Journal of Ginseng Research 48 (2024) 40-51

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Journal of Ginseng Research



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Research Article

Ginsenoside 20(S)-Rg3 reduces *KIF20A* expression and promotes CDC25A proteasomal degradation in epithelial ovarian cancer



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ARTICLE INFO

Article history: Received 16 November 2022 Received in revised form 15 June 2023 Accepted 25 June 2023 Available online 4 July 2023

Keywords: ginsenoside Rg3 ovarian cancer KIF20A CDC25A ubiquitination

ABSTRACT

Background: Ginsenoside 20(S)-Rg3 shows promising tumor-suppressive effects in ovarian cancer via inhibiting NF- κ B signaling. This study aimed to explore the downstream tumor suppressive mechanisms of ginsenoside Rg3 via this signaling pathway.

Materials and methods: A systematical screening was applied to examine the expression profile of 41 kinesin family member genes in ovarian cancer. The regulatory effect of ginsenoside Rg3 on *KIF20A* expression was studied. In addition, we explored interacting proteins of KIF20A and their molecular regulations in ovarian cancer. RNA-seq data from The Cancer Genome Atlas (TCGA) was used for bio-informatic analysis. Epithelial ovarian cancer cell lines SKOV3 and A2780 were used as *in vitro* and *in vivo* cell models. Commercial human ovarian cancer tissue arrays were used for immunohistochemistry staining.

Results: KIF20A is a biomarker of poor prognosis among the kinesin genes. It promotes ovarian cancer cell growth *in vitro* and *in vivo*. Ginsenoside Rg3 can suppress the transcription of *KIF20A*. GST pull-down and co-immunoprecipitation (IP) assays confirmed that KIF20A physically interacts with BTRC (β -TrCP1), a substrate recognition subunit for SCF^{β -TrCP} E3 ubiquitin ligase. *In vitro* ubiquitination and cycloheximide (CHX) chase assays showed that via interacting with BTRC, KIF20A reduces BTRC-mediated CDC25A poly-ubiquitination and enhances its stability. Ginsenoside Rg3 treatment partly abrogates *KIF20A* overexpression-induced CDC25A upregulation.

Conclusion: This study revealed a novel anti-tumor mechanism of ginsenoside Rg3. It can inhibit *KIF20A* transcription and promote CDC25A proteasomal degradation in epithelial ovarian cancer.

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1. Introduction

Epithelial ovarian cancer (EOC) is a fatal malignancy in women. It acts as a "silent killer" since the symptoms are only noticeable at relatively late clinical stages ("silent") and a high 5-year mortality rate ("killer") [1]. Most EOCs are highly sensitive to paclitaxel + platinum combination chemotherapy during initial treatment, but recurrence is inevitable due to the development of chemoresistance [2,3]. In the past decade, the application of Poly (ADP-ribose) polymerase (PARP) inhibitors significantly prolonged progression-free survival (PFS) in patients with Breast Cancer-Associated 1 and 2 (BRCA1/2) mutant ovarian cancer [4]. However, the BRCA1/2 mutation rate is around 16% to 24% in ovarian cancer patients in China [5,6]. Therefore, PARP inhibitors might not bring clinical benefits for more than 3/4 of ovarian cancer patients

https://doi.org/10.1016/j.jgr.2023.06.008

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without BRCA mutations. The major mechanism of paclitaxel and platinum drugs is to promote microtubular aggregation and interfere with cell mitosis, transport and motility [7]. Therefore, an indepth exploration of the biological characteristics of ovarian cancer cells in the process of mitosis is critical to overcome chemoresistance.

Ginsenoside 20(S)-Rg3 (ginsenoside Rg3) shows promising *in vitro* and *in vivo* tumor-suppressive effects in multiple cancers [8–10]. Ginsenoside Rg3 could induce cancer cell apoptosis [11,12], including ovarian cancer cells [13,14]. Besides, in ovarian cancer, it can inhibit hypoxia-induced epithelial-mesenchymal transition [15], indue autophagy [16], inhibit the Warburg effect [17], and suppress the expression of multiple tumor-promoting genes [17,18]. Therefore, it might be a potential candidate for adjuvant treatment. A clear understanding of the mechanisms underlying its anti-tumor effects would help promote its clinical application.

Mitosis is a highly regulated, highly ordered process. The precise progression of cytocentrosome isolation, spindle filament formation, chromosome collection, and cytoplasmic division requires the kinesin superfamily proteins (KIFs), a set of molecular motors [19]. The dysregulation of KIF proteins plays a key role in the development of human cancers [20,21]. In ovarian cancer, KIF14 expression is an independent biomarker of poor prognosis [22]. Inhibiting KIF5, an essential factor for spindle assembly, can suppress ovarian cancer growth [23]. *KIF20A* upregulation is associated with unfavorable clinical outcomes and tumor progression [24,25].

In this study, we systematically screened the KIF family member genes and confirmed *KIF20A* as a biomarker of poor prognosis and a functional tumor-promoting gene. Our bioinformatic analysis revealed that ginsenoside Rg3 might regulate *KIF20A* expression. Therefore, we further examined the effects of ginsenoside Rg3 on *KIF20A* transcription, the interacting proteins of KIF20A, and their molecular regulations in ovarian cancer.

2. Materials and methods

2.1. Bioinformatic analysis

RNA-seq data of 41 KIF family members from primary ovarian cancer cases in the cancer genome atlas (TCGA)-ovarian cancer (OV) (N = 419) and normal ovary and fallopian tube (N = 93) from the Genotype-Tissue Expression (GTEx) were extracted using the combined GTEx and TCGA dataset in UCSC Xena browser (https://xe nabrowser.net/) [26]. Immunohistochemistry (IHC) staining of KIF20A expression was checked using data from the Human Protein Atlas (HPA) (https://www.proteinatlas.org/) [27]. In this database, the protein expression score is determined by manually scoring immunohistochemical data for staining intensity and the fraction of stained cells. The staining intensity is classified as negative, weak, moderate, or strong, while the fraction of stained cells is categorized as <25%, 25-75%, or >75%. Each combination of intensity and fraction is then automatically converted into a protein expression level score. A negative score indicates that the protein was not detected, while a weak score (<25%) also indicates that the protein was not detected. A weak score combined with 25-75% or 75% is classified as low. A moderate score (<25%) is classified as low, while a moderate score combined with either 25-75% or 75% is classified as medium. A strong score (<25%) is classified as medium, while a strong score combined with either 25-75% or 75% is classified as high (https://www.proteinatlas.org/about/help#4). The association between KIF20A expression and the survival outcomes of patients with primary ovarian cancer was assessed using the Kaplan-Meier plotter (http://kmplot.com/analysis/index.php?p=service&cancer =ovar), using the optimal cutoff [28].

2.2. Cell culture and treatment

Human ovarian surface epithelial (HOSE) cells and epithelial ovarian cancer cell lines (SKOV3, A2780, OV90, and OVCAR3) were cultured following the methods introduced previously [29]. Lentiviral KIF20A shRNAs (shKIF20A) were constructed by HanBio Technology, based on pLKO.1-puro plasmid. The following sequences were used: shKIF20A#1. 5'-CGTACACCATTCAAGGTACTA-3', shKIF20A#2, 5'-GCTAGATGAAACAAGTCAATT-3', shKIF20A#3, 5'- GCCACTCACAAATTTACCTTT-3'. Lentiviruses expressing myctagged BTRC (myc-BTRC), flag-tagged KIF20A (flag-KIF20A), and RELA (NF-KB p65) were generated based on the pLenti-puro backbone. pLenti puro HA-Ubiquitin (HA-Ub) (Plasmid #74218) was obtained from Addgene (Cambridge, MA, USA). Lentivirus for infection was produced by co-transfecting with the lentivirus packaging plasmids (pSPAX2 and pMD2.G, HanBio Technology) in 293T cells, as we previously described [30]. Cells were infected at a multiplicity of infection (MOI) of 15, with the presence of 6 μ g/ml polybrene. Global protein translation inhibitor (cycloheximide, CHX) and the proteasome inhibitor MG132 were obtained from Selleck Chemicals. Ginsenoside Rg3 (purity>98%) was purchased from HerbSubstance (Chengdu, China).

2.3. Reverse transcription quantitative PCR (RT-qPCR)

In brief, cDNA was reversely transcribed using RNA samples extracted from cells and then used as the PCR assay template. Relative gene expression was normalized to *GAPDH*, by the $2^{-\Delta\Delta CT}$ method. The primers were as follows: *KIF20A*, forward: 5'-CAA-GAGGCAGACTTTGCGGCTA-3' and reverse: 5'-GCTCTGGTTCTTAC-GACCCACT-3'; *RELA*, forward: 5'-TGAACCGAAACTCTGGCAGCTG-3' and reverse: 5'-CATCAGCTTGCGAAAAGGAGCC-3'; *GAPDH*, forward: 5'-GTCTCCTCTGACTTCAACAGCG-3', and reverse, 5'-ACCACCCTGTT GCTGTAGCCAA-3'.

2.4. Western blotting

Cell samples were harvested, washed, and lysed using a lysis buffer containing protease inhibitors. After centrifugation, the supernatant was collected to determine protein concentration using a BCA kit (Beyotime). 30 µg protein samples were loaded into each lane. The following antibodies and dilutions were used, including anti-KIF20A (1:1000, 15911-1-AP, Proteintech, Wuhan, China), anti-BTRC (1:1000, 37-3400, ThermoFisher Scientific, Waltham, MA, USA), anti-Flag tag (1:5000, 66008-4-Ig, Proteintech), anti-CDC25A (1:1000, 55031-1-AP, Proteintech), anti-HA tag (1:5000, 51064-2-AP, Proteintech), anti-Myc tag (1:3000, 16286-1-AP, Proteintech), and anti- β -actin (sc-47778, Santa Cruz Biotechnology, Santa Cruz, CA, USA). HRP-conjugated secondary antibodies were used. Then, the signals were developed using the BeyoECL Star reagent (Beyotime) and a LAS-4000 imaging system (GE Healthcare, Piscataway, NJ, USA).

2.5. CCK-8 assays, colony formation, and cell cycle detection

48 h after lentiviral infections, SKOV3 and A2780 cells were seeded into 96-well plates at a density of 2,000 cells per well and were incubated for 24, 48, and 72 h. At each time point, the cell viability was measured using a CCK-8 Kit (Beyotime, Shanghai, China). 10 μ l of CCK-8 reagent was added to each well and incubated for 2 h. Then, absorbance at 450 nm was measured using a microplate reader.

For colony formation assays, SKOV3 and A2780 cells with or without *KIF20A* knockdown were seeded in 6-well plates (1000 cells/per well) and cultured for 10-14 days. Then, the plates were

washed, and the colonies were fixed with 4% formaldehyde and stained with 1.0% crystal violet.

Cell cycle distribution was assessed by Propidium Iodide (PI) staining. In brief, 48 h after lentiviral infection, cells were collected and washed twice with PBS and fixed with 70% ethanol at 4° C for 1h. Then, cells were resuspended in PBS with 50 µg/mL PI and 100 µg/mL RNase A. The cells were incubated at room temperature in the dark for 30 min. Then, cell cycle distribution was detected using flow cytometry (Novocyte Advanteon, Agilent, Santa Clara, CA, USA) and analyzed using NovoExpress software (version 1.5.4, Agilent).

2.6. Nude mouse xenograft model

Female Balb/c nude mice aged 4-6 weeks were purchased from Vital River Laboratory Animal Technology (Beijing, China). All animal protocols used were approved by the Institutional Animal Care and Use Committee of Shanxi Provincial People's Hospital, China (approval no. 2022-057). All animal housing and experiments were conducted in strict accordance with the institutional Guidelines for the Care and Use of Laboratory Animals. Mice were randomly divided into four groups (n = 6 per group). Approximately 2×10^6 of A2780 or SKOV3 cells with or without KIF20A knockdown or SKOV3 cells with KIF20A overexpression were inoculated subcutaneously in the left armpit of each mouse. For the ginsenoside Rg3 treatment group, Ginsenoside Rg3 was administered at 20 mg/ kg body weight to mice 3 times per week for 4 weeks via intraperitoneal injection. Tumors were measured every 3 days with a caliper. About 4 weeks after inoculation, xenograft tumors were removed, weighed, fixed, and sectioned. IHC staining was performed to check Ki-67 expression in tumor sections.

2.7. Glutathione-S-transferase (GST) pull-down and coimmunoprecipitation (IP) assays

The genes encoding BTRC, FBXW11, and FBXW7 were subcloned in pGEX-6p-1 between the EcoRI and XhoI restriction sites. GSTfusion proteins were expressed in E. coli BL21 (DE3). In brief, the ligation mixture was transformed into competent E. coli cells and plated on LB agar plates containing ampicillin. A single colony was picked and grown in LB broth containing ampicillin. When the OD600 of the LB medium reached 0.6-0.8, protein expression was induced by adding IPTG to a final concentration of 0.1 mM and continuing to incubate for 4 h at 37°C with shaking. The cells were harvested by centrifugation at 4,000 \times g for 10 min at 4°C, resuspended in lysis buffer containing protease inhibitors, and lysed by sonication. The lysates were centrifugated at $12,000 \times g$ for 15 min at 4°C to remove cell debris. The supernatant was collected and incubated with Glutathione-Sepharose beads for 1 h at 4°C with gentle shaking. Then, the beads were washed several times with lysis buffer to remove non-specifically bound proteins. The GSTtagged proteins were eluted from the beads by adding an elution buffer. Then, GST pull-down assays were performed using Pierce GST Protein Interaction Pull-Down Kit (ThermoFisher Scientific), following the protocol of the kit. The bait GST-tagged proteins were immobilized on the pierce spin column with equilibrated glutathione agarose. The supernatant from HEK293T cells overexpressing flag-tagged KIF20A (as prey protein) was prepared and added to the pierce spin column containing the immobilized GSTtagged proteins and then incubated at 4°C for 4 h with gentle rocking. Then, the column was washed several times and the baitprey proteins were eluted with the glutathione elution buffer. The eluted samples were subjected to western blotting assays. Co-IP assay was performed as we previously described [30], using mouse anti-BTRC (37-3400, ThermoFisher Scientific), rabbit antiKIF20A (15911-1-AP, Proteintech), and protein A agarose (sc-2001, Santa Cruz).

2.8. Immunofluorescent staining

Immunofluorescent staining was performed following the methods introduced previously [31]. In brief, cells were grown on coverslips. After about 50% confluence, cells were fixed and permeabilized. Then, the cells were washed and incubated with primary antibody against BTRC and KIF20A (mouse anti-BTRC, 1:200, 37-3400, ThermoFisher Scientific and rabbit anti-KIF20A, 1: 200, 15911-1-AP, Proteintech) at 4 °C overnight. The CoraLite594-conjugated Goat Anti-Mouse IgG(H + L) and CoraLite488-conjugated Goat Anti-Rabbit IgG(H + L) (Proteintech) were used as the secondary antibodies. Nuclei were stained with DAPI. Immunofluorescent images were acquired using IX83 (Olympus, Tokyo, Japan).

2.9. Statistical analysis

Welch's t-test was conducted to check the statistical difference between the two groups. One-way ANOVA with post-hoc Tukey test was performed for multiple-group comparisons. Log-rank test was performed in Kaplan-Meier (K-M) survival analysis. Pearson's r or Spearman's rho values were calculated to estimate correlations. p < 0.05 was considered statistically significant.

3. Results

3.1. Systematic screening identifies a link between KIF20A upregulation and unfavorable prognosis of ovarian cancer

To explore dysregulated KIF genes, we extracted RNA-seq data of 41 KIF family members from primary ovarian cancer cases in TCGA-OV (N = 419) and normal ovary and fallopian tube (N = 93) from GTEx (Fig. S1A). The dysregulated genes were identified by the following criteria: serous EOC (SEOC) vs. normal (log₂ fold change \geq 2) and adj. *p* < 0.05. After the screening, 14 candidates were identified, including *KIF18B, KIF20A, KIF14, KIF11, KIF18A, KIF2C, KIF15, KIFC1, KIF1A, KIF23, KIF12, KIF26B, KIF6,* and *NEK6* (Fig. S1B). K-M survival analysis using data from the Kaplan-Meier plotter confirmed that high *KIF20A* expression was associated with significantly worse PFS (HR: 1.35, 95%CI: 1.12-1.63, *p* = 0.0015) and OS (HR: 1.25, 95%CI: 1.06-1.46, *p* = 0.006) (Fig. 1A–B). To explore KIF20A expression at the protein level, we conducted IHC staining using a commercial ovarian cancer tissue assay. Results confirmed medium to high KIF20A expression, mainly in the nucleus (Fig. 1C).

Then, we examined the IHC staining of KIF20A in the Human Protein Atlas (HPA) [27]. In the HPA, KIF20A was examined in 12 ovarian cancer tissues using two antibodies (HPA036909 and HPA036010) (Fig. S2). Medium to high expression of KIF20A was observed in most of the tumor tissues (Fig. S2). Subcellular analysis showed that KIF20A is mainly distributed in the nucleus, with minor distribution in the cytoplasm (Fig. S2, top panels, enlarged areas).

3.2. Knockdown of KIF20A impairs ovarian cancer cell proliferation in vitro

KIF20A expression in normal human ovarian surface epithelial (HOSE) cells and multiple ovarian cancer cell lines, including SKOV3, A2780, OV90, and OVCAR3, were examined. Results showed that the tumor cell lines had significantly elevated KIF20A expression at the mRNA and protein levels than HOSE cells (Fig. S3A-B). SKOV3 and A2780 were selected as representative cell lines for

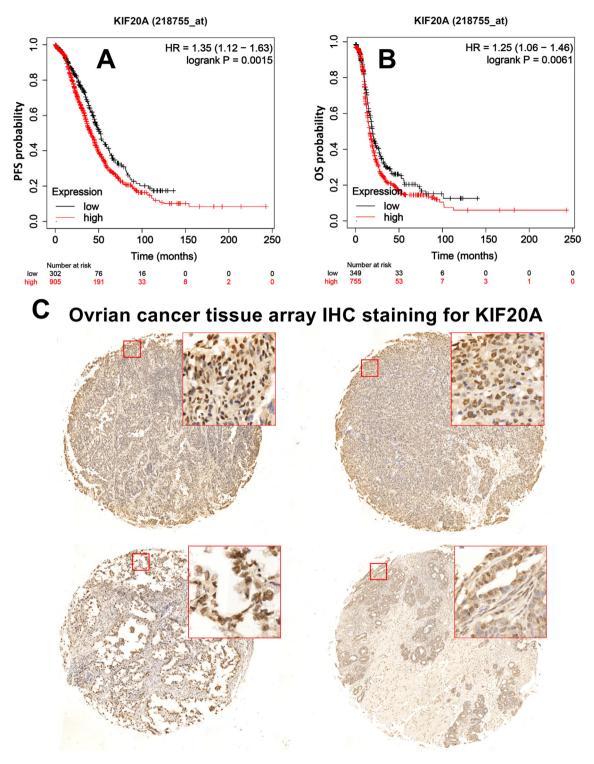


Fig. 1. Systematic screening identifies a link between *KIF20A* upregulation and unfavorable prognosis of ovarian cancer, **A-B.** K-M plotter was generated to compare the difference in PFS (C) and OS (D) between patients with high and low *KIF20A* expression with survival data from the Kaplan-Meier plotter. **C.** Representative images of KIF20A expression in commercial ovarian cancer tissue arrays. Enlarged tissue areas were provided to show the subcellular distribution of KIF20A.

further studies. These two cell lines were subjected to *KIF20A* knockdown or overexpression using lentiviruses (Fig. S1C-F). CCK-8 (Fig. 2A–B), colony formation (Fig. 2E–F), and flow cytometric analysis (Fig. 2H–J) showed that *KIF20A* knockdown significantly

reduced cell viability, colony formation, cells in the S phase, and increased G1 phase arrest of SKOV3 and A2780 cells (Fig. 2E–H). In comparison, *KIF20A* overexpression significantly enhanced proliferation and cell cycle progression (Fig. 2A–J).

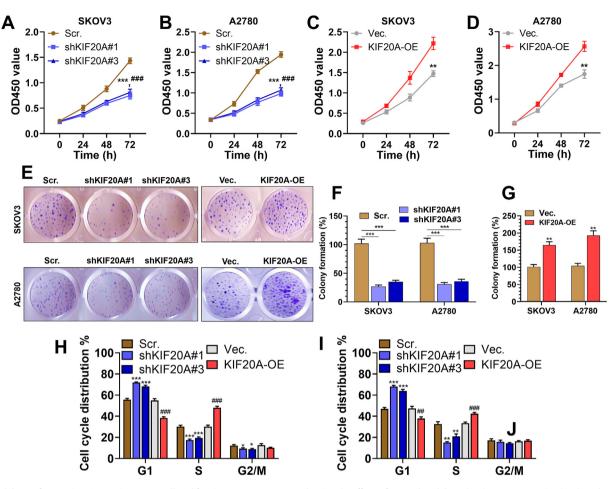


Fig. 2. Knockdown of *KIF20A* impairs ovarian cancer cell proliferation, **A-D.** CCK-8 assays showing the effects of *KIF20A* knockdown (A-B) or overexpression (C-D) on the viability of SKOV3 (A and C) and A2780 (B and D) cells. **E-I.** Colony formation (E-G) and flow cytometric analysis (H–I) were performed to show the effect of *KIF20A* knockdown or overexpression on colony formation and cell-cycle distribution of SKOV3 and A2780 cells. Data are expressed as mean \pm SD. *, comparison between scramble (scr.) control and shKIF20A. # comparison between vector (vec.) and KIF20A-OE. ## and **p < 0.01.

3.3. Ginsenoside Rg3 suppresses KIF20A expression in ovarian cancer cells

By performing KIF20A promoter scanning, we observed highpotential binding sites of NF-κB p65/RELA (Figure S4, bold green nucleobases). Therefore, we further checked the expressional correlation between KIF20A and RELA in primary ovarian cancer cases in TCGA. Correlation analysis confirmed a moderate positive correlation (Pearson's r = 0.50) (Fig. 3A). Ginsenoside Rg3 has welldocumented effects on inhibiting the activity of NF-kB p65 via suppressing its phosphorylation [32–34]. Therefore, we explored its effects on *KIF20A* expression in ovarian cancer cells. As expected. it suppressed KIF20A expression dose-dependently (Fig. 3B-C). To validate this finding, we overexpressed RELA in SKOV3 and A2780 cells (Fig. 3D-F). RELA overexpression was associated with increased NF-kB p65 phosphorylation (Fig. 3F-H) and increased KIF20A expression at the mRNA (Fig. 3D-E) and protein levels (Fig. 3F-H). Ginsenoside Rg3 treatment significantly weakened RELA overexpression-induced KIF20A upregulation (Fig. 3D-H).

3.4. KIF20A directly interacts with BTRC

To explore the potential functional regulation of KIF20A, we checked its interacting proteins using BioGRID (https://thebiogrid.org/). Only the proteins with minimum evidence ≥ 2 (at least two previous experimental evidence) were identified (Fig. 4A). Among

the candidates, BTRC (also known as β -TrCP1) and FBXW11 (β -TrCP2) were two potential candidates (Fig. 4A). BTRC serves as the substrate recognition subunit for SCF $^{\beta$ -TrCP E3 ubiquitin ligase, which specifically ubiquitinates phosphorylated substrates [35]. This E3 ligase exerts critical regulations on cell cycle progression and tumorigenesis by controlling the degradation of multiple essential cell cycle regulators [36].

To validate the specificity of the potential interactions, we generated recombinant pGEX-GST vectors expressing BTRC, FBXW11, and, another well-characterized F-box protein FBXW7. GST-fusion proteins were expressed in E. coli BL21 (DE3). Flag-KIF20A was expressed in 293T cells. Then, a GST pull-down assay was performed. Results showed that KIF20A exhibited a weak binding to FBXW11 and FBXW7 and a strong affinity to BTRC (Fig. 4B). The interaction between KIF20A and BTRC was also validated at the endogenous level. In the cell lysates from SKOV3 and A2780 cells, BTRC was identified in the KIF20A enriched fraction, and KIF20A was co-isolated with BTRC reciprocally (Fig. 4C–D). Immunofluorescent staining confirmed the co-localization between endogenous BTRC and KIF20A in the nucleus (Fig. 4E).

3.5. Ginsenoside Rg3 promotes CDC25A proteasomal degradation via suppressing KIF20A expression

Since we validated the interaction between KIF20A and BTRC, we hypothesized that KIF20A might exert specific regulation on the

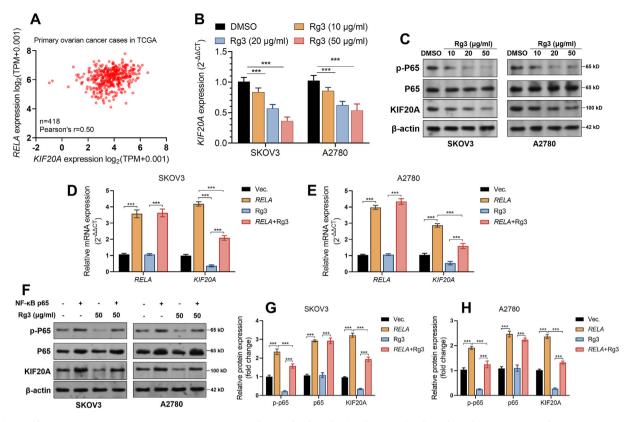


Fig. 3. Ginsenoside Rg3 suppresses *KIF20A* expression in ovarian cancer cells, **A.** A plot chart showing the expressional correlation between *KIF20A* and *RELA* in primary tumor cases in TCGA-OV. **B**–**C.** QRT-PCR (B) and western blotting assay (C) were performed to detect the expression of *KIF20A* in SKOV3 and A2780 cells 48 h after ginsenoside Rg3 treatment. **D**-**H.** QRT-PCR (D-E) and western blotting assay (F–H) were performed to detect the expression of *RELA* and *KIF20A* in SKOV3 and A2780 cells with *RELA* overexpression alone or in combination with ginsenoside Rg3 treatment (50 ng/ml for 48 h). ****p* < 0.001.

 $\text{SCF}^{\beta-\text{TrCP}-1}$ complex. To verify this hypothesis, we examined the expression of cell division cycle 25 A (CDC25A), a well-known $SCF^{\beta-TrCP-1}$ substrate [37] in SKOV3 cells. QRT-PCR assays confirmed that KIF20A knockdown or overexpression did not alter CDC25A transcription (S1 Fig. G-H). Western blotting data showed that KIF20A knockdown did not alter BTRC expression but reduced the expression of CDC25A (Fig. 5A, top panel). However, when MG132 was added. KIF20A knockdown could not induce CDC25A downregulation (Fig. 5A, bottom panel), suggesting that KIF20A might affect the proteasomal degradation of CDC25A. Therefore, we assessed the effect of KIF20A on SCF^{β -TrCP-1} ubiquitin ligase activity for CDC25A. In brief, SKOV3 cells were infected with lentiviruses with selective overexpression of HA-ubiquitin (HA-Ub), Myc-BTRC, and/or flag-KIF20A (Fig. 5B). The ubiquitination of CDC25A was checked after IP using an anti-CDC25A antibody. The myc-BTRC group had a higher level of high molecular-weight smeared bands of CDC25A, indicating increased CDC25A poly-ubiquitination (Fig. 5B). KIF20A overexpression attenuated CDC25A polyubiquitination (Fig. 5B). In comparison, its knockdown increased CDC25A poly-ubiquitination (Fig. 5C). CHX chase assay showed that KIF20A overexpression increased the stability of CDC25A (Fig. 5D-E). KIF20A knockdown shortened the half-life of CDC25A (Fig. 5F–G).

Ginsenoside Rg3 treatment reduced CDC25A protein levels in a dose-dependent manner (Fig. 5H), the effect of which was canceled by adding MG132 (Fig. 5I). In addition, it partly abrogated *KIF20A* overexpression-induced CDC25A upregulation (Fig. 5J). These findings imply that ginsenoside Rg3 can promote CDC25A proteasomal degradation by suppressing *KIF20A* expression.

3.6. Ginsenoside Rg3 impairs ovarian tumor growth in vivo

To explore the regulatory effect of KIF20A on *in vivo* growth ovarian tumors, we generated xenograft tumor models in nude mice. Ovarian tumors derived from SKOV3 or A2780 cells with *KIF20A* knockdown grew significantly slower than those without *KIF20A* knockdown (Fig. 6A–D). CDC25A expression was also significantly lower in the group with KIF20A knockdown (Fig. 6F–G). IHC staining of Ki-67 confirmed that the tumors with *KIF20A* knockdown had fewer cells with positive Ki-67 staining (Fig. 6H). To validate the tumor suppressive effect of ginsenoside Rg3 *in vivo*, we generated xenograft tumor models in nude mice using SKOV3 cells with *KIF20A* overexpression. KIF20A overexpression significantly promoted tumor growth, accompanied by CDC25A upregulation (Fig. 6I–J). However, ginsenoside Rg3 treatment significantly retarded *KIF20A* overexpression-induced tumor growth and decreased CDC25A expression (Fig. 6I–J).

3.7. KIF20A expression was positively correlated with CDC25A expression in human epithelial ovarian cancer tissues

To validate the correlation between KIF20A and CDC25A expression, we used commercial tissue microarrays (continuous sections, Bioaitech, Xi'an, China), containing 59 human epithelial ovarian cancer cases. IHC staining and the following analysis of IHC scores by Spearman's correlation observed a moderate positive correlation between KIF20A and CDC25A in the 59 tumor tissue cases (Spearman's rho = 0.49, Fig. 7A–B).

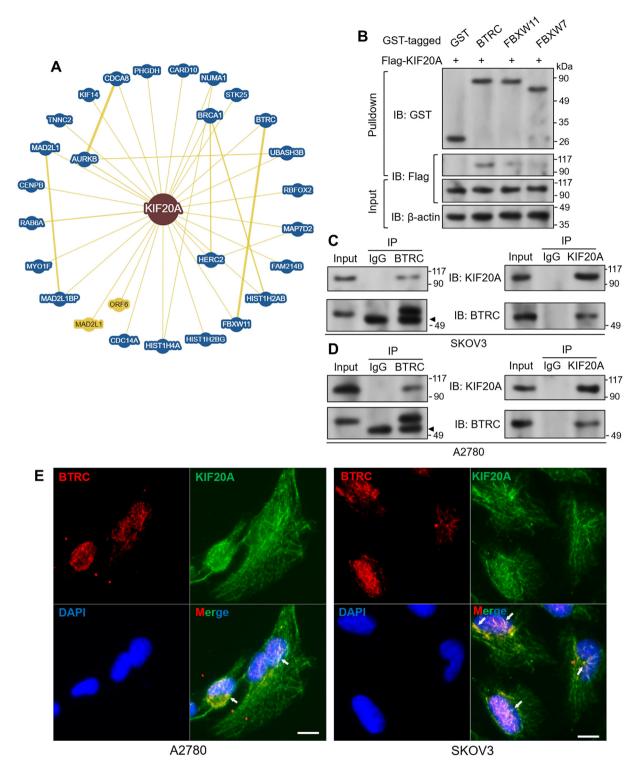


Fig. 4. KIF20A directly interacts with BTRC, **A.** Bioinformatic prediction of KIF20A interacting proteins. Prediction was performed using BioGRID. Only the proteins with minimum evidence ≥ 2 were identified as the candidates. **B.** Binding affinity of flag-KIF20A to the predicted E3 ligases. After various GST-fused proteins were expressed, a GST pull-down assay was performed. **C-D.** Co-IP was performed to show the interaction between KIF20A and BTRC at the endogenous level in SKOV3 (C) and A2780 (D) cells. IP was conducted with an anti-BTRC or anti-KIF20A antibody. Mouse IgG served as a negative control. Arrowheads: IgG heavy chain bands. **E.** Immunofluorescent staining was performed to visualize BTRC (red) and KIF20A (green) in SKOV3 and A2780 cells. Scale bar: 10 μ m.

4. Discussion

Via bioinformatic analysis, we confirmed that *KIF20A* is significantly upregulated in ovarian cancer, and its upregulation is a biomarker of prognosis. The human KIF20A encodes a protein

consisting of 890 amino acids. Aberrant *KIF20A* expression is associated with malignant behaviors and unfavorable clinical outcomes in multiple cancers [38–41], including ovarian cancer [24,25]. *KIF20A* was transcriptionally activated by FOXM1 in ovarian cancer and can promote the proliferation and invasion of ovarian

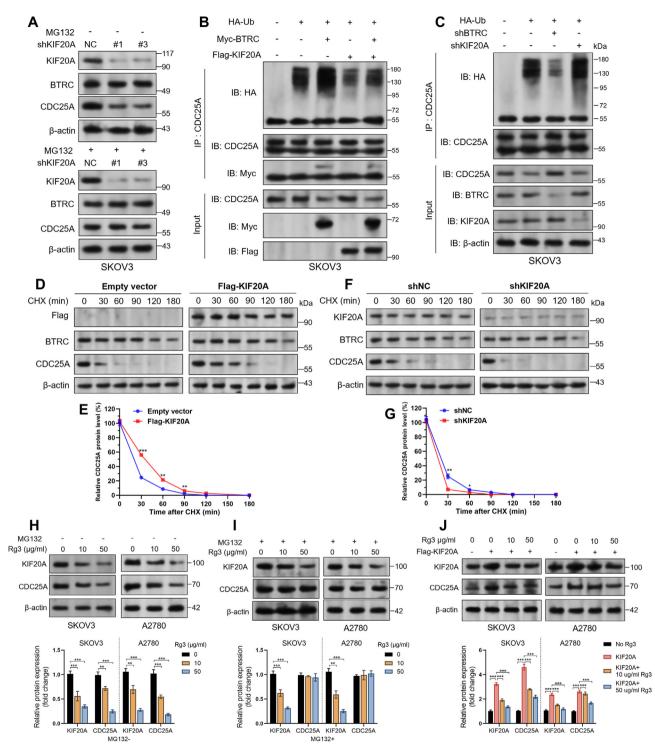


Fig. 5. Ginsenoside Rg3 promotes CDC25A proteasomal degradation via suppressing *KIF20A* expression, **A.** SKOV3 cells were subjected to lentiviral mediated *KIF20A* knockdown for 48 h, with or without the presence of MG132 (10 μ M for 2 h before harvest). **B**–**C.** Western blot of *in vitro* ubiquitination assay. SKOV3 cells were infected with indicating selective combination of pLenti-puro-HA-Ubiquitin, myc-BTRC and/or flag-tagged KIF20A (B) or were infected with indicating selective combination of pLenti-puro-HA-Ubiquitin and shBTRC or shKIF20A (C). 48 h later, cells were lysed and the cell lysates were subjected to IP with an anti-CDC25A antibody. **D-G.** SKOV3 cells were infected for KIF20A overexpression (D-E) or knockdown (F-G). Then, the cells were incubated in the presence of 20 μ M CHX for the indicated times (n = 3). Proteins were then analyzed by western blotting with the indicated antibodies. Relative levels of CDC25A (E and G) were determined from western blots using the ImageJ program based on the respective blots. **H**–**I.** Representative images (top panels) and quantitation (bottom panels) of western blotting analysis of KIF20A and CDC25A expression in SKOV3 and A2780 cells were subjected to ginsenoside Rg3 treatment for 48 h, with (I) or without (H) the presence of MG132 (10 μ M for 2 h before harvest). **J.** SKOV3 and A2780 cells were subjected to lentiviral-mediated *KIF20A* knockdown. 48 h later, cells in indicated groups were treated with ginsenoside Rg3 for another 48 h. Then, cell samples were collected for western blotting analysis of KIF20A and CDC25A expression. Data are expressed as mean \pm SD. Compared with the control group: *p < 0.05, **p < 0.01, ***p < 0.001.

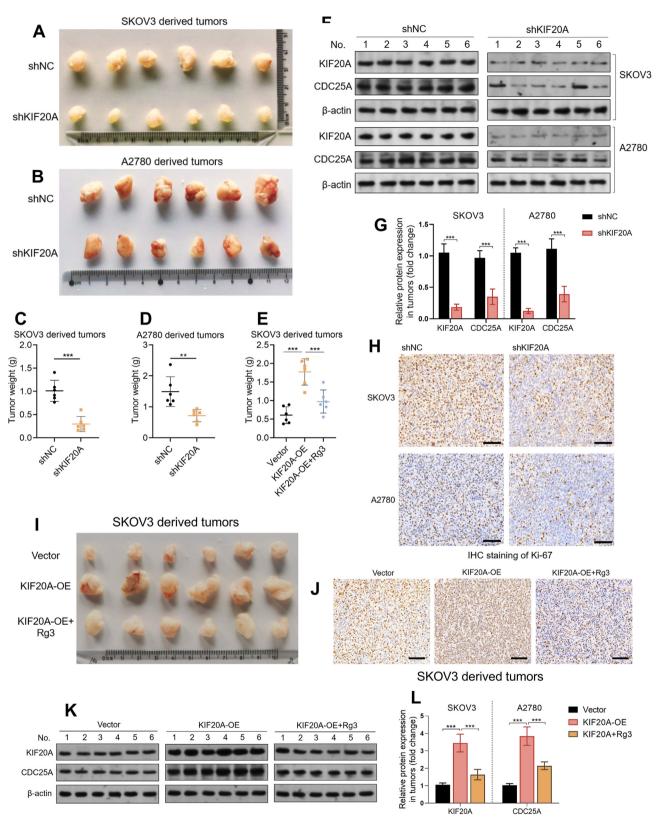
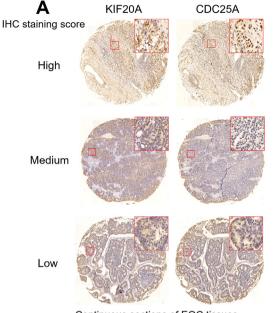


Fig. 6. The *in vivo* regulatory effect of KIF20A and its correlation with CDC25A in human epithelial ovarian cancer tissues, **A-D**. Xenograft tumors (A-D) and their weight (C-D), derived from SKOV3 (A) and A2780 (B) cells with or without *KIF20A* knockdown (n = 6). **F-G**. Representative images (F) and quantitation (G) of KIF20A and CDC25A proteins in tumor tissues in panel A, detected by western blotting. β -actin was used as a loading control. **H**. Representative images of immunohistochemical staining for Ki-67 in xenograft tumors (I) and their weight (E), derived from SKOV3 cells with *KIF20A* overexpression alone or in combination with ginsenoside Rg3 treatment (n = 6). **J**. Representative images of immunohistochemical staining for Ki-67 in xenograft tumor tissues in panel I. **K-L**. Representative images (K) and quantitation (L) of KIF20A and CDC25A proteins in tumor tissues in panel I, detected by western blotting. β -actin was used as a loading control. Data are expressed as mean \pm SD. Compared with the control group: **p < 0.01, ***p < 0.001. Panels H and J, scale bar: 100 µm.



	١.	

Correlation between the expression of KIF20A and CDC25A in EOC tissues

KIF20A staining	CE	- Total number				
score	Negative	Low	Medium	High		
Negative	0	1	0	0	1	
Low	3	5	10	4	22	
Medium	0	5	5	9	19	
High	0	0	5	12	17	
Total number	3	11	20	25	59	

Spearman's rho=0.49

Continuous sections of EOC tissues

Fig. 7. The correlation between KIF20A and CDC25A expression in human epithelial ovarian cancer tissues, A. Representative IHC staining images of high, medium, and low KIF20A (left panel) and CDC25A (right panel) expression in two continuous ovarian cancer tissue microarrays (A). B. Correlation between KIF20A and CDC25A staining scores in 59 ovarian cancer tissues. Spearman's correlation analysis was conducted.

cancer cells [25]. In this study, using A2780 and SKOV3 cells as *in vitro* and *in vivo* cell models, we confirmed that the knockdown of *KIF20A* can significantly suppress tumor cell growth. These findings suggest that KIF20A might act as an important player in the pathological development of ovarian cancer.

KIF20A expression might be activated by NF-κB/P65, and ginsenoside Rg3 has confirmed effects on inhibiting the activity of P65 [32–34]. These clues suggest that ginsenoside Rg3 might suppress *KIF20A* expression. Our *in vitro* studies confirmed that ginsenoside Rg3 could inhibit the phosphorylation of P65 and transcription of *KIF20A*. Since ginsenoside Rg3 shows potent tumor-suppressive effects in ovarian cancer [15–18], we infer that KIF20A might be a downstream effector of ginsenoside Rg3.

KIF20A exerts biological regulations mainly via interacting with other molecules [42,43]. It interacts with the chromosomal passenger complex (CPC) and mediates localization in anaphase [44]. It interacts with the Regulator of G Protein Signaling 3 (RGS3) and controls the division modes of neural progenitor cells during cortical neurogenesis [45]. Therefore, the current study focused on its interacting proteins in ovarian cancer. By applying GST pulldown and co-IP assays, we found that it physically interacts with BTRC, a substrate recognition subunit for SCF^{β -TrCP} E3 ubiquitin ligase. This protein can promote protein degradation by recognizing the phosphorylation of critical signaling molecules with crucial roles in cell cycle regulation, DNA damage response, and cancer progression [46,47]. SCF^{β -TrCP} E3 ubiquitin ligase can recognize phosphorylated AEBP2 and target it for ubiquitylation and proteasomal degradation, leading to cisplatin resistance in ovarian cancer [48].

Among the substrates of SCF^{β -TrCP} E3 ubiquitin ligase, CDC25A is a critical cell-cycle regulator, and its dysregulation is closely associated with chemoresistance in ovarian cancer [49]. CDC25A removes the inhibitory phosphorylation in cyclin-dependent kinase 4 (CDK4), CDK6, and CDK2 and promotes the cell-cycle progression during the G1/S and G2/M phases [50]. Inhibiting CDC25A using a small molecular inhibitor could sensitize ovarian cancer multicellular spheroids to chemotherapeutic agents [49]. The mechanisms underlying CDC25A upregulation are quite complex in cancer. Increased transcription, translation, and protein stability can elevate its expression in tumor cells. Some proteins can reduce CDC25A degradation via the ubiquitin-proteasome pathway via physical binding during cell cycle progression. For example, Rhoassociated coiled-coil-containing protein kinase 2 (Rock2) can interact with CDC25A and reduce its ubiquitination and degradation in hepatocellular carcinoma cells [51]. CENPW can slow CDC25A degradation by interacting with and destabilizing the $SCF^{\beta-TrCP}$ complex during the G2/M phase [52]. Therefore, we further explored whether KIF20A affects the stability of CDC25A. By performing in vitro ubiquitination and CHX chase assays, we confirmed that via interacting with BTRC, KIF20A could reduce BTRC-mediated CDC25A poly-ubiquitination and enhance its stability. In addition, we confirmed that ginsenoside Rg3 treatment could reduce CDC25A protein levels and abrogate KIF20A overexpression-induced CDC25A upregulation in SKOV3 and A2780 cells. Therefore, we infer that ginsenoside Rg3 can promote CDC25A proteasomal degradation by suppressing KIF20A expression.

5. Conclusion

In summary, *KIF20A* is a tumor-promoting gene in ovarian cancer. KIF20A physically interacts with BTRC, reduces BTRC-mediated CDC25A poly-ubiquitination, and enhances its stability. Ginsenoside Rg3 can inhibit *KIF20A* transcription, thereby promoting CDC25A proteasomal degradation. These findings revealed a novel anti-tumor mechanism of ginsenoside Rg3 in ovarian cancer.

Funding

This study was supported by Tianjin Key Medical Discipline (Specialty) Construction Project (TJYXZDXK-031A), Natural Science Foundation of Shanxi Province (grant no.202103021223422 and

202203021221261), and in part, by the National Natural Science Foundation of China (grant nos. 82073264).

Data availability statements

All data generated or analyzed during this study are included in this published article.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jgr.2023.06.008.

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