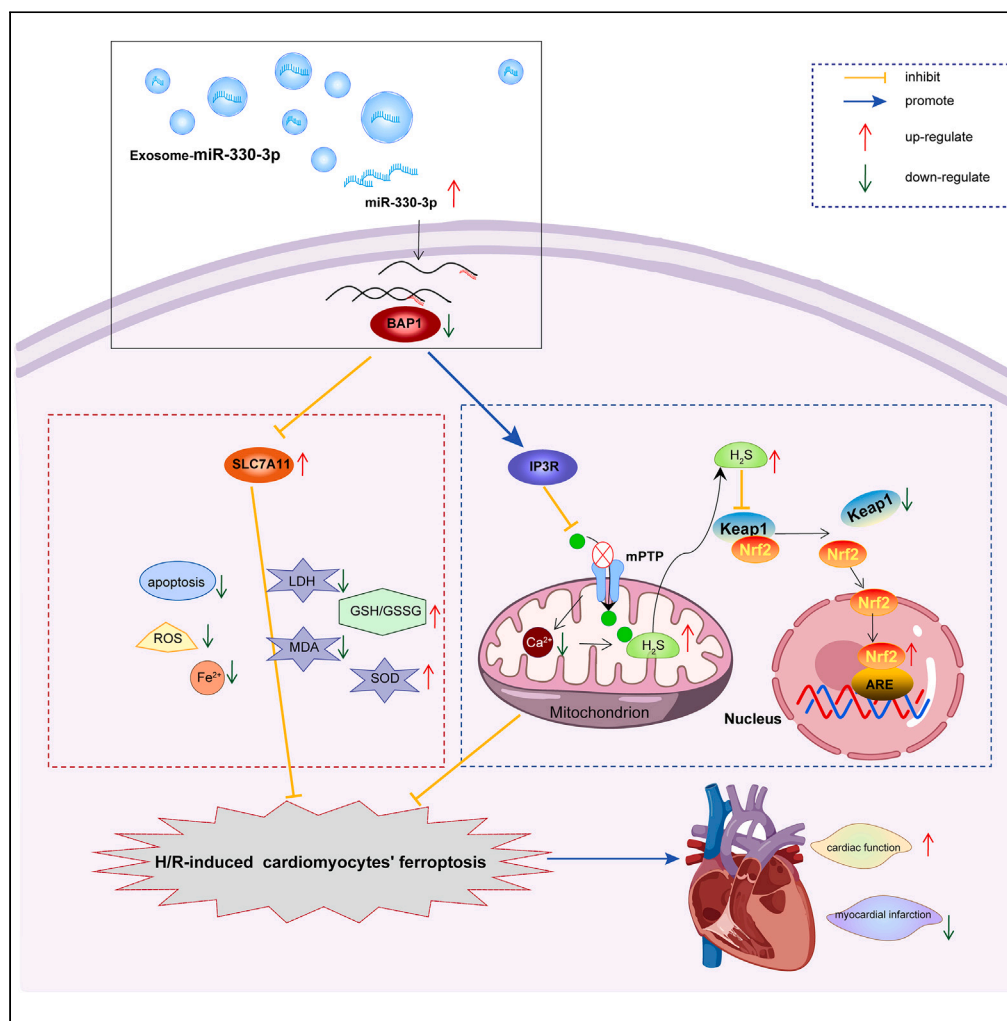


Article

GATA-4 overexpressing BMSC-derived exosomes suppress H/R-induced cardiomyocyte ferroptosis



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Highlights

Exos^{oe-GATA-4} upregulates miR-330-3p in H/R-induced cardiomyocytes

miR-330-3p targeted negative regulated BAP1, BAP1 downregulates SLC7A11

BAP1 interacted with IP3R causing mPTP opening and mitochondrial dysfunction

Exos^{oe-GATA-4} suppresses H/R-induced cardiomyocytes' ferroptosis and mPTP opening



Article

GATA-4 overexpressing BMSC-derived exosomes suppress H/R-induced cardiomyocyte ferroptosis

Zhiyuan Xiao,^{2,5} Si Li,^{3,5} Xinxin Wu,⁴ Xinhao Chen,³ Dan Yan,² and Jigang He^{1,6,*}

SUMMARY

Bone marrow mesenchymal stem cell (BMSC)-derived exosomes overexpressing GATA-4 (Exos^{oe-GATA-4}) can protect cardiac function. Mitochondrial permeability transition pore (mPTP) has a crucial role in ferroptosis. This study aimed to assess the mechanism of Exos^{oe-GATA-4} in myocardial ischemia/reperfusion (I/R) injury. Exos were successfully excreted, and 185 differential expression miRNAs were obtained using bioinformatics. The Exos^{oe-GATA-4} effectively suppressed hypoxia/reoxygenation (H/R)-induced cardiomyocytes' ferroptosis, while the effects were reversed by miR-330-3p inhibitor. miR-330-3p targeted negative regulated BAP1. The effects of miR-330-3p inhibitor were reversed by knock-down BAP1. Also, BAP1 reversed the effects of Exos^{oe-GATA-4} on H/R-induced cardiomyocytes' ferroptosis by downregulating SLC7A11. Mechanistically, BAP1 interacted with IP3R and increased cardiomyocytes' Ca²⁺ level, causing mPTP opening and mitochondrial dysfunction, promoting H/R-induced cardiomyocytes' ferroptosis. Moreover, hydrogen sulfide (H₂S) content was increased and regulated the Keap1/Nrf2 signaling pathway by Exos^{oe-GATA-4} treated. Exos^{oe-GATA-4} effectively suppresses H/R-induced cardiomyocytes' ferroptosis by upregulating miR-330-3p, which regulates the BAP1/SLC7A11/IP3R axis and inhibits mPTP opening.

INTRODUCTION

Cardiovascular diseases are the leading cause of death worldwide.¹ Acute myocardial infarction (AMI) is a serious condition caused by permanent damage to the heart muscle due to inadequate oxygen supply. At the moment, reperfusion remains the most effective treatment method for AMI²; timely reperfusion can salvage approximately 50% of severely ischemic myocardium.³ However, cardiomyocyte injury and death that occur after ischemia/reperfusion (I/R) treatment, such as ferroptosis and pyroptosis, are irreversible.⁴ Therefore, searching for effective treatment strategies to relieve cardiomyocyte injury after I/R is necessary for AMI patients.

Ferroptosis is a programmed cell death process characterized by a significant accumulation of lipid peroxides.⁵ Studies have found that ferroptosis has a crucial role in myocardial I/R injury. For example, in diabetic patients with myocardial injury, ferroptosis is involved in the occurrence of myocardial injury.⁶ In addition, Kajarabille et al. reported that ferroptosis inhibition can decrease the infarct size of transplanted I/R hearts and protect heart function.⁷ Solute carrier family 7 member 11 (SLC7A11) is a crucial regulated protein of iron overload-ferroptosis,⁸ which can increase cystine uptake and reduce the lipid peroxidation and ferroptosis that occur inside the cell.⁹ Moreover, Zhang et al. found that BRCA1-associated protein 1 (BAP1), an anti-cancer gene, can regulate the ferroptosis-related gene SLC7A11 mediated ferroptosis.¹⁰ Therefore, targeting SLC7A11 is a potential therapeutic strategy to prevent ferroptosis during myocardial I/R injury.

Mesenchymal stromal cells (MSCs) protect cardiac function by regulating cardioprotection, angiogenesis, and immunoregulation.¹¹ Moreover, studies have found that MSC-derived exosomes (MSC-Exos), rich in abundantly biologically active microRNAs, are essential for the capability of angiogenesis in treating myocardial infarction (MI).¹² In myocardial I/R injury, MSC-Exos can regulate the change between macrophages to M2 phenotype by miR-182 to relieve myocardial I/R injury.¹³ In addition, Gao et al. found that several microRNAs highly expressed in MSC-Exos, especially miR-125a-5p, can be an effective therapy in I/R cardiac repair.¹⁴

Mitochondrial stress and dysfunction participate in ferroptosis by regulating Fe²⁺ and reactive oxygen species (ROS).¹⁵ The opening of the mitochondrial permeability transition pore (mPTP), induced by Fe²⁺ and Ca²⁺,¹⁶ which by inhibiting is a crucial factor in protecting the heart from the death of myocardial cells during I/R.¹⁷ Previous research has confirmed that mPTP is the leading cause of cell death after reperfusion injury.¹⁸ Overload of Ca²⁺ leads to mPTP opening, further inducing superoxide production, increased ROS, and cell ferroptosis.^{19,20} Also,

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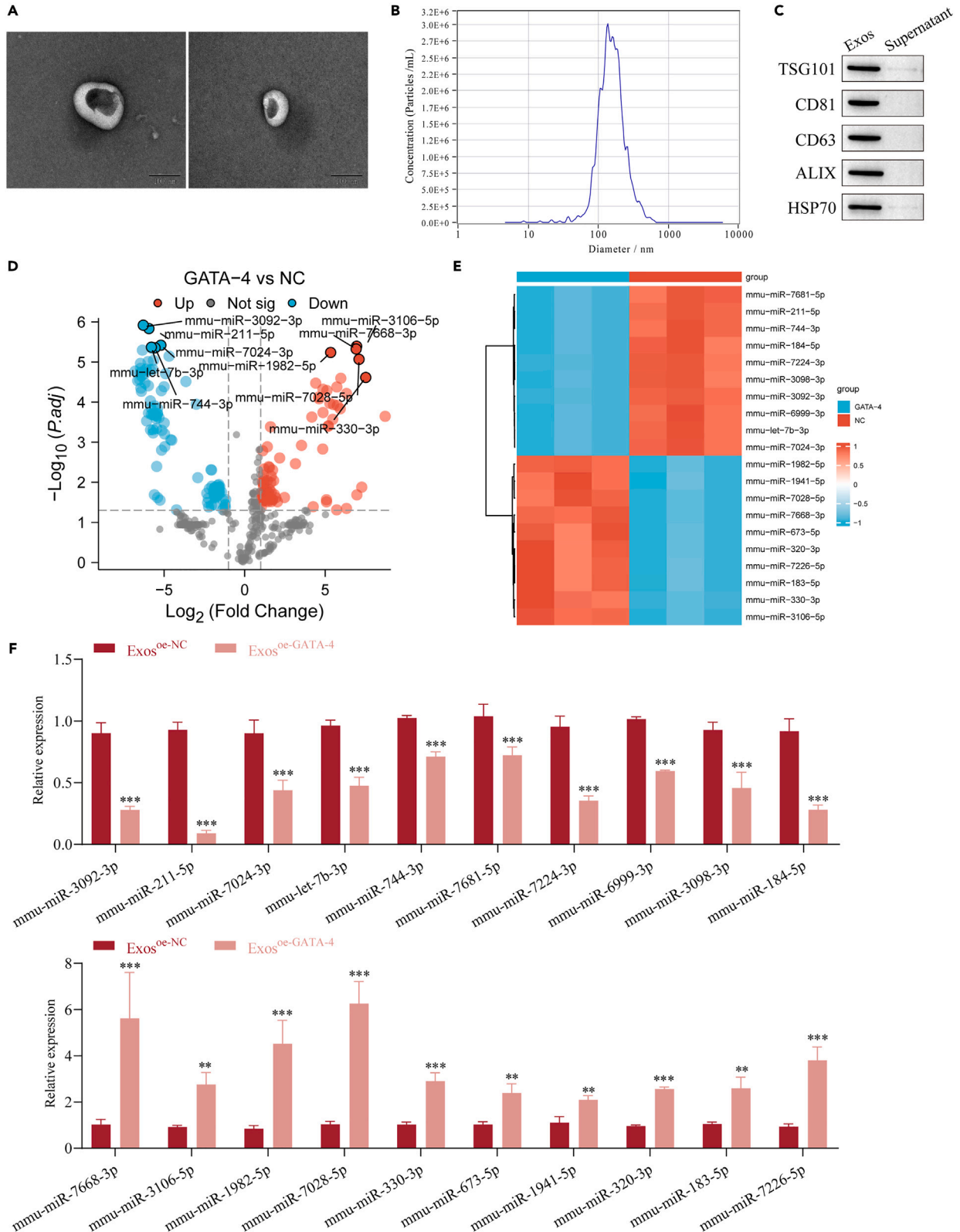


Figure 1. Differential expression miRNAs in BMSC-derived exosomes (Exos) overexpressing GATA-4 compared to BMSC-derived Exos^{oe-NC} group

(A) TEM image of Exos.

(B) NanoSight analysis.

(C) Western blot was used to evaluate exosome markers.

(D and E) Volcano plot (D) and heatmap (E) of differential expression miRNAs.

(F) RT-qPCR detected the expression levels of differential expression miRNAs. $n = 3$, ** $p < 0.01$, *** $p < 0.001$. Data are represented as mean \pm SD.

inositol 1,4,5-triphosphate receptor (IP3R) has been reported as a regulated factor of Ca^{2+} levels that can induce Ca^{2+} release and raise the levels of Ca^{2+} in the cytosolic, further improving mitochondrial intake.^{21,22} However, the mechanism of action of IP3R and mPTP has not been elucidated yet in myocardial I/R injury.

This study investigated the functional relationship between mPTP and myocardial I/R injury ferroptosis. Our results found that overexpression-GATA-4 BMSC-derived Exos effectively regulates the ferroptosis and is related to mPTP opening by BAP1/SLC7A11/IP3R axis via miR-330-3p, which also has an important role in cancer cell proliferation, apoptosis and migration, such as laryngeal squamous cell carcinoma,²³ gastric cancer,²⁴ and ovarian cancer.²⁵ Our findings elucidate an effective molecular mechanism of overexpression-GATA-4 BMSC-derived Exos in ferroptosis and identify the treatment strategy in myocardial I/R injury.

RESULTS

Differential expression miRNAs of overexpression-GATA-4 BMSC-derived exosome

Our previous study has confirmed that BMSC-derived exosomes (Exos) overexpressing GATA-4 can reduce anoxia-induced cardiomyocyte apoptosis and relieve myocardial infarction, in turn protecting cardiac function.²⁶ To further explore the exact mechanism involved in myocardial I/R injury, we extracted and identified the Exos. Exos showed a shape similar to a cup holder and a bilayer membrane (Figure 1A) with a particle size of 138.0 nm (Figure 1B; Data S1). Moreover, western blot was used to identify exosome markers, and it also had been verified that extracted Exos successfully (Figure 1C), TSG101, CD81, CD63, ALIX, and HSP70 only expressed in Exos.

Next, bioinformatics analysis was applied, and 185 differential expression miRNAs, including 104 downregulation and 81 upregulation, were detected (Table S1). The volcano plot is shown in Figure 1D, and the heatmap of each top 10 downregulation and upregulation differential expression miRNAs is shown in Figure 1E. Subsequently, we detected the expression of differential expression miRNAs; compared with Exos^{oe-NC} group, the expressions of mmu-miR-3092-3p, mmu-miR-211-5p, mmu-miR-7024-3p, mmu-let-7b-3p, mmu-miR-744-3p, mmu-miR-7681-5p, mmu-miR-7224-3p, mmu-miR-6999-3p, mmu-miR-3098-3p, and mmu-miR-184-5p were downregulated; the expressions of mmu-miR-7668-3p, mmu-miR-3106-5p, mmu-miR-1982-5p, mmu-miR-7028-5p, mmu-miR-330-3p, mmu-miR-673-5p, mmu-miR-1941-5p, mmu-miR-320-3p, mmu-miR-183-5p, and mmu-miR-7226-5p were upregulated in Exos overexpressing GATA-4 (Figure 1F).

BMSC-derived Exos overexpressing GATA-4 inhibits H/R-induced ferroptosis by upregulating miR-330-3p target-regulating BAP1

Based on preliminary research and studies, we identified miR-330-3p as a factor that may play an important role in cardiomyocyte I/R injury among many differential miRNAs, while the mechanism is unclear. Previous research has found that miR-330-3p plays a vital role in various cancers,^{27,28} while the function in myocardial I/R injury has not been clearly stated. miR-330-3p is one of the differentially expressed miRNAs that effectively mediate AMI pathogenesis.²⁹ Moreover, miR-330-3p has been confirmed to suppress hepatic ischemia/reperfusion by regulating mitophagy.³⁰ Therefore, miR-330-3p may be an important regulatory factor as a differentially expressed miRNA. The aforementioned results have confirmed that miR-330-3p had a high expression in BMSC-derived Exos overexpressing GATA-4. To understand the mechanism of action of the Exos in myocardial I/R injury, we established cardiomyocytes I/R injury model *in vitro* by hypoxia/reoxygenation (H/R) induction.³¹ To verify the success of the model construction, we performed reoxygenation for 2, 4, 6, and 8 h, and found increased malondialdehyde (MDA), ROS (Figures S1A and S1C) and apoptosis (Figure S1B), decreased superoxide dismutase (SOD) (Figure S1A) levels gradually as the reoxygenation time increased, had the best in 6 h. Subsequently, we evaluated the expression levels of hypoxia-inducible factor-1 α (HIF-1 α), B cell lymphoma-2 (Bcl-2), and Bcl-2-associated X (Bax) using RT-qPCR (Figure S1D) and western blot (Figure S1E), which showed that rose expression levels of HIF-1 α and Bax, while lower expression levels of Bcl-2 as the reoxygenation time increases, also had the best with 6 h. Therefore, we chose hypoxia for 18 h and reoxygenation for 6 h to construct an H/R model that was a success, and then transfected cardiomyocytes with an NC inhibitor or miR-330-3p inhibitor (Figure 2A). The expression of miR-330-3p (Figure 2B) and cell viability (Figure 2C) increased in cardiomyocytes with BMSC-Exos^{oe-NC}, while cell apoptosis decreased (Figure 2D); yet, this effect was more pronounced in cardiomyocytes with BMSC-Exos overexpressing GATA-4 (Exos^{oe-GATA-4}). After adding miR-330-3p inhibitor, the expression of miR-330-3p and cell viability decreased, while cell apoptosis increased.

Subsequently, we assessed the content of lactate dehydrogenase (LDH), MDA, glutathione (GSH)/ oxidized glutathione (GSSG), and SOD, and levels of ROS and Fe^{2+} . The results showed that BMSC-Exos^{oe-NC} had a particular effect on LDH, MDA, GSH/GSSG, SOD, ROS, and Fe^{2+} levels but it was not significant, while Exos^{oe-GATA-4} significantly reduced the content of LDH, and MDA increased the GSH/GSSG ratio and content of SOD (Figure 2E), and reduced the levels of ROS (Figure 2F) and Fe^{2+} (Figure 2G). On the contrary, transfection with miR-330-3p

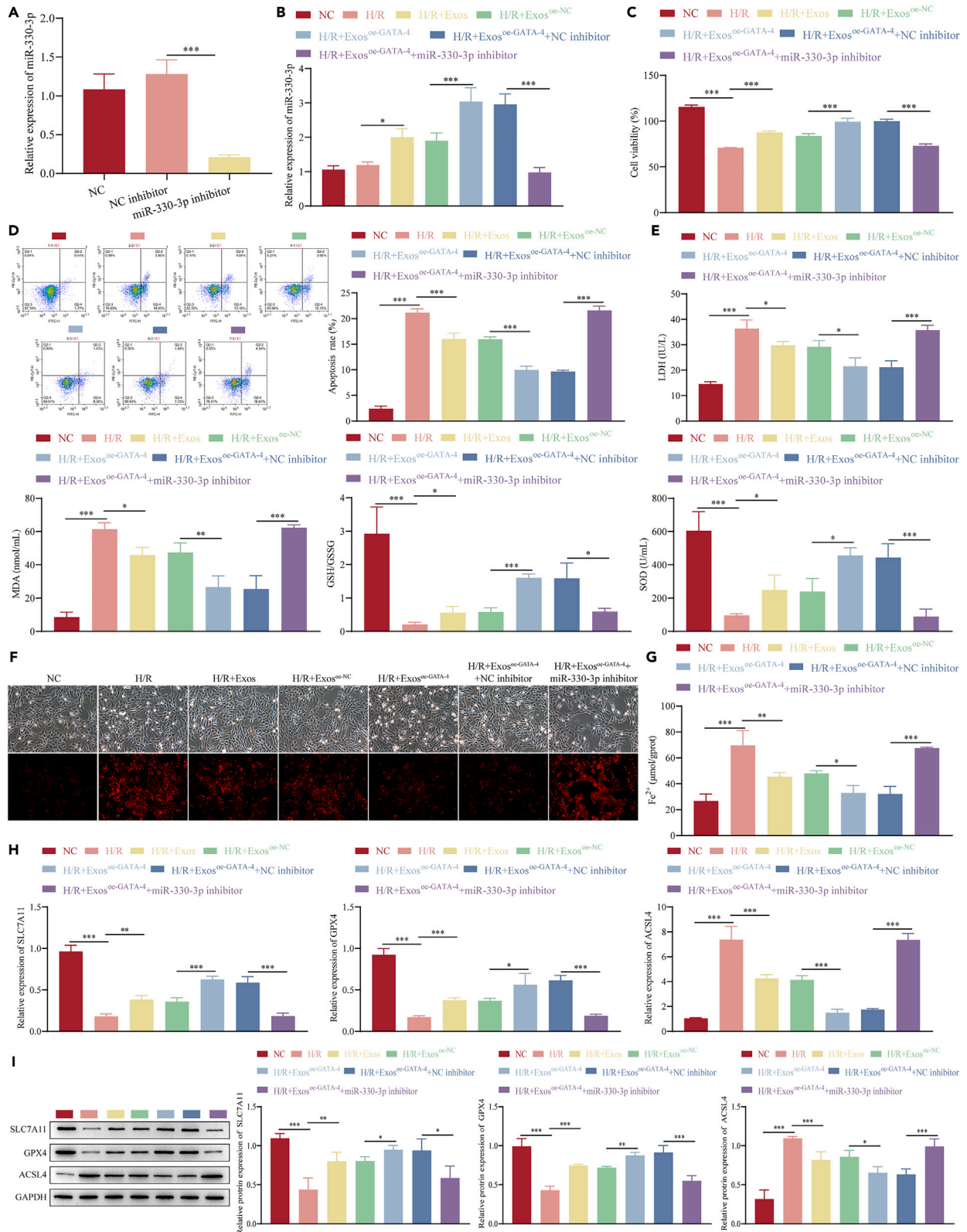


Figure 2. BMSC-derived exosomes overexpressing GATA-4 inhibits H/R-induced ferroptosis by upregulating miR-330-3p

(A and B) Transfection efficiency (A) and the expression of miR-330-3p (B) detected by RT-qPCR.

(C) CCK-8 assay.

(D) Flow cytometry assessing early and late cell apoptosis.

(E) The content of LDH, MDA, and GSH was detected by ELISA.

(F and G) The ROS (F) and Fe^{2+} (G) levels were detected by Kits assay.

(H and I) The expression levels of SLC7A11, GPX4, and ACSL4 were detected by RT-qPCR (H) and western blot (I). $n = 3$, $*p < 0.05$, $**p < 0.01$, $***p < 0.001$. Data are represented as mean \pm SD.

inhibitor reversed these effects; it increased the content of LDH and MDA, decreased the GSH/GSSG ratio and content of SOD and increased ROS and Fe^{2+} levels. The content of GSH and GSSG individually are shown in [Figure S2](#).

In addition, $\text{Exos}^{\text{oe-GATA-4}}$ regulated the key proteins involved in ferroptosis, increased the expression levels of SLC7A11 and GPX4, and decreased the ACSL4 ([Figures 2H and 2I](#)); these effects were reversed by miR-330-3p inhibitor. The aforementioned results indicated that $\text{Exos}^{\text{oe-GATA-4}}$ can suppress H/R-induced cardiomyocytes' ferroptosis by upregulating miR-330-3p.

To clarify the mechanism further, we predicted the target genes of miR-330-3p, a total of 3,965 genes ([Table S2](#)). Cytoscape software visualized the target relation of genes ([Figure 3A](#); [Table S3](#)). Interestingly, among them, BAP1's high expression is related to ferroptosis, which is a driver gene in ferroptosis, which can inhibit cystine uptake, decrease GSH levels, and increase ROS accumulation.^{10,32} Hence, we further verified the relationship between miR-330-3p and BAP1, and found that BAP1 was the target gene of miR-330-3p; the combined sequence shown in [Figure 3B](#) indicated that BAP1 contains targeted binding sites for miR-330-3p. The results of the dual-luciferase reporter assay showed that miR-330-3p mimic reduced the luciferase activity of BAP1-WT, while it did not affect BAP1-MUT ([Figure 3C](#)). AgO2-RIP assay further confirmed this relationship; miR-330-3p mimic increased the expression of BAP1 in the AgO2 group ([Figure 3D](#)). In summary, the results showed targeted binding between miR-330-3p and BAP1.

We then co-transfected si-NC and si-BAP1 into cardiomyocytes and examined the transfection efficiency by RT-qPCR ([Figure 3E](#)) and western blot ([Figure 3F](#)). $\text{Exos}^{\text{oe-GATA-4}}$ reduced the expression of BAP1, while miR-330-3p inhibitor reversed this process. When cells were co-transfected with si-BAP1, the expression level was further decreased ([Figures 3G and 3H](#)).

We further explored the effect of BAP1 in H/R-induced cardiomyocyte ferroptosis and found that the cell viability was decreased in cardiomyocytes with the $\text{Exos}^{\text{oe-GATA-4}} + \text{miR-330-3p}$ inhibitor. Yet, co-transfection of cardiomyocytes with si-BAP1 further increased the cell viability ([Figure 4A](#)). The miR-330-3p inhibitor promoted cell apoptosis; in contrast, this process was reversed after co-transfected with si-BAP1 ([Figure 4B](#)). Also, the $\text{Exos}^{\text{oe-GATA-4}} + \text{miR-330-3p}$ inhibitor group significantly increased the content of LDH and MDA, decreased the GSH/GSSG ratio and content of SOD, and raised the levels of ROS and Fe^{2+} ; while co-transfection with si-BAP1 reversed these effects ([Figures 4C–4E](#)). The content of GSH and GSSG individually are shown in [Figure S3](#). In addition, the $\text{Exos}^{\text{oe-GATA-4}} + \text{miR-330-3p}$ inhibitor group decreased the expression levels of SLC7A11 and GPX4 and increased the ACSL4, which was analyzed by RT-qPCR and western blot ([Figures 4F and 4G](#)); these effects were reversed by co-transfected si-BAP1. These results confirmed that $\text{Exos}^{\text{oe-GATA-4}}$ effectively suppressed H/R-induced cardiomyocytes' ferroptosis by miR-330-3p targeted negative regulated the expression of BAP1.

BAP1 reverses the inhibiting role of overexpression-GATA-4 BMSC-derived exosome H/R-induced cardiomyocytes ferroptosis by downregulating target gene SLC7A11

Interestingly, solute carrier family 7 member 11 (SLC7A11) is a crucial regulated protein of ferroptosis, which has been reported as the target gene of BAP1.^{10,33} Therefore, we further verified the mechanism of BAP1 and SLC7A11 in H/R-induced cardiomyocyte ferroptosis. Luciferase reporter assay showed that BAP1-WT could reduce the SLC7A11 promoter, while BAP1-MUT had no effect on the promoter. Also, knock down of BAP1 could increase the SLC7A11 promoter ([Figure 5A](#)).

We then transfected oe-NC and oe-BAP1 into cardiomyocytes and examined the transfection efficiency by RT-qPCR ([Figure 5B](#)) and western blot ([Figure 5C](#)). Western blot data showed that overexpression of BAP1 could reduce the expression of SLC7A11, while the knock down of BAP1 increased the expression ([Figure 5D](#)).

Then, we co-transfected oe-NC and oe-SLC7A11 into cardiomyocytes and examined the transfection efficiency by RT-qPCR ([Figure 5E](#)) and western blot ([Figure 5F](#)). $\text{Exos}^{\text{oe-GATA-4}}$ increased the expression of SLC7A11, while after transfection with oe-BAP1, expression levels decreased; when co-transfected with oe-SLC7A11, the expression level further increased ([Figures 5G and 5H](#)). These results show that BAP1 negatively regulates the expression of SLC7A11.

The CCK-8 assay showed that the effect of $\text{Exos}^{\text{oe-GATA-4}}$ on cell viability was reversed by overexpression of BAP1, while overexpression of SLC7A11 increased cell viability ([Figure 6A](#)). Also, overexpression of BAP1 promoted cell apoptosis, which was reversed by overexpression SLC7A11 ([Figure 6B](#)). Subsequently, the results showed that the $\text{Exos}^{\text{oe-GATA-4}} + \text{oe-BAP1}$ group significantly increased the content of LDH and MDA, decreased the GSH/GSSG ratio and content of SOD, and raised the levels of ROS and Fe^{2+} . On the contrary, co-transfection with oe-SLC7A11 reversed this process ([Figures 6C–6E](#)). The content of GSH and GSSG individually are shown in [Figure S4](#). In addition, overexpression of BAP1 reversed the effects of $\text{Exos}^{\text{oe-GATA-4}}$, decreased the expression levels of SLC7A11 and GPX4, and increased the ACSL4, which was analyzed by RT-qPCR and western blot ([Figures 6F and 6G](#)). Similarly, overexpression of SLC7A11 further reversed the effects. These results confirmed that BAP1 reverses the effects of $\text{Exos}^{\text{oe-GATA-4}}$ suppressed H/R-induced cardiomyocytes' ferroptosis by downregulating the expression of SLC7A11.

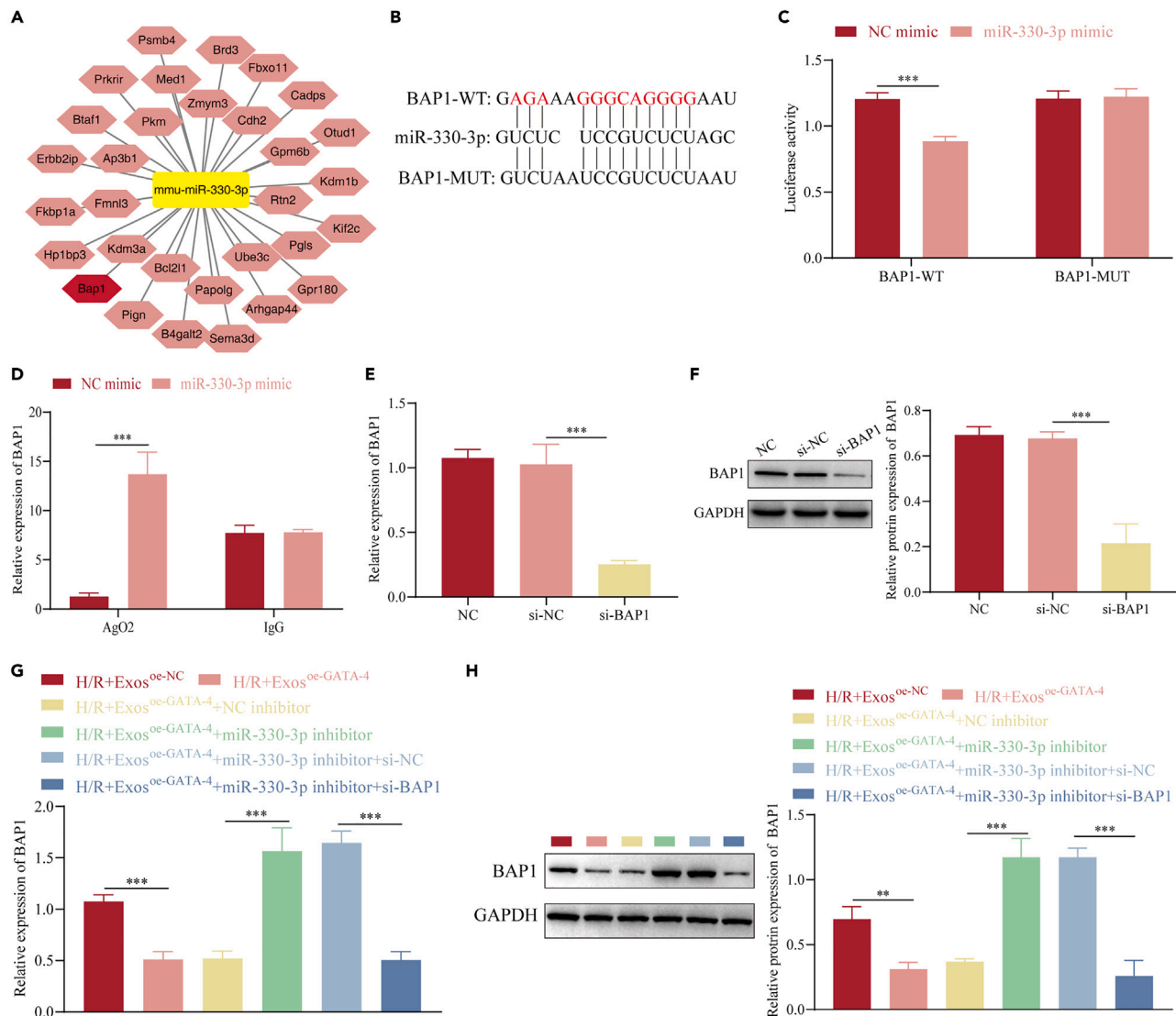


Figure 3. miR-330-3p target-regulating BAP1

(A) Cytoscape software visualization (only shows the 31 target genes).

(B) The combined sequence between miR-330-3p and BAP1.

(C) Dual-luciferase reporter assay.

(D) AgO2-RIP assay.

(E and F) Transfection efficiency of si-NC and si-BAP1 in cardiomyocytes was detected by (E) RT-qPCR and western blot (F).

(G and H) The expression levels of BAP1 were detected by RT-qPCR (G) and western blot (H). $n = 3$, $**p < 0.01$, $***p < 0.001$. Data are represented as mean \pm SD.

BAP1 induces cardiomyocytes Ca^{2+} overload, leading to mPTP activation and mitochondrial dysfunction by interacting with IP3R

The mitochondrial permeability transition pore (mPTP) has a crucial role in cardiomyocyte H/R injury; the increased Ca^{2+} induces mPTP opening and causes cardiomyocyte apoptosis.^{34,35} Inositol 1,4,5-triphosphate receptor (IP3R) has been confirmed to regulate cytosolic Ca^{2+} levels and promote the activation of mitochondrial calcium uniporter (MCU), involved in mPTP opening.^{21,36} In our study, co-immunoprecipitation (coIP) and glutathione S-transferase (GST) pull-down assays showed that in cardiomyocytes, BAP1 protein interacts with IP3R protein (Figure 7A), and GST-labeled BAP1 protein could pull down GST-labeled IP3R protein (Figure 7B). These results further confirmed a close interaction between BAP1 and IP3R. Overexpression of BAP1 significantly increased the expression of IP3R, while the knock down of BAP1 reduced the expression (Figures 7C and 7D).

We then transfected si-NC and si-IP3R into cardiomyocytes and examined the transfection efficiency by RT-qPCR (Figure 7E) and western blot (Figure 7F), the expression of IP3R was decreased after knock down of IP3R, which indicated that transfection was successful. The

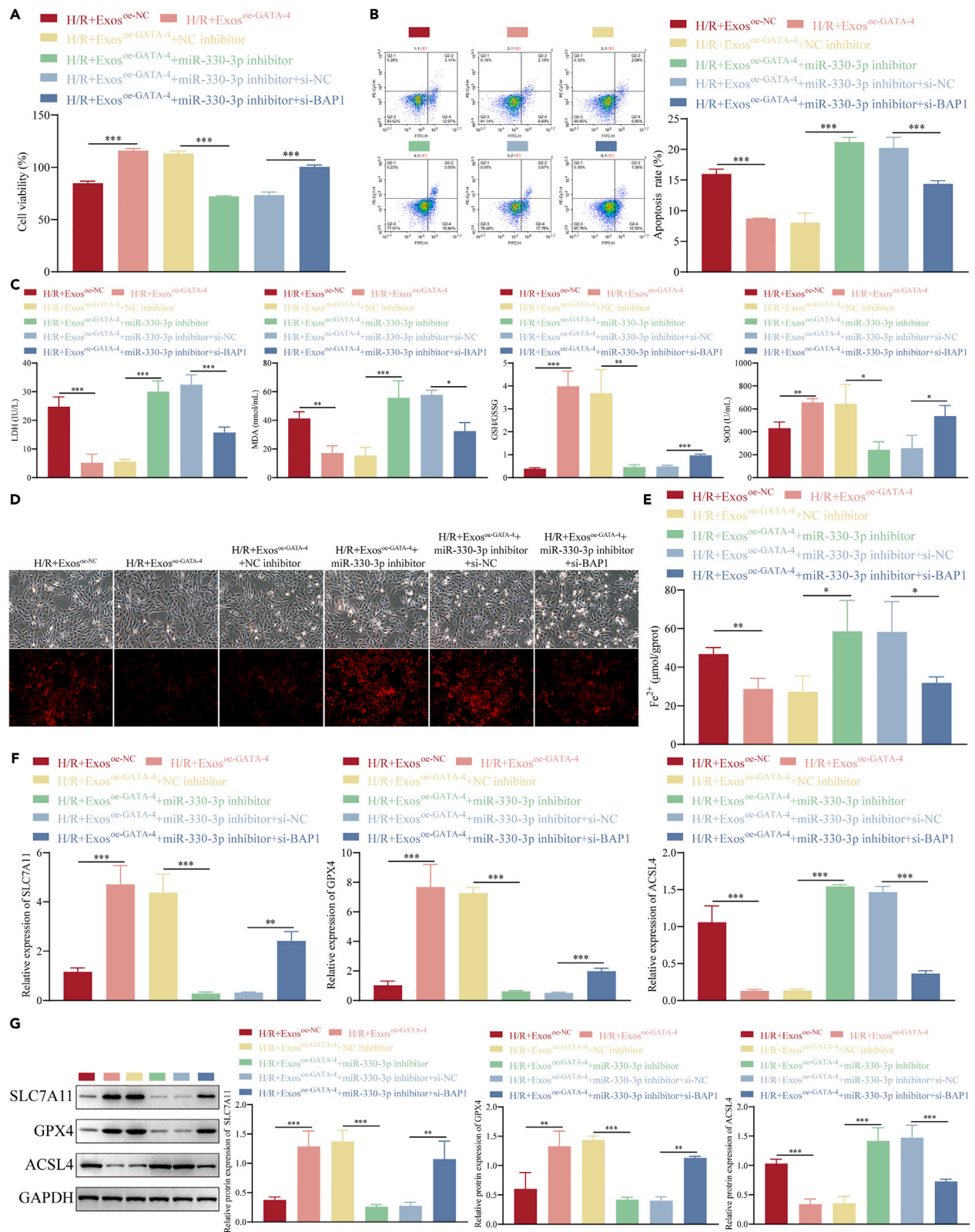


Figure 4. BMSC-derived exosomes overexpressing GATA-4 inhibits H/R-induced cardiomyocyte ferroptosis by miR-330-3p target-regulating BAP1

(A) CCK-8 assay.

(B) Early and late cell apoptosis detected by flow cytometry.

(C) The content of LDH, MDA, and GSH was detected by ELISA.

(D and E) The ROS (D) and Fe²⁺ (E) levels were detected by Kits assay.

(F and G) The expression levels of SLC7A11, GPX4 and ACSL4 were detected by RT-qPCR (F) and western blot (G). *n* = 3, **p* < 0.05, ***p* < 0.01, ****p* < 0.001. Data are represented as mean ± SD.

expression of IP3R was reduced in the Exos^{oe-GATA-4} group, while transfected oe-BAP1 increased these levels significantly. In addition, after being co-transfected with si-IP3R, the expression level of IP3R further decreased (Figures 7G and 7H).

To further explore the function of BAP1 and IP3R in mPTP opening, we analyzed the Ca²⁺ levels in cardiomyocytes. Exos^{oe-GATA-4} significantly decreased the level of Ca²⁺, while BAP1 overexpression reversed this process. In contrast, after co-transfected si-IP3R, the level was further reduced (Figure 7I). The mPTP opening analysis showed that Exos^{oe-GATA-4} significantly inhibited the mPTP opening, while the overexpression of BAP1 promoted mPTP opening. At the same time, knock down of IP3R relieved the function and inhibited mPTP opening (Figure 8A). Also, the MCU mRNA and protein expression levels were decreased in the Exos^{oe-GATA-4} group. After transfection with oe-BAP1, the levels further increased, while the knock down of IP3R reversed the effect of oe-BAP1 (Figures 8B and 8C). Similarly, JC-1 monomers and CyP-D fluorescence expression were decreased in the Exos^{oe-GATA-4} group; in the Exos^{oe-GATA-4} + oe-BAP1 group, the fluorescence expression was further increased, while after cells were co-transfected si-IP3R, the effects were inhibited (Figures 8D and 8E). Consistently, mitochondrial swelling and disruption of the bilayer membrane were seen in the Exos^{oe-GATA-4} + oe-BAP1 group but relieved in the Exos^{oe-GATA-4} + oe-BAP1 + si-IP3R group (Figure 8F). These results indicated that BAP1 increases cardiomyocytes' Ca²⁺ level, inducing mPTP opening and mitochondrial dysfunction through interactions with IP3R.

BAP1 induced mPTP opening reverses the inhibiting role of BMSC-derived Exos^{oe-GATA-4} on H/R-induced cardiomyocytes ferroptosis by interacting with IP3R

To further explore the function mechanism of mPTP opening in H/R-induced cardiomyocyte ferroptosis, cardiomyocytes were treated with mPTP inhibitor (CsA). Overexpression of BAP1 significantly reduced cell viability (Figure 9A) and promoted cell apoptosis (Figure 9B), while CsA reversed these results. Also, the Exos^{oe-GATA-4} + oe-BAP1 group significantly increased the content of LDH and MDA, decreased the GSH/GSSG ratio and content of SOD, and increased the levels of ROS and Fe²⁺; these effects were reversed by CsA (Figures 9C–9E). The content of GSH and GSSG individually are shown in Figure S5. Subsequently, the results of RT-qPCR and western blot also confirmed that CsA reversed the role of the Exos^{oe-GATA-4} + oe-BAP1 group, increased the expression levels of SLC7A11 and GPX4, and decreased the ACSL4 (Figures 9F and 9G). These results confirmed that overexpression-GATA-4 BMSC-derived exosome inhibits H/R-induced cardiomyocyte ferroptosis through BAP1 interacts with IP3R inhibited mPTP opening.

BMSC-derived Exos^{oe-GATA-4} inhibits H/R-induced cardiomyocytes ferroptosis related with keap1/Nrf2 signaling pathway

Previous studies have shown that H₂S can regulate the mPTP opening in cardiomyocytes,³⁷ and Ca²⁺ induces mPTP opening blocked by high levels of H₂S.³⁸ Moreover, H₂S production can further reduce lipid peroxide levels and inhibit ferroptosis,³⁹ which may be related to the keap1/Nrf2 signaling pathway.⁴⁰ In our study, we further observed that the hydrogen sulfide (H₂S) content increased in the Exos^{oe-GATA-4} group. Yet, after overexpressing BAP1, the H₂S content decreased. At the same time, CsA further increased the H₂S content (Figure 10A). In addition, the results of RT-qPCR and western blot showed that the expression levels of keap1 were decreased, and Nrf2 was increased in the Exos^{oe-GATA-4} group, while after overexpressing BAP1, keap1 increased and Nrf2 decreased. Similarly, these results were reversed by CsA (Figures 10B and 10C).

We further used immunofluorescence (IF) to review the expression situation of Nrf2 and found that expressed in the cytoplasm, while the Exos^{oe-GATA-4} group and Exos^{oe-GATA-4} + oe-BAP1 + CsA group increased the expression in the nucleus (Figure 10D). Therefore, our results showed that Exos^{oe-GATA-4} may have regulated the keap1/Nrf2 signaling pathway through released H₂S, inhibiting H/R-induced cardiomyocyte ferroptosis.

BMSC-derived Exos^{oe-GATA-4} inhibits I/R-induced cardiomyocytes ferroptosis by upregulating miR-330-3p in vivo

I/R mice model treated with Exos^{oe-NC}, Exos^{oe-GATA-4}, NC inhibitor, and miR-330-3p inhibitor by tail vein injection was assessed next. Compared with the Sham group, ejection fraction (EF) and fractional shortening (FS) levels decreased, and impaired cardiac function (Figure 11A) and infarction area increased (Figure 11B) in the I/R and I/R + Exos^{oe-NC} group, while these effects were relieved in the I/R + Exos^{oe-GATA-4} group. In contrast, in the I/R + Exos^{oe-GATA-4} + miR-330-3p inhibitor group, heart damage and infarction were more obvious.

Subsequently, we detected the levels of Fe²⁺ and MDA. In the I/R and I/R + Exos^{oe-NC} group, Fe²⁺ and MDA increased, while they decreased in the I/R + Exos^{oe-GATA-4} group. Conversely, in the I/R + Exos^{oe-GATA-4} + miR-330-3p inhibitor group, the levels of Fe²⁺ and MDA further increased (Figures 11C and 11D). At the same time, the GSH/GSSG level was decreased by I/R-induced, which was increased in the I/R + Exos^{oe-GATA-4} group; on the contrary, the I/R + Exos^{oe-GATA-4} + miR-330-3p inhibitor group further reduced that (Figure S6A). The results of RT-qPCR and western blot further showed that the expression levels of miR-330-3p, SLC7A11, and GPX4 were increased in the I/R + Exos^{oe-GATA-4} group; while BAP1, IP3R, and ACSL4 were decreased; in the I/R + Exos^{oe-GATA-4} + miR-330-3p inhibitor group these data were

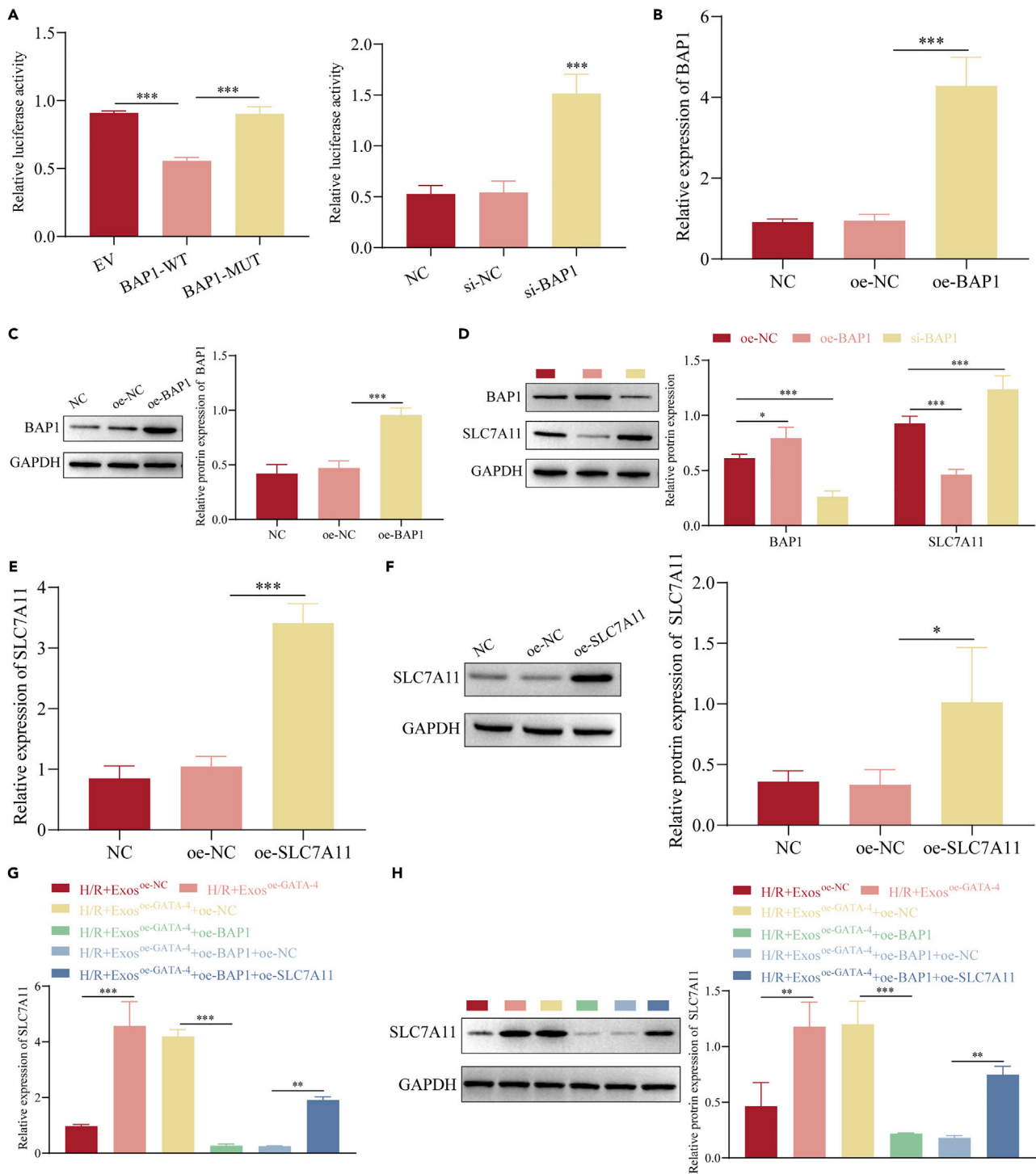


Figure 5. BAP1 negative regulated the expression of SLC7A11

(A) Luciferase reporter assay. AgO2-RIP assay.

(B and C) Transfection efficiency of oe-NC and oe-BAP1 in cardiomyocytes was detected by RT-qPCR (B) and western blot (C).

(D) The expression levels of BAP1 and SLC7A11 were detected by western blot.

(E and F) Transfection efficiency of oe-NC and oe-SLC7A11 in cardiomyocytes was detected by RT-qPCR (E) and western blot (F).

(G and H) The expression levels of SLC7A11 were detected by RT-qPCR (G) and western blot (H). $n = 3$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Data are represented as mean \pm SD.

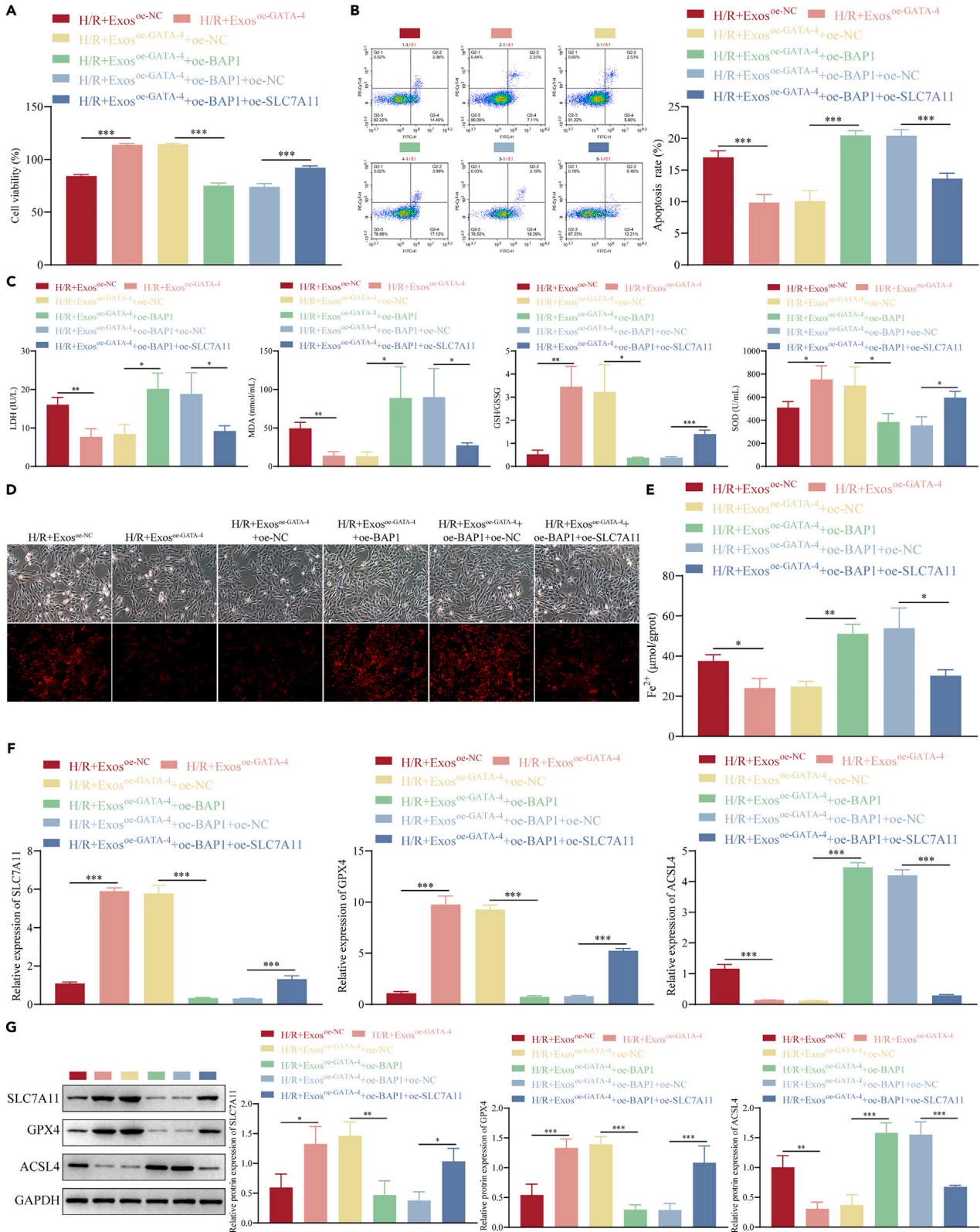


Figure 6. BAP1 reverses the inhibiting role of BMSC-derived exosome overexpressing GATA-4 on I/R-induced cardiomyocyte ferroptosis by downregulating target gene SLC7A11

(A) CCK-8 assay.

(B) Early and late cell apoptosis detected by flow cytometry.

(C) The content of LDH, MDA, and GSH was detected by ELISA.

(D and E) The ROS (D) and Fe^{2+} (E) levels were detected by Kits assay.

(F and G) The expression levels of SLC7A11, GPX4, and ACSL4 were detected by RT-qPCR (F) and western blot (G). $n = 3$, $*p < 0.05$, $**p < 0.01$, $***p < 0.001$. Data are represented as mean \pm SD.

reversed (Figure 11E). Moreover, we further estimated the expression of Keap1/Nrf2; the results of RT-qPCR (Figure S6B) and western blot (Figure S6C) showed the expression of Keap1 was increased, and Nrf2 was reduced by I/R-induced. Keap1 was further decreased, and Nrf2 was further rose by Exos^{oe-GATA-4}. The I/R+Exosoe-GATA-4+miR-330-3p inhibitor group showed a reversal trend. These results suggest that BMSC-derived exosome overexpressing GATA-4 inhibits I/R-induced cardiomyocyte ferroptosis by increasing the expression levels of miR-330-3p.

DISCUSSION

Our previous research demonstrated that BMSC-derived exosome overexpressing GATA-4 (Exos^{oe-GATA-4}) can protect cardiac function and inhibit cardiomyocyte apoptosis.²⁶ However, the specific mechanism of action of Exos^{oe-GATA-4} in myocardial I/R injury remains unclear. In this study, we successfully extracted and identified the Exos and obtained 185 differential expression miRNAs by bioinformatics analysis, including 104 downregulated and 81 upregulated miRNAs. Among the upregulated miRNAs, we assessed mmu-miR-330-3p further. miR-330-3p has a crucial role in I/R injury and apoptosis.³⁰ However, its function in myocardial I/R injury is still not fully understood. Herein, we found that Exos^{oe-GATA-4} can inhibit I/R-induced cardiomyocyte ferroptosis by upregulating the expression of miR-330-3p and related to Ca^{2+} overload and mPTP opening.

miRNAs in Exos regulate function during intercellular communication.⁴¹ BMSC-derived Exos has multiple functions; for example, they promote skeletal muscle regeneration,⁴² participate in lung cancer metastasis,⁴³ and can ameliorate osteoarthritis.⁴⁴ They also have a crucial role in cardiomyocyte injury. Mao et al. confirmed that miR-183-5p found in BMSC-derived Exos inhibits cardiomyocyte apoptosis and protects myocardial I/R injury.⁴⁵ Previous studies have also shown that miR-330-3p is a differentially expressed miRNA in kynurenine-treated BMSC cultures.⁴⁶ This is consistent with our findings, which show that miR-330-3p is one of the upregulation differential expression miRNAs in Exos^{oe-GATA-4}. BMSC-derived exosomes are a valid treatment method for ischemic injury; BMSC-derived Exos miR-148b-3p further strengthen BMSC-derived Exos effects, which are used in treating cerebral ischemia.⁴⁷ Therefore, miRNA is a crucial regulatory factor for the BMSC-derived Exos role. Exos also exert a role in cancer by inhibiting miR-330-3p.⁴⁸ Previous research has found that miR-330-3p plays a vital role in various cancers,^{27,28} while the function in myocardial I/R injury has not been clearly stated. miR-330-3p is one of the differentially expressed miRNAs that effectively mediate AMI pathogenesis.²⁹ However, the Exos^{oe-GATA-4} and miR-330-3p functions in I/R-induced cardiomyocyte ferroptosis have not been reported. Interestingly, hypoxia-preconditioned brain cells (brain-EVs)-derived extracellular vesicles decreased infarct size in neonatal hypoxic-ischemic brain injury (HIBI) and consistently expressed miR-330-3p,⁴⁹ this seems to coincide with our results. This study discovered that Exos^{oe-GATA-4} could effectively suppress H/R-induced cardiomyocytes' ferroptosis by upregulating miR-330-3p. Moreover, Exosoe-GATA-4 also increased the GSH/GSSH ratio and reduced ROS accumulation. ROS accumulation induces myocardial cell injury and is related to low GSH content, which can participate in clearance.^{50,51} GSH plays a vital role in maintaining redox homeostasis in cardiomyocytes. Disruption of redox homeostasis is evidenced by a significant decrease in GSH content and accumulation of GSSG and ROS in the myocardium. GSH has been confirmed to relieve myocardial injury by inhibiting ferroptosis. Maintaining an optimal GSH/GSSG ratio in the myocardium is essential for maintaining homeostatic cell survival. Moreover, GSH and glutathione peroxidase 4 (GPX4) are intimately associated with ferroptosis.⁵² ROS and GSH are the core participants in ferroptosis; GSH depletion and GPX4 inactivation have been confirmed to lead to ferroptosis.⁵³

miR-330-3p plays multiple effects by regulating direct targets, such as in glioma cells, miR-330-3p inhibits cell proliferation and migration by regulating the target gene CELF1,⁵⁴ miR-330-3p promotes the non-small-cell lung cancer (NSCLC) malignant progression through targeting GRIA3.⁵⁵ Our study also found that BAP1 is the target gene of miR-330-3p. BAP1 functions as a tumor suppressor and is essential in cellular metabolism.⁵⁶ Also, BAP1 participates in ferroptosis,⁵⁷ which is a driver gene in ferroptosis, which can inhibit cystine uptake, decrease GSH levels, and increase ROS accumulation.^{10,32} Our results further confirmed that the effects of Exos^{oe-GATA-4} suppress H/R-induced cardiomyocytes' ferroptosis through miR-330-3p targeted negative regulated BAP1, at the same time, increase the GSH/GSSG ratio and reduce ROS accumulation. It is widely acknowledged that GPX4 and SLC7A11 are critical regulatory proteins involved in ferroptosis. Loss of GSH is a key mechanism in ferroptosis occurrence; SLC7A11 has been confirmed to be necessary for intracellular GSH production to inhibit ferroptosis.⁵⁸ SLC7A11 overexpression can relieve ferroptosis in various cancer cells^{59,60} and myocardial cells.⁶¹ Furthermore, we further demonstrated that BAP1 is capable of reducing the expression of SLC7A11. BAP1 reverses the suppressing effects of Exos^{oe-GATA-4} on H/R-induced cardiomyocytes' ferroptosis by downregulating the expression of SLC7A11, decreasing the GSH/GSSH ratio. BAP1 has been demonstrated to regulate SLC7A11 expression and ferroptosis in previous research, BAP1 regulates the expression of SLC7A11 independently of other transcription factors. BAP1 reduces the presence of H2A ubiquitination (H2Aub) on the SLC7A11 promoter and suppresses the expression of SLC7A11 in a deubiquitinating-dependent manner. Additionally, BAP1 hinders cystine uptake by repressing SLC7A11 expression, which leads to

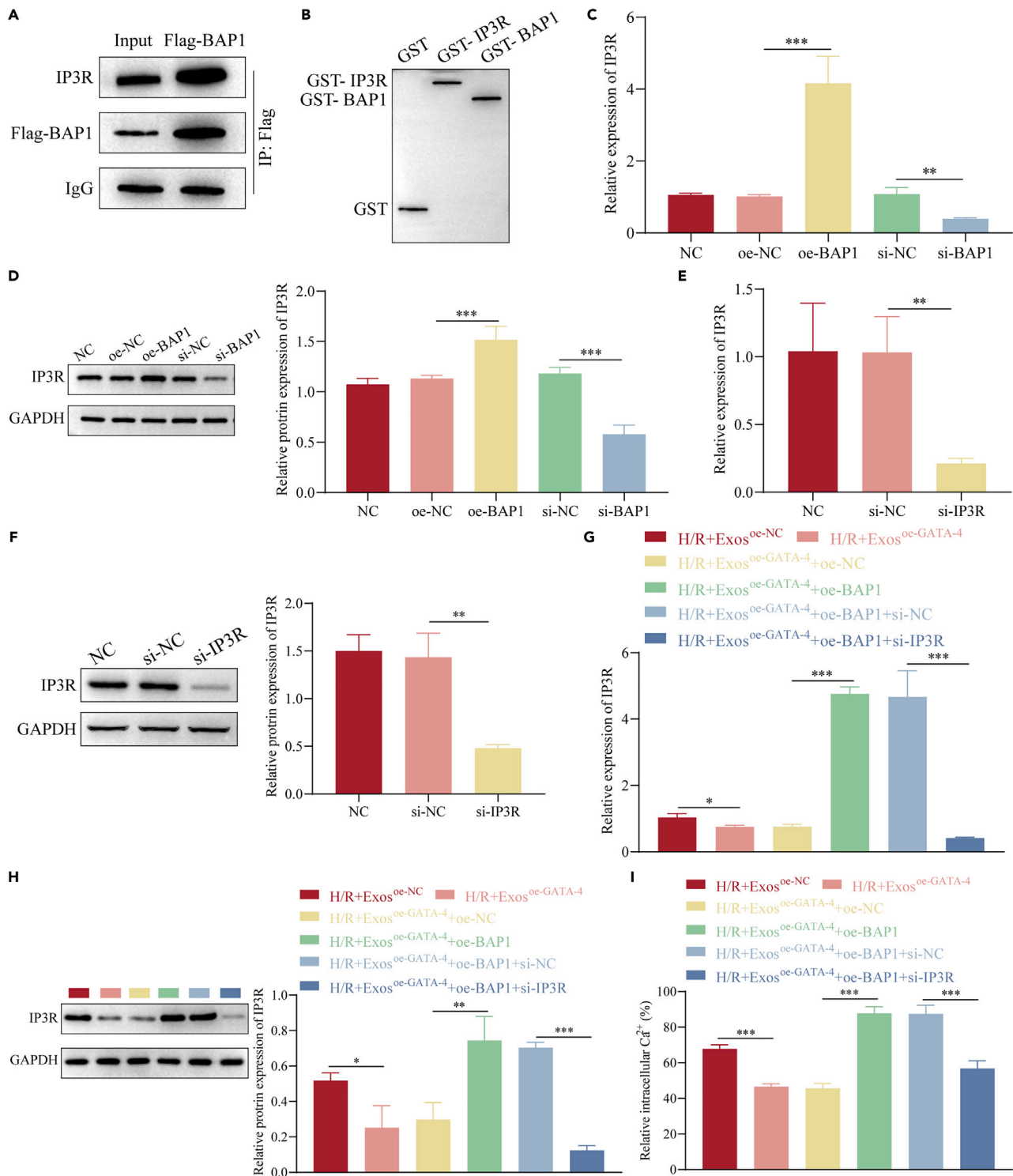


Figure 7. BAP1 interacts with IP3R

(A) CoIP assay.

(B) GST pull-down assay.

(C and D) The expression levels of IP3R were detected by (C) RT-qPCR and western blot (D).

(E and F) Transfection efficiency of si-NC and si-IP3R in cardiomyocytes was detected by RT-qPCR (E) and western blot (F).

(G and H) The expression levels of IP3R were detected by RT-qPCR (G) and western blot (H).

(I) The Ca^{2+} levels were detected by Kits assay. $n = 3$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Data are represented as mean \pm SD.

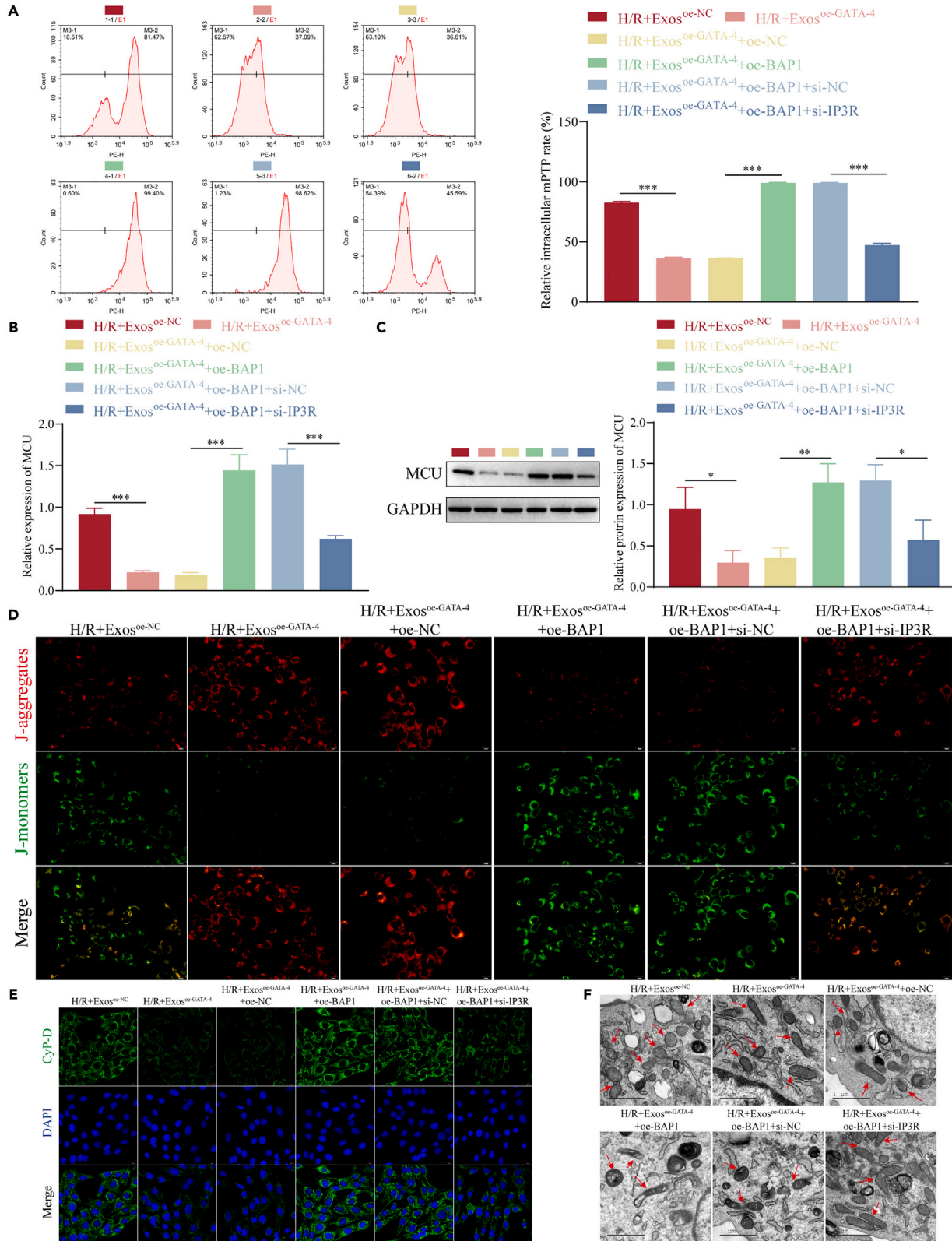


Figure 8. BAP1 induces cardiomyocytes Ca^{2+} overload, leading to mPTP activation and mitochondrial dysfunction through interaction with IP3R

(A) mPTP assessment by flow cytometry.

(B and C) The expression level of MCU was detected by RT-qPCR (B) and western blot (C).

(D) Mitochondrial membrane potential assay (scale bar: 20 μm).

(E) IF detected the fluorescence intensity of CyP-D (scale bar: 20 μm).

(F) TEM was reviewed for mitochondrial morphology (scale bar: 1 μm). $n = 3$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Data are represented as mean \pm SD.

increased lipid peroxidation and ferroptosis.^{10,33} However, our study did not further confirm the specific mechanism of action of BAP1 targeting to negatively regulate SCL7A11 expression, and subsequent studies are needed to further elucidate how BAP1 regulates SCL7A11 through experiments, chromatin immunoprecipitation sequencing (ChIP-seq) analysis, and high-throughput sequencing.

In addition, studies have discovered that the expression level of BAP1 relates to intracellular Ca^{2+} concentrations.⁶² The balance of Ca^{2+} intracellular has a crucial role in mitochondrial dysfunction and cell death.⁶³ The excessive Ca^{2+} levels induce mPTP opening, which is dependent on Ca^{2+} , causing cell death.⁶⁴ The mPTP opens during myocardial I/R injury, during which Ca^{2+} rises and the ROS increases. Thus, target mPTP therapies have an important role in cardioprotection.⁶⁵ Liu et al. confirmed that IP3R increases the Ca^{2+} level, activates the mPTP opening and mitochondrial dysfunction, and induces the ferroptosis of kidney injury.⁶⁶ Interestingly, BAP1 interacts with the IP3R protein^{67,68} to regulate Ca^{2+} and cell death, which is also confirmed in our study. In this study, we observed that BAP1 increased cardiomyocytes' Ca^{2+} level, causing mPTP opening and mitochondrial dysfunction through interactions with IP3R, and reversed the function of Exos^{oe-GATA-4} inhibited H/R-induced cardiomyocytes ferroptosis. Therefore, Exos^{oe-GATA-4} inhibits H/R-induced cardiomyocyte ferroptosis through BAP1, which interacts with IP3R-inhibited mPTP opening. Similarly, Mewton et al. found that infarct size is reduced, and cardiac function is improved after treatment of CsA,⁶⁹ which is an mPTP inhibitor. Finally, in the I/R mice model, Exos^{oe-GATA-4} relieved impaired cardiac function, and decreased infarction area inhibited I/R-induced cardiomyocyte ferroptosis by regulating miR-330-3p, BAP1 and IP3R expression levels.

In this study, we further observed the change in H_2S content in the Exos^{oe-GATA-4} group; the H_2S content was decreased during mPTP opening. H_2S has a vital role in H/R-induced cardiomyocyte injury,³⁷ and Ca^{2+} induces mPTP opening blocked by high levels of H_2S .³⁸ H_2S production can further reduce lipid peroxide levels and inhibit ferroptosis.³⁹ In addition, studies have shown that in H_2S regulation of the keap1/Nrf2 signaling pathway in cardiomyocytes, H_2S increases the expression of Nrf2 and simultaneously reduces the expression of keap1.⁷⁰ Similarly, in this study, the H_2S content was increased, the expression levels of keap1 were decreased, and Nrf2 was increased in the Exos^{oe-GATA-4} group. H_2S can induce Nrf2 dissociation from Keap1, leading to enhanced Nrf2 nuclear translocation.⁷¹ We further discovered that the expression of Nrf2 was raised in the nucleus. We speculate that Nrf2 enters the nucleus when H_2S content is increased. This is consistent with Li's study, which reported that Nrf2 enters the nucleus after dissociating from keap1 during oxidative stress.⁷² The keap1/Nrf2 signaling pathway is the key regulation of ferroptosis.⁷³ Keap1/Nrf2 is considered an important oxidative stress regulatory pathway for cardiomyocyte damage and relates to ferroptosis.⁷⁴ Therefore, our data suggest that Exos^{oe-GATA-4} may regulate the keap1/Nrf2 signaling pathway by releasing H_2S , in turn inhibiting H/R-induced cardiomyocyte ferroptosis.

In summary, our study found that Exos^{oe-GATA-4} suppresses H/R-induced cardiomyocyte ferroptosis through miR-330-3p, which regulates BAP1/SCL7A11/IP3R axis and mitochondrial permeability transition pore opening. In addition, these effects may connect to H_2S regulated the keap1/Nrf2 signaling pathway. Our results had much significance in treating Exos^{oe-GATA-4} in myocardial I/R injury. However, further research still needs to explore the H_2S -mediated keap1/Nrf2 signaling pathway mechanism, and clinical research is needed to confirm our results further.

Conclusions

In this study, we successfully extracted overexpressing GATA-4 BMSC-derived exosome Exos and explored the function and mechanism of the Exos in H/R-induced cardiomyocytes' ferroptosis. These findings showed that Exos^{oe-GATA-4} effectively suppressed H/R-induced cardiomyocytes' ferroptosis through upregulation of miR-330-3p, to target negative regulated the expression of BAP1. BAP1 can regulate the expression of SCL7A11 to affect H/R-induced cardiomyocytes' ferroptosis or interact with IP3R and increase cardiomyocytes' Ca^{2+} level, causing mPTP opening, promoting H/R-induced cardiomyocytes' ferroptosis. Our findings shed light on the potential of Exos^{oe-GATA-4} as a treatment for H/R-induced cardiomyocyte ferroptosis and as an effective target for it.

Limitations of the study

This study did not further confirm the specific mechanism of action of how BAP1 regulates SCL7A11 expression, and subsequent studies are needed to further elucidate through experiments, ChIP-seq analysis, and high-throughput sequencing. Moreover, the results of this study were only confirmed at the cellular and mouse levels, and clinical research is needed to confirm our results further.

RESOURCE AVAILABILITY

Lead contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by the lead contact, Jigang He (chouchou0708@aliyun.com).

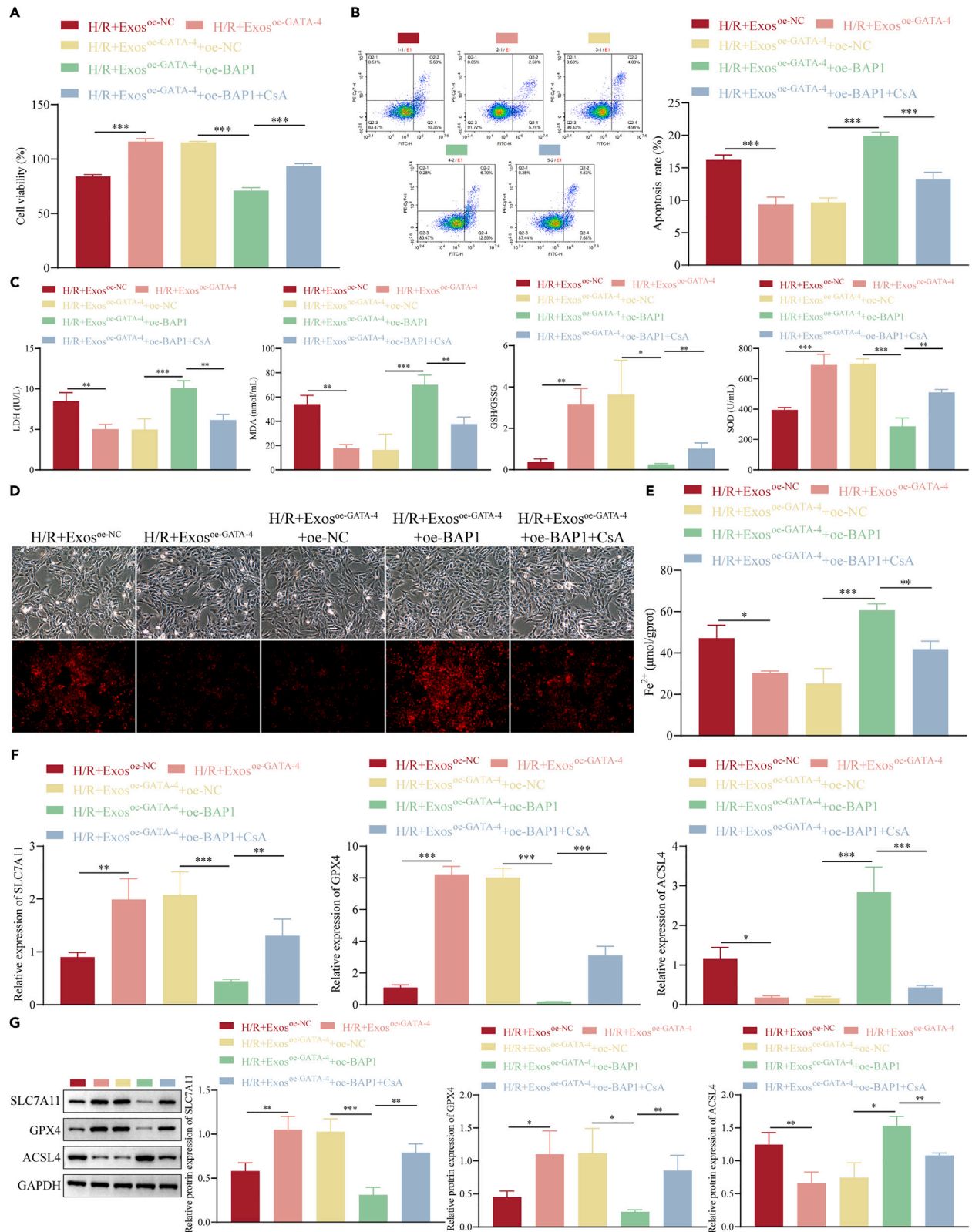


Figure 9. BAP1 induces mPTP opening, which reverses the inhibiting role of BMSC-derived Exos^{oe-GATA-4} on H/R-induced cardiomyocyte ferroptosis through interaction with IP3R

(A) CCK-8 assay.

(B) Early and late cell apoptosis detected by flow cytometry.

(C) Levels of LDH, MDA, and GSH were detected by ELISA.

(D and E) The ROS (D) and Fe²⁺ (E) levels were assessed using Kits assay.

(F and G) The expression levels of SLC7A11, GPX4, and ACSL4 were detected by RT-qPCR (F) and western blot (G). *n* = 3, **p* < 0.05, ***p* < 0.01, ****p* < 0.001. Data are represented as mean ± SD.

Materials availability

This study did not generate new unique reagents.

Data and code availability

- All data produced in this study are included in the published article.
- This work does not report original code.
- Any information needed to re-analyze the data reported in this paper is available upon request from the primary contact.

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AUTHOR CONTRIBUTIONS

Conceived and designed the experiments, J.H. and Z.X.; performed the experiments, J.H., X.W., and X.C.; analyzed the data, D.Y.; contributed reagents/materials/analysis tools, X.C. and S.L.; writing – original draft, X.W. and J.H.; writing – review & editing, J.H. and Z.X.

DECLARATION OF INTERESTS

All authors declare no competing interests.

STAR★METHODS

Detailed methods are provided in the online version of this paper and include the following:

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- **METHOD DETAILS**
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SUPPLEMENTAL INFORMATION

Supplemental information can be found online at <https://doi.org/10.1016/j.isci.2024.110784>.

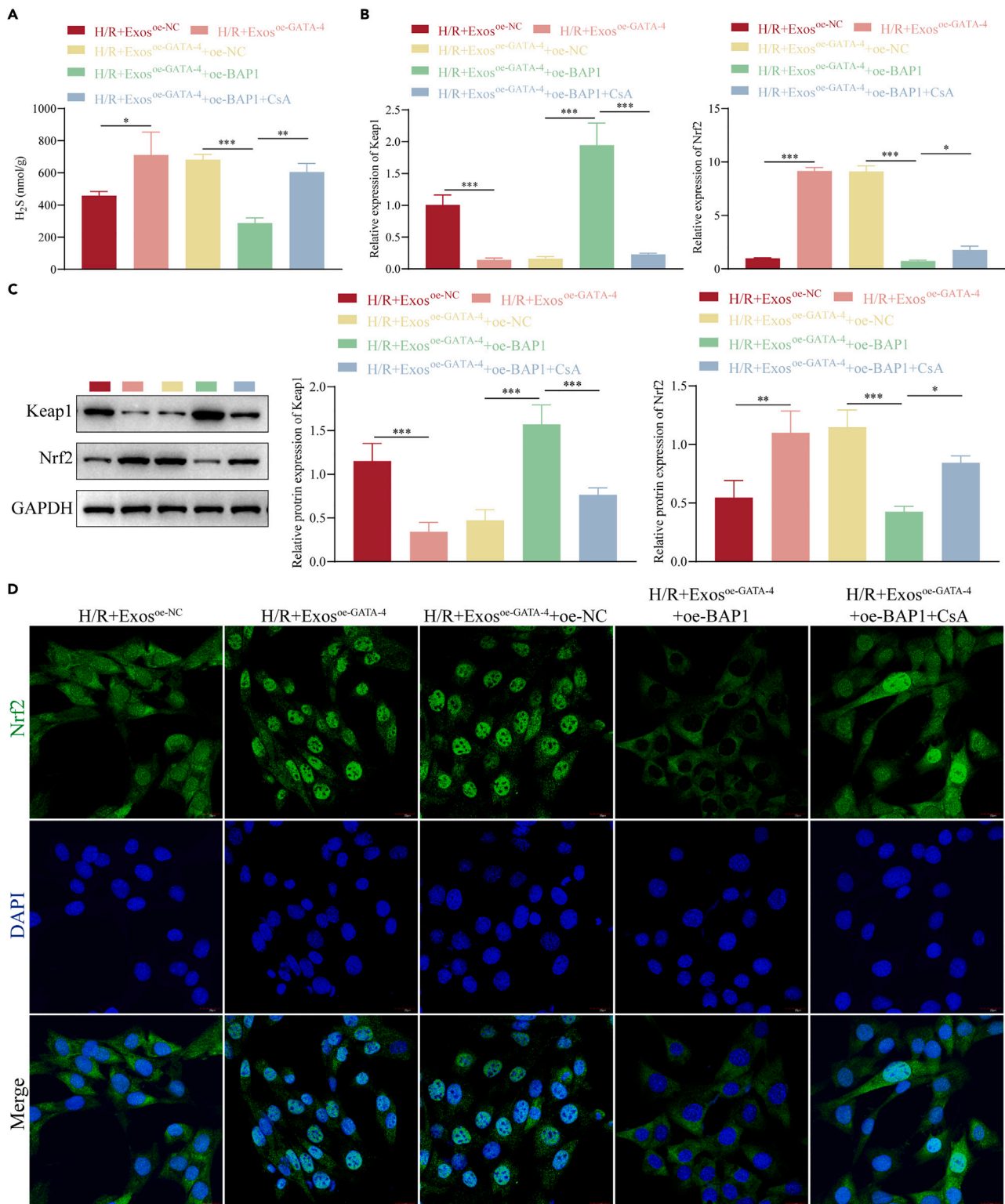


Figure 10. BMSC-derived Exos^{oe-GATA-4} inhibits H/R-induced cardiomyocytes ferroptosis related to Keap1/Nrf2 signaling pathway

(A) The content of H₂S was assessed using Kits assay.

(B and C) The expression levels of Keap1 and Nrf2 were detected using RT-qPCR (B) and western blot (C).

(D) The expression of Nrf2 was detected using IF (scale bar: 20 μm). n = 3, *p < 0.05, **p < 0.01, ***p < 0.001. Data are represented as mean ± SD.

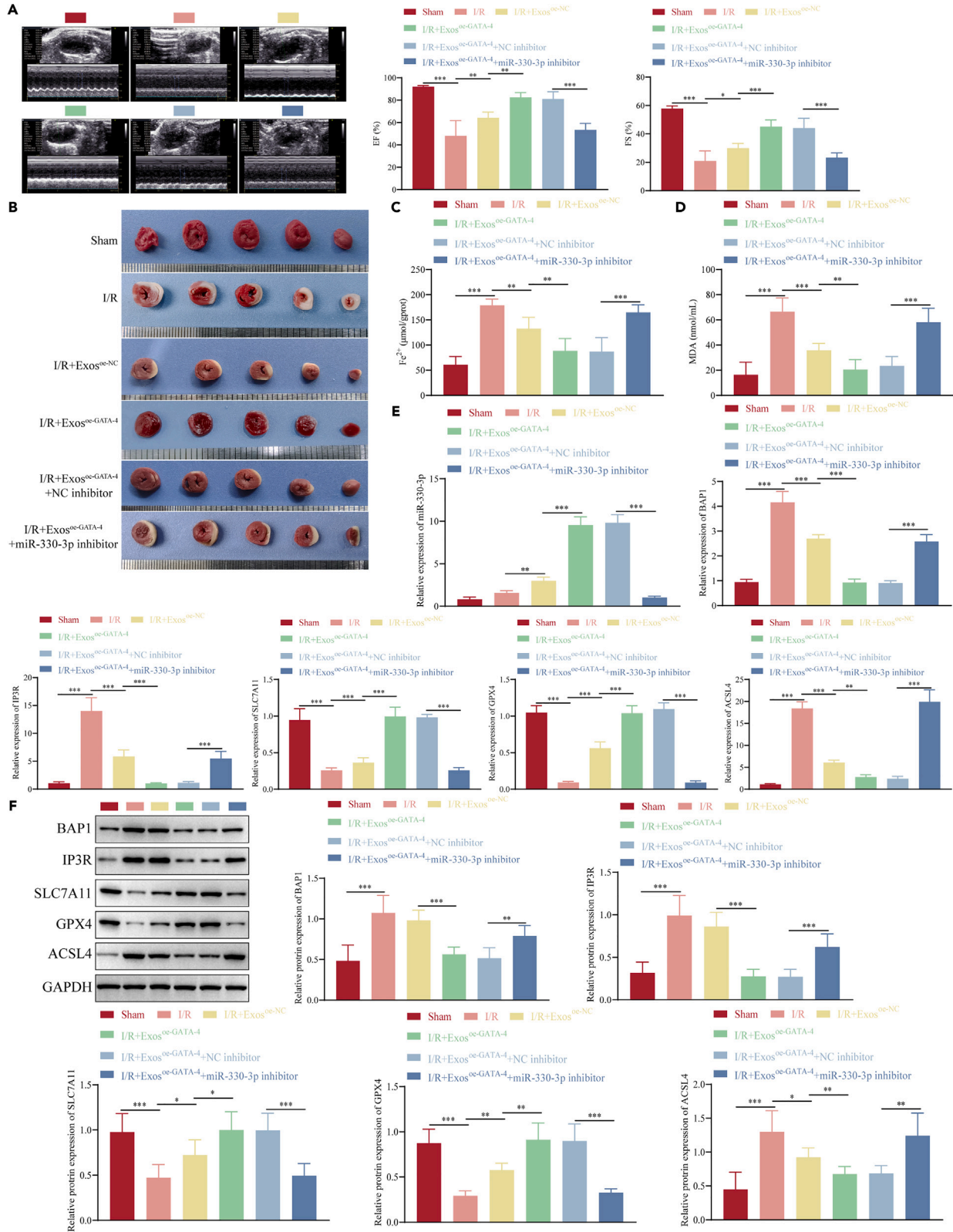


Figure 11. BMSC-derived Exos^{oe-GATA-4} inhibits I/R-induced cardiomyocyte ferroptosis by upregulated miR-330-3p in vivo

(A) An ultrasonic cardiogram estimated cardiac function.

(B) The TTC staining.

(C and D) The Fe²⁺ (C) and MDA (D) levels were assessed using Kits assay.

(E) The mRNA expression levels of miR-330-3p, BAP1, IP3R, SLC7A11, GPX4, and ACSL4 were detected by RT-qPCR.

(F) The protein expressions of BAP1, IP3R, SLC7A11, GPX4, and ACSL4 were detected by western blot. $n = 6$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Data are represented as mean \pm SD.

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STAR★METHODS

KEY RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Antibodies		
anti-SLC7A11	Abcam	ab175186; RRID : AB_2722749
anti-GPX4	Abcam	ab125066; RRID : AB_10973901
anti-ACSL4	Abcam	ab155282; RRID : AB_2714020
anti-BAP1	Abcam	ab255611
anti-Keap1	bioass	bs-3648R; RRID : AB_10856809
anti-Nrf2	bioass	bs-1074R; RRID : AB_10855421
anti-IP3R	Abcam	ab252536
anti-MCU	MedChemExpress	HY-P80216
anti-HIF-1 α	Abcam	ab179483; RRID : AB_2732807
anti-Bcl-2	Abcam	ab182858; RRID : AB_2715467
anti-Bax	Abcam	ab32503; RRID : AB_725631
antibodies conjugated with HRP	Abcam	ab205718; RRID : AB_2819160
β -actin	Abcam	ab8226; RRID : AB_306371
GAPDH	Abcam	ab9485; RRID : AB_570852
anti-CyP-D	Abcam	ab110324; RRID : AB_10864110
anti-Nrf2	Affinity	BF8017; RRID : AB_3083515
Bacterial and virus strains		
Lentivirus	This paper	N/A
Biological samples		
Cardiac tissue in mice	This paper	N/A
Chemicals, peptides, and recombinant proteins		
Bone marrow mesenchymal stem cell growth medium	Cyagen Biosciences	MUXMX-90011
FBS	Gibco	10099-141
PBS	ZSGB-Bio	ZLI-9061
Lipofectamine 3000 reagent	Invitrogen	L3000150
Cyclosporin A	MedChemExpress	59865-13-3
TRlzol reagent	Invitrogen	15596026
MEM medium	gibco	11095080
Double-antibody	gibco	1902417
SYBR Green PCR Master Mix	ThermoFisher	K0253
RIPA buffer	Sigma-Aldrich	V900854
PVDF membrane	Millipore	IPVH00010
BSA	biofroxx	4240GR100
Critical commercial assays		
mirVana purification miRNA Isolation Kit	Invitrogen	AM1561
TRlzol reagent	Invitrogen	15596026
One Step Prime Script miRNA cDNA Synthesis Kit	Takara	6110A
CCK-8 test kit	Biyuntian	C0037
Annexin-V-FITC/PI apoptosis kit	7seapharmtech	A005-4
LDH assay kit	Enzyme-linked	ml002267

(Continued on next page)

Continued

REAGENT or RESOURCE	SOURCE	IDENTIFIER
MDA assay kit	Enzyme-linked	m1077384
GSH assay kit	Enzyme-linked	m1002260
GSSG assay kit	Enzyme-linked	m1057674
SOD assay kit	Enzyme-linked	m1001998
CellROX™ Deep Red kit	ThermoFisher	C10422
Ferrous Ion Content Assay Kit	Solarbio	BC5415
Fluo-8 calcium flux assay kit	Abcam	ab112129
H ₂ S content Assay Kit	Solarbio	BC2055
mPTP assay kit	Beyotime	C2009S
JC-1 Mitochondrial Membrane Potential Assay Kit	MedChemExpress	HY-K0601
Dual Luciferase assay kit	Biyuntian	RG027
Magna RIP™ RNA-Binding Protein Immunoprecipitation Kit	Millipore	17-700
ECL chemiluminescence assay kit	Biyuntian	P0018S
TTC staining kit	Solebao	T8170
miRNA Complete Labeling and Hyb Kit	Agilent	5190-0456

Experimental models: Cell lines

mouse cardiomyocytes HL-1	Zhong Qiao Xin Zhou Biotechnology Co., Ltd	ZQ0920
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Experimental models: Organisms/strains

BALB/c mice	SPF	N/A
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Oligonucleotides

Primers for qPCR, see Data S3	This Paper	N/A
NC inhibitor/mimic	RiboBio	N/A
miR-330-3p inhibitor/mimic	RiboBio	N/A
oe-/si-BAP1	RiboBio	N/A
oe-SLC7A11	RiboBio	N/A
si-IP3R	RiboBio	N/A

Software and algorithms

Adobe Photoshop	Adobe	https://www.adobe.com/es/
Graphpad Prism8	GraphPad Prism Software, Inc	https://www.graphpad.com/
ImageJ	ImageJ	https://imagej.net/ij/
Cytoscape	Cytoscape	https://cytoscape.org/
R language	The R Project for Statistical Computing	https://www.r-project.org/

Other

Agilent chip scanner	This paper	G2565CA
Agilent Feature Extraction software	This paper	N/A

EXPERIMENTAL MODEL AND STUDY PARTICIPANT DETAILS

Mouse models

60 BALB/c mice (20 ± 2 g, 4–6 weeks old) were purchased from SPF (Beijing) Biotechnology Co., Ltd. All the animals were housed in an environment with a temperature of 22 ± 1°C, a relative humidity of 50 ± 1%, and a light/dark cycle of 12/12 h. All animal studies (including the mice euthanasia procedure) were done in compliance with the regulations and guidelines of Yunnan Labreal Biotech Co., Ltd. animal care and conducted according to the AAALAC and the IACUC guidelines (IACUC Issue No. PZ20220504). Male and female mice did not affect the experiment and were therefore included in each experiment.

All experiment procedures in this study were approved and performed in accordance with the guidelines of the French Ministry of Agriculture's Animal Ethics Committee (EC Directive 2010/63/EU and French Decree 2013-118). The animal experiment of was received approval from the Experimental Animal Ethics Committee of Yunnan Labreal biotech Co., Ltd (IACUC Issue No. PZ20220504). The approved

project: Overexpressing GATA-4 mesenchymal stem cell derived exosome remodeling mitochondrial function in infarcted cardiomyocytes suppresses cardiomyocyte ferroptosis via Ap2m1/p66shc. Approval number: PZ20220504, 05/07/2020.

Cell lines culture

The mouse cardiomyocytes HL-1 (ZQ0920) was purchased from China Shanghai Zhong Qiao Xin Zhou Biotechnology Co., Ltd. Cells were cultured in MEM (Gibco, USA) supplemented with 10% fetal bovine serum (FBS, Gibco, USA) and 1% double-antibody (Gibco). Cells were incubated at 37°C in a 5%CO₂ humidified atmosphere. The cells were not cultured for longer than 2 months.

METHOD DETAILS

BMSC extraction

BMSCs were extracted by the femur and tibia of mice as previously reported⁷⁵ and co-incubated with bone marrow mesenchymal stem cell growth medium (MUXMX-90011, Cyagen Biosciences, Sunnyvale, CA, USA) containing 10% FBS. The specific procedures have been previously described in our previous publication.²⁶ P9 cells were selected for follow-up experiments.

Extraction and identification of exosomes

Collecting transfected BMSCs were cultured in medium with BMSC growth medium without FBS for 48 h and then centrifuged 1 h at 110,000×g and 4°C. After removing the supernatant, added the phosphate buffer saline (PBS) was resuspended through centrifugation for 1 h at 110,000×g at 4°C. Transmission electron microscopy (TEM) and nanosight analysis⁴³ were employed to observe and analyze the exosome morphology.

Cell transfection and treatment

Lentivirus overexpressing GATA-4²⁶ (Genomeditech, Shanghai, Chian) and oe-NC, as well as NC inhibitor/mimic, miR-330-3p inhibitor/mimic, oe-/si-NC, oe-/si-BAP1, oe-/si-SLC7A11, and si-IP3R (RiboBio, Guangzhou, China) were used to transduce BMSCs and cardiomyocytes using lipofectamine 3000 reagent (Invitrogen Life Technologies, Carlsbad, CA, USA), following the manufacturer's instructions. The expression levels of genes and proteins were assessed by RT-qPCR or Western blot 24 h after transfection. Cyclosporin A (CsA, mPTP inhibition, 59865-13-3) was purchased from China, Shanghai, MedChemExpress Co., Ltd.

Bioinformatics analysis

Six exosome groups transfected with lentivirus overexpressing GATA-4 and oe-NC were randomly selected ($N = 3$). Total RNA was extracted using TRIzol reagent (Invitrogen, 15596026). The quality test for total RNA was performed using the formaldehyde-denatured gel electrophoretic assay. Next, we purified the RNA using the mirVana purification miRNA Isolation Kit (AM1561). The miRNA Complete Labeling and Hyb Kit (5190-0456, Agilent, China) was then applied to dephosphorylate and label the RNA. After hybridization, slides were washed with 0.2 SDS and 2×SSC. We scanned the slides using the Agilent chip scanner (G2565CA) and the Agilent Feature Extraction (v10.7) software to analyze the hybrid images and extract the data. Then gene expression differences and statistically significant p -values were calculated using GeneSpringGX software. Moreover, raw and normalized signal values with corresponding annotation information of all samples are shown in Table S4. Because of had 3 or more samples, the samples are clustered according to the correlation of their expression patterns (Table S5). Subsequently, the limma package of the R script⁷⁶ was used to analyze the differentially expressed genes (DEGs), and the ggplot2 and heatmap package, respectively, map volcanoes and heat maps. Screening criteria were $|\log_2FC| > 1$ and adjusted p -value < 0.05 .

Cell hypoxia/reoxygenation (H/R) model and co-culture

Cell hypoxia/reoxygenation (H/R) model was established as previously described.³¹ HL-1 was cultured in a hypoxia cell culture incubator for 18 h in the glucose-free medium. Then, cells were placed in a 95% O₂ and 5% CO₂ incubator for 6 h. Subsequently, 1 mL of exosomes (5 μg/mL) was added in co-culture with 1×10^5 HL-1, including the Exos from BMSCs, BMSCs expressing oe-NC, and BMSCs overexpressing GATA-4.

RT-qPCR

A total RNA was extracted using a TRIzol reagent. RNA was then subjected to reverse transcription to form cDNA using the One Step Prime Script miRNA cDNA Synthesis Kit (Takara, Kyoto, Japan). For RT-qPCR procedures, we followed the instructions provided by the manufacturer of the SYBR Green PCR Master Mix (ThermoFisher, USA). The sequences of RT-qPCR primers are shown in Data S3. Finally, the $2^{-\Delta\Delta Ct}$ method was used to calculate the value, with GAPDH, U6 or β -actin as the internal reference.

Western blot

The proteins in tissue samples and cells of each group were extracted using RIPA buffer (Sigma-Aldrich, USA) containing 1% protease inhibitor and phosphatase inhibitor. Proteins were then separated using 10% SDS-PAGE gel and transferred to a polyvinylidene fluoride (PVDF) membrane (Millipore, MA, USA). The membrane was sealed with 5% skim milk at room temperature for 2 h and then incubated overnight at 4°C

with the following primary antibodies: anti-SLC7A11 (1:10000, ab175186, Abcam, UK), anti-GPX4 (1:1000, ab125066, Abcam, UK), anti-ACSL4 (1:1000, ab155282, Abcam, UK), anti-BAP1 (1:2000, ab255611, Abcam, UK), anti-Kelch-like ECH-associated protein 1 (Keap1, 1:1000, bs-3648R, bioss), anti-Nuclear factor erythroid 2-related factor 2 (Nrf2, 1:1000, bs-1074R, bioss), anti-IP3R (1:1000, ab252536, Abcam, UK), anti-MCU (1:500, HY-P80216, MedChemExpress), anti-HIF-1 α (1:5000, ab179483, Abcam, UK), anti-Bcl-2 (1:2000, ab182858, Abcam, UK), and anti-Bax (1:1000, ab32503, Abcam, UK). Next, samples were washed and incubated with second antibodies conjugated with HRP (1:2000, ab205718, Abcam, UK) at room temperature for 1 h. ECL chemiluminescence solution development was used for exposure and observation. Antibody against GAPDH (1:2500, ab9485, Abcam, UK) or β -actin (1:1000, ab8226, Abcam, UK) as the control. Protein band analysis was done using ImageJ.

CCK-8 assay

The cell viability was detected using the CCK-8 test kit (Biyuntian, Beijing, China). Cells were cultured in a 96-well plate at a concentration of 3×10^3 cells per well for 1, 2 and 3 h. After each time point, 10 μ L of CCK-8 solution was added to each well and incubated at 37°C. The absorbance values were measured at 450 nm using an enzyme labeling instrument (SM600, UTRAO).

Flow cytometry

The cells from each group were collected and rinsed with 200 μ L of PBS solution. Early and late cell apoptosis was measured using the Annexin-V-FITC/PI apoptosis kit (7seapharmtech, Shanghai, China) following the manufacturer's instructions. Briefly, 5 μ L of Annexin V-FITC and 5 μ L of PI were added to each well and incubated for 15 min in a dark chamber. After that, apoptosis was detected by using FACScan flow cytometry.

The levels of lactate dehydrogenase (LDH), malondialdehyde (MDA), reduced glutathione GSH/oxidized glutathione (GSSG), superoxide dismutase (SOD) and ROS

The ELISA Kits of lactate dehydrogenase (LDH) assay kit (ml002267), malondialdehyde (MDA) assay kit (ml077384), reduced glutathione (GSH) assay kit (ml002260), oxidized glutathione (GSSG) assay kit (ml057674), and superoxide dismutase (SOD) assay kit (ml001998) were purchased from China Shanghai Enzyme-linked Biotechnology Co., Ltd. CellROX Deep Red kit (C10422) was purchased from USA Thermo Fisher Scientific Co., Ltd. Specific operation referenced the instructions of kits.

The levels assay of Fe²⁺, Ca²⁺ and H₂S

The Ferrous Ion Content Assay Kit (BC5415, Solarbio), Fluo-8 calcium flux assay kit (ab112129, Abcam), and H₂S content Assay Kit (BC2055, Solarbio), were used to measure the concentration of Fe²⁺, Ca²⁺ and H₂S, respectively, following the referenced the manufacturer's protocol. The microplate reader was used to detect the OD.

Analysis of the mPTP

The mPTP assay kit (C2009S) was purchased from China Shanghai Beyotime Biotechnology Co., Ltd. Briefly, cells were mixed with corresponding reagents after being centrifuged at 1000 g for 5 min. Next, cells (1×10^6) were cultured for 30 min in the dark, re-centrifuged at 1000 g for 5 min and then mixed with 400 μ L buffer. After that, FACScan flow cytometry was used to evaluate the mPTP situation.

Mitochondrial membrane potential assay

The JC-1 Mitochondrial Membrane Potential Assay Kit (HY-K0601, MedChemExpress) was used to analyze the situation of mitochondrial membrane potential following a previously described approach⁷⁷ research. A fluorescence microscope was used to detect green fluorescence J-monomers and red J-aggregates. The microtome stained with uranyl acetate and lead citrate sections were reviewed for mitochondrial morphology under a TEM (JEM-2000EX, JEOL, Japan).

Immunofluorescence (IF) experiment

The cells were placed onto a 24-well plate at a density of 2×10^4 cells per well. After 24 h, the cells were washed twice with PBS, fixed with 4% paraformaldehyde, permeabilized for 10 min, and blocked with bovine serum albumin (BSA) for 1 h. The cells were then double-stained with anti-Cyp-D (ab110324, Abcam, UK) or anti-Nrf2 (BF8017, Affinity) overnight at 4°C and then incubated with corresponding secondary antibodies for 1 h, followed by DAPI staining. Finally, the stained cells were observed and photographed under a fluorescence microscope (400857, Nikon, Japan).

Luciferase reporter assay

The luciferase reporter vector was cloned by BAP1-3' untranslated region (UTR) containing the miR-330-3p binding site to generate wild type (WT) luciferase reporter plasmid, or SLC7A11 promoter was cloned by luciferase reporter pGL3 vector. After 24 h, the collected cells were lysed. The dual luciferase assay kit (Biyuntian, Beijing, China) detected the luciferase activity.

AgO2-RIP assay

The cells transfected with NC mimic, miR-330-3p mimic, after 24 h, Magna RIP RNA-Binding Protein Immunoprecipitation Kit (17-700, Millipore, Burlington, MA, USA) used to RIP analysis. The level of miR-330-3p was assessed using RT-qPCR.

Coimmunoprecipitation (CO-IP)

Cells were first lysed with IP lysis buffer and centrifuged, after which the supernatant was collected and incubated with protein A/G Sepharose (Santa Cruz Biotechnology) with the anti-BAP1 and anti-IP3R for 60 min. Then, all IPs were set overnight at 4°C. After centrifuging the beads and washing steps, the immune precipitates were assessed using Western Blot.

Pull-down assay

The pull-down assay was performed as previously described.^{78,79} In short, biotin labeling with BAP1 or antisense RNA was mixed with 500 μ L CO-IP buffer to dissolve. Then, 3 μ g of biotinylated DNA oligoprobe or antisense probes were incubated with 50 μ L streptavidin C1 magnetic beads (Invitrogen) for 1 h. SDS-PAGE was used to analyze the bound proteins in the pull-down material.

Ischemia and reperfusion (I/R) mice model

Mice were randomly divided into an ischemia and reperfusion (I/R) group and a Sham group. The animal groups were assigned random numbers using the Rand () function in Microsoft Excel. All mice were anesthetized using isoflurane inhalation (1.5%–2%). The I/R group was reperfused for 3 h after a left anterior descending coronary artery (LAD) of 45 min, following a protocol described in a previous study,⁸⁰ while the reperfusion was not performed in the Sham group. Next, both groups were treated with Exos^{oe-NC}, Exos^{oe-GATA-4}, NC inhibitor, or miR-330-3p inhibitor by tail vein injection for 3 days. Experimental mice were respectively divided into 6 different groups ($n = 6$ mice per group): Sham group, I/R group, I/R+Exos^{oe-NC} group, I/R+Exos^{oe-GATA-4} group, I/R+Exos^{oe-GATA-4}+NC inhibitor group and I/R+Exos^{oe-GATA-4}+ miR-330-3p inhibitor group.

An ultrasonic cardiogram (PHILIPS, EPIQ 7C) estimated cardiac function 3 days post-modeling. After the mice were then euthanized by cervical dislocation after anaesthetization. The 2,3,5-triphenyl tetrazolium chloride (TTC, T8170, Beijing Solebao Biotechnology Co., Ltd., Beijing, China) staining method was implemented to determine the size of a myocardial infarct.

QUANTIFICATION AND STATISTICAL ANALYSIS

The data in this paper was presented as mean \pm standard deviation (mean \pm SD). GraphPad Prism 8 was used to analyze and plot the data. T-test was used to compare two groups, One-way ANOVA was used to compare multiple groups, and two-way ANOVA was used for pairwise comparison between groups. A p value < 0.05 was considered statistically significant.

ADDITIONAL RESOURCES

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.