and tap water. Animal care and handling was in accordance with the Colorado State University Animal Care and Use Committee guidelines.

For fetal tissue collections, female and male mice were housed together overnight, and the following day considered to be embryonic day 0 (E0) if vaginal plugs were observed. At the appropriate age, pregnant dams were deeply anesthetized with ketamine/xylazine (80 and 8 mg/kg, respectively), embryos were removed individually by Cesarean section, and a crown-rump-length measurement was taken to verify gestational age (approximately 10 mm at E13, 14 mm at E15, and 19 mm at E17) (19). GnRH-eGFP mice were homozygous for eGFP (CBB6/F1 background), and heterozygous Sf1 mice (C57BL/6 background) were bred to produce WT and KO embryos. Tissue from each fetus was collected prior to perfusion for genotyping PCR using primers for Sry to determine genetic sex, and primers for Sf1 to identify Sf1 KO animals (20). After removal, each pup was perfused transcardially with 2 ml 4% paraformaldehyde in 0.1 M phosphate buffer (PB; pH = 7.4) using a hand held 10 ml syringe. Heads were post-fixed overnight in fresh perfusion fixative then stored at 4°C in 0.1 M PB prior to sectioning.

For post-natal tissues, post-natal day (P) 12 and P35 animals were anesthetized with ketamine/xylazine (80 and 8 mg/kg, respectively) and perfused with 10 ml Heparin/Saline followed by 10 ml 4% paraformaldehyde. Heads/brains were post-fixed overnight as above and stored in 0.1 M PB prior to sectioning.

PROBES FOR IN SITU HYBRIDIZATION

The templates for generating DIG-labeled riboprobes to Kiss1 and KissIr were obtained from Invitrogen Corporation as cDNAs in the vector pT7T3-Pac, and prepared using DIG RNA labeling mix (Roche Applied Sciences #11277073910) according to manufacturer’s instructions. Antisense riboprobes to Kiss1 were transcribed from an EcoRI-linearized cDNA (GenBank accession #AA023588) that includes the entire kisspeptin pre-protein coding sequence (base pairs 38–416 of reference sequence NM_178260). KissIr antisense riboprobes were generated from EcoRI-linearized cDNA (accession #BF470621) complementary to base pairs 1716–2842 of KissIr reference sequence NM_053244), representing nearly the entire KissIr coding sequence with the exception of 234 base pairs within alternatively spliced exon 4. Sense probes were generated from the same plasmids linearized with NotI. No reaction product was observed in sections incubated with sense probes using ISH.

IN SITU HYBRIDIZATION

In situ hybridization was performed as described previously (21) using free-floating tissue sections. Brains were embedded in 5% agarose containing 1% diethyl pyrocarbonate (DEPC; Sigma, D5758) and sectioned at 100 µm using a vibrating microtome (Leica VT1000s) and collected in 0.05 M phosphate buffered saline (PBS) containing 1% DEPC. All sections from fetal brains were collected in one mesh-bottomed container (referred to as a boat) while sections from post-natal brains were alternated between two boats. Sections were then treated with 6% hydrogen peroxide in 0.05 M PB containing 1% Tween-20 and 1% DEPC (PBT) for 1 h followed by three 5 min washes in PBT. After washing, sections were treated with 10 µg/ml proteinase K (Sigma, P2308) in PBT for 15 min, 10 min in 2 mg/ml glycine in PBT, and two 5 min washes in PBT. Next, sections were post-fixed in 4% paraformaldehyde/0.2% glutaraldehyde in PBT for 20 min and washed twice for 5 min in PBT. All incubations and washes up to this point were done on a shaker at room temperature. Following post-fixing, sections were transferred to scintillation vials containing 2 ml of 50% formamide in saline-sodium citrate (SSC; Sigma, S6639) buffer containing 8.8 U/ml heparin (Sigma, H9399), 0.05 mg/ml yeast tRNA (Sigma, R5636), and 0.024 mg/ml dextran sulfate (Sigma, D8906) (collectively pre-hybridization solution) for 1 h shaking at 60°C. DIG labeled riboprobes (1 µg/ml) were denatured by incubating for 5 min in an 85°C water bath and added to the vials containing the sections. Probes were hybridized overnight on a shaker at 60°C.
The following day, sections were transferred back into boats and washed three times for 30 min in a 50% formamide/25% SSC solution, then three times for 30 min in 50% formamide/10% SSC (all while shaking at 60°C). Sections were then washed three times for 5 min in Tris buffered saline (TBS) containing 1% Tween-20 (TBST) then pre-blocked in 10% sheep serum in TBST for 1 h (shaking at room temperature). Sections were then incubated overnight (while shaking at 4°C) in a solution of 1% sheep serum in TBST containing alkaline phosphatase conjugated anti-DIG antibody (Roche, 11093274910) at a concentration of 1:2000.

On the third day, sections were washed three times for 5 min, then five times for 1 h in TBST on a shaker at room temperature, and incubated overnight at 4°C in TBST. On the final day, sections were washed at room temperature three times for 15 min in a solution of 0.1 M NaCl, 0.1 M Tris (pH = 9.5), 0.05 M MgCl₂, and 1% Tween-20 (collectively NTMT). Sections were then incubated on a shaker in the dark at room temperature in a solution containing 10% polyvinyl alcohol, 1 mM Levamisol (Vector Laboratories, Burlingame, CA 94010, USA), 2% NBT/BCIP (Roche, 11681451001), 0.1 M Tris (pH = 9.5), 0.1 M NaCl, and 0.005 M MgCl₂ (color detection mix). Sections were left in the color detection mix until dark purple reaction product was visible under a dissecting microscope, at which point the reaction was terminated for all tissues of the same age. To stop the color reaction, sections were washed twice for 5 min in NTMT in the dark, incubated in 0.1 M TBS containing 0.001 M EDTA for 30 min, and finally twice for 10 min in PBT (on a shaker at room temperature). The procedures were designed to process all tissues at the same time to facilitate qualitative comparisons between different genotypes.

IMMUNOHISTOCHEMISTRY

Immunocytochemical procedures were standard and performed as described previously (22). Briefly, 50 µm serial sections from 4% paraformaldehyde perfusion-fixed peri-pubertal (P35) or fetal (E17) brains were cut using a vibrating microtome (Leica VT1000s) and collected into mesh-bottomed boats. Sections were pretreated with 0.1 M glycine then 0.5% sodium borohydride in 0.05 M PBS. Sections were blocked with 5% normal goat serum (NGS) and 1% hydrogen peroxide in 0.05 M PBS. Sections were incubated with rabbit derived KISS1 antibody directed against rodent kisspeptin-10 (provided by Dr. Alain Caraty) at a final dilution of 1:10,000 for two nights (23). Primary antibody was localized with a biotinylated donkey anti-rabbit secondary antibody (Jackson Immunoresearch, #016-160-084) at a concentration of 1:500. IHC was developed using Cy3-conjugated streptavidin (Jackson Immunoresearch #016-160-084) at a concentration of 1:500.

QUANTITATIVE REVERSE TRANSCRIPTION REAL-TIME PCR

Tissue was collected fresh from fetuses (E17) and adults (~P50) and flash frozen on dry ice then stored at ~80°C until homogenized on a dissecting microscope, at which point the reaction was terminated for all tissues of the same age. To stop the color reaction, sections were washed twice for 5 min in NTMT in the dark, incubated in 0.1 M TBS containing 0.001 M EDTA for 30 min, and finally twice for 10 min in PBT (on a shaker at room temperature). The procedures were designed to process all tissues at the same time to facilitate qualitative comparisons between different genotypes. 

RNA was isolated using the Qiagen RNeasy Mini Kit (Qiagen Sciences, #74104). Briefly, excised brain pieces were pulverized using a motorized tissue grinder and RNase free tubes and disposable pestles (VWR cat. #47747-370 and #47747-366), then homogenized in the supplied homogenization buffer and procedures were followed according to manufacturer’s instructions. Once eluted, the RNA concentration and purity of each sample was determined by spectrophotometry and samples were stored at ~80°C until reverse transcription (RT). 

For GnRH-eGFP mice, RT was performed using the Thermo Verso RT kit (Fisher cat #AB1453B) using random hexamer primers for first strand synthesis according to manufacturer’s instructions. For Sf1 KO mice, RT was performed using the qScript cDNA Synthesis kit (Quanta Biosciences cat #95047) which contains a mixture of random hexamers and oligo(dT). To insure uniformity between samples, all RNA isolates were diluted to 100 ng/µl of which 5 µl (500 ng total RNA) was added to each 20 µl reaction. RT was performed less than 24 h prior to QPCR to minimize potential sample degradation.

DUAL-LABEL ISH/IHC

Dual-label ISH/IHC experiments were carried out exactly as single-label experiments with the exception that the two protocols were run in series. In this case, ISH for KissIr was performed first, followed immediately by IHC for GnRH. Primary antibody for these experiments was rabbit-anti-GnRH (Affinity Bioreagents #PA1-121) used at a concentration of 1:200. For visualization, the IHC was developed using Cy3-conjugated streptavidin (Jackson Immunoresearch #016-160-084) at a concentration of 1:500.

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Knoll et al. Kisspeptin development in fetal mouse brain October 2013 | Volume 4 | Article 140 | 3
For GnRH-eGFP animals, QPCR was performed using HotStart-IT SYBR Green QPCR Master Mix (2X; USB Corporation, Cleveland, OH 44146, USA). According to the HotStart-IT protocol, 20 µl reactions were run with 2 µl cDNA. For Sfl KO animals, 20 µl reactions were run with Light Cycler 480 SYBR Green I Master Mix kit (Roche cat #04-707-516001) using 4 µl cDNA in each 20 µl reaction. All QPCR experiments were performed in a LightCycler 480 system (Roche Applied Sciences). Cycling parameters were as follows: hot start at 95°C for 1 min; 45 cycles of amplification/quantification at 95°C for 10 s, 60°C for 30 s, and 72°C for 30 s during which time fluorescence was measured. Melting curve analysis was performed using continuous fluorescence acquisition from 65–97°C. These cycling parameters generated intron spanning regions of Kiss1 and Rn18s (reference gene) to investigate the gene of interest and monitor amplification efficiency. The two sets of primers used for this experiment were as follows: Kiss1 forward 5′-TGATCTCAATGGCTTCTTGCGACG-3′ and reverse 5′-CTTCTCGATACCGGATTC CTTT-3′; Rn18s forward 5′-AGGGGAGGGGGTGTAAGAGA-3′ and reverse 5′-GGACAGGACTA GGGCGAACA-3′.

For absolute quantification of kisspeptin transcript, the same plasmid used to generate the Kiss1 probe was used as a standard. Since each plasmid contains a single copy of the Kiss1 gene, and using an approximation of the total molecular weight of the plasmid (~3.7E−12 µg/copy) the concentration of plasmid was calculated in terms of number of copies per µl of solution. A 10-fold serial dilution series was used to generate a standard curve ranging from ~1E11 copies/µl (0.4 µg/µl) to ~100 copies/µl. This dilution series was run in the same plate as each experiment and was used to generate a standard curve from which the concentration (in number of copies/well) was calculated for each sample. This number was then used to calculate the number of copies of Kiss1 in E17 and adult male and female brains [copies/well ÷ (microliter cDNA/well) = copies/microliter cDNA] ÷ (microliter RNA/20 µl cDNA) = copies/microliter RNA × Dilution Factor = copies/microliter RNA (undiluted) × Total RNA Volume = Total Copies/dissection.

To control for contamination, several controls were used. First, pieces of cortex not expected to express Kiss1 were collected from each brain at the time of tissue collection. These tissues were treated the same as all other tissue pieces and did not generate a signal above background during QPCR. During the RT, two additional controls were used; one reaction with no RNA, and one with RNA (from an adult female rostral POA) but no reverse transcriptase. Controls from each of the previous steps were run through all subsequent steps. Real-time PCR controls included all of the previous controls and one reaction containing no cDNA (water control). None of the negative controls produced a signal above background in QPCR (data not shown). Finally, standards and samples were run in triplicate to verify accuracy; calculated crossing point variance was below 2% for replicated samples.

STATISTICAL ANALYSIS

For each age group in each experiment three animals of each sex and genotype from a minimum of two different litters were used for quantitative analysis. To determine the number of cells expressing kisspeptin, all cells (with obvious nuclear voids) with visible reaction product in all sections from a given brain were manually counted at high magnification by an investigator blind to the sex of each animal. For fetal brains this meant counting all sections from the entire brain (all sections collected in a single boat) while for older animals it meant counting all sections from half of the brain (sections were alternated between two boats). The reason for collecting all sections from the embryonic brains was to ensure that important sections were not lost due to the smaller size of the brains. For comparison purposes, the total number of cells counted for each embryonic brain was divided in half to generate the equivalent of the number of cells per half-brain. This method was validated by alternating sections from a subset of fetal brains into two boats and counting the number of cells per half-brain; the resultant average was approximately equal to the average of half the total cells per whole brain.

For QPCR, the crossing point was determined according to the absolute quantification/second derivative maximum method in the LightCycler 480 SW 1.5 software. From this number, the total copy number was calculated based upon the previously described standard curve. To verify the results of the standard curve absolute quantification method, relative expression analysis was performed by normalizing Kiss1 to Rn18s signal. Both methods generated similar results and the absolute quantification method results were selected for presentation. Cycling parameters were set up such that the exponential amplification phase had been reached for all positive samples (45 cycles total). Any sample that did not exhibit an appropriate amplification curve, a single melt curve, or that came up after 40 cycles was assumed to be a false signal and was not analyzed. Negative control samples were never observed to generate a signal before 40 cycles.

Statistical analysis was performed using SPSS 13.0 or JMP 10.0 for Mac OSX. For cell count analysis, the total number of cells per half-brain and the sex of the animal were analyzed by two-way ANOVA for sex and age. For QPCR data from Sfly embryos two-way ANOVA for sex and genotype was used, with Least Square Means Student’s t as a post hoc test. For adult animals, even though there were two regions per animal, due to the greater variance in the rostral/POA region compared to the caudal/ARC region, one-way ANOVA was conducted on the rostral region separately from a two-way analysis in the caudal/ARC region.

RESULTS

Kiss1/KISS1 AND Kiss1r REGIONAL LOCALIZATION IN THE FETAL BRAIN

Kiss1 was detected by ISH at E13 in a few cells (arrows in Figure 1 left) near the ME. Two days later (E15) the total number of cells expressing Kiss1 had greatly increased (from approximately 30 cells/half-brain to approximately 400 cells/half-brain), although the distribution remained similar (Figure 1). Cells containing Kiss1 were found in approximately eight sequential sections, representing a distance of greater than 800 µm in all ages examined.

Expression of Kiss1r was detected at E13 in both sexes by ISH. At this age, the only cells containing Kiss1r were found in the nasal compartment in a pattern similar to the pattern of migrating GnRH neurons. By E15 a large proportion of this population...
Knoll et al. Kisspeptin development in fetal mouse brain

FIGURE 1 | Kiss1 and Kiss1r are expressed as early as E13. Developmental changes in the expression of Kiss1 (top four images) and Kiss1r (bottom four images) are shown in digital images from sagittal sections of female mice at E13 (left) and E15 (right). Smaller images are higher magnifications of the same sections displayed immediately above them. Note the change in location of the Kiss1r positive cells from the nasal compartment to the forebrain between E13 and E15 reminiscent of the migrating GnRH neuron population. Arrows indicate the location of mRNA positive cells. CP, cribriform plate; Pit, pituitary; VNO, vomeronasal organ. Scale Bars: black = 1 mm, white = 200 µm.

Knoll et al. Kisspeptin development in fetal mouse brain

of cells had apparently migrated to and across the cribriform plate into the ventral forebrain (Figure 1), again suggestive of migrating GnRH neurons. With each successive age, the pattern of Kiss1r expression matched the typical distribution of GnRH neurons, with older animals having a high density of Kiss1r expression around the diagonal band of Broca (DBB) and surrounding the organum vasculosum of the lamina terminalis (OVLT) as well as a more dispersed expression as far caudal as the optic chiasm. In addition, Kiss1r containing cells were seen in a highly restricted population of cells in the habenula as early as E17 (data not shown). No sex differences were observed in Kiss1r expressing cells at any age or in any region (data not shown).

To verify that the cells seen to express Kiss1r in previous experiments were GnRH neurons, dual-label ISH/IHC were performed on E15 (Figure 2). As illustrated, GnRH immunoreactivity was seen in a pattern corresponding to that of the Kiss1r expression pattern at the same age (compare with Figure 1). High magnification images of fluorescently labeled GnRH (B) and DIG labeled Kiss1r (C) shows that, in fact, cells expressing Kiss1r at E15 were migrating GnRH neurons.

To determine if Kiss1 is translated into processed KISS1 peptide during development, serial sections from fetal (E17) brains were examined by IHC. Immunoreactive kisspeptin (KISS1; Figures 3B,D) was detected using an antiserum raised against the biologically active decapeptide. A similar distribution to that seen using ISH was observed (Figures 3A,C). In fetal mice, KISS1 was only found in a distribution of cells in the ARC, and cell bodies were clearly identifiable in fetal ARC.

RELATIVE DIFFERENCES IN KISS1 LOCALIZATION PATTERNS IN MOUSE FETAL AND EARLY POST-NATAL BRAIN

For the ages of E15 (Figure 2) and E17 (Figure 4) the pattern of cells expressing Kiss1 remained unchanged. In addition, there appeared no sex difference in the number of cells expressing Kiss1 (E15 not shown; E17, Figure 4). At P12, the number of cells expressing Kiss1 was dramatically higher in the female compared
to the male. This is the only age examined at which there was a significant sex difference in the detectable number of cells expressing Kiss1 in and around the ARC [Figure 4; F(1,4) = 8.2, p < 0.05]. There was no sex difference in the number of cells expressing Kiss1 at E13, E15, E17, or P35 (Figure 4).

In rostral sections, Kiss1 was first detected using ISH in a few cells at P12 (Figure 5). As with the more caudal ARC population, there was a distribution of cells in the rostral sections that begins near the opening of the third ventricle and extends caudally in a continuous cluster beyond the level of the anterior commissure. For the entire distribution, Kiss1 was found in cell bodies along a narrow periventricular strip noted as the rostral periventricular region of the third ventricle (RP3V) (4). At P12 there was not a statistically significant sex difference in the number of cells found in the rostral population of cells. At P35 there appeared dramatically more cells in RP3V sections in both sexes as well as a significant sex difference in the number of cells found in these sections [Figure 5; F(1,4) = 262.0, p < 0.01], but no difference in the total number of cells in the ARC sections [Figure 5; F(1,4) = 1.83, p = 0.25].

SEX DIFFERENCES IN ABSOLUTE Kiss1 AMOUNT IN FETAL AND ADULT MOUSE BRAIN

Quantitative reverse transcription real-time PCR was used to assess the absolute level of Kiss1 in E17 and P50 (young adult) male and female GnRH-eGFP mice. As previous results suggested, and in agreement with the ISH data, adult cells expressed nearly four times as much Kiss1 as males in the RP3V [Figure 6; F(1,4) = 9.77; p < 0.05]. In the caudal hypothalamic region of the adult animals, females were found to express more than twice as much transcript as males [Figure 6; F(1,4) = 43.1, p < 0.01]. A similar difference was found in the E17 animals, when Kiss1 expression is restricted to the caudal region around the ARC, with females expressing more than twice as much Kiss1 as males [Figure 6; F(1,6) = 22.1; p < 0.01]. Females were not examined at the time of dissection to determine estrous stage. In a final comparison, and in agreement with the increase in cell count with age, the level of Kiss1 expression was significantly different between fetal and adult animals [Figure 6; age effect: F(1,10) = 41.01, p < 0.01; sex by age effect; F(1,10) = 10.26, p < 0.01].

POTENTIAL SOURCE OF SEX DIFFERENCES IN Kiss1 IN FETAL MOUSE BRAIN

To determine if the sex difference of Kiss1 in ARC neurons was related to steroid hormones or gonadal status of fetal mice, we conducted Kiss1 ISH analyses of Sf1 KO XY mice (agonadal due to disruption of the Sf1 gene but genetically male) compared with XY and XX WT littermates. Sf1 KO mice die shortly after birth due to the absence of adrenal hormones, and thus without glucocorticoid supplementation these animals can only be evaluated at embryonic ages (24, 25). However, the advantage of using these animals is that the effects of total gonadal ablation can be achieved from the earliest stage of development, before surgical gonadectomy is possible. In each experiment, sections from Sf1 KO XY mice were most comparable to sections from WT XX mice by qualitative visual inspection of the optical density of reaction product (Figure 7). Cells observed in sections from WT XY mice were consistently lighter in color than either WT XX or XY Sf1 KO mice.

To verify that the visual ISH difference represents an actual difference in Kiss1, QPCR was performed on cDNA from hypothalamic tissue dissections from E17 XY and XX Sf1 KO and WT littermates. There was a sex difference in Kiss1 copy number between XY and XX WT mice from the Sf1 KO line (p < 0.05 post hoc) that was similar to the results from the previous QPCR experiments using GnRH-eGFP animals. Importantly, there was a significant sex by genotype interaction [Figure 7; F(1,8) = 6.56; p = 0.034] with XY WT mice expressing significantly less Kiss1 than XY KO, but with no difference between XX WT and XX KO. Thus the impact of the KO was only seen in males that may have had functional gonads.

DISCUSSION

An increasing number of studies have indicated the importance of kisspeptin signaling for both the onset of puberty and the promotion of normal adult reproduction (1, 26). Several have demonstrated the sex-steroid dependence of peri-pubertal changes in Kiss1 expression and sexually dimorphic Kiss1 expression in the rostral hypothalamus (11, 27). However, despite the pre-pubertal sex differences in circulating sex steroids, most notably at certain perinatal “critical periods,” until recently few studies have investigated the early developmental expression of Kiss1 and its cognate receptor KISS1R (12, 28).

In the last few years a growing body of research has begun to shed light on the emerging understanding that the kisspeptin system is actively regulated long before puberty. Several recent reports have examined the expression of Kiss1 early in life. In a study of the ontogeny of kisspeptin neurons using BrdU birth dating in rats, these neurons differentiate locally within the region of the ARC beginning around E12.5 (29). Kiss1 was present in hypothalamic micropatches and KISS1 immunoreactive cells and fibers were detected as early as E14.5. Importantly, by showing that the
number of cells increased early in development (E14.5–18.5) and then decreased (E18.5–22.5) the data suggests pre-natal regulation of the kisspeptin system. Similar to these results, Kiss1 expressing neurons were detected via ISH soon after birth (first reported for P3) in the ARC of rats and there were transient sex differences in the number of Kiss1 cells, with females having significantly more cells at certain times than their male littermates (30). Finally, in mice examined for Kiss1 expression on the day of birth, both the number of Kiss1 positive cells and the amount of Kiss1 per cell were higher in females than males (31). Interestingly, by examining the levels of circulating testosterone and using transgenic models with disrupted kisspeptin or GnRH signaling, the authors demonstrated that sex differences in gonadal steroid production arise independent of KISS1/KISS1R and GnRH.

In the current series of experiments, Kiss1 and Kiss1r were detected in E13 mouse brain tissue. Using IHC it was further demonstrated that Kiss1 is translated into immunoreactive peptide as early as E17 and potentially earlier. This result is similar to findings of pre-natal kisspeptin expression in rats (29). The differences with our results, most notably that a small number of KISS1 IR cells and fibers were found in the RP3V pre-natally in rats, are likely due to species variation or differences in detection technique. The current results replicate earlier studies showing the sexually dimorphic number of Kiss1 expressing cells in the ARC and RP3V of mice and rats (5, 31, 32), but importantly show that there is already a sexually dimorphic pattern within the fetal ARC, whether examined qualitatively by visual inspection of colorimetric ISH (see Figure 7) or quantitatively using QPCR. Our data show sex differences in the amount of ARC Kiss1 at all ages examined, with RP3V expression only detected after birth. By using Sfi KO mice that do not develop gonads, the early dependence of Kiss1 levels on gonadal status is strongly suggested. Although it is possible that knocking out Sfi causes changes in Kiss1 expression in gonad independent manner – such as preventing signaling within the mediobasal hypothalamus itself – this is unlikely considering that XX knockouts (KO) were not significantly different from their WT littermates. The demonstration of regulated Kiss1 expression early in development suggests functional relevance that merits further investigation.

In an effort to better understand the development of sex differences in the brain’s reproductive axis, the developmental profile of Kiss1 expression using ISH was determined. Expression of Kiss1 was found at E13 followed by a dramatic increase in the number of detectable cells positive for Kiss1 by E15. This increase demonstrates an early expression of Kiss1, and also suggests a temporally coordinated up-regulation. From E15 to P0 there was no significant change in either the number of cells found to express Kiss1 or in the distribution pattern of these cells around the ARC (i.e., ~400 cells/half-brain distributed over ~800 µm rostrocaudally). Protein translation from Kiss1 was verified by IHC for KISS1 in E17 and adult animals where immunoreactive product was seen in a pattern similar to that seen with ISH. At all ages examined, mRNA coding...
for the kisspeptin receptor KISS1R also was detected. The presence of both the ligand and cognate receptor establishes the possibility that a functional signaling system exists not only prior to puberty, but also well before birth. KISS1R is highly selective for kisspeptin when compared with all other RF-amide peptides. Similar to previous results, at E13 these cells were found exclusively in the nasal compartment in a distribution pattern that strongly resembles the migrating GnRH neuron population (33). Co-localization of immunoreactive GnRH and Kiss1r in E15 animals confirmed that cells seen to contain Kiss1r are, in fact, migrating GnRH neurons. Unfortunately, the absence of verified antibodies against KISS1R prevented the examination of the translation status of KISS1R.

Projections from neurons in the ARC may develop relatively late (34, 35). This would make ARC KISS1 an unlikely source of ligand for migrating GnRH neurons at embryonic ages, particularly when they are in the nasal compartment expressing Kiss1r. Previous results showing the efficacy of peripheral kisspeptin administration suggest that systemic, endocrine-like signaling, as opposed to synaptic release, could potentially play a role in development (36). Other peripheral sources of kisspeptin are possible (e.g., placenta), which would suggest that signaling is not for the purpose of providing a directional cue for migrating GnRH neurons but could possibly influence axon targeting (37). Similar to previous findings, one additional population of Kiss1r expressing cells was found in the habenula (38). These cells are located at the approximate border of the medial and lateral divisions of the habenula and were seen from E17 on (though not noted in younger animals). It is interesting to note the role of the habenula in physiological changes related to seasonality and specifically in seasonal breeders (36, 39, 40). While it remains to be determined where the ligand would come from to reach cells in the habenula expressing KISS1R, one possible source is the “estrogen concentrating cells” of the POA that send projections to the habenula (41–43). This also raises the possibility that patients with inactivating mutations of KISS1R or KISS1 may exhibit phenotypes other than those manifested in the reproductive system.

The data from older animals in the current study confirms the pattern of Kiss1 expression that has been reported previously (5,
Specifically, Kiss1 was observed in the ARC in both sexes at all post-natal ages in a pattern very similar to the fetal pattern. At P12 there was a significant sex difference in the number of Kiss1 expressing cells in the ARC, with females having more cells than males. Since the number of cells in males is similar to that of females by the next time point (P35) it could simply indicate a sex difference in maturational rate, which would not be unusual for the development of brain characteristics (45). Similarly, it is possible that all post-natal sex differences observed in the ARC are due to differences in circulating sex steroids; several studies have shown that sex differences in Kiss1 expression in the RP3V are eliminated in mice and rats that have artificially equal levels of sex steroids (5, 14). Interestingly, P12 is the first age at which Kiss1 expression was detected in a few cells in rostral sections. This result is similar to previously published research showing detection of Kiss1 at P10 (32). At this age, possibly due to the apparently low level of message or the relatively low number of cells, there was no sex difference in the number of Kiss1 containing cells seen in the RP3V. By contrast, at around the time of puberty onset (P35) there was a dramatic sex difference in the number of Kiss1 expressing cells in the RP3V, with females having far more cells than males.

In the current study, data from three different approaches suggest that the level of Kiss1 in the ARC is a reliable sex difference in development and adulthood. First, qualitative differences were noted between males and females based on the optical density of ISH reaction product. Second, quantitative QPCR produced complementary results. The complementary nature of both ISH and QPCR assay was particularly evident at E17. Although the number of cells positive for Kiss1 in the ARC appeared similar according to ISH, females had absolute levels of Kiss1 ∼ twofold greater than males according to QPCR and this difference remained at P35. As a verification of the method, the sex difference in adult Kiss1...
levels within the more rostral RP3V was approximately fourfold as expected from data in reports for either whole hypothalamus or RP3V, respectively (28, 46). It should be noted that the adult females used for QRCR experiments were not examined to determine which stage of the estrous cycle they were in at the time of sacrifice, nor were circulating levels of sex steroids measured to mine which stage of the estrous cycle they were in at the time of sacrifice. After a significant interaction between sex and genotype, *p < 0.05 indicates a specific of XY KO to XX WT. 3V, third ventricle; ME, median eminence. Scale bar = 100 µm.

FIGURE 7 | Pre-natal Kiss1 expression is gonad dependent. Digital images of coronal sections in (A) show that E17 Sf1 KO XY resemble WT XX more than WT XY mice by qualitative inspection of ISH reaction product. qPCR quantification of Kiss1 (B) reveals a significant effect of sex by genotype with WT males expressing less Kiss1 than KO males or females of either genotype (n = 3 per group; mean ± SEM). After a significant interaction between sex and genotype, *p < 0.05 indicates a specific of XY KO to XX WT. 3V, third ventricle; ME, median eminence. Scale bar = 100 µm.

In summary, Kiss1 and Kiss1r were detected in fetal mice early in development. Kiss1r was co-localized with GnRH in the nasal compartment and rostral forebrain during GnRH neuron migration, while Kiss1 was found selectively in cells within the developing ARC. At E17 Kiss1 was observed in the same region and distribution as the mRNA. Kiss1 expression was both qualitatively and quantitatively sexually dimorphic, and likely related to hormone exposure prior to birth. The sex difference in this region is maintained into adulthood, although the exact cause and function of this early kisspeptin expression remains to be elucidated.

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Kisspeptin development in fetal mouse brain

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Knoll et al.
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