MiRNA-143 mediates the proliferative signaling pathway of FSH and regulates estradiol production

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Abstract

MicroRNAs (miRNAs) play important regulatory roles in many cellular processes. MiR-143 is highly enriched in the mouse ovary, but its roles and underlying mechanisms are not well understood. In the current study, we show that miR-143 is located in granulosa cells of primary, secondary and antral follicles. To explore the specific functions of miR-143, we transfected miR-143 inhibitor into primary cultured granulosa cells to study the loss of function of miR-143 and the results showed that miR-143 silencing significantly increased estradiol production and steroidogenesis-related gene expression. Moreover, our in vivo and in vitro studies showed that follicular stimulating hormone (FSH) significantly decreased miR-143 expression. This function of miR-143 is accomplished by its binding to the 3′-UTR of KRAS mRNA. Furthermore, our results demonstrated that miR-143 acts as a negative regulating molecule mediating the signaling pathway of FSH and affecting estradiol production by targeting KRAS. MiR-143 also negatively acts in regulating granulosa cells proliferation and cell cycle-related genes expression. These findings indicate that miR-143 plays vital roles in FSH-induced estradiol production and granulosa cell proliferation, providing a novel mechanism that involves miRNA in regulating granulosa cell functions.

Introduction

Follicles are the functional units of the ovary that consist of oocytes and one or more layers of somatic granulosa cells. Ovarian follicular development is dependent on the proliferation and differentiation of the granulosa cells (Craig et al. 2007), and the estradiol synthesized from the granulosa cells is required for the structure and function of female reproductive tissues. Many extra- and intra-ovarian factors have been implicated in granulosa cell proliferation and estradiol synthesis, such as the pituitary gonadotropin, including the follicular stimulating hormone (FSH) and luteinizing hormone (LH) (Frishman et al. 1992).

MicroRNA (miRNA) are conserved, short non-coding RNAs (19-25bp) that act as important cellular regulators, influencing cell proliferation, apoptosis and differentiation (Mattes et al. 2007, Farazi et al. 2008). MiRNA precursors (pre-miRNAs) are generated in the nucleus, and are then cleaved to a mature functional miRNA by Dicer, the ribonuclease 3 (Hong et al. 2008). Mature miRNAs bind the 3′-untranslated regions
(3'-UTR) of target mRNAs thus promoting targeted mRNA degradation, translational repression or both (Stefani & Slack 2006, Sirotkin et al. 2009).

The role of miRNA in mammalian reproduction has been explored in several studies. It has been reported that Dicer is expressed in both oocytes and granulosa cells of the mouse ovary’s follicle (Lei et al. 2010). Conditional inactivation of Dicer1 in follicular granulosa cells leads to increased primordial follicle pool endowment and accelerates early follicle recruitment. More degenerated follicles have been found in Dicer1 KO mouse ovaries. (Hong et al. 2008). In addition, significant differences between KO and WT mouse ovaries were noted in the expression of certain follicle development-related genes, such as CYP19A1, which is the gene that encodes aromatase (Hong et al. 2008, Nagaraja et al. 2008, Stocco 2008), indicating that miRNAs are mechanistically involved in ovarian functions.

MiR-143 is a short RNA molecule, which is highly conserved in vertebrates (Song et al. 2011). Functional studies of miR-143 have been mainly focused on cardiac morphogenesis and cancer tissues (Chen et al. 2009, Wu et al. 2013). It has been documented that miR-143 suppresses the development of cancers by inhibiting cell proliferation (Xu et al. 2011a) and that miR-143 expression is reduced in several types of tumors, including colorectal cancer (Chen et al. 2009), prostate cancer (Clape et al. 2009) and human ovarian cancer (Iorio et al. 2007b).

Under normal physiological conditions, miR-143 is expressed in pregranulosa cells during primordial follicle formation which occurs between 17.5 dpc and approximately 4–5 dpp, and is also expressed in granulosa cells of primary, secondary and antral follicles in the mouse ovary. These cells participate in murine primordial follicle formation (Zhang et al. 2013) and play roles in FSH-induced folliculogenesis (Yao et al. 2009).

The V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog, also known as KRAS, is a key molecule in the EGFR/RAS/mitogen-activated protein kinase (MAPK) pathway (Malumbres & Barbacid 2003). KRAS has been found to be associated with cell proliferation and migration in response to growth factors (Downward 2003). Previous studies revealed that KRAS is a direct target of miR-143 in colorectal tumorigenesis and prostate cancer (Chen et al. 2009, Xu et al. 2011a).

In the present study, we found that miR-143 is mainly expressed in mouse ovarian granulosa cells and functions as a mediator of the FSH signaling pathway to regulate estradiol synthesis and secretion by targeting KRAS. Additionally, miR-143 is critical in regulating the cell proliferation in ovarian granulosa cells.

Materials and methods

Animals

Mice for this study were purchased from the Animal Institute of the Chinese Medical Academy (Beijing, China) and raised in standard temperature (25 ± 1°C) and light (12 h light, 12 h darkness cycle) conditions. All animal procedures were approved by the Chinese Association for Laboratory Animal Sciences. Female mice (Kun Ming white) at approximately 21 days were injected intraperitoneally with 10 U of pregnant mare serum gonadotropin (PMSG) to stimulate follicular development.

In situ hybridization (ISH)

MiR-143 ISH was carried out by using digoxigenin-labeled locked nucleic acid (LNA) probes. Mmu-MiR-143-3p miRCURY LNA microRNA detection probes (TGAGCTACAGTCTTTCTCTCA) and scrambled probes (CATTAATGTCGGACAACTCAAT) were purchased from Exiqon (MA, USA). The LNA probes were labeled with digoxigenin using a DIG oligonucleotide tailing kit (Roche) following the manufacturer’s instructions. After the ovaries were collected, all of the samples were fixed in 4% paraformaldehyde (PFA) in phosphate-buffered saline (PBS) treated with diethyl pyrocarbonate. The cryosections (10 µm thick) were prepared, and ISH was carried out as described previously (Obernosterer et al. 2007). The sections were examined under a DMRB light microscope (Leica).

Isolation of granulosa cells and cell culture

Granulosa cell isolation was performed as described previously (Hanoux et al. 2007, Fiedler et al. 2008, Teng et al. 2015). The ovaries were cleaned of the surrounding marginal tissue under a stereomicroscope and washed twice with DMEM/F12 medium. Granulosa cells were collected immediately by puncturing follicles from the isolated ovary, which had been cleaned as above with a 25-gauge needle in a Falcon dish. Granulosa cell suspensions were then centrifuged at 1200 × g for 5 min and resuspended in DMEM/F12 medium supplemented with 10% fetal bovine serum (FBS) (GIBICO, Carlsbad, CA, USA), 100IU/ml penicillin and 100 µg streptomycin.
sulfate. The cells were then counted, and viability was assessed. For the assay, cells were plated (1.0×10^5 cells/well) onto 6-well plates for 24 h at 37°C in a humidified atmosphere of 5% CO₂. After being cultured for 48 h, the primary granulosa cells were transfected.

MicroRNA and siRNA transfections

The transfections of the miR-143 inhibitor or mimics (Shanghai GenePharma Co., Ltd, China) were performed using Lipofectamine 2000 (Invitrogen) according to the manufacturer’s instructions. Six hours after transfection, the cells were collected for real-time PCR (RT-PCR) or cell proliferation analysis. The following oligos were used for cell transfection: NC-inhibitor (NC)-in (5'-CAGUAUUUGUGUAGUCAAA3'); mmu-miR-143 inhibitor (5'-GAGCUACAGUGCUUCAUCUA-3'); mmu-miR-143 mimics (5'-UGAGAUGAACGCUGUCUC-3', Reverse:5'-GCAGUGACAGUUCUCAU-3'); NC-mimics (NC -mi) (Forward: 3'-UUCCCGAAGCUGUCAGUTT-3'; Reverse: 5'-ACUGUAGCACUGUCCGAGA-ATF-3').

Real-time PCR

According to the protocol provided by the manufacturer, the total RNA of the granulosa cells was isolated using the Trizol Reagent (Takara, Tokyo, Japan). U6 RNA was used for normalization of microRNA expression. Reverse transcriptase reactions contained the purified total RNA (0.3 µg) and 50 nM RT primer (the RT-miR-143 stem-loop primer: CTCACTGTGGTCTGGAGTGCTGGCAATTC AGTGGAGGCTACA and the RT-U6 stem-loop primer: AAGCCTTTAACAAGGAGA-3'). M-MLV Reverse Transcriptase (Promega) was used according to the manufacturer’s instructions. The 15 µL reactions were incubated in a DNA Thermal Cycler 4800 for 30 min at 16°C, 30 min at 42°C and 5 min at 85°C. Real-time PCR was performed using a standard Takara SYBR Premix Ex Taq protocol on an Applied Biosystems 7500 Real-time PCR System (Applied Biosystems). The primer sequences are listed in Table 1, and the conditions were as follows: 95°C for 10 min, followed by 40 cycles of 95°C for 15 s and 60°C for 1 min. The relative abundance of the genes was determined using the 2-ΔΔCT method (Schmittgen 2001) with GAPDH as the reference gene using ABI PRISM 7500 equipped software (Applied Biosystems). All the experiments were performed in at least triplicate. The validation of the real-time PCR assays were conducted, and the results were showed in the Supplementary Figure 1 (see section on supplementary data given at the end of this article).

BrdU analysis

After transfecting with inhibitors and mimics and cultured as above, the granulosa cells were further cultured with 5′-bromo-2′-deoxy-uridine (BrdU, final concentration 20µg/ml) for 3h. They were then fixed, permeabilized and treated with 10% goat serum and incubated with biotinylated goat anti-mouse IgG and HRP-conjugated streptavidin (1:500, Jackson ImmunoResearch Laboratories, Inc., West Grove, PA, USA) at RT for 2h. Visualization was done using diaminobenzidine (DAB) with hematoxylin counterstaining. At least five random fields per well were counted for the labeled cells in three separate experiments. The BrdU labeling index was defined as the ratio of the number of BrdU-positive nuclei to the number of total nuclei within the fields.

Table 1 Sequences of the primers applied for real-time PCR.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Sequence of primers (5′→3′)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cyclin B1</td>
<td>F: TGGCCTCACAAAAAGCAGATGA R: GCTGTGGCAGCGTTCATTC</td>
</tr>
<tr>
<td>Cyclin D2</td>
<td>F: AACGGTCCAGAGAGAAAA R: AGGTGTAGCAGGACTTCA</td>
</tr>
<tr>
<td>Cyclin E2</td>
<td>F: AGGAGGCTATAAAGGACACC R: CATTTTATCGAGTAGGTGGCG</td>
</tr>
<tr>
<td>Cdk 4</td>
<td>F: CCCGCTGGTATGCTGCTCT R: CACTTGTCAACTGGGAGG</td>
</tr>
<tr>
<td>Kras</td>
<td>F: GCTGTGCCAGCGTGCTAATC R: CTCGCTTCGGCAGCAC</td>
</tr>
<tr>
<td>Cdk 6</td>
<td>F: GAGGGTGCTTCAAGACCGCACCC R: AGGAGGCTATAAAGGACACC</td>
</tr>
<tr>
<td>Star</td>
<td>F: AGTTGCTATGCTTCTTTGG R: TCAGCTTCCAGAAACCCGTTCA</td>
</tr>
<tr>
<td>3B-hsd</td>
<td>F: CACCTGTCAGACTGGGAGG R: GAGAAGACCAAGGAGATT</td>
</tr>
<tr>
<td>P450ccc</td>
<td>F: ACGTGATCAGAGCTTCA R: AGGAGGCTATAAAGGACACC</td>
</tr>
<tr>
<td>Cyp19a1</td>
<td>F: CATTTTATCGAGTAGGTGGCG R: AGGAGGCTATAAAGGACACC</td>
</tr>
<tr>
<td>17B-hsd1</td>
<td>F: GACGGTTCACAGACCCGTTCA R: CACCAACCAGACCGTTCAAT</td>
</tr>
<tr>
<td>U6</td>
<td>F: GCTGGTTCTGGGAGCGTCA R: AAGCCTTCCAGAAATTTGT</td>
</tr>
<tr>
<td>GAPDH</td>
<td>F: GTGTGCTTCCTGGAGCTTCA R: GGGTGTTCCAGGGTTTCTTA</td>
</tr>
</tbody>
</table>

F, forward primer; R, reverse primer.
Table 2

<table>
<thead>
<tr>
<th>CREBS-3 UTR</th>
<th>Mut-CREBS-3 UTR</th>
<th>KRAS-3 UTR</th>
<th>Mut-KRAS-3 UTR</th>
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<td>tctgcctttcacaaaatatagggcataacagtggccctgtggtctctgtccctgctggactatgaggactggatgtctgtctgatttttaagcaaatcactgtctgcttggttttgacggcatgcaagacattaacctcccagccgtg</td>
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<td>aaatatcatcagctgagagctgtctgtctgtcatgtcttcatggcttgccatggttttgactttgggtctctggtggtctggagacacttcatcctccagaaccccgctgtaaatag agagctgtctgtctgtctttgactttgggtctctggtggtctggagacacttcatcctccagaaccccgctgtaaatag</td>
<td>aaatatcatcagctgagagctgtctgtctgtcatgtcttcatggcttgccatggttttgactttgggtctctggtggtctggagacacttcatcctccagaaccccgctgtaaatag agagctgtctgtctgtctttgactttgggtctctggtggtctggagacacttcatcctccagaaccccgctgtaaatag</td>
</tr>
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Radioimmunoassay (RIA)

Transfected granulosa cells were cultured in FBS-free DMEM/F12 (phenol red-free) medium for 24 h. The medium was then collected for measuring estradiol and progesterone levels, and the cells were lysed in 1 mL Trizol for gene determination. Estradiol/progesterone radioimmunoassay reagents were provided by the Beijing North Institute Biological Technology (Beijing, China). Experiments were performed at least three times. The experiment was performed according to the manufacturer’s instructions. The minimum detectable concentration was 5 pg/mL for estradiol and 0.2 ng/mL for progesterone. For each radioimmunoassay, the intra- and interassay coefficients of variation were less than 10% and 15%, respectively.

Western blot

Granulosa cells were lysed with RIPA buffer (50 mM Tris–HCl pH 7.4, 150 mM NaCl, 1% TritonX-100, 1% sodium deoxycholate, 0.1% SDS) containing 1 mM phenylmethylsulfonyl fluoride (PMSF). The protein concentration of each group was determined by using the BCA assay reagent (Vigorous Biotechnology, Beijing, China) according to the manufacturer’s recommendations. Equal amounts of protein (50 μg) were electrophoresed on an 11% sodium dodecyl sulfate–polyacrylamide gel (SDS-PAGE), and the proteins were transferred to polyvinylidene difluoride (PVDF) membrane (Bio-Rad Laboratories). The membrane was blocked with 5% (w/v) nonfat dry milk in 0.05 M, pH 7.4 tris-buffered saline (TBS) for 3 h and incubated with the KRAS antibody (1:1000, abs115469, absin, Shanghai, China) and an internal control GAPDH, the internal control was replaced with TUBLIN antibody (1:500, 6G7, Developmental Studies Hybridoma Bank). The PVDF membrane was then washed three times for 30 min in TBST (0.1% Tween-20 in TBS) and incubated for 2 h with horseradish peroxidase-conjugated goat antirabbit IgG. After washing for 30 min with 3 changes of TBST, the membrane was treated with the Pierce™ ECL 2 Western blot substrate (Thermo scientific). The relative intensity of each blot was assessed and analyzed with the Alphalmager 2200 software package. The intensity values pertaining to each group were normalized against the optical density of GAPDH corresponding to the same group within a single gel and expressed in terms of the means ± s.e.m. of 3 independent experiments.

Human embryonic kidney 293T cells culture and Luciferase reporter assay

The human embryonic kidney 293T cell line (293T) was grown in Dulbecco’s modified Eagle’s medium (DMEM; GIBCO) containing 10% (V/V) FBS (GIBCO, Grand Island, NY, USA) and 1% penicillin streptomycin. The cells were also incubated at 37°C in a humidified atmosphere of 5% CO2.

The dual-luciferase reporter genes were constructed using the psiCHECKTM-2 vector (Promega) and the 3′-UTR sequences of mouse CREBS and KRAS. The KRAS 3′-UTR fragment cloning was done using overlap PCR (Table 2), and Renilla luciferase 3′ UTR was introduced between the NotI and Xhol sites. The firefly luciferase vector was used for internal reference. The 293T cells were transfected using Lipofectamine2000 with a mixture containing 200 ng/mL of the dual-luciferase reporter plasmid and 40 nM miR-143 mimics. Cells were transfected with the mut-KRAS vector, serving as a control for normalization. Luciferase activity was measured by a Modulus™ II microplate multimode reader.
reader (Promega), 24 h post transfection using a Dual-Lucy Assay Kit (Vigorous Biotechnology Beijing Co., Ltd, China). All transfections were repeated independently at least three times.

Statistical analysis

All experiments were independently performed three times with different cell preparations in each experiment. Qualitative data reported are representative results obtained from the replicate experiments and presented as mean±S.E.M. Statistical analysis was performed using SPSS 10.0 (SPSS, Inc.). The t-test was used to compare the treatment and control samples, and one-way analysis of variance (ANOVA) was used when more than two groups were compared. When differences were observed using ANOVA, pairwise comparisons were made using the t-test. A P value<0.05 was considered to be statistically significant.

Results

MiR-143 expression in the mouse ovary

In order to identify the functions of miR-143 in the mouse ovary, we initially examined miR-143 expression in the mouse ovary by real-time PCR and ISH. The real-time PCR results showed that miR-143 was expressed at very low levels from E11.5 to E15.5, after which ovarian miR-143 expression levels sharply increased and persisted until the adult mouse (Fig. 1A). We further examined the expression of miR-143 in granulosa cells and oocytes by using real-time PCR, and the result revealed that the expression levels of miR-143 in granulosa cells are significantly higher than those in oocytes (P < 0.01) (Fig. 1B).

We then localized miR-143 expression in the adult ovary by using a digoxingenin-labeled LNA probe (a scrambled probe was used as a negative control), and the results showed that the miR-143 ISH signal was localized to granulosa cells of primary, secondary and antral follicles (Fig. 1C).

MiR-143 regulates estradiol production

Since the main function of granulosa cells is to secrete estradiol and progesterone, which modulate the structure and function of female reproductive tissues, we hypothesized that miR-143 is involved in regulating estradiol and progesterone production. To confirm this deduction, the miR-143 in the cultured granulosa cells was, respectively, overexpressed and knocked down by transfecting the miR-143 inhibitor and mimics. The results showed that the miR-143 inhibitor downregulated miR-143 by 78.6%, while the mimics upregulated miR-143 expression 56-fold (Fig. 2A). Meanwhile, we assessed the effects of the miR-143 inhibitor and mimics on estradiol production in the cultured granulosa cells, and the results revealed that miR-143 mimics decreased estradiol level by 15%. In contrast, the miR-143 inhibitor considerably increased estradiol release by 30% (P < 0.05) (Fig. 2B). It was out of our expectation that neither the miR-143 inhibitor nor the mimics would have a significant effect on progesterone secretion (P > 0.05) (Fig. 2C).

We further analyzed the effect of the miR-143 inhibitor and mimics on the expression of genes related to the estradiol synthesis, including STAR, P450scc, 3B-HSD, CYP19A1 and 17B-HSD1 in isolated granulosa cells. The results show that the miR-143 inhibitor upregulated 3B-HSD, CYP19A1 and 17B-HSD1 expressions not only at mRNA level but also at protein level. (Fig. 2D, E, G, H, I).
MiR-143 regulates estradiol and steroidogenesis-related genes expression. Periovulatory granulosa cells from large follicles stimulating by PMSG were cultured. (A) Overexpression and inhibition efficiency of miR-143 mimics or inhibitor, transfected into granulosa cells after 24 h. NC-in/NC-mi, miRNA inhibitor/mimics nonsense control, inhibitor: miR-143 inhibitor; mimics: miR-143 mimics. Results are mean ± s.e.m. of 3 independent experiments, ***P < 0.001 (t-test). (B) and (C) Granulosa cells were transfected with miR-143 mimics and mimics control, or miR-143 inhibitor and inhibitor control. The culture media were collected for measuring estradiol and progesterone levels at 24 h after transfection. Results are mean ± s.e.m. of 4 independent experiments, ***P < 0.001 (t-test). (D) and (E) mRNA levels of steroidogenesis-related enzymes expression in the granulosa cells were measured by real-time PCR after being transfected with an inhibitor and mimics for 24 h. Results are mean ± s.e.m. of 3 independent experiments done in triplicate and normalized to their respective control (*P < 0.05; **P < 0.01 and ***P < 0.001, by ANOVA. NS, not statistically significant). (F) Analysis of the 3B-HSD protein. Granulosa cells were transfected for 24 h and protein extracts were analyzed by Western blotting. (G) Quantification of 3B-HSD protein levels. Results are mean ± s.e.m. of 4 independent experiments; (*P < 0.05, by t-test). Granulosa cells transfected with miR-143 mimics and mimics control, or miR-143 inhibitor and inhibitor control for 24 h. (H) Western blotting analysis of CYP19A1 in granulosa cells transfected with miR-143 mimics and mimics control, or miR-143 inhibitor and inhibitor control for 24 h. (I) Quantification of CYP19A1 protein levels. Results are mean ± s.e.m. of 3 independent experiments; (*P < 0.05, by t-test). (J) Western blotting analysis of 17B-HSD in granulosa cells transfected with miR-143 mimics and mimics control, or miR-143 inhibitor and inhibitor control for 24 h. (K) Quantification of 17B-HSD protein levels. Results are mean ± s.e.m. of 4 independent experiments; (*P < 0.05, by t-test).
I and J), and conversely, the miR-143 mimic decreased 3B-HSD, CYP19A1 and 17β-HSD1 mRNA and protein levels ($P < 0.05, P < 0.01$) (Fig. 2E, F, G, H, I and J). However, miR-143 has no effect on STAR and P450scc expressions ($P > 0.05$) (Fig 2D and E). These data demonstrated that miR-143 negatively regulated steroidogenesis-related gene and protein expression.

**FSH decreased miR-143 expression in vivo and in cultured granulosa cells in vitro**

It is known that FSH is one of the most important hormones that regulate the ovary’s functions, including steroidogenesis. We thus hypothesized that FSH induces steroidogenesis by affecting miR-143 expression. To confirm this assumption, we assayed the ovary’s miR-143 expression. There was no significant change except that the miR-143 level was significantly lower at estrous stage (Fig. 3A). However, 10U (Wei et al. 2015) of PMSG decreased miR-143 levels after 48 h treatment (Fig. 3B).

Furthermore, the separated mouse granulosa cells were cultured in DMEM/F12 medium with the addition of 100 ng/ml FSH (Wayne et al. 2007). MiR-143 levels were assayed after 0 (control) 6h, 12h and 24h of FSH treatment, and the effect of FSH on miR-143 expression was measured. The FSH treatment decreased miR-143 levels about 83%, 70% and 88%, respectively (Fig. 3C). We then treated the cultured granulosa cells with 0, 1, 10 and 100 ng/ml FSH for 6 h and assayed the miR-143 levels. The results showed that 10 and 100 ng/ml FSH significantly decreased miR-143 expressions ($P < 0.05, P < 0.01$), but 1 ng/ml FSH had no obvious effects on miR-143 expression (Fig. 3D). These data revealed that the inhibiting effect of FSH on miR-143 expression was closely related to the FSH dose and treatment time.

Since FSH influences CYP19A1 expression and estradiol secretion through different signal pathways,
such as PKA, PKC, ERK1/2 and P38 (Meroni et al. 2004, Hunzicker-Dunn et al. 2012, Fa et al. 2013, Chen et al. 2014), we determined to find out the signaling pathway in which miR-143 is regulated by FSH. Cultured granulosa cells were separately pretreated with CH (a PKC inhibitor), H89 (a PKA inhibitor), PD98059 (an ERK1/2 inhibitor), SP600125 (a JNK inhibitor) and SB203580 (a P38 inhibitor) for 1 h, and then treated with 100 ng/ml FSH for 6 h. MiR-143 expression was then assayed by real-time PCR. The results showed that miR-143 expression was rescued by H89 and CH treatments. However, the other inhibitors had no effects on miR-143 expression. This suggested that FSH decreased miR-143 expression through the PKA or PKC pathways (Fig. 3E).

The expression level of miR-143 after incubating mouse granulosa cells with LH (1 U/ml) for 0, 6, 12 and 24 h was examined by real-time PCR, and the results revealed that LH had an enhancing effect on miR-143 expression after the cells were cultured for 6, 12 and 24 h (Fig. 3F). These data revealed that LH upregulated the expression of miR-143.

**MiR-143 mediates the FSH signaling pathway influencing estradiol production**

FSH is a key factor influencing estradiol production. To confirm that miR-143 is involved in the FSH signaling pathway, cultured granulosa cells were transfected with miR-143 mimics and miR-143 inhibitor for 24 h and then treated with 100 ng/ml FSH for 12 h. CYP19A1 expression and estradiol levels were then measured. The results showed that miR-143 inhibitor increased both basal and FSH-enhanced estradiol production and CYP19A1 expression (Fig. 4A and C). We also found that as expected, FSH increased estradiol secretion and upregulated CYP19A1 expression in cells transfected with negative control mimics, but this effect vanished in cells that overexpressed miR-143 (Fig. 4B and D). These results demonstrated that miR-143 negatively regulated FSH’s stimulatory action on estradiol production.

**MiR-143 is involved in granulosa cell proliferation**

Estradiol levels generally change through two pathways, one is the cell state, such as the status of enzymes important for the synthesis of estradiol, another is through a change in the number of cells that secrete estradiol. The above experiments have verified the effects of miR-143 on the expression of estradiol synthesis-related genes. To explore the effects of miR-143 on granulosa cell proliferation, BrdU staining was carried out after transfection of miR-143 mimics or miR-143 inhibitor for 24 h or 48 h (Supplementary Fig. 2). We counted BrdU-positive cells in more than 5000 cells per treatment. There was roughly 44% less BrdU-positive cells in miR-143 mimics than in the control group (P < 0.05). MiR-143 silencing significantly increased the number of cells compared to the controls (P < 0.01) (Fig. 5A and B).

Furthermore, we analyzed the effect of miR-143 on the expression of genes related to the cell cycle, including Cyclin B1, D2, E2 and Cdk 4 and 6 in isolated granulosa cells after transfection with the miR-143 inhibitor and mimics. The results showed that the miR-143 inhibitor increased Cyclin B1, D2, E2 and Cdk4, 6 mRNA levels (P < 0.01, P < 0.001) (Fig. 5C), and conversely, miR-143 mimics decreased Cyclin B1, D2, E2 and Cdk4, 6 mRNA levels (P < 0.05, P < 0.01) (Fig. 5D). These data demonstrated that miR-143 negatively regulated the proliferation of granulosa cells.

![Figure 4](image)

**Figure 4**

MiR-143 is involved in the FSH signaling pathway. Periovulatory granulosa cells from large follicles stimulating by PMSG were cultured. (A) and (B) Estradiol secreted by granulosa cells. The cells were transfected with either miR-143 inhibitors or miR-143 mimics. Twenty-four hours later, the cells were treated with FSH (100 ng/ml) for 12 h. Results are mean ± s.e.m. of 4 independent experiments, *P < 0.05 (t-test). (C) and (D) mRNA levels of CYP19A1. Results are mean ± s.e.m. of 4 independent experiments done in triplicate and normalized to their respective control. (*P < 0.05; **P < 0.01 by ANOVA).
**KRAS is a direct target of miR-143**

To determine the potential target of miR-143 affecting estradiol synthesis and granulosa cells proliferation in mouse granulosa cells, we used computational prediction algorithms, including miRanda and pictar. Among the putative target genes, KRAS plays important role in cell proliferation and CREB5 responses to the PKA signaling. In addition, previous reports have showed that KRAS is a target of miR-143 in other organs (Chen et al. 2009, Xu et al. 2011b, Wu et al. 2013). We predicted that CREB5 and KRAS were candidates of miR-143 targeting genes (Fig. 6A). The 3’ UTR of CREB5 and KRAS mRNA were then inserted downstream from the Renilla luciferase coding region in the reporter vector (Table 2, Fig. 6B and C). A 3’ UTR of CREB5 mRNA with eight mutated nucleic acids and a 3’ UTR of KRAS mRNA with six mutated nucleic acids in the seed sequence were used as negative controls (Table 2, Fig. 6B). Each reporter construct was separately co-transfected into 293T cells with the miR-143 mimicking molecules. Compared to the mut-KRAS-3’UTR control, the luciferase activity declined by about 40% after the transfection with miR-143 mimics and the KRAS-3’UTR reporter vector (Fig. 6E). However, there was no difference between the NC-mimics and the miR-143 mimics group after transfecting the cells with the CREB5-3’UTR reporter vector (Fig. 6D). Further functional analysis indicated that miR-143 overexpression in granulosa cells resulted in a reduction of KRAS protein levels, whereas the inhibition of miR-143 significantly increased the KRAS protein levels (Fig. 6G and H) without affecting KRAS mRNA levels (Fig. 6F). These results indicated that KRAS is the direct target gene of miR-143.

**KRAS is involved in the signaling pathway of FSH that regulates estradiol production**

To identify whether KRAS is involved in the signaling pathway of FSH that regulates estradiol production, cultured granulosa cells were treated with 0 ng/mL, 1 ng/mL, 10 ng/mL and 100 ng/mL FSH for 6h, and KRAS expression was assayed. The results showed that FSH sharply increased KRAS mRNA levels at 10 ng/mL and 100 ng/mL, and there was no obvious influence at 1 ng/mL (Fig. 7A). Western blot analysis also showed that FSH significantly upregulated KRAS protein levels at 10 ng/mL and 100 ng/mL (Fig. 7B and C). However, in the presence of miR-143 mimics, FSH fails to increase KRAS expression (Fig. D and E). We then constructed three kinds of KRAS siRNA and chose the KRAS siRNA1 which had the highest inhibition on KRAS mRNA (Fig. 7F). KRAS siRNA1 partly inhibited the effect of FSH on estradiol levels by 45% (Fig. 7G). These preliminary results demonstrated that KRAS plays an important role in mediating the regulatory effect of FSH on estradiol production.
Discussion

We detected miR-143 expression in the mouse ovary from 17.5dpf to 4dpp, the period of primordial follicle formation (Zhang et al. 2013). Previous studies revealed that miR-143 is located in granulosa cells of primary, secondary and antral follicles in the mouse ovary (Yao et al. 2009). However, the functions of miR-143 in the postnatal ovary have not been established. Our results presented here show that miR-143 is located in the granulosa cells of the mouse ovary, which infers that miR-143 plays important role in regulating the follicular development through its effect on granulosa cell proliferation and related ovarian hormone secretion. Furthermore, by using a silencing and overexpression approach, we demonstrate that miR-143 negatively regulates granulosa cell proliferation and mediates FSH-induced estradiol production by targeting KRAS. Our results revealed that miR-143 mimics decreased estradiol level by 15% and the miR-143 inhibitor considerably increased estradiol release by 30%. While a 15–30% variation in estradiol levels is a moderate change, as hormones play a role by regulating the amount and activity of regulatory factors and can amplify the regulatory signal, this can lead to significant changes in the body. In addition, the earliest occurrence of any disease is caused by a long-term minimal alteration.

Figure 6

MiR-143 binds to KRAS-3'UTR, which regulates its protein expression. (A) The predicted miR-143 binding site in CREB5-3'UTR and KRAS-3'UTR from www.mirNA.org. (B) Schematic of inserted CREB5-3'UTR and KRAS-3'UTRs sequences. (C) The psi-CHECKTM-2 reporter vector map. (D) and (E) Relative luminescence intensity detected by the Modulus TMII microplate multimode reader after miR-143 mimics and dual-luciferase vector were co-transfected into 293T cells for 24h. Results are means ± S.E.M. of three independent experiments done in triplicate and normalized to their respective control. (**) P < 0.01. NS, not statistically significant). (F) Quantification of KRAS mRNA levels. Periovulatory granulosa cells from large follicles stimulating by PMSG were cultured. Granulosa cells were transfected with an NC-inhibitor (NC-in), miR-143 inhibitor, NC-mimics (NC-mi), miR-143 mimics for 6h. The data are mean ± S.E.M. for multiple separate transfactions (n = 3). (NS, not statistically significant by t-test). (G) Analysis of the KRAS protein. Granulosa cells were transfected an NC-inhibitor (NC-in), miR-143 inhibitor, NC-mimics (NC-mi), miR-143 mimics for 24h and protein extracts were analyzed by Western blotting. (H) Quantification of KRAS protein levels. Results are mean ± S.E.M. of three independent experiments (* P < 0.05; NS, not significant). Data are presented as mean ± S.E.M. (n = 3) (P < 0.05, by t-test).
For example, polycystic ovary syndrome is triggered by endocrine disorders. Detailed in vivo experiments are required to further investigate the physiological function of miR-143 in the ovary.

MiR-143 expression has been detected in different tissues, such as the ventricular chamber (Deacon et al. 2010) and several types of tumors (Chen et al. 2009, Clape et al. 2009), and functional studies have shown that miR-143 is required for the ventricular chamber formation (Deacon et al. 2010), and tumor cells proliferation (Iorio et al. 2007a). In this study, the expression of miR-143 in the developing mouse ovary sharply increased at 17.5 dpc, when primordial follicle begins to formation, and persisted until the adult mouse. ISH results showed that miR-143 is expressed in the granulosa cells of primary, secondary and antral follicles, and indicated that miR-143 plays an important role in granulosa cell functions.

FSH has been implicated in regulating granulosa cells proliferation/differentiation and estradiol secretion, which are critical for the structure and function of female reproductive tissues (Pasapera et al. 2005). Previous reports have shown that several miRNAs are under control of FSH in granulosa cells, including miR-143 (Yao et al. 2009). We therefore postulated that miR-143 participates in FSH-induced estradiol production in granulosa cells. RIA and real-time PCR results revealed that the estradiol levels and the mRNA levels of steroidogenic enzymes, including 3B-HSD, CYP19A1, and 17B-HSD1, increased when miR-143 was silenced, suggesting that miR-143 acts as a negative regulating molecule in estradiol synthesis and secretion in granulosa cells.

FSH has long been considered as a key regulating factor of estradiol production by the granulosa cells during the development of the dominant follicle.
(Erickson 1983). In the estradiol pathway, FSH induces the expression of P450arom (the CYP19 gene) and the type 1 17B-hydroxysteroid dehydrogenase (17B-HSD), which metabolize theca-derived androstenedione to estradiol (Erickson 1983). In the current study, the expression levels of miR-143 decreased in the estrous stage of the ovarian estrous cycle and injecting the ovary with PMSG, when the FSH levels were high in vivo. Furthermore, FSH decreased miR-143 expression in cultured granulosa cells through the PKA-ERK1/2 signaling pathway in vitro, which subsequently decreased aromatase activity and estradiol production.

In order to assess whether the effect of FSH on estradiol production depends on miR-143, we examined FSH-induced estradiol production with a miR-143 inhibitor or mimics. Our results revealed that the miR-143 inhibitor increases both basal and FSH-enhanced estradiol production and increases the mRNA levels of estradiol-generating enzymes, including CYP19A1 and 17B-HSD1, suggesting that miR-143 plays a negative regulatory role in FSH-induced estradiol synthesis and production.

It is well documented that miR-143 is an anti-proliferation gene in many cancer cells (Chen et al. 2009, Clape et al. 2009). Since follicular development is accompanied by a large proliferation of their surrounding granulosa cells, we thus postulated that miR-143 is involved in the proliferative regulation of granulosa cells. Our results demonstrate that there is a sharp reduction in granulosa cell proliferation and in the expression of the genes that are closely associated with cell proliferation when miR-143 was overexpressed, and the reverse happened when we inhibited miR-143. These results demonstrate that miR-143 plays a negative role in regulating granulosa cell proliferation similar to its function in cancer cells. However, further in vivo experiments are required to further elucidate the physiological function of miR-143 in the ovary.

Effective inhibition of mRNA translation by microRNAs is known to be mediated by binding to specific 3′UTR sites. KRAS 3′UTR has a miR-143 binding sequence. KRAS is a small G-protein that is correlated with colorectal cancer cell proliferation (Fan et al. 2009, Liu et al. 2011), and KRAS is the target gene of miR-143 in colorectal tumorigenesis (Chen et al. 2009). Moreover, KRAS is highly expressed in granulosa cells, which is involved in follicle development and ovulation (Fan et al. 2008). Here, we demonstrated that miR-143 directly binds the KRAS gene. Furthermore, our in vitro experiments have shown that FSH downregulated miR-143 and upregulated KRAS in granulosa cells. miR-143 repressed the luciferase reporter gene expression by targeting the 3′UTR binding site in vitro, indicating a direct interaction site between miR-143 and 3′UTR of KRAS.

KRAS, an oncogene, is suggested to play a pivotal role in the transduction of several growth or differentiation factor stimuli. It has been reported that the expression levels of KRAS are related to the malignant degree of cancers, including glioma, breast cancer, melanoma and other cancers (Fitzgerald et al. 2015, Ze-An Qiu1 2016). In this study, FSH increased KRAS protein expression through the downregulation of miR-143, and KRAS mediated the roles of miR-143 to influence estradiol production and function. These results not only validate the functional relevance of KRAS (a target gene of miR-143) in FSH/miR-143-stimulated mouse granulosa cells, but also provide a new molecular mechanism on FSH regulation of KRAS. It was reported that miR-143 decrease prostate cancer cells proliferation and migration and enhances their sensitivity to docetaxel through suppression KRAS (Xu et al. 2011a). In the current study, we demonstrate that miR-143 negatively regulates the proliferation of granulosa cells and its target gene is KRAS. These results indicated that KRAS may be a link between miR143 and proliferation.

In conclusion, we have shown that miR-143 is highly expressed in the mouse ovarian granulosa cells, and it acts as a negative mediator to regulate FSH-induced estradiol production by targeting KRAS. In addition, miR-143 also regulates granulosa cells proliferation. In the light of our study, tissue-specific microRNAs, such as miR-143, can be used as novel targets for physiological or pharmacological interventions in diseases resulting from abnormal ovarian granulosa cell proliferative and hormone secretion.

**Supplementary data**
This is linked to the online version of the paper at http://dx.doi.org/10.1530/JOE-16-0488.

**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.

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Author contribution statement
Sheng Cui conceived and designed the experiments; Li Zhang and Xiaoxin Zhang carried out the experiments; Li Zhang, Xuejing Zhang and Xiaoxin Zhang analyzed the data; Xiaoxin Zhang and Lei Li provided the reagents/materials/analysis tools; and Sheng Cui and Li Zhang wrote the manuscript.

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