miR-124-3p regulates angiogenesis in peripheral arterial disease by targeting STAT3

YEFEI SHI1*, XU XU1*, PEIPEI LUAN1, WENXIN KOU1, MINGJIE LI2, QING YU1, JIANHUI ZHUANG1, Yawei Xu1, WENHUI PENG1 and WEIXIA JIAN2

1Department of Cardiology, Shanghai Tenth People's Hospital, Tongji University School of Medicine, Shanghai 200072; 2Department of Endocrinology, Xinhua Hospital Affiliated to Shanghai Jiaotong University, School of Medicine, Shanghai 200092, P.R. China

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Abstract. Peripheral arterial disease (PAD) is the third leading cause of cardiovascular morbidity worldwide, after coronary artery disease and stroke. As endogenous regulators of gene expression, microRNAs (miRs) are implicated in the development and progression of various diseases, including types of cancer, autoimmune diseases and heart diseases. In the present study, the role of miR-124-3p in PAD was investigated. The reverse transcription-quantitative PCR results indicated that the expression levels of miR-124-3p were significantly increased in the ischemic tissue of the hindlimb ischemia (HLI) model and in hypoxic human umbilical vein endothelial cells compared with the corresponding control groups. Proliferation, wound healing and tube formation assays demonstrated the inhibition of miR-124-3p on angiogenesis in vitro and the HLI model indicated the same function of miR-124-3p in vivo. A dual-luciferase reporter revealed STAT3 as the target of miR-124-3p. The expression levels of miR-124-3p in human blood were negatively correlated with ankle-brachial index, which is an index for the evaluation of the severity of PAD. Collectively, the present study indicated that miR-124-3p was a critical regulator of angiogenesis in PAD, and a potential diagnostic, prognostic and therapeutic target for PAD.

Introduction

Peripheral arterial disease (PAD) is a common peripheral circulatory problem, in which narrowed arteries occur, especially in the lower extremities (1,2). PAD has been reported as a highly age-related vascular disease, typically occurring in patients aged 60-70 years, which leads to health problems (3). Surgical and catheter-based revascularization that target primary occluded macro vessels are the primary conventional treatment strategies for PAD. Unfortunately, these high-cost methods result in limited improvement in the microcirculation, due to complications that occur in patients with PAD (4). Angiogenesis is a process of the endothelium, by which a new vessel is formed from the old one (5). Therapeutic angiogenesis has been studied for two decades, focusing on the overexpression of growth factors, which have been identified as factors that evoke angiogenesis in vitro in PAD, including vascular endothelial growth factor (VEGF) and hepatocyte growth factor (6,7). However, almost none of the trials met the expected goal, including significant clinical remission, which has led researchers to investigate other molecules that are responsible for the limited effects.

MicroRNAs (miRNAs/miRs), a class of ~22 nucleotide-long, small non-coding RNAs, regulate gene expression by repressing post-transcription to modulate cell fate decisions (8,9). miRNAs were first defined as endogenous regulators for a variety of cellular physiologic and pathologic processes (10). To date, 2,654 mature human miRNAs have been identified (11). Recently, certain miRNAs have been identified to be associated with ischemia-reperfusion injury (12,13). A number of identified miRNAs have been reported to serve as endogenous negative regulators of angiogenesis. For example, the antiangiogenesis function of miR-92a has been verified in vitro and in vivo (14,15). However, whether other miRNAs serve the same role as miR-92a is not completely understood. miR-124-3p has been reported to regulate glioma angiogenesis (16,17) and participate in ischemic diseases (18,19). Nevertheless, there are limited studies on the role of miR-124-3p in PAD. Therefore, the present study investigated the effect of miR-124-3p on endothelial cells (ECs) and PAD.

In the present study, the role of miR-124-3p in PAD was investigated in the blood of patients with PAD, as well as in...
the ECs and in the hindlimb ischemia model. In addition, the target of miR-124-3p was identified in the present study.

Materials and methods

Cell culture, stimulation and transfection. Human umbilical vein ECs (HUVECs; cat. no. 8000; ScienCell Research Laboratories, Inc.) were cultured and stimulated at 37°C in 5% CO₂ in Endothelial Cell Medium (cat. no. 1001; ScienCell Research Laboratories, Inc.) supplemented with 5% FBS (cat. no. 0025; ScienCell Research Laboratories, Inc.), 1% endothelial cell growth supplement (cat. no. 1052; ScienCell Research Laboratories, Inc.) and 1% penicillin/streptomycin solution (cat. no. 0503; ScienCell Research Laboratories, Inc.).

Cobalt (II) chloride hexahydrate (500 µM, cat. no. C8661; Sigma-Aldrich; Merck KGaA) was used to stimulate HUVECs at 37°C in 5% CO₂ for 24 or 48 h when cells reach 90% confluence. At ~80% confluence, HUVECs were transfected with mimic (50 nM; Guangzhou Ribobio Co., Ltd.), inhibitor (100 nM; Guangzhou Ribobio Co., Ltd.), small interfering (si)RNA (25 nM; Shanghai GenePharma Co., Ltd.) or corresponding negative controls (NCs, 25 nM; Shanghai GenePharma Co., Ltd.) for 36 h using Lipofectamine® 2000 (cat. no. 11668019; Invitrogen; Thermo Fisher Scientific, Inc.) according to the manufacturer's instructions. The sequences of the mimics, inhibitors and siRNAs were as follows: NC mimic forward, 5'-UUUGUAUCACAAAGAGACUG-3' and reverse, 5'-CAGUACUUUGUGAUAACA-3'; miR-124-3p mimic forward, 5'-UAAGGCACGCUGGUGAUGUC-3' and reverse, 5'-GGCAUUACCACCGUGCCCUAA-3'; NC inhibitor, 5'-CAGUACUUAUGUGAUAACA-3'; miR-124-3p inhibitor, 5'-GGCAUUACCACCGUGCCCUAA-3'; si-NC forward, 5'-UUCUCCGAAACGUGCACGU-3' and reverse, 5'-ACGUGACACGUGUCCGGA-3'; si-STAT3 forward, 5'-CCCCGGAAAUUUAACACUU-3' and reverse, 5'-AGAAUGUUAUAUUCGGGG-3'.

RNA isolation and reverse transcription-quantitative PCR (RT-qPCR). Total RNA was isolated from human blood, HUVECs, and the blood of HLI model mice using TRIzol® (cat. no. 15596026; Invitrogen; Thermo Fisher Scientific, Inc.) according to the manufacturer's instructions. Total RNA (1 µg) was reverse transcribed into cDNA using the PrimeScript RT Reagent kit (cat. no. RR037A; Takara Bio, Inc.) as follows: 37°C for 15 min, 85°C for 5 sec and 4°C thereafter. Subsequently, qPCR was performed using KAPA Biosystems (cat. no. K0220S; Thermo Fisher Scientific) as follows: 95°C for 3 min, then 40 cycles of 95°C for 30 sec and 60°C for 30 sec. miRNA and mRNA expression levels were quantified using the 2−ΔΔCq method (20) and normalized to the internal reference genes U6 and GAPDH, respectively. Stem-loop primers of miR-124-3p and U6 were purchased from Guangzhou Ribobio Co., Ltd. The primer sequences of miR-124-3p, U6, STAT3 and GAPDH were as follows: miR-124-3p forward, 5'-TCTTTAAGGCACCGGGTG-3' and reverse, TATGTTTTTACGACTGTGTGAT; U6 forward, 5'-CTCGGTTCGACGCCGACA-3' and reverse, 5'-AACGCTTCTACGATTTGCCGT-3'; STAT3 forward, 5'-CAGCAGCTTGCACACGAGTGA-3' and reverse, 5'-AAAACACAAAGTGGCATGTGA-3'; and GAPDH forward, 5'-GGAGCGGATCCCTCCAAAT-3' and reverse, 5'-GCGTGTGTCACTTCTCATT-3'.

Proliferation assay. Cell proliferation was determined using the Edu Cell Proliferation kit (cat. no. C10339; Invitrogen; Thermo Fisher Scientific, Inc.). Following 12 h serum starvation, HUVECs were incubated with Edu-labeling mixture (10 µM) in combination with recombinant human VEGFA-165 (50 ng/ml; cat. no. 0025; PeproTech, Inc.) for 12 h at 37°C in 5% CO₂. Images (four pictures of each group) were captured by an Olympus IX83 fluorescence microscope (Olympus Corporation) at 10x magnification. The rate of cell proliferation was calculated using the following formula: Number of Edu⁺ cells/total number of cells in each field.

Wound healing assay. At ~90% confluence, the limit of HUVEC proliferation, a scratch was made in the center of each well using the tip of a 200 µl pipette. Subsequently, serum-starved HUVECs were cultured with VEGFA-165 (50 ng/ml). Images of the wounds were captured at 0 and 24 h by an Olympus CKX53 inverted microscope at 4x magnification (Olympus Corporation). Cell migration was analyzed using ImageJ software (version 1.52a; National Institutes of Health).

Tube formation assay. For the assay, 96-well plates were pre-coated with Matrigel (cat. no. 354230; Corning, Inc.) at 37°C for 30 min, and then HUVECs were seeded (2x10⁴ cells/well) into the Matrigel. Following culture with VEGFA-165 (50 ng/ml) for 8 h at 37°C in 5% CO₂, images were captured to detect tube formation by an Olympus CKX53 inverted microscope at 4x magnification (Olympus Corporation). The total tube length was assessed using ImageJ software (version 1.52a; National Institutes of Health).

Dual-luciferase reporter assay. The target of miR-124-3p was predicted using TargetScan (version 7.1, http://www.targetscan.org). The 3'-untranslated region (3'-UTR) luciferase reporter construct of STAT3 was cloned downstream of the Renilla luciferase gene in the psi-check2 vector (Hanbio Biotechnology Co., Ltd.). 293T cells (cat. no. CRL-11268; American Type Culture Collection) were seeded into a 96-well plate with density of 80%. Subsequently, 293T cells were co-transfected with 5 pmol miR-124-3p mimic or NC mimic and 0.16 µg STAT3-wild-type (WT) or STAT3-mutant (Mut) using Lipofectamine® 2000 (cat. no. 11668019; Invitrogen; Thermo Fisher Scientific, Inc.). At 48 h post-transfection, luciferase activities were detected using the Dual-Luciferase Reporter Assay System (cat. no. E1910; Promega Corporation). Firefly luciferase activities were normalized to Renilla luciferase activities.

Protein extraction and western blotting. Total protein was extracted from HUVECs using Cell Lysis Buffer (cat. no. 9803s; Cell Signaling Technology, Inc.) with protease inhibitors (cat. no. 04693159001; Roche Diagnostics). The bicinchoninic acid method was used for protein determination. Protein (10 µg) was separated via 8% SDS-PAGE and transferred to PVDF membranes, which were blocked with 5% bovine serum albumin at room temperature for 1 h.
Subsequently, the membranes were incubated overnight at 4°C with the following primary antibodies: STAT3 (1:1,000; cat. no. 9139; Cell Signaling Technology, Inc.) and GAPDH (1:5,000; cat. no. 60004-1-Ig; ProteinTech Group, Inc.). Following primary incubation, the membranes were incubated with horseradish peroxidase-conjugated secondary antibodies (anti-mouse IgG, 1:2,000, cat. no. ab205719, Abcam) at room temperature for 1 h. Protein bands were visualized using chemiluminescence (cat. no. 180-5001; Tanon Science and Technology Co., Ltd.) and detected using the Amersham Imager 600 system (GE Healthcare Life Sciences). Protein expression was semi-quantified using ImageJ software (version 1.52a; National Institutes of Health) with GAPDH as the loading control.

**HLI model and detection of perfusion recovery.** A total of 50 eight-week-old male mice (18 to 22 g) were used for HLI model. The HLI model was established as previously described (21). Briefly, mice were anesthetized with an intraperitoneal injection of ketamine (80 mg/kg) and xylazine (5 mg/kg). Excision and ligation were performed on the left femoral artery. For the sham operation, excision was performed on the contralateral hindlimb. miR-124-3p was overexpressed using agomir-R-124-3p and inhibited using antagomiR-R-124-3p. Accordingly, mice were injected with 5 nmol agomir-R-124-3p or agomiR-NC (Guangzhou RiboBio Co., Ltd.) into two sites of the gastrocnemius and one site of the tibialis anterior muscle on day 0, 7, 14 and 21 post- HLI. In addition, 8 mg/kg agomir-R-124-3p or agomiR-NC (Guangzhou RiboBio Co., Ltd.) were injected via a tail vein injection on day 0, 7, 14 and 21 post- HLI and quantified using moorLDI Image software (version 5.3; Moor Instruments Ltd.). Perfusion in the ischemic limb was normalized to the sham limb for each mouse. The mice were anesthetized by isoflurane (5%) inhalation and euthanized by CO2 (100%) inhalation at a rate of 30% volume/minute. Animal studies were conducted in compliance with the Guide for the Care and Use of Laboratory Animals published by the NIH (23) and approved by the Ethics Committee of the Shanghai Tenth People's Hospital (approval no. 2019-K-153).

Statistical analysis. Data are presented as the mean ± standard deviation. Comparisons between two groups were analyzed using the unpaired Student’s t-test. Comparisons among multiple groups were analyzed using one-way or two-way ANOVA followed by Bonferroni’s post hoc test. The parameters from baseline characteristics of patients with PAD and non-PAD individuals were analyzed using the χ² test (age, BMI and blood lipid were excluded). Pearson's correlation analysis was performed to investigate the correlation between ABI and the expression level of miR-124-3p. Statistical analyses were performed using GraphPad Prism software (version 6.01; GraphPad Software, Inc.). P<0.05 was considered to indicate a statistically significant difference. All experiments were repeated ≥3 times.

Results

Expression levels of miR-124-3p are increased in the HLI model and hypoxic HUVECs. To identify the role of miR-124-3p in the HLI model, the dynamic expression of miR-124-3p was detected in the ligated ischemic gastrocnemius. Total...
RNA was extracted from the gastrocnemius and blood of HLI model mice. The RT-qPCR results suggested that the levels of miR-124-3p in the ischemic gastrocnemius were significantly upregulated on day 2 compared with day 0 (day 2, 7.50±2.00 vs. day 0, 1.01±0.20; Fig. 1A). However, the levels of miR-124-3p in the blood peaked on day 3 (day 3, 4.48±1.26 vs. day 0, 1.05±0.43; Fig. 1B). Hypoxia-inducible factor-α (HIF-α) is a powerful inducer of angiogenesis (26,27). Cobalt has been reported to mimic hypoxia by preventing the degradation of HIF-α (28). Therefore, cobalt was used to mimic hypoxia in HUVECs. The levels of miR-124-3p were significantly increased following cobalt-induced hypoxia (500 µM) at 48 h compared with 0 h (48 h, 38.54±11.88 vs. 0 h, 1.01±0.16; Fig. 1C). Collectively, the results indicated that miR-124-3p levels were increased in HUVECs and tissues under hypoxic conditions, which suggested that miR-124-3p might be essential for the progression of HLI.

**miR-124-3p impairs the functions of VEGFA-165-treated HUVECs.** VEGFA-165-stimulated ECs display enhanced proliferation, migration and stability for angiogenesis (29). Moreover, the aforementioned results provided evidence for investigating the functions of miR-124-3p in angiogenesis (29). Therefore, miR-124-3p mimic was used to overexpress miR-124-3p, whereas miR-124-3p inhibitor was used to knock down miR-124-3p. At 48 h post-transfection, the expression levels of miR-124-3p were measured via RT-qPCR. Compared with the corresponding NCs, miR-124-3p was successfully overexpressed by mimic and knocked down by inhibitor in HUVECs (Fig. 2A). To investigate the effect of miR-124-3p mimic and
inhibitor, alterations to the cell phenotype were examined. miR-124-3p mimic significantly inhibited HUVEC proliferation compared with NC mimic, whereas miR-124-3p inhibitor significantly enhanced HUVEC proliferation compared with NC inhibitor (Fig. 2B and C). Subsequently, the effect of miR-124-3p on HUVEC migration was analyzed. The wound healing assay results indicated that HUVEC migration was significantly inhibited by miR-124-3p mimic compared with NC mimic, but significantly enhanced by miR-124-3p inhibitor compared with NC inhibitor (Fig. 2D and F). The tube formation assay was conducted to evaluate the effect of miR-124-3p on angiogenesis. miR-124-3p mimic significantly inhibited tube formation compared with NC mimic, whereas miR-124-3p inhibitor significantly enhanced tube formation compared with NC inhibitor (Fig. 2E and G). Therefore, the results suggested that miR-124-3p impaired HUVEC functions in vitro.

STAT3 is a target of miR-124-3p. TargetScan indicated that STAT3 was a potential target of miR-124-3p (Fig. 3A). STAT3 is a member of the STAT protein family, and emerging evidence has suggested that it is a regulator of angiogenesis (30). To verify STAT3 as a target of miR-124-3p, luciferase reporter plasmids containing miR-124-3p binding sites in the 3'-UTRs of STAT3 were constructed. The dual-luciferase reporter assay results indicated that miR-124-3p mimic significantly decreased the luciferase activities of STAT3-WT compared with NC mimic (Fig. 3C). Therefore, the results suggested that miR-124-3p impaired HUVEC functions in vitro.

miR-124-3p expression is increased in patients with PAD. The aforementioned results indicated that the expression of

<table>
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<tr>
<th>Variable</th>
<th>Non-PAD (n=47)</th>
<th>PAD (n=49)</th>
<th>P-value</th>
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<tr>
<td>Age (years)</td>
<td>62.60±11.88</td>
<td>65.90±8.00</td>
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<td>Gender (male)</td>
<td>22 (46.81%)</td>
<td>29 (59.18%)</td>
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<td>BMI (kg/m²)</td>
<td>24.16±2.87</td>
<td>24.28±1.87</td>
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<td>Smoking</td>
<td>11 (23.40%)</td>
<td>28 (57.14%)</td>
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<tr>
<td>Blood lipid</td>
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<tr>
<td>Total cholesterol (mmol/l)</td>
<td>4.22±1.02</td>
<td>4.70±1.45</td>
<td>0.059</td>
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<tr>
<td>Triglyceride (mmol/l)</td>
<td>1.99±0.84</td>
<td>1.70±0.87</td>
<td>0.092</td>
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<tr>
<td>High-density lipoprotein (mmol/l)</td>
<td>1.21±0.27</td>
<td>1.43±0.50</td>
<td>0.008</td>
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<tr>
<td>Low-density lipoprotein (mmol/l)</td>
<td>2.74±0.86</td>
<td>2.89±0.98</td>
<td>0.413</td>
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<td>Medical history</td>
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<tr>
<td>Coronary heart disease</td>
<td>9 (19.14%)</td>
<td>24 (48.98%)</td>
<td>0.003</td>
</tr>
<tr>
<td>Diabetes</td>
<td>31 (65.96%)</td>
<td>46 (93.88%)</td>
<td>0.001</td>
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<tr>
<td>Hypertension</td>
<td>24 (51.06%)</td>
<td>33 (67.35%)</td>
<td>0.146</td>
</tr>
<tr>
<td>Statins</td>
<td>18 (38.30%)</td>
<td>28 (57.14%)</td>
<td>0.071</td>
</tr>
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</table>

Data are presented as the mean ± SD or n (%). Age, BMI and blood lipid variables were analyzed using the Student's t-test. All other parameters were analyzed using the χ² test. PAD, peripheral arterial disease; BMI, body mass index.
miR-124-3p in the tissues and blood of the HLI model displayed a similar peak time, and increased miR-124-3p expression markedly inhibited angiogenesis in ligated legs, suggesting that blood-derived miR-124-3p might serve as a marker of serious PAD. To investigate the hypothesis, 49 patients with PAD and 47 healthy individuals were enrolled in the present study. The baseline characteristics of the patients are presented in Table I. RT-qPCR was conducted to detect the levels of miR-124-3p in human blood. The levels of miR-124-3p in patients with PAD were significantly higher compared with non-PAD individuals (1.85-fold; PAD, 2.03±0.65 vs. non-PAD, 1.10±0.47; Fig. 5A). ABI is an index for the assessment of the severity of PAD (31,32). Pearson's correlation analysis indicated that the levels of miR-124-3p in the blood were negatively correlated with ABI scores (r=−0.6248; Fig. 5B), suggesting that miR-124-3p expression levels were positively correlated with the severity of PAD.

Discussion

The concept of therapeutic angiogenesis for PAD has been around for decades, but the advances made thus far fall far below expectations. A potential reason for the lack of effective results from therapeutic angiogenesis could be the complicated self-regulation of cells in the microenvironment (33,34). miRNAs are a type of small molecule that can serve as endogenous regulators of cells (8,9). Although miRNAs have been reported to be widely involved in the regulation of diseases, such as cancers (35), autoimmune diseases (36), central nervous system injuries (37) and heart diseases (38), there is limited information on the involvement of miRNAs in PAD. miR-124-3p was initially reported to be highly expressed in brain tissues (39), serving a critical role in neuronal differentiation (40). Further studies investigated other functions of miR-124-3p. According to Ando et al (15), miR-124-3p...
suppressed tumor development by inhibiting angiogenesis. Shi et al. (16) also demonstrated that miR-124-3p might predict acute myocardial infarction, suggesting that miR-124-3p might serve as a regulator of angiogenesis. Therefore, the aforementioned studies highlighted the importance of investigating the correlation between miR-124-3p and angiogenesis in PAD.

In the present study, the results indicated that miR-124-3p was upregulated under hypoxic conditions both in vivo and in vitro compared with the corresponding control groups. Moreover, compared with the NC groups, miR-124-3p overexpression significantly suppressed HUVEC functions and impaired perfusion recovery in the HLI model. STAT3 has been recognized as a regulator of angiogenesis beyond inflammation (41). The functions of STAT3 are precisely regulated by multiple chaperonins under specific conditions. For example, canonical STAT3 signaling is associated with JAK-STAT signaling, whereby STAT3 is phosphorylated on tyrosine 750 (Y750), facilitating STAT3 homodimerization, nuclear translocation, DNA binding and initiation of transcription (42). The noncanonical nuclear activities, including acetylation (43), alkylation (44), methylation (45), ubiquitination (46) and glutathionylation (44), have been implicated in STAT3 transcriptional

Figure 4. miR-124-3p impairs perfusion recovery and capillary density in the HLI model. miR-124-3p was overexpressed using agomiR-124-3p or knocked down using antagomiR-124-3p in the HLI model. (A) Representative images of perfusion recovery in the HLI model. Dark blue represents low or no perfusion and red represents the highest degree of perfusion. Scale bar, 1 cm. The effects of (B) agomiR-124-3p and (C) antagomiR-124-3p on perfusion recovery were quantified using moorLDI Image Processing software. (D) Representative images of CD31+ capillaries of the ischemic gastrocnemius on day 14 post-HLI. Scale bar, 50 µm. (E) Quantification of the capillary density of gastrocnemius. The experiments were repeated four times. **P<0.01. miR, microRNA; HLI, hindlimb ischemia.

Figure 5. miR-124-3p expression levels are increased in patients with PAD. (A) Relative expression of miR-124-3p in the blood of non-PAD individuals (n=47) and patients with PAD (n=49). (B) Correlation analysis between ABI and the relative expression of miR-124-3p in the blood of patients with PAD and non-PAD individuals (n=96; r=-0.6248). ***P<0.01. miR, microRNA; PAD, peripheral arterial disease; ABI, ankle-brachial index.
activity in various cells. Certain studies have reported the axis of miR-124-3p/STAT3 (47-49), but to the best of our knowledge, no previous study has focused on the functions of STAT3 in EC proliferation. Inhibition of the STAT3 signaling pathway impairs angiogenesis and perfusion recovery in the muscles of patients with PAD (50). In addition, an increasing number of studies have verified that STAT3 was involved in the regulation of tumor angiogenesis by modulating the expression of VEGF (51,52). The results of the present study indicated that miR-124-3p overexpression significantly decreased STAT3 expression levels and inhibited HUVEC proliferation compared with NC mimic. Furthermore, it has been reported that STAT3 could bind with Yes-associated protein to regulate the mRNA expression levels of angiopoietin-2 in ECs (53,54). Therefore, the aforementioned results suggested that miR-124-3p regulated angiogenesis following ischemic injury in mouse hindlimbs by targeting STAT3.

Another interesting finding of the present study was that the levels of circulating miR-124-3p were negatively correlated with ABI, the index for PAD severity. ABI is a non-invasive physical index that provides the standard for the evaluation of PAD severity (31). ABI is less sensitive in conditions associated with vessel stiffness (55); therefore, the expression of miR-124-3p in the blood might serve as an improved marker for screening patients than ABI. However, the role of miR-124-3p in the progression of PAD requires further investigation with additional samples. In addition, the long-term outcome of patients with increased miR-124-3p expression requires further investigation.

Although previous studies have reported possible roles of miR-124-3p in ischemic diseases (27-28), there were several novel aspects of the present study. First, the potential role of miR-124-3p was identified in the HLI model. Secondly, the results indicated that the levels of miR-124-3p in human blood were positively correlated with the severity of PAD, which suggested that miR-124-3p might serve as a strong potential target for the evaluation and treatment of PAD. Therefore, the aforementioned findings may aid with the clinical translation of the present study.

In conclusion, the present study provided evidence for the link between miR-124-3p and PAD. miR-124 regulates angiogenesis by decreasing STAT3 expression. Although miRNA-based therapeutics are still being developed, the results of the present study are encouraging and suggested the potential of miR-124 as a diagnostic, prognostic and therapeutic target for PAD in the future.

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Availability of data and materials

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

Authors' contributions

WP and WJ designed the study. YS and XX performed the experiments, analyzed the data and wrote the manuscript. PL, WK, ML, QY, JZ and YX were responsible for collecting blood samples, baseline characteristics of patients and analyzing the data of population study. All authors read and approved the final manuscript, and agreed to be accountable for the work in ensuring that questions related to the integrity of any part of the work were appropriately investigated and resolved.

Ethics approval and consent to participate

Written informed consent was obtained from all patients. The present study was approved by the Ethics Committee of Shanghai Tenth People's Hospital, Shanghai, China (approval no. 2019-K-153). Animal experiments were approved by the Laboratory Animal Ethics Committee of Shanghai Tenth People's Hospital, Shanghai, China (approval no. SHDSYY-2019-2149).

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

References

Critical function of Bmx/Etk in


