GATA augments GNRH-mediated increases in Adcyap1 gene expression in pituitary gonadotrope cells

Robin L Thomas, Natalie M Crawford, Constance M Grafer, Weiming Zheng and Lisa M Halvorson
Division of Reproductive Endocrinology and Infertility, Department of Obstetrics and Gynecology, University of Texas Southwestern Medical Center, 5323 Harry Hines Boulevard, Dallas, Texas 75390-9032, USA

Correspondence should be addressed to L M Halvorson
Email lisa.halvorson@utsouthwestern.edu

Abstract
Pituitary adenylate cyclase-activating polypeptide 1 (PACAP or ADCYAP1) regulates gonadotropin biosynthesis and secretion, both alone and in conjunction with GNRH. Initially identified as a hypothalamic-releasing factor, ADCYAP1 subsequently has been identified in pituitary gonadotropes, suggesting it may act as an autocrine–paracrine factor in this tissue. GNRH has been shown to increase pituitary Adcyap1 gene expression through the interaction of CREB and jun/fos with CRE/AP1 cis-elements in the proximal promoter. In these studies, we were interested in identifying additional transcription factors and cognate cis-elements which regulate Adcyap1 gene promoter activity and chose to focus on the GATA family of transcription factors known to be critical for both pituitary cell differentiation and gonadotropin subunit expression. By transient transfection and electrophoretic mobility shift assay analysis, we demonstrate that GATA2 and GATA4 stimulate Adcyap1 promoter activity via a GATA cis-element located at position −191 in the rat Adcyap1 gene promoter. Furthermore, we show that addition of GATA2 or GATA4 significantly augments GNRH-mediated stimulation of Adcyap1 gene promoter activity in the gonadotrope LjT2 cell line. Conversely, blunting GATA expression with specific siRNA inhibits the ability of GNRH to stimulate ADCYAP1 mRNA levels in these cells. These data demonstrate a complex interaction between GNRH and GATA on ADCYAP1 expression, providing important new insights into the regulation of gonadotrope function.

Introduction
Proper functioning of the hypothalamic–pituitary–gonadal axis requires the complex interplay of gonadotropin-releasing hormone (GNRH), steroids, and other regulatory factors. In addition to the well-characterized effects of hypothalamic GNRH, the neuropeptide adenylate cyclase-activating polypeptide 1 (ADCYAP1; also known as PACAP) also regulates gonadotropin gene expression. ADCYAP1 is secreted by hypothalamic neurons into the pituitary portal vasculature, binding to specific G protein-coupled receptors on pituitary cell membranes and activating the cAMP/protein kinase A signaling pathway (Sherwood et al. 2000, Vaudry et al. 2000). ADCYAP1 increases gonadotropin biosynthesis and secretion, alone and in synergy with GNRH (Culler & Paschall 1991,
Schermerus et al. 1994, Tsuji & Winters 1995, Winters et al. 1996, Purwana et al. 2010, Kanasaki et al. 2013). ADCYAP1 has been shown to increase α-subunit, Lhb, Fshb, and Gnrh gene promoter activity and mRNA levels in gonadotropes (Schermerus et al. 1994, Tsuji & Winters 1995, Winters et al. 1996, Burrin et al. 1998, Katayama et al. 2000, Cheng & Leung 2001, Ngan et al. 2001, Pincas et al. 2001b, Fujii et al. 2002, Ferris et al. 2007, Purwana et al. 2010). Although less potent than GNRH, ADCYAP1 also stimulates luteinizing hormone (LH) and follicle-stimulating hormone (FSH) secretion by primary pituitary cells and the gonadotrope cell line (Osuga et al. 1996, Burrin et al. 1998, Katayama et al. 2000). These stimulatory effects of ADCYAP1 on LH secretion in rats have been confirmed in vivo (Osuga et al. 1992, Radloff-Schlimme et al. 1998). GNRH and ADCYAP1 exert cooperative effects on gonadotropin function via multiple mechanisms including alterations in receptor expression. As shown by Kanasaki et al. (2009), treatment of gonadotrope cells with either pulsatile GNRH or ADCYAP1 stimulates both GNRH receptor (GnRHR) and PACAP receptor type 1 (Adcyap1r1) gene expression.

Although, originally identified as a hypothalamic-releasing factor, ADCYAP1 subsequently has been determined to have widespread distribution and function, including expression in the CNS and peripheral nervous system, smooth muscle, adrenal gland, placenta, anterior and posterior pituitary, ovaries, and testes (Arimura & Shioda 1995). Within the anterior pituitary gland, both gonadotropes and the folliculostellate cells have been shown to synthesize and secrete ADCYAP1 peptide (Koves et al. 1998, Jin et al. 2001, Szabo et al. 2002, Heinlmann et al. 2008). Therefore, ADCYAP1 both acts on and is secreted by pituitary cells, forming a functional autocrine–paracrine loop in this tissue.

A limited number of studies have begun to elucidate the hormonal factors which regulate Adcyap1 gene expression. Estradiol and progesterone have been suggested to stimulate Adcyap1 expression in the hypothalamus and ovary (Ha et al. 2000, Park et al. 2000, Apostolakis et al. 2004, Moore et al. 2005). Additional studies have shown the ability of LH and FSH to promote Adcyap1 expression in human granulosa–luteal cells obtained from patients undergoing IVF (Morelli et al. 2008). LH, FSH, human chorionic gonadotropin, and GNRH have also been shown to increase Adcyap1 mRNA levels in the ovary (Ko et al. 1999, Lee et al. 1999, Park et al. 2001).

GNRH has also been demonstrated to increase ADCYAP1 biosynthesis in the pituitary. As shown by our group and others, Adcyap1 promoter activity and mRNA levels are markedly increased by static or pulsatile GNRH treatment in an immortalized gonadotrope cell line (Grafer et al. 2009, Purwana et al. 2010, Kanasaki et al. 2011). This stimulatory effect has been confirmed in rat primary pituitary cell cultures in which a threefold increase in Adcyap1 mRNA levels has been observed in response to GNRH treatment (C M Grafer and L M Halvorson, 2009, unpublished observations). We have reported that the GNRH response is mediated via the PKA, PKC, and MAPK intracellular signaling pathways acting via three DNA-regulatory elements, a CRE site located at position −205 and two AP1 sites located at positions −275 and −448, in the proximal Adcyap1 promoter (Grafer et al. 2009). Furthermore, these studies demonstrated a role for CREB and the AP1 proteins, jun and fos, in mediating this response. This work was the first to identify specific transcription factors and associated cis-elements with the importance for pituitary Adcyap1 gene expression. We, therefore, were interested in identifying additional transcription factors with the importance for expression of this gene.

The GATA family of transcription factors has been shown to regulate gene expression at all levels of the reproductive axis. Although originally characterized in the hematopoietic and cardiac systems, GATA factors are now known to be expressed in hypothalamic GNRH neurons, the pituitary, the ovary, and the testes (LaVoie 2003, Viger et al. 2008). Vertebrates express six different GATA family members. The amino acid sequence of these factors is highly conserved with ~80% homology in the zinc finger DNA-binding domains. As indicated by their name, the GATA factors bind to the consensus motif GATA, although they have also been reported to bind nucleotide sequences containing core GATC or GATT elements (Merika & Orkin 1993, Nakagawa et al. 2001).

Within the pituitary gland, GATA transcription factors have been shown to be critical for both pituitary cell differentiation and function. During development, GATA2 directs cells toward the gonadotrope lineage and away from the thyrotrope lineage through reciprocal interactions with Pit1 (Dasen et al. 1999). Functional GATA cis-elements have also been identified in the promoter regions of the common α- and Fshb-subunit genes, as well as the Gnrh gene (Steger et al. 1994, Pincas et al. 2001a, Lo et al. 2011). Our laboratory has recently demonstrated that the adult mouse pituitary expresses GATA4 in addition to GATA2 and that both of these factors stimulate gonadotropin Lhb gene expression in the LβT2 gonadotrope cell line (Lo et al. 2011).
For the studies reported here, we hypothesized that GATA transcription factors play a role in the regulation of Adcyap1 gene expression in pituitary gonadotropes. Our results demonstrate the ability of both GATA2 and GATA4 to stimulate basal and GNRH-induced Adcyap1 gene expression via a GATA response element located at position —191 relative to the transcriptional start site in the proximal rat Adcyap1 gene promoter.

Subjects and methods

RNA extraction and RT

Total RNA was prepared from cultured gonadotrope LβT2 cells using TRI Reagent (Ambion, Inc., Austin, TX, USA) according to the manufacturer’s instructions. Total RNA samples were DNase-treated using the Turbo DNA-free Kit (Ambion, Inc.) and reverse transcribed using Superscript II reverse transcriptase (Invitrogen, Inc.) primed with random hexamer. A parallel reaction lacking RT was used as an additional negative control. LβT2 cells were generously provided by Dr P L Mellon (University of California, San Diego, CA, USA).

Quantitative real-time PCR

cDNA (10–100 ng/reaction) was amplified in triplicate in a 384-well plate on a 7900HT Sequence Detection System (Applied Biosystems) using Applied Biosystems TaqMan Universal PCR Master Mix and gene-specific TaqMan Gene Expression Assay primer/probe sets with universal cycling conditions (Table 1). Each reaction was run in 15 μl total volume. The expression of each target gene was normalized to 18S transcript expression in each sample. The relative target gene expression levels among treatments were calculated using the comparative Ct method as described in Applied Biosystems User Bulletin No. 2.

Table 1  PCR primers used in this study

<table>
<thead>
<tr>
<th>Name of oligonucleotides</th>
<th>Sequences (mutated residues underlined)</th>
</tr>
</thead>
<tbody>
<tr>
<td>EMSA WT (−209/−167)</td>
<td>5′-ATGCTGACGTCTTTTACTGATACCCGGATATTACGTGACTGGG-3′</td>
</tr>
<tr>
<td>Mutant −191 GATA</td>
<td>5′-ATGCTGACGTCTTTTACTGCCACCCGGATATTACGTGACTGGG-3′</td>
</tr>
<tr>
<td>Mutant −205 CRE</td>
<td>5′-ATGCTGACGTCTTTTACTGATACCCGGATATTACGTGACTGGG-3′</td>
</tr>
<tr>
<td>Mutant −179 CRE</td>
<td>5′-ATGCTGACGTCTTTTACTGATACCCGGATATTACGTGACTGGG-3′</td>
</tr>
<tr>
<td>Mutant 205/−179 CRE</td>
<td>5′-ATGCTGACGTCTTTTACTGATACCCGGATATTACGTGACTGGG-3′</td>
</tr>
<tr>
<td>Mutagenesis Mutant −191 GATA</td>
<td>5′-ATGCTGACGTCTTTTACTGATACCCGGATATTACGTGACTGGG-3′</td>
</tr>
<tr>
<td>Mutant −191 GATA/−205 CRE</td>
<td>5′-ATGCTGACGTCTTTTACTGATACCCGGATATTACGTGACTGGG-3′</td>
</tr>
<tr>
<td>Mutant −191 GATA/−179 CRE</td>
<td>5′-ATGCTGACGTCTTTTACTGATACCCGGATATTACGTGACTGGG-3′</td>
</tr>
<tr>
<td>Mutant −191 GATA/−205 CRE/−179 CRE</td>
<td>5′-ATGCTGACGTCTTTTACTGATACCCGGATATTACGTGACTGGG-3′</td>
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Plasmids

The rat Adcyap1 gene promoter spanning region −1916 to +906 relative to the transcription start site and exon 1A (gene ID: 24166) was subcloned into the pGL3-Basic luciferase reporter vector (Promega) (cDNA was kindly provided by Drs S L White and K M Braas (University of Vermont College of Medicine, Burlington, VT)). A CRE site mutant (mutCRE(−205)) was also provided containing an AC to TG mutations present at position —203. Additional deletion constructs and site-directed mutations were generated by the PCR or the QuikChange Site-directed Mutagenesis Kit (Stratagene, La Jolla, CA, USA). The fidelity of all constructs was verified by nucleotide sequencing. The cDNAs encoding mouse GATA2 and GATA4 were provided by D F Gordon and S Hammes, respectively, and were subcloned into pcDNA3.1(+) (Invitrogen, Inc.).

Transient transfection of cell lines

Green monkey kidney fibroblast cells (CV1) were maintained in monolayer culture in low glucose DMEM supplemented with 10% fetal bovine serum (FBS) (v/v) and 1% penicillin/streptomycin (v/v) at 37 °C in humidified 5% CO2/95% air. CV1 cells (6–7×10^4 cells/well) were cultured overnight in 12-well plates. Using the calcium phosphate precipitation method, each well was transfected with 400 ng/well of ADCYAP1 reporter vector and 0–30 ng/well of GATA2 or GATA4 expression vectors as indicated in the dose–response experiment (Fig. 1). For subsequent CV1 experiments, cells received 30 ng of GATA2 and 10 ng of GATA4 expression vector. The GATA response of the empty luciferase reporter vector was less than threefold (data not shown).

For LβT2 transfection experiments, cells were maintained in high glucose DMEM supplemented with
GNRH analog [des-Gly10, D-Ala6]-LH-RH ethylamide acetate hydrate (10 nM or as indicated; Sigma–Aldrich) or vehicle before harvest. Cotransfection of LβT2 and CV1 cells with 48 ng/well of a pSV-β-galactosidase plasmid (Promega) allowed correction for differences in transfection efficiency within the experiments. Cells were harvested 48 h after transfection for total RNA isolation for quantitative real-time PCR (qPCR) analysis. Each combination of siRNA and hormonal treatment was tested in duplicate in three experiments.

For each experiment, qPCR data was calculated using the comparative $C_T$ method and calibrator values were chosen to set the averages of replicate vehicle-treated or GNRH-treated, non-targeting (NTA) siRNA samples equal to 100. The various experimental vehicle-treated or GNRH-treated samples were then expressed relative to their appropriately treated NTA controls.

Statistical analysis

Statistical analysis was performed using the SigmaStat Software Package (SPSS Science). Data were analyzed for normality followed by ANOVA. The Tukey’s test was used for post hoc comparisons. The t-test was used where only two groups were involved. Statistical significance was set at $P<0.05$.

Results

GATA2 and GATA4 stimulate Adcyap1 gene promoter activity in CV1 cells

In order to study the effects of GATA transcription factors on Adcyap1 promoter activity, transient transfection of the full-length rat Adcyap1 (−1916/+906) gene promoter

Data are shown as the mean ± S.E.M. from at least three experiments with three replicates performed within each experiment.
fused to the pGL3 luciferase reporter was conducted in CV1 cells. These cells are an immortalized green monkey kidney fibroblast cell line essentially devoid of any endogenous GATA (Robert et al. 2006). Dose–response experiments demonstrated maximal GATA2 (26±two-fold) stimulation of full-length rat Adcyap1 gene promoter activity at 30 ng/well and maximal GATA4 (42±nine-fold) stimulation of full-length rat Adcyap1 gene promoter activity at 10 ng/well (Fig. 1). These maximal doses were chosen for subsequent transfection experiments in the CV1 cell line.

**The GATA response maps to positions −242 to −172 of the rat Adcyap1 gene promoter**

We next wished to determine the region of the Adcyap1 gene promoter that confers GATA responsiveness. Transient transfection of serial 5′ deletions of the rat Adcyap1 gene demonstrated a dramatic loss of GATA2 and GATA4 responsiveness between nucleotide positions −402 and −77 (79±2 and 89±2%, respectively, compared with the −1916/+906 Adcyap1 promoter construct; Fig. 2A). A significant loss of GATA4 responsiveness was also observed with deletion between positions −915 and −402 (Fig. 2A). We chose to focus on the downstream region as it conferred both GATA2 and GATA4 effects.

As shown in Fig. 2B, a series of intermediate 5′-truncations between region −402 and −77 were tested to further localize the GATA-responsive region. Both the GATA2 and GATA4 responses were significantly decreased with deletion between positions −242 and −172 (80±9 and 72±6%, respectively, compared with the −402/+906 Adcyap1 promoter construct).

**Identification of a putative GATA binding site in the rat Adcyap1 gene promoter**

By sequence homology, three GATA-like elements, located at positions −210, −191, and −184, were identified within region −242 to −172. By electrophoretic mobility shift assay (EMSA), in vitro translated and endogenous LβT2, GATA2, and GATA4 proteins did not bind to a nucleotide probe spanning either position −210 or −184 (data not shown). However, as shown in Fig. 3B, in vitro translated GATA2 and GATA4 (lanes 2 and 4 respectively) bound to the WT probe spanning position −191. The presence of GATA2 or GATA4 in the identified complex was confirmed by the addition of specific antibodies for the corresponding protein (lanes 3 and 5). Endogenous GATA2 and GATA4 present in LβT2 nuclear extracts were also found to interact with this region of the Adcyap1 gene promoter (Fig. 3C). The loss of intensity of this complex with addition of the GATA2 antibody (lane 2) or GATA4 antibody (lane 3) verified the presence of GATA in this complex.

Interestingly, the −191 GATA site is flanked by two sites located at positions −205 and −179 with homology to the consensus CRE cis-element (Fig. 3A). Our laboratory has previously demonstrated CREB binding to the −205 CRE site, with mutation of this site blunting the ability of...
GATA proteins bind to CRE sites which flank the GATA cis-element.

Cold competition EMSA experiments were then performed in which LβT2 nuclear extract was incubated with the −209/−167 oligonucleotide probe and excess unlabeled oligonucleotides were added to determine their ability to compete for GATA binding (Fig. 3D). The oligonucleotides which were used contain the CRE and GATA sites present as WT or with the indicated mutations in the putative cis-elements. Mutation in the putative −191 GATA site eliminated the ability of the oligonucleotide to compete for GATA binding, but did not substantially alter the ability of CREB proteins to bind. Conversely, the ability of GATA to interact with the promoter region was not impacted by mutations in the CRE sites. Interestingly, mutations in both CRE sites were required to prevent CREB binding in this region.

**Mutations in the −205 CRE, −191 GATA, and −179 CRE sites, singly or in combination, decrease GATA2 and GATA4 effect**

We next wished to study the functional significance of mutation in the putative GATA and CRE sites on Adcyap1 gene promoter activity. Transient transfection of GATA2 or GATA4 expression vectors and reporter constructs containing the WT full-length (−1916/+906) rat Adcyap1 gene promoter or constructs containing mutations in these sites were conducted in CV1 fibroblast cells (Fig. 4).

Mutation at the putative −191 GATA cis-element decreased GATA2 and GATA4 stimulated Adcyap1 promoter activity by 50 ± 5 and 53 ± 6%, respectively, compared with WT. Mutation of the −205 CRE decreased GATA2 and GATA4 stimulated Adcyap1 promoter activity by 41 ± 3 and 41 ± 8%, respectively, while mutation at the −179 CRE decreased GATA2 and GATA4 stimulated

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Figure 3
GATA2 and GATA4 bind to the proximal rat Adcyap1 gene promoter on electrophoretic mobility shift assay (EMSA). (A) Depiction of the putative GATA cis-element and flanking CRE sites in the rat Adcyap1 gene promoter. (B) Binding by in vitro translated GATA2, GATA4, or unprogrammed reticulocyte lysate (RL) to a 5′-labeled oligonucleotide probe spanning positions −209 to −167 in the rat Adcyap1 gene promoter. (C) Interaction of GATA2 and GATA4 present in LβT2 gonadotrope nuclear extracts with the −209/−167 oligonucleotide probe. Antibodies directed against GATA2, GATA4, or CREB family members were added to the incubation mixture as indicated. (D) LβT2 nuclear extract was incubated with the WT −209/−167 Adcyap1 oligonucleotide probe and unlabeled oligonucleotide containing the WT sequence or with mutations in the CRE or GATA sites. Oligonucleotide competitors were added at 200-, 40-, and 8-fold molar excess. Shown are representative EMSA which have been performed a minimum of three times.
shown an important role for GNRH in mediating Adcyap1 promoter activity. We now wanted to confirm this observation in gonadotrope cell line as these cells express high levels of endogenous GATA protein (Lo et al. 2011).

As observed in the CV1 cells, a dramatic loss of Adcyap1 promoter activity occurred with truncation from position −402 to −77. The simultaneous loss of the GNRH response was expected as this region is known to contain the −205 CRE site as well as a −275 AP1 site, both of which have been shown to be critical for mediating the GNRH effect (Grafer et al. 2009). Additional transfection experiments compared the WT full-length rat Adcyap1 gene promoter to a reporter construct containing a mutation in the −191 GATA site. The presence of this mutation eliminated the ability of both GATA2 and GATA4 to stimulate the Adcyap1 promoter either alone or in the presence of GNRH, while the GNRH response was maintained (Fig. 5C and D). These data demonstrate that an intact −191 GATA site is required for cooperative activation of the rat Adcyap1 promoter by GATA and GNRH treatment.

siRNA knockdown of endogenous GATA2 or GATA4 blunts GNRH-stimulated Adcyap1 gene expression

As GATA2 and GATA4 significantly increase the ability of GNRH to stimulate Adcyap1 promoter activity, we reasoned that decreasing intracellular expression of these factors using a siRNA approach should blunt the ability of GNRH to stimulate endogenous Adcyap1 gene expression in LβT2 cells. As shown in Fig. 6, GNRH-induced Adcyap1 mRNA levels were significantly decreased in the presence of siRNAs directed against Gata2 or Gata4 (59±4 and 52±3%, respectively, relative to the NTA control siRNA). These data strongly support a requirement for GATA transcription factors in achieving maximal GNRH-stimulated Adcyap1 gene expression. No effect was observed on vehicle-treated Adcyap1 expression, likely due to the fact that Adcyap1 mRNA levels are very low in the basal state, preventing the ability to detect a further decrease (data not shown).

The average decrease in Gata2 mRNA levels using siRNAs directed against Gata2 was 51±4 and 55±4% in the absence and presence of GNRH respectively. The average decrease in Gata4 mRNA levels using siRNAs directed against Gata4 was 67±2 and 70±2% in absence and presence of GNRH respectively (data not shown). We have previously demonstrated a 60–70% decrease in GATA protein expression using an identical protocol (Lo et al. 2011).

Figure 4
Site-directed mutations in the −191 GATA, −205 CRE, or −179 CRE sites, either singly or in combination, blunt GATA-stimulated Adcyap1 promoter activity. CV1 cells were transiently transfected with GATA2 or GATA4 expression vectors and the full-length (−1916/+906) rat Adcyap1 gene promoter (WT) or constructs containing mutations in the −191 GATA, −205 CRE, and/or −179 CRE sites fused to a luciferase reporter vector. Vector only refers to the empty luciferase reporter construct, pGL3. The response in all mutated constructs was significantly decreased compared with the full-length construct (P < 0.001). All experiments were performed a minimum of three times with data expressed as the mean ± S.E.M.

Adcyap1 promoter activity by 48±4 and 36±6% respectively. Combinatorial mutations of the GATA and CRE cis-elements further decreased GATA-stimulated Adcyap1 promoter activity. Compared with the WT, all constructs containing mutations significantly decreased the effects of both GATA2 and GATA4 on Adcyap1 promoter activity (P < 0.001). These data demonstrate that the −191 GATA, −205 CRE, and −179 CRE sites all play an important role in GATA-mediated stimulation of the rat Adcyap1 promoter.

GNRH and GATA act cooperatively to stimulate Adcyap1 promoter activity in LβT2 gonadotrope cells

Having demonstrated the ability of GATA to increase Adcyap1 promoter activity in the CV1 fibroblast cell line, we now wanted to confirm this observation in gonadotrope LβT2 cells. Furthermore, as we have previously shown an important role for GNRH in mediating Adcyap1 promoter activity, the GATA response was tested following treatment with GNRH or vehicle for 6 h. Overexpression of GATA2 (Fig. 5A) or GATA4 (Fig. 5B) significantly increased the stimulatory effect of GNRH on Adcyap1 promoter activity. Note that the GATA response is lower in the gonadotrope cell line as these cells express high levels of endogenous GATA protein (Lo et al. 2011).
GATA augments pituitary Adcyap1 expression

Discussion

Initially described as a hypothalamic neuropeptide, ADCYAP1 is now known to be expressed in a wide range of tissues in which it exerts multiple physiologic effects. Despite growing interest in this peptide, surprisingly little is known about the transcription factors and associated DNA-regulatory regions which mediate expression of the Adcyap1 gene. We have previously reported that GNRH stimulates pituitary Adcyap1 promoter activity via CREB and the AP1 proteins (Grafer et al. 2009). We now add GATA to the list of transcription factors known to play a critical role in basal and GNRH-stimulated expression of the Adcyap1 gene.

Although highly homologous, GATA family members have been observed to vary in their effects on specific gene promoters as well as their activity within individual cell types and across physiologic states. This functional specificity has been attributed to differences in expression levels of the individual GATA proteins, as well as differences in the expression of cofactors and other transcription factors with which GATA factors are known to interact. In line with these prior observations, our results demonstrate that while GATA2 and GATA4 both markedly increase rat Adcyap1 promoter activity, subtle differences may exist in regards to the importance of specific nucleotide regions for achieving maximal stimulation. For example, deletion from nucleotide position −915 to −402 substantially decreased GATA4-mediated transactivation, but not GATA2, suggesting the presence of a cis-element in this region with specificity for GATA4 (Fig. 2). Characterization of this region will be of interest in future studies.

Our studies demonstrate that the CRE elements which flank the −191 GATA cis-element contribute to GATA-mediated stimulation of the Adcyap1 gene promoter, suggesting the presence of complex interactions between CREB and GATA factors on this promoter. Hong et al. (2006) have reported that GATA3 can form protein–protein bonds with CREB and a similar physical interaction may reasonably be postulated to occur with GATA2 and GATA4. In addition, they demonstrated that mutation of the CRE site markedly blunted the ability of GATA to stimulate expression of the tyrosine hydroxylase gene. Similarly, mutation of the CRE sites in the Adcyap1 promoter sequence blunts GATA-mediated stimulation. The proximity of the CRE and GATA sites suggests that the CREB and GATA proteins may bind to their respective DNA elements and to each other simultaneously to generate a maximal response. Of note, the EMSA
Adcyap1 stimulation of does not alter GATA4 protein expression and may actually reduce GATA protein expression. We have performed preliminary experiments which the simplest would be a GNRH-mediated increase in GATA response.

Figure 6
Effect of siRNA knockdown of GATA2 or GATA4 on GNRH-induced Adcyap1 mRNA expression. LβT2 cells were transfected with 100 nM of a non-targeting siRNA (NTA) or with 100 nM of siRNA directed against GATA2 or GATA4 followed by treatment with 100 nM GNRH for 6 h. Mouse Adcyap1 or siRNA target gene mRNA levels were quantified by qPCR. Results are expressed as percent relative to Adcyap1 expression in the GNRH-treated NTA transfected cells and represent the results from three experiments. *P<0.001 vs non-targeting control siRNA.

competition experiments did not suggest that binding by one factor was dependent on binding by the other, but subtle effects may be missed by this approach. Further studies with DNA-binding mutants and protein-DNA dimerization mutants will be required to characterize the mechanism by which the CRE sites contribute to the GATA response.

Perhaps surprisingly, endogenous Adcyap1 mRNA levels are very low in the LβT2 cell line despite the presence of significant amounts of GATA protein. This observation may be a reflection of the balance between stimulatory and inhibitory factors which regulate Adcyap1 promoter activity. At this time, a limited number of transcription factors have been identified which act on this promoter and it is quite possible that these cells also express high levels of a yet unidentified inhibitory factor. Of interest, Adcyap1 mRNA levels are much more readily detected in the αT3-1 gonadotrope cell line which is generally considered to be less differentiated than the LβT2 cell line, suggesting gain of an inhibitory factor with pituitary development (Grafer et al. 2009).

As shown in Fig. 5, GNRH augments GATA-mediated stimulation of Adcyap1 gene promoter activity. Multiple mechanisms can be postulated for this interaction of which the simplest would be a GNRH-mediated increase in GATA protein expression. We have performed preliminary experiments which suggest that 6 h of GNRH treatment does not alter GATA4 protein expression and may actually decrease GATA2 protein levels in LβT2 cells (data not shown). Kamesaki et al. (1996) observed a decrease in GATA1 protein and simultaneous increase in GATA2 protein expression in an erythroid cell line following activation of the PKC system with phorbol ester treatment. As increase in PKC activity results in an arrest in erythroid cell differentiation, they postulated that this quantitative switch in the ratio of GATA proteins was critical for the regulation of genes which mediate differentiation. Our dose–response data suggest that GATA4 may be more active than GATA2 at lower concentrations, albeit with caveats regarding possible differences in protein expression between constructs. Therefore, it is tempting to speculate that a decrease in GATA2 would allow for greater access of the more transcriptionally active GATA4 to the −191 GATA site.

GATA proteins also undergo hormonally mediated post-translational modifications, including acetylation and phosphorylation, which most commonly increase their functional activity (Towatari et al. 1995, Tremblay & Viger 2003, Hayakawa et al. 2004, Wang et al. 2005). It has been reported that GATA proteins can be phosphorylated following the activation of the PKA, PKC, or MAPK intracellular signaling systems, all pathways known to be activated by GNRH treatment (Liu et al. 2002, Fowkes et al. 2003, Haisenleder et al. 2003, Coss et al. 2007). Using two gonadotrope cell lines, αT3-1 and LβT2, Fowkes et al. (2002) demonstrated an increase in GATA binding to a consensus GATA nucleotide probe following activation of the MAPK (MEK) signaling system; however, it was not determined whether this was due to an increase in GATA protein levels or alteration in DNA-binding affinity. It is therefore possible that GNRH may increase transcriptional activity of one or both of the GATA proteins via post-transcriptional modifications rather than substantial changes in protein expression.

We have previously demonstrated that GNRH-mediated increases in rat Adcyap1 gene promoter activity depend, in large part, on the presence of an intact AP1-like site at position −275 as well as a CRE-like cis-element at position −205 (Grafer et al. 2009). As a general rule, the AP1 family of jun and fos proteins is expressed at low levels before hormonal stimulation, while transcriptional activity of the constitutively expressed CREB family members is modulated by phosphorylation state. Interestingly, GNRH treatment leads to the recruitment of the AP1 proteins, jun and fos, to both of these sites without detectable increases in phospho-CREB binding. These sites may be better described as composite AP1/CRE sites. The ability of the −179 CRE site to bind AP1 proteins was not investigated as the mutation only modestly blunted the
GNRH response. In any case, GATA family members have been shown to functionally interact with both AP1 family members and CREB proteins (Kawana et al. 1995, Hong et al. 2006). We, therefore, postulate a complex interaction between GATA proteins and both AP1 and CREB proteins acting at multiple sites in the proximal Adcyap1 gene promoter.

In summary, the data presented here demonstrate a central role for both GATA2 and GATA4 in mediating Adcyap1 gene expression in pituitary gonadotropes. Although we focused on a pituitary cell model, our finding may also be relevant to other cell types. For example, expressions of both ADCYAP1 (Gras et al. 1996, Scaldaferri et al. 1996, Shiода et al. 1996, Lee et al. 1999) and GATA transcription factors (LaVoie 2003) have also been demonstrated in ovarian granulosa cells and theca-interstitial cells. We propose that GATA transcription factors play an instrumental role in the regulation of Adcyap1 gene expression, and therefore, normal reproductive function.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

Funding
This work was supported by the National Institutes of Health Grant R01 HD054782 (to L M H).

Acknowledgements
We thank Drs Karen Braas and Victor May, who were instrumental in the development of the rat Adcyap1 promoter constructs that launched these studies.

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Received in final form 15 August 2013
Accepted 6 September 2013
Accepted Preprint published online 9 September 2013