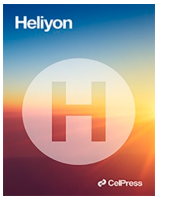
Heliyon 10 (2024) e37714

Contents lists available at ScienceDirect

Heliyon

journal homepage: www.cell.com/heliyon



Research article

TRIM72 inhibits cell migration and epithelial-mesenchymal transition by attenuating FAK/akt signaling in colorectal cancer

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ARTICLE INFO

Keywords:
TRIM72
Migration
Epithelial-mesenchymal transition
FAK/Akt
Colorectal cancer

ABSTRACT

TRIM72 (MG53), a membrane repair protein with E3-ligase activity, plays a crucial role in colorectal cancer (CRC). This study examined TRIM72 expression in primary CRC tumors and paired liver metastases using RT-PCR. Findings revealed significantly lower TRIM72 levels in liver metastases compared to primary tumors ($p < 0.001$). Aberrant TRIM72 expression correlated with lymph node metastasis and advanced clinical stages. Overexpression of TRIM72 inhibited CRC cell migration, intravasation, and EMT in vitro and in vivo, while TRIM72 knockout increased migration and invasion. TRIM72 interacted with Focal Adhesion Kinase (FAK), implicating the FAK/Akt signaling axis in colon cancer spread. Lower TRIM72 levels were associated with reduced survival rates, highlighting its potential as a prognostic marker and therapeutic target in CRC.

1. Introduction

Colorectal cancer (CRC) ranks among the deadliest cancer worldwide, with incidence rates on the rise [1]. Despite advances in surgical, diagnostic, and therapeutic approaches, postoperative recurrence and metastasis continue to challenge long-term survival in CRC patients. Each year, the global burden of CRC grows, with over 1.8 million new cases reported and 20 % of patients presenting metastatic disease right at diagnosis [2]. This underscores the urgent need for a more profound understanding of the mechanisms driving CRC progression, which could pave the way for novel therapeutic targets and diagnostic biomarkers.

The extracellular matrix (ECM), a crucial structural element in the tumor microenvironment, has been gaining recognition for its role in cancer metastasis. This biochemically active network interacts with cell membrane integrin receptors through focal adhesion molecules, triggering focal adhesion kinase (FAK) cascade [3]. This process amplifies signaling pathways driving cell migration and

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https://doi.org/10.1016/j.heliyon.2024.e37714
Received 2 July 2024; Received in revised form 3 September 2024; Accepted 9 September 2024
Available online 11 September 2024

epithelial-mesenchymal transition (EMT) in colorectal cancer (CRC) cells [4–6]. As a central hub in these pathways, FAK presents a promising target for therapeutic intervention [7,8].

TRIM72 is a member of the TRIM superfamily of proteins, characterized by a conserved structure that includes a RING finger domain, a B-Box motif, and a coiled-coil region [9]. As with other TRIM proteins, TRIM72 participates in the ubiquitination process, determining protein fate within cells. For example, ubiquitination at lysine residue K48 leads to proteasomal degradation, whereas K63-linked polyubiquitination regulates various non-proteasomal pathways [10]. TRIM72 is mainly expressed in the cell membrane and predominantly facilitates repair [11–13]. However, increasing evidence shows TRIM72 dysregulation across various cancers, where it plays a significant role in tumorigenesis and progression, including in tongue and lung cancers [14–16]. A recent in vivo genome-wide CRISPR/Cas9 screen identified several loss-of-function mutations that promote tumor growth and lung metastasis [17]. Among the genes identified are both well-known tumor suppressors and novel candidates, including Neurofibromin 2 (Nf2, Merlin), Phosphatase and Tensin Homolog (Pten), Cyclin-dependent kinase inhibitor 2a (Cdkn2a), TRIM72, Fibrinogen Alpha Chain (Fga), miR-152, and miR-345. Trim72 is an E3 ubiquitin ligase, and its role in cancer metastasis is largely unknown.

In this study, we reveal that TRIM72 is downregulated in colorectal cancer (CRC), and this reduction correlates with poor prognosis. Notably, knocking out TRIM72 in the benign HCT116 colorectal cell line induced epithelial-mesenchymal transition (EMT), boosting cell migration and invasion both in vitro and in vivo. In contrast, overexpressing TRIM72 curbed these aggressive behaviors. We found that TRIM72 directly interacts with FAK, promoting its ubiquitination and degradation, which suppresses the FAK/AKT signaling pathway. These findings position TRIM72 as a critical regulator of CRC metastasis and a promising target for therapeutic intervention.

2. Methods

2.1. Clinical samples

Sixty-three tissue samples from CRC patients were obtained from the Department of Pathology at The Fourth Affiliated Hospital of Guangzhou Medical University, China. Clinical staging was based on the eighth edition of the AJCC guidelines. The study received ethical approval from the Guangzhou Medical University Ethics Committee, with informed consent obtained from all participants.

2.2. Cell culture

Human colon cancer cell lines (Lovo, SW480, and HCT116) were sourced from the American Type Culture Collection (ATCC) and cultured in DMEM supplemented with 10 % fetal bovine serum (FBS), 100 U/mL penicillin, and 100 μg/mL streptomycin. Cells were incubated in a humidified atmosphere with 5 % CO2. MG132, a proteasome inhibitor, was purchased from TargetMol (Shanghai) and prepared at 20 mM in DMSO.

2.3. Quantitative reverse transcription-polymerase chain reaction (RT-qPCR)

Total RNA was reverse transcribed into cDNA using the GoScript™ Reverse Transcription System (Promega). Real-time PCR was conducted with the Promega GoTaq® qPCR Master Mix on an ABI7500 system (Thermo Fisher). Gene expression was normalized to GAPDH, and relative expression levels were calculated using the 2-△△Ct method. Primer sequences were as follows: Forward Primer: TCCCTGTTGTCAGGCATCTAC, Reverse Primer: TTCTTCCACACCTGGAATTTG; GAPDH Forward Primer: CATGGGTGTGAACCATGAGA, Reverse Primer: GTCTTCTGGGTGGCAGTGAT.

2.4. Plasmids

Human wild-type (WT) TRIM72 expression vectors pLVX-EF1a-EGFP-Puro-CMV-TRIM72-3FLAG (also for lentivirus production), and the fusion plasmid vectors pCDEF-HA-Ub, pcDNA3.1-PTK2-MYC were constructed by Umine-bio Tech Co., Ltd. Guangzhou, China. TRIM72 CRISPR/Cas9 KO Plasmid (h2) (sc-403554-KO-2) was purchased from SANTA CRUZ BIOTECHNOLOGY, INC. Transfections were carried out using Lipo8000™ Transfection Reagent (Beyotime, Shanghai, China) in accordance with the manufacturer's instructions.

2.5. Wound-healing assay

We employed wound-healing assay to assess the impact of TRIM72 on CRC cell migration.

TRIM72 was overexpressed in highly metastatic Lovo and SW480 cells, while it was knocked out in the benign HCT116 cell line, which naturally has high TRIM72 expression, using CRISPR/Cas9. Cells were cultured in 6-well plates until 80 % confluent, then scratched with a sterile pipette tip and rinsed with PBS. Scratch closure was monitored at 0 and 48 h using a Zeiss Axioskop 2 plus microscope (Carl Zeiss, Thornwood, NY, USA).

2.6. Transwell invasion assay

Cancer cell invasion was evaluated using transwell chambers with 8 μm pores (Corning) following the manufacturer's protocol. The

upper chamber was first coated with Matrigel and incubated at 37 °C for 1 h. Subsequently, 0.5 × 10^4 cells in serum-free medium were added to the upper chamber, while DMEM with 10 % FBS was placed in the lower chamber. After 24 h, non-invasive cells on the upper membrane surface were removed. The invasive cells on the lower surface were fixed with methanol, stained with crystal violet, and counted using a Zeiss Axioskop 2 plus microscope.

2.7. Zebrafish metastatic xenograft model

Zebrafish experiments adhered to institutional guidelines, with approval from the Animal Experimentations Ethics Committee, Southern Medical University. Wild-type AB zebrafish embryos were generated through natural mating and kept in a light-controlled environment with a 14:10 h light/dark cycle. Embryos were maintained in 0.3 % phenylthiourea (PTU) and injected with 50 CM-DiI-labelled CRC cells after anesthetization. Following injection, embryos recovered for 1 h at room temperature before being incubated at 33 °C for the remainder of the experiment.

2.8. Western blot analysis

Western blotting was conducted using standard protocols [30] using primary and secondary antibodies (Supplementary Table 1). Signals were detected using the enhanced chemiluminescence substrate kit, BeyoECL Moon (Beyotime, China).

2.9. Co-immunoprecipitation (Co-IP)

Cells were lysed with IP lysis buffer containing protease inhibitors (Absin, abs9116, China). The lysate was incubated overnight at 4 °C with the target-specific antibody (1 μg) (Supplementary Table 1). Complexes were then incubated with 40 μL BeyoMag™ Protein A + G Magnetic Beads (Beyotime, China) for 30 min at room temperature. After washing with PBS containing 0.1 % Tween 20 (pH 7.4), samples were denatured and analyzed by Western blot, followed by incubation with primary antibodies (Supplementary Table 1).

2.10. Immunohistochemical analysis

Colorectal and metastatic hepatic tumor samples were surgically resected at The Fourth Affiliated Hospital of Guangzhou Medical University, with informed consent from all patients. Specimens were fixed in 4 % formalin, embedded in paraffin, and sectioned at 4 μm thickness. Sections were incubated overnight at 4 °C with TRIM72 primary antibodies (Santa Cruz, A-10), followed by washing and incubation with HRP-polymer-conjugated secondary antibodies (ZSGB-BIO, China) for 1 h at room temperature. DAB staining was performed for 3 min, and nuclei were counterstained with hematoxylin.

2.11. Statistical analysis

All experiments were independently repeated three times. Data analysis was performed using GraphPad Prism 6.0 (GraphPad, La Jolla, CA, USA). Survival data were analyzed with SPSS Statistics software (version 13.0; SS Inc, Chicago, IL).

Table 1
Clinical and pathological information of colorectal cancer patients with low or high TRIM72 expression.

Characteristic	Low TRIM72 expression (n = 25)	High TRIM72 expression (n = 38)	p value
Age	63.02(36–91)	60.88(43–80)	0.789
Gender	Male:14(56.0 %)	20(52.6 %)	0.793
	Female:11(44.0 %)	18(47.4 %)	
Grade	Well differentiated:0(0 %)	6(15.8 %)	0.097
	Moderately differentiated: 23(92.0 %)	28(73.7 %)	
	Poorly differentiated: 2(8.0 %)	4(10.5 %)	
T stage	T1:0(0 %)	7(18.4 %)	0.069
	T2:1(4.0 %)	0(0 %)	
	T3:20(80.0 %)	28(73.7 %)	
	T4:4(16.0 %)	3(7.9 %)	
N stage	N0:5(20.0 %)	30(78.9 %)	0.000
	N1:15(60.0 %)	2(5.2 %)	
	N2:5(20.0 %)	3(7.9 %)	
M stage	M0: 22(88.0 %)	38(100.0 %)	0.058
	M1: 3(12.0 %)	0(0.0 %)	
Lymph node metastasis	No: 4(16.0 %)	30(78.9.0 %)	0.000
	Yes: 21(84.0 %)	8(21.1 %)	
Clinical stage	I:1(4.0 %)	6(15.8 %)	0.000
	II:2(8.0 %)	23(60.5 %)	
	III:19(76.0 %)	8(21.1 %)	
	IV:3(12.0 %)	1(2.6 %)	

3. Results

3.1. TRIM72 is a potential prognostic indicator in patients with colorectal cancer

To uncover the clinical significance of TRIM72, we analyzed its correlation with clinicopathological features in a cohort of 63 colorectal cancer (CRC) patients. As shown in Table 1, TRIM72 expression was inversely correlated with lymph node metastasis and clinical stage. Immunohistochemical (IHC) staining further revealed that TRIM72 expression was correlated with tumor differentiation, with lower levels observed in poorly differentiated CRC tissues (Fig. 1A).

Next, we compared TRIM72 expression and the survival chance of patients in our cohort. Interestingly, we observed a significant correlation between low TRIM72 expression and overall survival (Fig. 1B). An additional dataset of 597 colorectal cancer patients was selected from the protein atlas database and analyzed. Although initial analysis showed no significant correlation with prognosis ($p > 0.05$) (Fig. 1C), re-analysis excluding rectal cancer patients revealed a strong association between TRIM72 expression and patient survival ($p < 0.001$) (Fig. 1D). Our data positions TRIM72 as a potential prognostic indicator in CRC.

3.2. TRIM72 is underexpressed in metastatic colorectal cancer cells

Over 70 % of primary colorectal cancers spread to the liver (hepatic metastasis), dramatically reducing patient survival rates [18]. To understand the function of TRIM72 in colorectal cancer (CRC), we analyzed CRC patients' samples. 10 primary CRC tissue and corresponding liver metastases tissue samples from the same patients were analyzed using RT-QPCR. We examined TRIM72 expression in primary colon cancer tumors and liver metastases using the RT-QPCR. The result showed that cells in the liver metastases have lower TRIM72 expression, suggesting that reduced TRIM72 expression might contribute to liver metastasis of colon cancer (Fig. 2A). To gain further insight into how TRIM72 may influence CRC migration, metastatic CRC cell lines Lovo and SW480 were seeded into the Boyden Chamber (Fig. 2B). After 24 h, cells that had not migrated remained on the upper chamber surface, while the migrated cells were collected. qPCR analysis showed that migrated cells had significantly lower TRIM72 expression compared to the unmigrated cells in the two CRC cells (Fig. 2C). In summary, these results suggest that TRIM72 could be a valuable prognostic marker for managing CRC, with low TRIM72 expression potentially contributing to CRC metastasis.

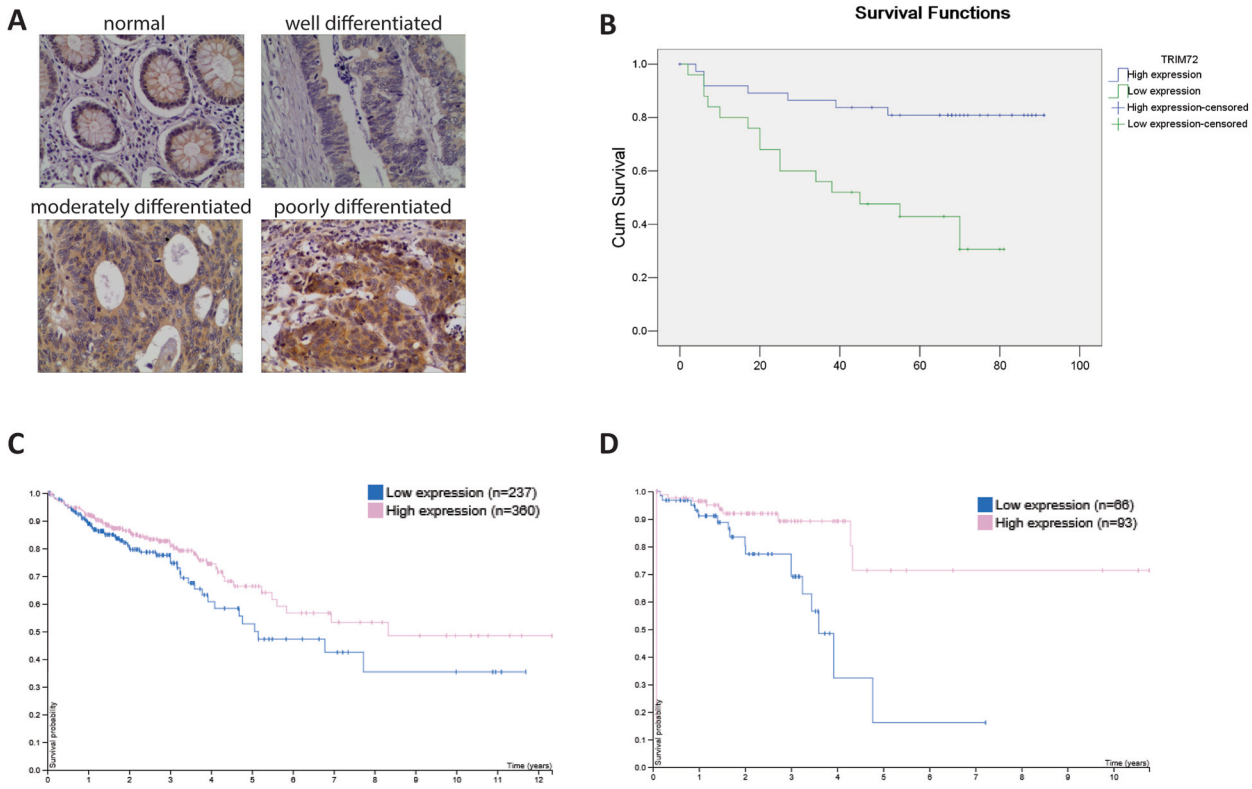

Fig. 1. TRIM72 is a potential prognostic indicator in patients with colorectal cancer.
(A) TRIM72 expression is inversely related to tumor differentiation. Representative pictures of TRIM72 expression in normal and colon cancer patient tissue samples. Scale bar 50 mm (B) The relationship between TRIM72 expression and patient survival in our cohort. Low TRIM72 expression is associated with poor survival chances. (C, D) Analysis of colon cancer dataset on the human protein atlas database. Low TRIM72 expression is also linked to poor survival chances.

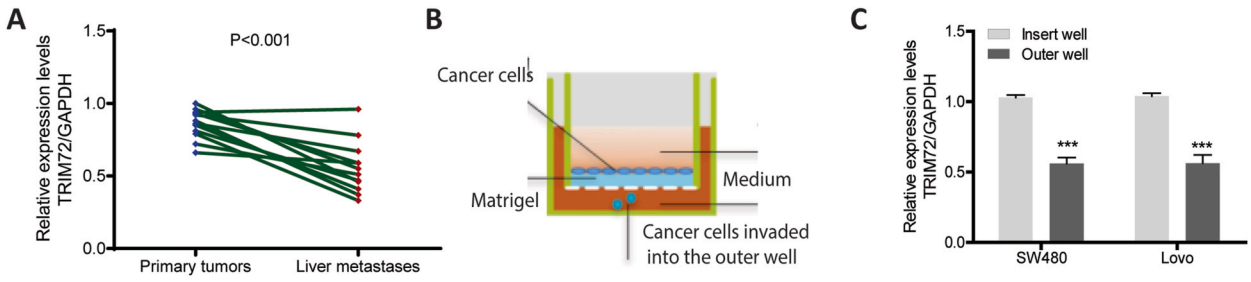

Fig. 2. TRIM72 is underexpressed in metastatic colorectal cancer cells.
(A) Real-time PCR analyses were performed to examine TRIM72 expression in primary colon tumor and paired liver metastases. ($n = 10$, $P < 0.001$) (B) Schematic representation of transwell invasion assay. (C) Colon cancer cells were seeded into the transwell membrane. After 24 h, the cells in the outer and inner part of the transwell membrane were collected and subjected to RT-PCR using TRIM72 primers.***$P < 0.001$, Data are presented as mean ± SD ($n \geq 3$).

3.3. TRIM72 inhibits migration of colorectal cancer cells in vitro

To explore the relationship between TRIM72 and migration of colorectal cancer, we performed wound healing and invasion assays. To do this, we assessed the expression of TRIM72 in several colorectal cells (Fig. S1A). We overexpressed TRIM72 in high metastatic cells, Lovo, SW480, while TRIM72 was knocked out in benign HCT116 which has a high TRIM72 basal expression using CRISPR/Cas9 (Fig. S1B). Similarly, we overexpressed TRIM72 in two metastatic CRC cell lines, Lovo and SW480, using a lentiviral packaged TRIM72 plasmid (Fig. S1C). Colon cancer cell lines, Lovo and SW480, both have a higher metastatic potential than HCT116. Western blotting analysis was performed to detect TRIM72 expression in the TRIM72 knockout and overexpression cells (Fig. S1D). In cells overexpressing TRIM72, we observed that wound healing was significantly slower than control cells (Fig. 3A–C). In contrast, TRIM72 knockout in HCT116 markedly increased wound healing compared to control cells (Fig. 3E). Next, we performed a transwell assay to confirm this observation. Similarly, TRIM72 expression reduced cell migration of both Lovo and SW480 in the transwell assay (Fig. 3B–D), whereas TRIM72 knockout in HCT116 increased cell migration (Fig. 3F). These results confirm that TRIM72 can inhibit the migration of CRC cells.

3.4. TRIM72 restricts intravasation of colorectal cancer cells in embryonic zebrafish

To validate the in vitro results, we established a zebrafish metastatic xenograft model using dil-labelled control, TRIM72 knockout or overexpression cells. Consistent with in vitro results, TRIM72 overexpression decreased the number of distant metastatic cells (Fig. 4A). Conversely, TRIM72 knockout increased the number of distant metastatic cells in the tail region of Zebrafish compared to the control group (shown by the white arrow) (Fig. 4B). In sum, the zebrafish metastatic xenograft model showed that TRIM72 can restrict the intravasation of colorectal cancer cells.

To validate the in vitro findings, we established a zebrafish metastatic xenograft model using dil-labelled control, TRIM72 knockout, and TRIM72 overexpression cells. Consistent with the in vitro results, TRIM72 overexpression reduced the number of distant metastatic cells (Fig. 4A). In contrast, TRIM72 knockout led to an increase in the number of distant metastatic cells in the tail region of the zebrafish, as indicated by the white arrow (Fig. 4B). Overall, the zebrafish metastatic xenograft model demonstrated that TRIM72 can limit the intravasation of colorectal cancer cells.

3.5. TRIM72 suppresses EMT progression of colorectal cancer cells by attenuating FAK/Akt signaling pathway

It is well established that epithelial-mesenchymal transition (EMT) plays a crucial role in colon cancer metastasis [19,20]. Low E-cadherin expression, a marker of EMT, is positively correlated with a malignant phenotype in colon cancer cells [21,22]. Given our earlier findings on TRIM72's regulatory effects on CRC cell migration, we next investigated TRIM72's influence on EMT gene expression in CRC cells. To do this, Lovo and SW480 were transfected with TRIM72 or control plasmid and subjected to western blotting. Notably, TRIM72 overexpression led to a downregulation of mesenchymal markers vimentin and N-cadherin, and an upregulation of the epithelial marker E-cadherin in both Lovo and SW480 cells (Fig. 5A). Conversely, TRIM72 knockout resulted in an increase in vimentin and N-cadherin expression, and a decrease in E-cadherin expression (Fig. 5B). This data suggest that TRIM72 suppressed CRC cell metastasis by inhibiting EMT phenotypic transition.

We next sought to elucidate the mechanism by which TRIM72 regulates CRC migration. The FAK/AKT pathway is upregulated in colorectal cancer and linked to metastasis and poor prognosis [23,24]. Previous studies have shown that FAK expression could be regulated by E3 ligase activity [25–27]. Next, we examined whether TRIM72 can interact with FAK. Interestingly, our co-immunoprecipitation results revealed an interaction between TRIM72 and FAK in the two cell lines (Fig. 5C). We further assessed whether TRIM72 overexpression or knockout could regulate the FAK/AKT signaling pathway. Further analysis showed that TRIM72 overexpression significantly reduced FAK levels, whereas TRIM72 knockout increased FAK expression (Fig. 5D, Fig. S2A), suggesting that TRIM72 may interact with FAK to promote its degradation via the ubiquitin-proteasome pathway. Interestingly, we observed

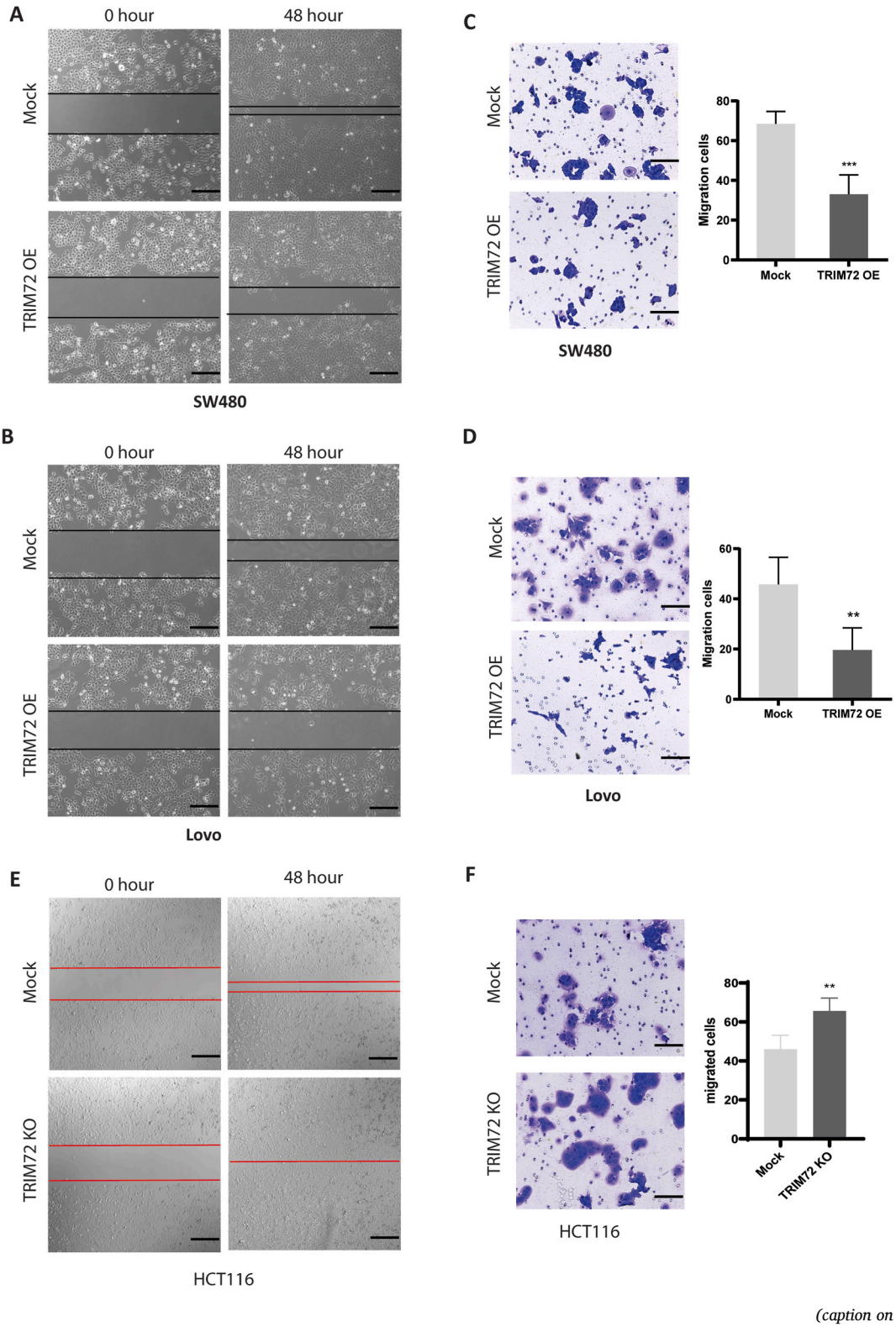

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Fig. 3. TRIM72 inhibits migration of colorectal cancer cells in vitro.
(A, B) TRIM72 was overexpressed in two colon cancer cells, SW480 (A) and Lovo (B). The migration ability of the TRIM72 overexpression cells and the control cells was analyzed by wound healing. (C, D) Transwell migration assay for TRIM72 overexpression cells, SW480 (C) and Lovo (D). Twenty-four hours after seeding, the migrated cells were fixed, stained, and photographed. Scale bar, 100 μm (E) HCT116 TRIM72 knockout cells were established using CRISPR technique. The migration ability of the knockout and control cells was analyzed by wound healing. (F) Transwell migration assay for TRIM72 knockout cells, HCT116. Twenty-four hours after seeding, the migrated cells were fixed, stained and photographed. Scale bar, 100 μm *P < 0.05, ***P < 0.001, Data are presented as mean ± SD.

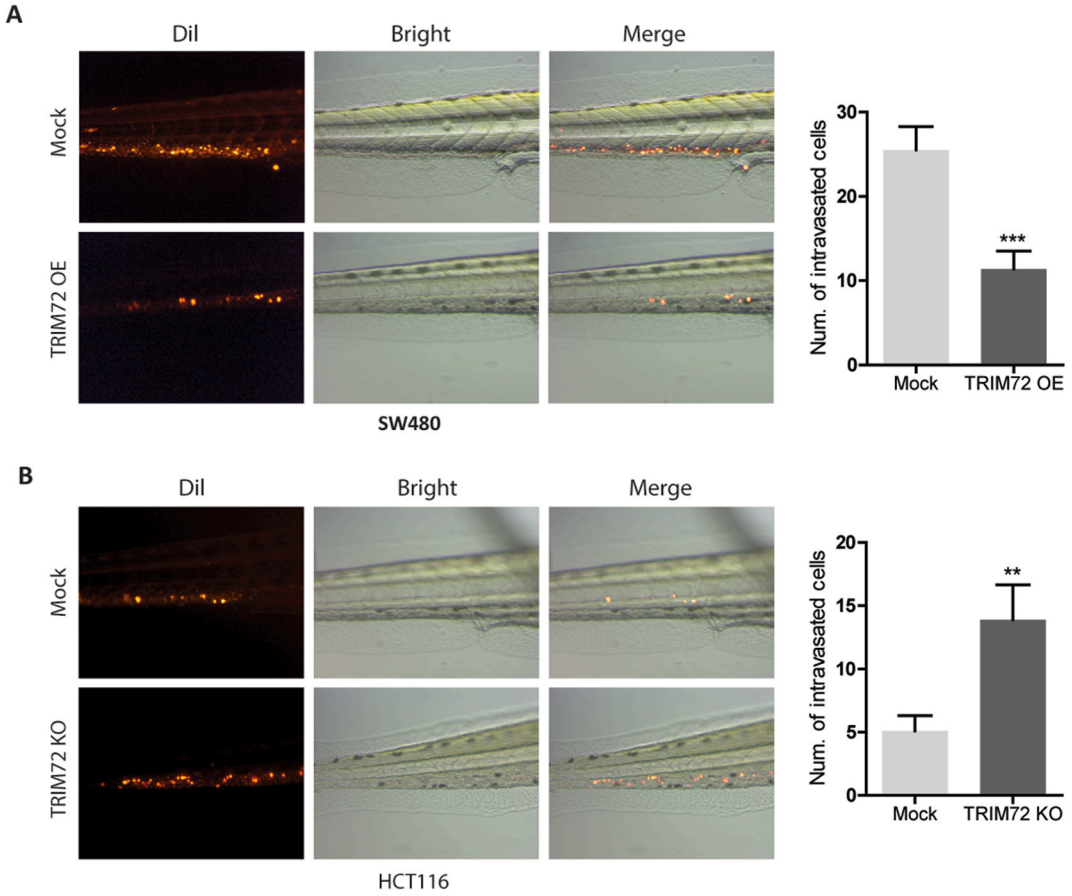

Fig. 4. TRIM72 restricts intravasation of colorectal cancer cells in embryonic Zebrafish.
(A) SW480 colon cancer cells overexpressing TRIM72 or control plasmid were labelled with cell tracker and microinjected into zebrafish embryos. (B) HCT116 TRIM72 knockout or control cells were labelled with a cell tracker and microinjected into zebrafish embryos. Scale bar, 500 μm **P < 0.01, ***P < 0.001, Data are presented as mean ± SD (n ≥ 3).

increased ubiquitin-FAK bands upon TRIM72 overexpression (Fig. 5E). In sum, these results suggest that TRIM72 directly binds to FAK, promoting its proteasomal degradation to inhibit CRC migration.

4. Discussion

In this study, we uncovered the previously unknown role of TRIM72 in colorectal cancer (CRC). We demonstrated that TRIM72 is downregulated in CRC patients, with its expression negatively correlating with both lymph node metastasis and advanced clinical/TNM stages. TRIM72 was initially identified as a regulator of cell membrane repair, and recent studies have highlighted that high TRIM72 expression is associated with poor CRC prognosis [28,29]. Despite these findings, the mechanisms underlying its role in CRC have remained largely unexplored until now. Our study reveals that TRIM72 functions as a tumor suppressor in CRC. Through the overexpression of TRIM72 in high metastatic CRC cell lines (Lovo, SW480) and knockout in HCT116 cells—which inherently express high levels of TRIM72—using CRISPR/Cas9, we uncovered a novel biological function of TRIM72. Our functional assays indicate that TRIM72 interacts with and promotes the degradation of focal adhesion kinase (FAK) via the ubiquitin-proteasome pathway, thereby inhibiting CRC metastasis.

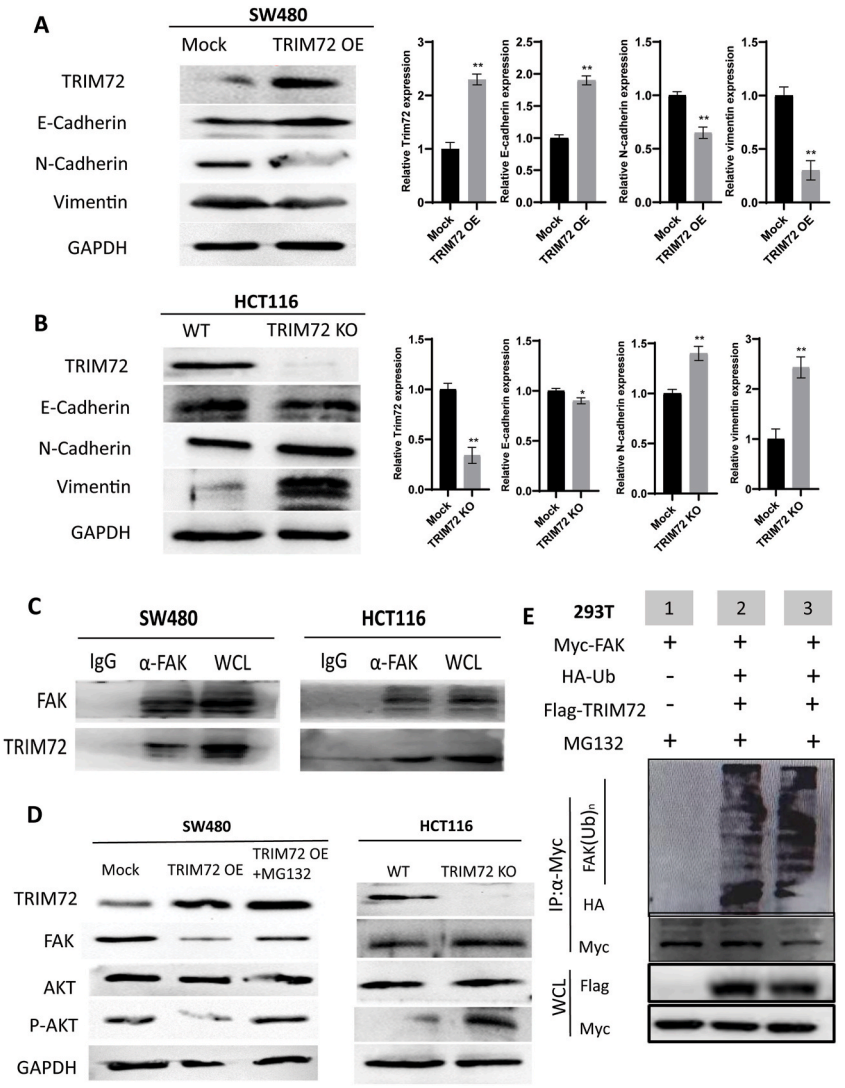

Fig. 5. TRIM72 suppresses EMT progression of colorectal cancer cells by attenuating FAK/Akt signaling pathway.
(A) Western blot assay was used to determine the expression of E-cadherin, N-cadherin, and vimentin, in SW480 colon cancer cells overexpressing TRIM72, or control plasmid. Quantitation of relevant protein levels were shown in right pane (n.s., not significant; *P < 0.05, **P < 0.01, ***P < 0.001; n = 3). (B) Western blot assay was used to determine the expression of E-cadherin, N-cadherin, and vimentin in HCT116 TRIM72 knockout or control cells. Quantitation of relevant protein levels were shown in right pane (n.s., not significant; *P < 0.05, **P < 0.01, ***P < 0.001; n = 3). (C) Circulating tumor cells were isolated from colon cancer patients, and the expression of TRIM72, vimentin and other marker was determined using immunofluorescence. (D) Co-immunoprecipitation of TRIM72 and FAK proteins in two colon cancer cells, SW480 and HCT116. (E) Western blot assay was used to determine the expression of FAK, AKT, and p-AKT in TRIM72 overexpression cells treated with or without mg132. (F) 293T cells were co-transfected with Myc-FAK, Myc-TRIM72, Ub-Ha as shown for 24 h and subsequently treated with or without MG132 for 12 h. The cells were lysed and subjected to IP with anti-Myc-conjugated beads. The immunoprecipitated proteins were subjected to western analysis using the indicated antibodies.

Our findings underscore the complex and multifaceted nature of cancer metastasis, which poses significant challenges to CRC treatment. Metastasis involves a series of steps that often result in cancer spreading to lymph nodes, lungs, and liver, causing disease progression despite initial treatment successes [35–37]. The role of extracellular matrix (ECM)-integrin interactions in cellular transformation and metastasis is well-established [11]. Activation of the ECM-integrin complex leads to FAK phosphorylation and subsequent activation of the Akt and PI3K signaling pathways [6,7]. Our data shows that TRIM72 overexpression attenuates FAK/Akt signaling activation, promotes mesenchymal-to-epithelial transition, and reduces CRC cell migration and invasion, both in vitro and in vivo. In contrast, the knockout of TRIM72 in HCT116 cells significantly increased the expression of mesenchymal markers, underscoring TRIM72's role as a tumor suppressor and its ability to inhibit metastasis in CRC. Through these findings, our study positions TRIM72 as a potential tumor suppressor and lays the groundwork for possible therapeutic strategies targeting TRIM72.

Biomarkers continue to play a crucial role in the management of colorectal cancer (CRC) treatment strategies. Our study provides

evidence suggesting that TRIM72 expression levels could serve as a predictive marker for CRC patient survival outcomes. By analyzing data from our CRC cohort and two online genomic databases, we identified a consistent negative correlation between TRIM72 expression and survival probabilities in CRC patients. These results align with recent research indicating that lower TRIM72 expression is associated with poorer prognosis in CRC patients [28,29].

Our study advances this understanding by demonstrating, for the first time, that silencing TRIM72 not only impairs the migratory abilities of colon cancer cells but also initiates epithelial-mesenchymal transition (EMT) programs through the activation of the FAK/AKT signaling pathway. Using both cellular models and zebrafish metastasis assays, we have elucidated TRIM72's role in regulating CRC metastasis. Additionally, our investigation into the differential expression patterns of TRIM72 within pathological tissue samples further supports the hypothesis that TRIM72 could hold significant clinical relevance in the context of CRC. It is important to acknowledge a limitation within our study; the regulatory mechanisms of TRIM72 in CRC were not examined within animal models. This area represents a potential avenue for future research, which could provide deeper insights into the biological mechanisms of TRIM72 in CRC progression and metastasis.

5. Conclusions

Our results offer new insights into the mechanisms underlying colon cancer metastasis. We have demonstrated that TRIM72, traditionally known as a membrane repair protein, also plays a role in regulating CRC migration and has the potential to serve as a prognostic marker.

Funding

The work was partially supported by grants from Guangdong Basic and Applied Basic Research Foundation, China (2021A1515010713); President Foundation of the Third Affiliated Hospital, Southern Medical University (YM2021001); Science and Technology Program of Guangzhou, China (202102080542); Zengcheng Technology Innovation Support Fund, Guangzhou, China (2024ZCKJ08).

Data availability statement

Data included in article/supp. material/referenced in article, and the datasets used and/or analyzed during the current study are available from the corresponding author upon reasonable request.

The interactive survival scatter plot & Survival analysis data of TRIM72 in colorectal carcinoma are available via the human protein atlas database (https://www.proteinatlas.org/ENSG00000177238-TRIM72/pathology/colorectal+cancer#ihc).

Ethics approval & consent to participate

This study was approved by the Ethics Committee of The Fourth Affiliated Hospital of Guangzhou Medical University (2024-H-005), and all patients signed informed consent.

All animal experiments were performed in compliance with the institutional guidelines and prior approval from the Animal Experimentations Ethics Committee, Southern Medical University for the care and use of experimental animals.

Patient consent for publicatuion

Not applicable.

CRediT authorship contribution statement

Oluwasijibomi Damola Faleti: Writing – original draft, Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Yibing Gong:** Software, Methodology, Investigation, Formal analysis, Data curation. **Jingyi Long:** Visualization, Software, Methodology, Investigation, Formal analysis, Data curation. **Qingshuang Luo:** Methodology, Investigation. **Haiqi Tan:** Methodology, Investigation. **Simin Deng:** Methodology. **Lizhen Qiu:** Resources, Data curation. **Xiaoming Lyu:** Writing – review & editing, Validation, Supervision, Resources, Project administration, Funding acquisition, Data curation, Conceptualization. **Jinke Yao:** Validation, Resources, Funding acquisition, Data curation, Conceptualization. **Gongfa Wu:** Writing – review & editing, Validation, Supervision, Resources, Project administration, Methodology, Funding acquisition, Data curation, Conceptualization.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:Xiaoming Lyu reports financial support was provided by Guangdong Basic and Applied Basic Research Foundation, China. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

We extend our gratitude to our colleagues in the Department of Laboratory Medicine at The Third Affiliated Hospital, Southern Medical University, for their dedicated work and kind assistance in SARS-CoV-2 screening.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.heliyon.2024.e37714.

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