# ORIGINAL ARTICLE

# Oestrogen induces epithelial-mesenchymal transition in endometriosis via circ\_0004712/miR-148a-3p sponge function

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### Abstract

Endometriosis is a common, chronic gynaecologic disease affecting up to 10% of women in their reproductive age and leading to pain and infertility. Oestrogen  $(E_2)$ -induced epithelial-mesenchymal transition (EMT) process has been considered as a key factor of endometriosis development. Recently, the dysregulated circular RNAs (circRNAs) have been discovered in endometriosis tissues. However, the molecular mechanism of circR-NAs on the E<sub>2</sub>-induced EMT process in endometriosis is still unknown. Here, we demonstrated that circ\_0004712 up-regulated by E<sub>2</sub> treatment in endometrial epithelial cells. Knock-down the expression of circ\_0004712 significantly suppressed E2-induced cell migration activity. Meanwhile, we identified miR-148a-3p as a potential target miRNA of circ 0004712. Inhibited the expression of miR-148a-3p could recovered the effect of circ\_0004712 knock-down in E2-treated endometrial epithelial. Furthermore, Western blot assay showed that E2 treatment could increase the expression and activity of β-catenin, snail and N-cadherin and reduce the expression of E-cadherin. The expression and activity of  $\beta$ -catenin pathway were recovered by circ\_0004712 knock-down or miR-148a-3p overexpression. Altogether, the results demonstrate that circ\_0004712/ miR-148a-3p plays an important role in E2-induced EMT process in the development of endometriosis, and the molecular mechanism may be associated with the β-catenin pathway. This work highlighted the importance of circRNAs in the development of endometriosis and provide a new biomarker for diagnosis and therapies.

### KEYWORDS

circ\_0004712, EMT, endometriosis, miR-148a-3p,  $\beta$ -catenin

He and Liu are Co-first authors.

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Endometriosis is a chronic disease in reproductive age women, which characterized as the ectopic growth of endometrial-like tissues outside the uterine cavity, resulted in chronic pelvic pain and infertility.<sup>1</sup> Due to the lack of effective biomarkers and treatment options, this chronic disease severely impairs patients' quality of life and imposes a lot of economic burden.<sup>2</sup> Therefore, exploring the effective markers for identifying the mechanisms related to exact pathogenesis of endometriosis is very important for improving the diagnosis and therapies.

Previous studies have demonstrated that abnormal oestrogen ( $E_2$ ) secretion is associated with the pathogenesis of endometriosis.<sup>3-5</sup> Using aromatase inhibitor to suppress the activity of aromatase, which is a key enzyme to produce oestrogen, has been demonstrated to be an effective treatment for this disease.<sup>6</sup> However, the molecular mechanism of  $E_2$  on the development of endometriosis has not been fully clarified. Recent study found that  $\rm E_2$  could induce epithelial-mesenchymal transition (EMT) process during the development of endometriosis.^7

Epithelial-mesenchymal transition is a biological process that promotes the polarized epithelial cell to process a mesenchymal phenotype, in which the epithelial cell obtain the ability of migration, invasion and re-localization.<sup>8</sup> The abnormal activation of EMT programs is considered as a key factor in tumour invasiveness and metastasis, and other pathological processes.<sup>9</sup> Many studies revealed that an enhanced EMT-like process was occurred in the establishment of ovarian endometriosis,<sup>10-12</sup> but the molecular mechanism of oestrogen on inducing EMT process of endometrial epithelial cells still unknown.

Circular RNAs (circRNAs) are a number of non-coding RNAs, which have been considered as a gene regulator at transcriptional or post-transcriptional level.<sup>13</sup> Because of its structure, it can stable expressed in cells and often act as miRNAs inhibitors by sponging miRNAs. Therefore, circRNAs could be potential biological regulators for recognizing the molecular mechanisms of disease and finding effective diagnostic biomarkers or therapeutic targets.

**TABLE 1**The primers used for qPCR

Symbol	Sequences (5'-3')
GAPDH-F	ACAACTTTGGTATCGTGGAAGG
GAPDH-R	GCCATCACGCCACAGTTTC
circ-F	AGCAGCACGATGTGGA
circ-R	CCTTTTTCTTGGTGCCAATC
miR-F	GCGCTCAGTGCACTACAGAA
miR-R	AACTGGTGTCGTGGAGTCGGC
miR-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACACAAAG
U6-F	CTCGCTTCGGCAGCACA
U6-R	AACGCTTCACGAATTTGCGT





**FIGURE 1** Effect of  $E_2$  on the expression of circ\_0004712 and cell migration. A, The expression of circ\_0004712 in  $E_2$ -treated Ishikawa and End1/E6E7 cells was tested by qPCR. Results show as mean ± SD. B, Cell migration of Ishikawa and End1/E6E7 cells after  $E_2$  treatment was analysed by transwell assay



**FIGURE 2** Effect of circ\_0004712 on cell migration. A, The expression of circ\_0004712 in Ishikawa and End1/ E6E7 cells after for specific siRNA for circ-0004712 (si-circ) or negative control siRNA (NC) transfection was tested by qPCR. Results show as mean  $\pm$  SD. \*\*Means *P* < 0.05. B, Cell migration of E<sub>2</sub> treated or untreated Ishikawa and End1/ E6E7 cells after si-circ or NC transfection was analysed by transwell assay

Previous study identified that circ\_0004712 was significantly up-regulated in endometriosis,<sup>14</sup> but the biological functions of circ\_0004712 still unknown. The aim of present study was explored the potential functions of circ\_0004712 in the process of  $E_2$ -induced EMT in endometriosis development.

### 2 | MATERIALS AND METHODS

### 2.1 | Cell culture, treatment and transfection

Ishikawa cell and End1/E6E7 cell was obtained from American Type Culture Collection (ATCC; Manassas, VA, USA). Cells were cultured in Dulbecco's modified Eagle's medium (DMEM, Gibico, Carlsbad, CA, USA) supplemented with 10% foetal bovine serum (FBS, Gibico, USA), 50 U/mL penicillin and 50 mg/mL streptomycin. Cells maintained at 37°C in a 5% CO<sub>2</sub> humidified incubator.

 $\rm E_2$  was purchased from Sigma (E-2758) and dissolved in dimethyl sulfoxide (DMSO). Cells were treated with different concentrations

(0,  $10^{-12}$ ,  $10^{-10}$ ,  $10^{-8}$  and  $10^{-6}$  mol/L) of E<sub>2</sub> and incubated 48 hours. The cells were incubated with serum-free medium for 24 hours before E<sub>2</sub> treatment.

The small interfering RNAs (siRNAs) targeting to the circ\_0004712 (5'-AACCTATATCAGGTACAACAT-3'), miR-148a-3p mimics, miR-148a-3p inhibitor, miRNA negative control (NC) were designed and synthesized by Genepharma (Shanghai, China). Cells were transfected using Lipofectamine 2000 Reagent (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's protocol.

# 2.2 | qPCR

Total RNAs were isolated from treated cells by Trizol reagent (Invitrogen, Carlsbad, CA, USA). The first strand of cDNA was obtained by PrimeScript RT Master Mix (Takara, Dalian, China). Specific gene expression was detected by SYBR Premix Ex Taq (Takara) using ABI PRISM 7500 Sequence Detection System (Life Technologies, Grand Island, NY, USA). The relative expression data



**FIGURE 3** Circ\_0004712 directly suppresses the expression of miR-148a-3p. A, The target sites of circ\_0004712 and miR-148a-3p. B, The expression of miR-148a-3p in E<sub>2</sub>-treated Ishikawa and End1/E6E7 cells was tested by qPCR. C, The expression of miR-148a-3p in E<sub>2</sub>-treated orE<sub>2</sub>-untreated Ishikawa and End1/E6E7 cells after for si-circ or NC transfection was tested by qPCR. D, Relative luciferase activity in Ishikawa and End1/E6E7 cells transfected with miR-NC or miR-mimics and circ-wild-type (wt) or circ-mutation (mut), respectively. Results show as mean ± SD. \*\*Means compared with control group, P < 0.05. ##Means compared with E<sub>2</sub>-treated group, P < 0.05

were normalized and analysed by the equation  $2^{-\Delta C_t}$ . The primers are shown in Table 1. GAPDH was used for circ\_0004712 normalizing, and U6 were used for miR-148a-3p normalizing.

# 2.3 | Transwell assay

Cell migration was tested by 24-well transwell chambers containing polycarbonate filters with a pore size of 8  $\mu$ m (Corning Costar, USA). Before culture, cells were resuspended in 200  $\mu$ L serum-free DMEM at the concentrate of 10<sup>5</sup> Cells/mL. Then, cells were seeded on the upper parts of the 24-well plate, which contains 500  $\mu$ L DMEM with 20% FBS at lower parts, and incubated at 37°C. The cells were fixed and stained in a 0.1% crystal violet solution for 15 minutes after 24 hours incubation. The stained migrated cells on the underside were photographed using microscopy (Nikon, Japan).

# 2.4 | Due-luciferase assay

The sequences of wild-type circ\_0004712 (circ-WT), mutation circ\_0004712 (circ-Mut), wild-type of 3'-UTR of SOS2 (SOS2-WT), mutation of 3'-UTR of SOS2 (SOS2-Mut) and were cloned into

psiCHECK-2 vector (Promega, Madison, WI, USA), respectively. The plasmid was co-transfected with miR-148a-3p mimics or NC into cells for 48 hours. The luciferase activities were detected using the Dual-Glo Luciferase Assay System (Promega). Firefly luciferase was used as a reporter gene for normalized control.

### 2.5 | Western blot assay

Treated cells were lysed in radio-immunoprecipitation assay (RIPA) buffer (Beyotime, Hangzhou, China) supplemented with PMSF (Sigma) for total protein extracting. The concentration of total protein was quantified using BCA protein assay kit (Beyotime). Equal protein ( $60 \mu g$ ) was separated by 10% SDS-PAGE and transferred onto a PVDF membrane (0.45  $\mu m$ ; Millipore). Following blocking with 5% non-fat milk, the membrane was incubated overnight at 4°C with E-cadherin (1:1000; ab40772, Abcam), N-cadherin (1:1000; ab18203, Abcam),  $\beta$ -catenin (1:1000; ab16051, Abcam), p- $\beta$ -catenin (1:1000; ab11350, Abcam), Snail (1:1000; ab167609, Abcam), SOS2 (1:1000; ab154999, Abcam) and GAPDH (1:4000; ab181602, Abcam), then secondary antibodies at room temperature for 1 hour. After that, the band was exposed by ECL system (Thermo Fisher Scientific, USA) and analysed by Quantity One software (Bio-Rad, San Diego, CA, USA).

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**FIGURE 4** Effect of circ\_0004712/miR-148a-3p on cell migration. A, Cell migration of  $E_2$ -treated or $E_2$ -untreated ishikawa and End1/ E6E7 cells after NC, si-circ and/or miR mimics transfection was analysed by transwell assay, respectively. B, Protein expression of E-cadherin and N-cadherin in  $E_2$ -treated or $E_2$ -untreated ishikawa and End1/E6E7 cells after NC, si-circ and/or miR mimics transfection was analysed by Western blot assay. C, Protein expression of  $\beta$ -catenin, p- $\beta$ -catenin and Snail in  $E_2$ -treated or  $E_2$ -untreated ishikawa and End1/E6E7 cells after NC, si-circ and/or miR mimics transfection was analysed by Western blot assay. Results show as mean ± SD. \*\*Means compared with control group, P < 0.05. ##Means compared with  $E_2$ -treated group, P < 0.05

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**FIGURE 5** miR-148a-3p directly suppresses the expression of SOS2. A, Venn diagram showed overlapped target genes of miR-148a-3p in three databases. B, Relative luciferase activity in Ishikawa and End1/E6E7 cells transfected with miR-NC or miR-mimics and SOS2-wild-type (wt) or SOS2-mutation (mut), respectively. C, The protein expression of SOS2 in E<sub>2</sub>-treated Ishikawa and End1/E6E7 cells was tested by Western blot. D, Cell migration of E<sub>2</sub>-treated or untreated Ishikawa and End1/E6E7 cells after NC, si-SOS2 and/or miR inhibitor transfection was analysed by transwell assay, respectively. E, Protein expression of E-cadherin and N-cadherin in E<sub>2</sub>-treated or E<sub>2</sub>-untreated Ishikawa and End1/E6E7 cells after NC, si-SOS2 and/or miR inhibitor transfection was analysed by Western blot. Results show as mean  $\pm$  SD. \*\*Means compared with control group, *P* < 0.05. ##Means compared with E<sub>2</sub>-treated group, *P* < 0.05

### 2.6 | Statistical analysis

All statistical analyses were performed using GraphPad Prism 8.0 (GraphPad Software Inc). Unpaired two-sided *t* test was performed for analysing the between-group differences. The data were expressed as mean  $\pm$  SD P values of less than 0.05 were considered statistically significant. All experiments for statistical analyses were repeated for triple times.

# 3 | RESULTS

# 3.1 | circ\_0004712 up-regulated by $E_2$ treating in endometrial epithelial cells

To explore the relationship between  $E_2$ -induced EMT and circ\_0004712 expression, we preformed different concentration of  $E_2$  (10<sup>-12</sup>, 10<sup>-10</sup>, 10<sup>-8</sup>, 10<sup>-6</sup>mol/L) treatment in endometrial epithelial cell lines. After 48 hours treatment, the expression of circ\_0004712 was significantly up-regulated as a dose-dependent manner in both of Ishikawa and End1/E6E7 cells (Figure 1A). Transwell assay showed  $E_2$  treatment markedly induced the migration activity as a dose-dependent manner (Figure 1B).

# 3.2 | circ\_0004712 promotes cell migration in endometrial epithelial cells after $E_2$ treatment

To study the potential biological effects of circ\_0004712 on E<sub>2</sub>.induced EMT process, we synthesized a specific interference RNA oligonucleotide (si-circ) to knock down endogenous expression of circ\_0004712 in endometrial cells after E<sub>2</sub> (10<sup>-8</sup> mol/L) treatment. qPCR results showed the expression of circ\_0004712 were significantly decreased by si-circ transfection in E<sub>2</sub>-treated Ishikawa and End1/E6E7 cells (Figure 2A). Transwell assay showed that knock-down circ\_0004712 significantly suppressed E<sub>2</sub>-induced cell migration activity (Figure 2B). Overall, the results suggested that high expression of circ\_00471 was related with E<sub>2</sub>-induced EMT progress.

# 3.3 | circ\_0004712 targeted to miR-148a-3p

Many evidences revealed that circRNAs could sponge miRNAs to regulate the expression of the target genes. Thus, we predicted the potential target miRNAs of circ\_0004712 by bioinformatics. MiR-148a-3p have a binding site to circ\_0004712 (Figure 3A), and the expression of miR-148a-3p was significantly down-regulated after  $E_2$  treatment as a dose-dependent manner (Figure 3B). Furthermore, the expression of miR-148a-3p was significantly reduced by circ-000471 knocking down (Figure 3C). The dual-luciferase assay further demonstrated the directly binding site between circ\_0004712 and miR-148a-3p (Figure 3D). Compared with control group, miR-148a-3p significantly reduced the relative luciferase activity, and no significant effect on luciferase activity when co-transfected with mutated plasmids. These results suggested that circ\_0004712 could bind to miR-148a-3p to modulate the  $E_2$ -induced EMT process in endometrial epithelial cells.

# 3.4 | circ\_0004712/miR-148a-3p regulated EMT process via β-catenin pathway

To further study the molecular mechanism of circ\_0004712/miR-148a-3p on E<sub>2</sub>-induced EMT process, cells were treated with E<sub>2</sub> and transfected with si-circ and/or miR-148a-3p mimics, respectively. Transwell assay revealed that inhibiting the expression of circ\_0004712 or increasing the expression of miR-148a-3p could significantly suppress the migration capacity in E2-treated endometrial epithelial cells (Figure 4A). Furthermore, the effect of circ\_0004712 knock-down on cell migration could be recovered by miR-148a-3p inhibitor. Western blot assay showed that E2 treatment could increase the expression and activity of  $\beta$ -catenin pathway and N-cadherin and reduce the expression of E-cadherin (Figure 4B). The expression and activity of β-catenin pathway were recovered by si-circ or miRNA mimics transfecting (Figure 4C). These results suggested that circ\_0004712 and miR-148a-3p had opposite effects on EMT process, and circ\_0004712 could suppress the expression of miR-148a-3p. The molecular mechanism of circ\_0004712/miR-148a-3p on the E2-induced EMT process may be associated with the  $\beta$ -catenin pathway.

# 3.5 | miR-148a-3p targets to SOS2

miRNAs could bind to the 3'-UTR of target genes. Thus, we predicted the target genes of miR-148a-3p through three databases (miRTar-Base, targetscan7.2, and miRDB) and found three common genes (ARL8B, GLRX5 and SOS2) in these three databases (Figure 5A). In these three genes, SOS2 (Son of sevenless 2) was associated with EMT process.<sup>15</sup> Thus, we tested the expression of SOS2 in E<sub>2</sub>treated Ishikawa and End1/E6E7 cells. The results of Western blot showed the expression of SOS2 was significantly increased after E<sub>2</sub>



treatment as a dose-dependent manner (Figure 5C). The dual-luciferase assay further demonstrated the directly binding site between miR-148a-3p and SOS2 (Figure 5B). Transwell assay revealed that knock-down the expression of SOS2 could significantly suppress the migration capacity in  $E_2$ -treated endometrial epithelial cells and recovered the effect of miR-148a-3p inhibitor on the cell migration (Figure 5D). To further explore the effect of miR-148a-3p/SOS2 on the regulating the EMT process, we tested the expression of N-cadherin and E-cadherin. The results of Western blot showed that the expression of N-cadherin and E-cadherin were recovered by si-SOS2 transfecting (Figure 5E). These results suggested that SOS2 was the target of miR-148a-3p involved in the circ\_0004712mediated  $E_2$ -induced EMT process in endometrial cells.

# 4 | DISCUSSION

Endometriosis is a common, chronic gynaecologic disease affecting women in their reproductive age and leading to pain and infertility.<sup>16</sup> Identifying the accrue biomarkers and specific therapeutic targets for the early diagnosis and treatment is immediately needed. Increasing evidences have highlighted circRNAs as important molecular biomarkers and gene regulators. Recently, the expression profile of circRNAs in endometriosis has been reported,<sup>14,17</sup> and these studies indicated that dysregulated circRNAs might be potential molecular targets for clinical diagnosis and therapy. However, the molecular mechanism of these circRNAs is still unclear. Here, we studied the roles of an up-regulated circRNAs (circ\_0004712) on the  $E_2$ -induced EMT process in endometrial cells.

Epithelial-mesenchymal transition in endometrial cells is important for endometriosis establishment.<sup>11</sup> As a reproductive tissue, endometrial cells located in high level of oestrogen. Thus, endometriosis has been considered as an oestrogen-dependent disease.<sup>18</sup> Many studies demonstrated that oestrogen could induce in many cancers and adenomyosis.<sup>19-21</sup> Recent studies also suggested that oestrogen promotes EMT process during the development of endometriosis.<sup>7,10</sup> However, the relationship between dysregulated circRNAs and oestrogen-induced EMT in endometriosis remain largely unknown. Here, our results showed that the expression of circ\_0004712 was significantly increased in endometrial epithelial cells after E<sub>2</sub> treatment. Meanwhile, knock-down the expression of circ\_0004712 could markedly suppress cell migration activity in endometrial cells. These results revealed that circ\_0004712 involved in regulating the E<sub>2</sub>-induced EMT process.

circRNAs containing the target site could bind to specific miR-NAs to inhibit the expression and function of miRNAs.<sup>22</sup> In this work, circ\_0004712 act as a sponge of miR-148a-3p. Up-regulating the expression of miR-148a-3p could suppress cell migration as well as circ\_0004712 knocking down. Recent studies suggested that overexpression of miR-148a-3p could suppress the process of EMT in cancer cells.<sup>23-25</sup> Thus, circ\_0004712 might sponge miR-148a-3p to promote EMT during E<sub>2</sub> treatment in endometrial cells.

miRNAs regulate the cellular process by suppressing the expression of target genes via directly binding to the 3'-UTR of the genes.<sup>26</sup> In our study, we demonstrated SOS2 was a target gene of miR-148a-3p involved in the  $E_2$ -induced EMT process. SOS2 is a number of SOS (Son of sevenless) family, which is the Ras-specific guanine nucleotide-exchange factor. SOS2 enhances the activation of Ras and regulates many cellular process, such as cell proliferation and migration.<sup>27</sup> Previous study suggested that inhibiting the expression of SOS2 could suppress the cell proliferation and EMT process by down-regulating MAPK/Erk pathway in non-small-cell lung cancer cells.<sup>15</sup> In our study, we also found the expression of SOS2 increased in endometrial cells after  $E_2$  treatment and demonstrated the binding ship between SOS2 and miR-148a-3p. Furthermore, inhibiting the expression of SOS2 could suppress cell migration after  $E_2$  treatment. Thus, SOS2 acted as the target gene of miR-148a-3p involved in the  $E_3$ -induced EMT process in endometrial cells.

The up-regulation of N-cadherin and Vimentin and down-regulation of E-cadherin are the most influential biomarkers of EMT.<sup>8</sup>  $E_2$  have been demonstrated to reduce the expression of E-cadherin <sup>28</sup> and activate  $\beta$ -catenin signalling to promote EMT process.<sup>29</sup> Our results also revealed  $E_2$  could activate  $\beta$ -catenin signalling. Furthermore, knocking down the expression of circ\_0004712 and over-expression of miR-148a-3p suppressed activation of  $\beta$ -catenin signalling, subsequently up-regulated E-cadherin expression and down-regulate N-cadherin expression after  $E_2$  treatment in endometrial epithelial cells. Reducing the expression of miR-148a-3p could recover the effect of circ\_0004712 knocking down. Furthermore, we also found inhibiting the expression of SOS2 could recover the effect of miR-148a-3p knocking down on the expression of N-cadherin and E-cadherin. However, the precise relationship between SOS2 and  $\beta$ -catenin signalling needs more experiments to illustrate.

In conclusion, this work demonstrated  $E_2$  could promote EMT to enhance cell migration in the development of endometriosis by up-regulating circ\_0004712 expression levels. Circ\_0004712 sponged miR-148a-3p to activate the  $\beta$ -catenin signalling to promote EMT process. These findings revealed the important effect of circRNAs on endometriosis and provided new biomarker for early diagnosis and therapeutic targets for the treatment of endometriosis.

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### CONFLICTS OF INTEREST

The authors declare no conflict of interest.

## AUTHOR CONTRIBUTION

Xin He: Methodology (equal); Visualization (equal); Writing-original draft (lead). Nana Liu: Investigation (equal); Methodology (equal); Visualization (equal); Writing-original draft (supporting). Tianyi Mu:

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Formal analysis (equal); Investigation (equal); Software (equal). Dan Lu: Data curation (equal); Investigation (lead). Chanwei Jia: Formal analysis (equal); Investigation (equal). Yushu Wang: Formal analysis (equal); Software (equal). Chenghong Yin: Formal analysis (equal); Software (equal). Lingyan Liu: Validation (equal); Visualization (equal). liying zhou: Validation (equal); Visualization (equal). Xiaowu Huang: Conceptualization (supporting); Funding acquisition (equal); Resources (equal); Supervision (lead); Validation (lead); Writingreview & editing (supporting). Yanmin Ma: Conceptualization (supporting); Funding acquisition (equal); Project administration (lead); Resources (equal); Supervision (lead); Writing-review & editing (lead).

#### DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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