Integrative analysis reveals essential mRNA, long non-coding RNA (lncRNA), and circular RNA (circRNA) in paroxysmal and persistent atrial fibrillation patients

Haoliang Sun#, Junjie Zhang1, Yongfeng Shao

Department of Cardiovascular Surgery, the First Affiliated Hospital of Nanjing Medical University; Jiangsu-China
1Department of Cardiothoracic Surgery, Changzhou Wujin People’s Hospital; Jiangsu-China

ABSTRACT

Objective: This study aimed to investigate the functions of mRNA, long non-coding RNA (lncRNA), and circular RNA (circRNA) in paroxysmal and persistent atrial fibrillation (AF) patients.

Methods: A total of 9 left atrial appendage (LAA) tissues were collected from patients with AF (ParoAF patients = 3 and PersAF patients = 3) and donors (n=3). Genes and circRNAs were identified by per kilobase per million reads (RPKM) and number of circular reads/number of mapped reads/read length (SRPBM), respectively. Differentially expressed mRNAs (DE mRNAs), lncRNAs (DE lncRNAs), and circRNAs (DE circRNAs) were identified by | log2 (Fold Change) | ≥ 2 and p-value < 0.05. Gene Ontology (GO) and the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses were performed. Protein-protein, mRNA-lncRNA, and circRNA-miRNA interaction networks were constructed. In addition, logistic analysis was conducted among AF and circRNAs.

Results: A total of 285 (116 up-regulated and 169 down-regulated) and 275 (110 up-regulated and 165 down-regulated) DE mRNAs, 575 (276 up-regulated and 299 down-regulated) and 583 (330 up-regulated and 253 down-regulated) DE lncRNAs, and 83 (48 up-regulated and 35 down-regulated) and 99 (58 up-regulated and 41 down-regulated) circRNAs were detected in ParoAF and PersAF, respectively, as compared with control. MAPK signal pathway as well as voltage-dependent, L type, and alpha 1C subunit calcium channel (CACNA1C) might participate in AF occurrence by preventing atrial parasympathetic remodeling. Collagen type I alpha 1 (COL1A1) and COL1A2 mostly participated in the enriched GO and KEGG terms and connected with most of the DE mRNAs. The expression of chr10:69902697|69948883 was a protective factor against PersAF after adjusting for age (p=0.022, 95% CI: 0.003–0.634).

Conclusion: We found that some mRNAs, lncRNAs, circRNAs, and pathways play essential roles in AF pathogenesis and development. Moreover, one protective factor against PersAF was detected.

Keywords: atrial fibrillation, RNA-Seq, pathway, mRNA, lncRNA, circRNA

Cite this article as: Sun H, Zhang J, Shao Y. Integrative analysis reveals essential mRNA, long non-coding RNA (lncRNA), and circular RNA (circRNA) in paroxysmal and persistent atrial fibrillation patients. Anatol J Cardiol 2021; 25: 414-28.

Introduction

Atrial fibrillation (AF) is the most common type of arrhythmia, which affected 37.574 million individuals worldwide in 2017 (1). AF increases the probability of thromboembolism, ischemic stroke, congestive heart failure, psychological distress, and death (2). It impairs the quality of life of patients severely, especially patients who require open-heart surgery (3). There are three kinds of AF, which include paroxysmal AF (ParoAF), persistent AF (PersAF), and permanent AF (4). PersAF appears to be more reliant on fibroblast proliferation and myocyte-fibroblast coupling when compared with ParoAF, which is mainly due to primary on pulmonary vein triggers (5). The mechanisms related to occurrence and development of ParoAF and PersAF have been studied continuously for a long time.

In recent years, next-generation sequencing (NGS) provided a more efficient way to study AF. There are growing evidences

#These authors contributed equally to this work.

Address for Correspondence: Yongfeng Shao, MD, Department of Cardiovascular Surgery, the First Affiliated Hospital of Nanjing Medical University, No. 300, Guangzhou Road, Nanjing/210029, Jiangsu-China
Phone: +86-13851536726 E-mail: shaoyongfeng_2019@163.com
Accepted Date: 22.12.2020 Available Online Date: 21.05.2021
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DOI:10.14744/AnatolJCardiol.2020.57295
that genome-wide association, microRNA (miRNA), mRNA, long non-coding RNA (lncRNA), and circular RNA (circRNA) play essential roles in pathogenesis and development of AF (6-11). For instance, miR29 was shown to play a crucial role in atrial fibrotic remodeling and may also been considered as a biomarker and/or therapeutic target (6). Sinner et al. (9) provided five novel loci for AF, which might be novel molecular targets for future biological and pharmacological investigation.

LncRNA longer than 200 nucleotides in length with non-protein coding function has attracted the attention of researchers (12). LncRNA plays a central role in many functions during heart development and various heart diseases, including cardiac hypertrophy, cardiac fibrosis (CF), AF, and heart failure (HF) (13-16). CircRNA is a non-coding RNA that regulates gene expression and acts as miRNA “sponges” by competing with endogenous RNA (ceRNA) to suppress the activity of specific miRNA (17). Moreover, circRNAs serve as biomarkers for many diseases (18). In the study by Hu et al. (19), they detected several circRNAs that might be associated with inflammatory responses in AF. However, RNA-related studies on ParoAF and PersAF patients are still inadequate.

To identify the differentially expressed mRNAs (DE mRNAs), lncRNAs (DE lncRNAs), and circRNAs (DE circRNAs) on ParoAF and PersAF left atrial appendages (LAA) in patients were investigated and studied through high-throughput RNA sequencing (RNA-Seq). We performed Gene Ontology (GO) and the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analyses for functional annotation of the DE mRNAs, mRNAs near the DE lncRNAs, and host genes of DE circRNAs were performed. Finally, the protein-protein, mRNA-lncRNA, and ceRNA interaction network was constructed. These results will provide valuable genes and pathways, which regulate the occurrence and development of AF.

**Methods**

**Sample collection**

The LAA of the donors was recruited. A total of 9 LAA tissues collected from the hearts of patients with AF (ParoAF patients=3 and PersAF patients=3) and donors (n=3) were used for NGS sequencing. All the healthy donors had sinus rhythm and were in good condition. The ParoAF and PersAF LAA tissues were selected from the maze surgery of AF patients.

**RNA extraction**

The LAA tissues were washed with ddH₂O, cut into small pieces with a clean scalpel, and then snapped into liquid nitrogen for at least 4 h and finally stored at −80° until use. TRIzol Reagent (Invitrogen, Carlsbad, CA, USA) was used for total RNA extraction. The total amount was quantified and the quality was assessed. Samples with RNA amount >5 μg, RNA integrity number >7, and OD₂₆₀/₂₈₀ >1.9 were employed for library preparation.

**Library preparation and sequencing**

Ribosomal RNA (rRNA) in each RNA sample was deleted using RiboMinus kit (Thermo Fish, Waltham, MA, USA). Next, each RNA sample was quantified and applied for library preparation using TruSeq RNA Library Preparation Kit v2 (Illumina Inc, USA). All libraries were loaded into one lane on Illumina HiSeq X Ten (Illumina Inc, USA) platform, followed by 2 × 150 bp paired-end sequencing.

**Bioinformatics analysis of DE mRNAs, DE lncRNAs, and DE circRNAs**

FastQC (v0.11.5, http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) was used to process raw sequencing data. Clean reads were mapped onto Homo sapiens (assembly GRCh38. P12) using TopHat (v2.0.12, https://ccb.jhu.edu/software/tophat/index.shtml), followed by assembly using Cufflinks (v2.2.1, http://cufflinks.cbcb.umd.edu). Transcripts with reads per kilobase of exon per million read mapped (RPKM > 0) were retained for further analysis. For circRNA detection, RNA sequencing data were analyzed by CircRNA Identifier (CIRI) and an algorithm for de novo circRNA identification (20). Junction reads and circRNA candidates in SAM files were scanned twice by CIRI. CircRNAs that have junction reads ≥2 and appeared in at least two samples were regarded as high-confidence circRNAs. Finally, edgeR (http://www.bioconductor.org/packages/release/bioc/html/edgeR.html) was utilized to identify the DE mRNAs, DE lncRNAs, and DE circRNAs by pairwise comparisons, with the threshold of |Log₂ Fold Change (FC)| ≥2 and p-value < 0.05.

**GO and KEGG pathway enrichment analyses**

We focused on the neighboring target genes of DE lncRNAs. We searched mRNAs nearest to DE lncRNAs both in upstream and downstream. Each circRNA was annotated to the linear host mRNA according to their position relationship on the chromosome. We used the linear host mRNA as the proxy of its related circRNAs.

GO (http://geneontology.org/) enrichment analysis was performed on all DE mRNAs, mRNAs nearby the DE lncRNAs, and host genes of DE circRNAs, with corrected p-value <0.05 as a threshold.

KEGG database (https://www.kegg.jp/) was applied for pathway mapping. KEGG pathway enrichment analysis identified
metabolic pathways or signaling pathways significantly enriched in all DE mRNAs, mRNAs nearby the DE IncRNAs, and host genes of DE circRNAs in the whole genome using KOBAS, taking p-value <0.05 as a threshold to identify the enrichment pathway. We further plotted the network of top ten KEGG pathways and mRNA in ParoAF and PersAF using Cytoscape software v3.6.1.

Interaction networks

We constructed the protein-protein interaction network of DE mRNAs in ParoAF_Control and PersAF_Control. STRING database (https://string-db.org/cgi/input.pl) was used for the interaction correlation study and only those with correlation (r) >0.7 were displayed. The DE mRNAs, which were also targeted by DE IncRNAs, were selected for the mRNA-IncRNA network study.

The common DE circRNAs in ParoAF_Control and PersAF_Control were selected for the circRNA-miRNA interaction network analysis. The miRNAs binding to circRNAs were identified in miRanda (v3.3a, http://www.microrna.org). CircRNAs with more miRNA binding sites were screened as candidate “sponge” circRNAs and used to construct the ceRNA interaction network. Cytoscape software v3.6.1 was used for the network drawing.

Samples used for validation

Quantitative real-time polymerase chain reaction (qRT-PCR) was performed to validate the results of sequencing analysis on the DE IncRNAs and DE mRNAs in samples of Control, ParoAF, and PersAF. RNA samples were prepared as previously mentioned. The synthesis of the first-strand cDNA was compounded using PrimeScript™ RT reagent kit (Takara, Otsu, Shiga, Japan), followed by amplification using AceQ qPCR SYBR Green Master Mix (Vazyme Biotech Co., Nanjing, China) on ABI 7500 system RT-PCR instrument (Applied Biosystems, FosterCity, CA, USA). Expression levels of collagen type I alpha 1 (COL1A1), FK506 binding protein 5 (FKBP5), collagen type I alpha 2 (COL1A2), and RP11-442H21.2 were validated by qRT-PCR in the samples and ParoAF patients and 4 genes COL1A1, COL1A2, chemokine (C-C motif) ligand 5 (CCL5), and CTA-134P22.2 were detected in control samples and PersAF patients. The mRNAs and IncRNAs expression levels were calculated by the $2^{-\Delta\Delta Ct}$ method.

Forty LAA samples isolated from the donors (n = 20, control) and patients with PersAF (n = 20) were used for validation of circRNA expression. The primary clinical characteristics including, age, body mass index (BMI), left ventricular ejection fraction (LVEF), left atrium (LA), left ventricular diastolic dimension (LVDD), left ventricular systolic diameter (LVSD), and ventricular rate was collected from patients. RNA samples were extracted using previously reported methods. The expression levels of circRNAs including, chr10: 69881195|69882097 and chr10: 69902697|69948883, were detected by qRT-PCR in heart samples from healthy donors and PersAF subjects. Primers were designed and presented in Table 1. Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) was used as the housekeeping gene. HiScript II one Step qRT-PCR Probe Kit (Vazyme Biotech Co., Nanjing, China) was used for the measurement. qRT-PCR was performed with ABI 7500 RT-PCR system (Thermo Fisher Scientific). The specific generation of the expressed PCR product was validated by melting curve analysis. The expression levels of circRNAs were calculated using the $2^{-\Delta\Delta Ct}$ method.

### Statistical analysis

All statistical analyses were performed using IBM SPSS Statistics v22.0 (IBM Corp., Armonk, NY, USA) or GraphPad Prism version 8 (GraphPad Software, San Diego, CA). Comparison among three groups was performed by applying the non-parametric Kruskal–Wallis H test, followed by Mann–Whitney U-test. Data were presented as median (interquartile range). Comparison between two groups was performed using the non-parametric Mann–Whitney U-test, followed by Dunn’s test. Normal data were presented as median (interquartile range). Logistics regression analysis was performed to determine the risk factors for AF after adjusting for age. P-value <0.05 was considered as statistically significant.

### Results

#### Clinical characteristics

There were no significant differences in age, BMI, LVDD, LVSD, systolic blood pressure, diastolic blood pressure, CHA2DS2-VASc score, HAS-BLED score, and EHRA across control donors, ParoAF, and PersAF patients (p>0.05, Table 2).

#### Differentially expressed mRNAs, IncRNAs, and circRNAs

A total of 285 (116 up-regulated and 169 down-regulated) and 275 (110 up-regulated and 165 down-regulated) DE mRNAs were detected in ParoAF and PersAF, respectively, when compared to control (Fig. 1a, 1b). A total of 63 common DE mRNAs were expressed in ParoAF_Control and PersAF_Control (Fig. 1c). The DE mRNAs of ParoAF_Control and PersAF_Control are provided in Supplementary Files 1, 2, respectively.

A total of 575 (276 up-regulated and 299 down-regulated) and 583 (330 up-regulated and 253 down-regulated) DE IncRNAs were detected in ParoAF and PersAF, respectively, when compared to the control (Fig. 1d, 1e). A total of 116 common DE IncRNAs were expressed in ParoAF_Control and PersAF_Control (Fig. 1f). The DE mRNAs of ParoAF_Control and PersAF_Control are provided in Supplementary Files 3, 4, respectively.
A total of 83 (48 up-regulated, 35 down-regulated) and 99 (58 up-regulated, 41 down-regulated) circRNAs were DE in ParoAF and PersAF, respectively, when compared with control samples (ParoAF_Control and PersAF_Control), including 14 common circRNAs (Fig. 1g-1i). The total DE circRNAs of ParoAF_Control and PersAF_Control are listed in Supplementary Files 5 and 6.

Table 2. Clinical characteristics of subjects used for the sequencing

| Items                        | Control (n=3) | ParoAF (n=3) | PersAF (n=3) | P-value |
|------------------------------|---------------|--------------|--------------|---------|
| Age (years)                  |               |              |              |         |
|                             | 39.00 (38.00–42.00) | 54.00 (47.00–60.00) | 57.00 (51.00–64.00) | 0.061a  |
| Gender (F/M)                 | 1/2           | 1/2          | 1/2          |         |
| BMI (kg/m²)                  |               |              |              |         |
|                             | 21.70 (18.80–24.40) | 23.07 (22.10–24.00) | 25.17 (24.50–26.00) | 0.141a  |
| LA (mm)                      |               |              |              |         |
|                             | 35.00 (34.00–38.00) | 37.00 (30.00–42.00) | 42.00 (40.00–51.00) | 0.641a  |
| LVDD (mm)                    |               |              |              |         |
|                             | 46.00 (39.00–48.00) | 46.00 (45.00–49.00) | 44.00 (44.00–48.00) | 0.219a  |
| LVSD (mm)                    |               |              |              |         |
|                             | 28.00 (24.00–30.00) | 30.00 (30.00–36.00) | 30.00 (28.00–31.00) | 0.079a  |
| Ventricular rate             |               |              |              |         |
|                             | 54.00 (50.00–64.00) | 85.00 (81.00–108.00) | 76.00 (65.00–80.00) | 0.275a  |
| Systolic blood pressure      |               |              |              |         |
|                             | 127.00 (118.00–130.00) | 112.00 (101.00–129.00) | 119.00 (111.00–134.00) | 0.436a  |
| Diastolic blood pressure     |               |              |              |         |
|                             | 78.00 (70.00–87.00) | 84.00 (72.00–92.00) | 84.00 (70.00–95.00) | 0.297a  |
| CHA²DS²-VASc score           | -             | 3.00 (2.00–5.00) | 2.00 (1.00–3.00) | 0.478b  |
| HASBLED score                | -             | 4.00 (3.00–5.00) | 2.00 (1.00–5.00) | 0.988b  |
| EHRA                         | -             | I(1)/II(2)    | I(1)/II(2)    |         |

Values are expressed as median (interquartile range). P-value <0.05 was considered as statistically significant. (a) Differences were analyzed by non-parametric Kruskal–Wallis H test, followed by the Mann–Whitney U-test. (b) Differences were analyzed by non-parametric Mann–Whitney U-test, followed by Dunn’s test.

BMI - body mass index; LA - left atrium; LVDD - left ventricular diastolic dimension; LVSD - left ventricular systolic diameter; CHA²DS²-VASc contains congestive heart failure/LV dysfunction, hypertension, age ≥75, diabetes mellitus, stroke/TIA/TE, Vascular disease, age ≥65–74, and sex category. HAS-BLED contains parameters of hypertension, abnormal renal function, abnormal liver function, previous stroke, bleeding history or predisposition, history of labile international normalized ratio, age ≥65, concomitant aspirin or nonsteroidal anti-inflammatory drug therapy, and substantial alcohol intake. EHRA - European Heart Rhythm Association; PersAF - persistent atrial fibrillation; ParoAF - paroxysmal atrial fibrillation

Table 3. Clinical characteristics of Control donors and PersAF patients

| Items                        | Control (n=20) | PersAF (n=20) | P-value |
|------------------------------|---------------|--------------|---------|
| Age (years)                  |               |              |         |
|                             | 31.00 (25.00–40.75) | 65.00 (55.25–69.50) | <1.00E-04  |
| BMI (kg/m²)                  |               |              |         |
|                             | 23.50 (20.85–25.32) | 26.10 (24.12–27.87) | 0.028   |
| LA (mm)                      |               |              |         |
|                             | 35.00 (33.00–37.75) | 42.50 (39.00–46.00) | <1.00E-04  |
| LVDD (mm)                    |               |              |         |
|                             | 47.00 (45.25–48.00) | 46.50 (45.00–50.00) | 0.565   |
| LVSD (mm)                    |               |              |         |
|                             | 30.00 (28.25–31.75) | 30.00 (29.00–32.00) | 0.841   |
| Ventricular rate             |               |              |         |
|                             | 69.00 (62.00–70.75) | 84.50 (72.50–89.75) | 0.024   |
| Systolic blood pressure      |               |              |         |
|                             | 115.50 (108.00–125.00) | 122.00 (106.25–128.25) | 0.665   |
| Diastolic blood pressure     |               |              |         |
|                             | 74.50 (72.00–78.00) | 78.50 (74.25–83.50) | 0.761   |
| CHA²DS²-VASc score           | -             | 2.50 (2.00–4.00) | -       |
| HASBLED score                | -             | 3.00 (1.25–3.00) | -       |
| EHRA                         | -             | I(3)/II(16)/III(1) | -       |
| chr10:69881195|69882097      | 0.30 (0.19–0.49) | 0.025 (0.00–0.13) | 0.004   |
| chr10:69902697|69948883      | 0.02 (0.00–0.09) | 0.47 (0.23–0.77) | <1.00E-04  |

Values are expressed as median (interquartile range). Differences were analyzed by non-parametric Mann–Whitney U-test, followed by Dunn’s test. P-value <0.05 was considered as statistically significant. BMI - body mass index; LA - left atrium; LVDD - left ventricular diastolic dimension; LVSD - left ventricular systolic diameter; CHA²DS²-VASc contains congestive heart failure/LV dysfunction, hypertension, age ≥75, diabetes mellitus, stroke/TIA/TE, Vascular disease, age ≥65–74, and sex category. HAS-BLED contains parameters of hypertension, abnormal renal function, abnormal liver function, previous stroke, bleeding history or predisposition, history of labile international normalized ratio, age ≥65, concomitant aspirin or nonsteroidal anti-inflammatory drug therapy, and substantial alcohol intake. EHRA - European Heart Rhythm Association; PersAF - persistent atrial fibrillation; ParoAF - paroxysmal atrial fibrillation
Fig. 2). HECT and RLD domain containing E3 ubiquitin-protein ligase 4 (HERC4), muscular LMNA-interacting protein (MLIP), and titin (TTN) had three circRNA isoforms. It was worth noting that chloride channel nucleotide-sensitive 1A (CLNS1A) and myopalladin (MYPN) produced circRNA isoforms with opposite expression patterns in PersAF patients when compared to control (Fig. 2). CLNS1A was the host gene of hsa_circ_0008342 and hsa_circ_0000343. MYPN was the host gene of...
chr10:69881195|69882097 and chr10:69902697|69948883. Among all the genes that had the same expression patterns, laminin, alpha 2 (LAMA2), dystrophin (DMD), anoctamin 5 (ANO5), and HERC4 varied greatly on the level of expression (Fig. 2).

Since the association of MYPN with muscle diseases including hypertrophic cardiomyopathy, the two circRNA isoforms of it (chr10:69881195|69882097 and chr10:69902697|69948883) had opposite expression profiles in PersAF compared with control. In the validation cohort, there was significant difference in age (p<0.0001), BMI (p=0.028), LA (p<0.0001), ventricular rate (p=0.024), and expression levels of chr10:69881195|69882097 (p=0.004) and chr10:69902697|69948883 (p=0.001, Table 3) between control and PersAF samples. The expression level of chr10:69881195|69882097 and chr10:69902697|69948883 was significantly down-regulated and up-regulated, respectively, in patients with PersAF compared with donors (Control). Logistics regression analysis showed that expression of chr10:69881195|69882097 was not associated with PersAF after adjusting for patients’ age, while chr10:69902697|69948883 was a protective factor against PersAF (95% CI: 0.003–0.634, p=0.022, Table 4).

GO and KEGG pathway analysis on DE mRNAs
With the criterion of corrected p-value <0.05, there were only two GO terms selected in ParoAF_Control and they were “extracellular matrix” and “platelet-derived growth factor binding.” COL1A2, COL6A1, COL3A1, and COL2A1 participated in the two enriched GO terms. COL1A2, COL6A1, and COL3A1 were up-regulated in ParoAF when compared to control. COL2A1 was down-regulated in ParoAF when compared to control. With the same criterion, “collagen type I” and “platelet-derived growth factor binding” were enriched in PersAF_Control, while COL1A2 and COL1A1 were enriched in both GO terms. Both COL1A2 and COL1A1 were up-regulated in PersAF when compared to control.

KEGG pathway enrichment analysis revealed that the top enriched pathways were “ECM-receptor interaction,” “protein digestion and absorption,” “PI3K-Akt signaling pathway Focal adhesion Amoebiasis,” “TGF-beta signaling pathway” and “Amoebiasis” in ParoAF patients when compared to control donors (Fig. 3a). Up-regulated DE mRNAs, such as COL1A1, COL1A2, and laminin, beta 2 (LAMB2), participated in most of the top ten pathways (Fig. 3b). Down-regulated DE mRNA COL2A1 was involved in most of the top ten pathways. DE mRNAs, decorin (DCN), SMAD specific E3 ubiquitin-protein ligase 2 (SMURF2), and interferon gamma (IFNG), participated in TGF-β signaling pathway.

The top enriched pathways were “Insulin resistance,” “Protein digestion and absorption,” “Type I diabetes mellitus,” “herpes simplex infection,” and “Antigen processing and presentation Dorso-ventral axis formation” in PersAF patients when compared to control donors, with IFNG (up-regulated), major
histocompatibility complex class IC (HLA-C, up-regulated), interferon regulatory factor 9 (IRF9, down-regulated) being the mostly involved DE mRNAs (Fig. 3c, 3d).

**GO and KEGG functions on DE IncRNAs through cis**

We searched mRNAs nearest to DE IncRNAs both upstream and downstream and analyzed their function through GO and KEGG. We listed the top ten GO terms both upstream and downstream in Table 5. The most enriched GO terms of upstream were “phosphoric diester hydrolase activity,” “regulation of nucleotide metabolic process,” and “cytoskeleton.” They were “sequence-specific DNA binding RNA polymerase II transcription factor activity,” “response to dietary excess,” and “positive regulation of gene expression” of downstream.

Otherwise, 23 and 47 KEGG pathways were also enriched in upstream and downstream mRNAs with the threshold of \( p \)-value < 0.05, respectively. The upstream mRNAs were mainly enriched in “Ras signaling pathway,” “MAPK signaling pathway,” and “PPAR signaling pathway” (Fig. 4a). Genes Mitogen-activated protein kinase 10 (MAPK10) and phospholipase A2 group IVA (PLA2G4A) were related to more pathways than others in the upstream mRNAs (Fig. 4b). While the downstream mRNAs were involved in “Arrhythmogenic right ventricular cardiomyopathy (ARVC),” “Signaling pathways regulating pluripotency of stem cells,” as well as “Glycine, serine, and threonine metabolism” (Fig. 4c). For downstream mRNAs, calcium channel voltage-dependent L-type alpha 1C subunit (CACNA1C), ATPase Ca\(^{++}\) transporting cardiac muscle slow twitch 2 (ATP2A2), catenin (cadherin-associated protein) beta 1 88kDa (CTNNB1), phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha (PIK3CA), and protein kinase cAMP-dependent catalytic gamma (PRKACG) were involved in not less than four top ten pathways (Fig. 4d).

**GO and KEGG pathway analysis on host genes of DE circRNAs**

GO analysis indicated that the host genes of DE circRNAs in ParoAF_Control were mainly enriched in response to muscle stretch, I band, contractile fiber part, myofibril, and contractile fiber (\( p \)-value <0.05). In addition, the host genes of DE circRNAs in PersAF_Control were mainly enriched in Z disc, I band, actinin
binding, and cardiac muscle cell differentiation, a muscle system process (p-value <0.05). Through GO analysis, we noted that the host genes were mainly related to fiber and muscle.

Pathways, such as dilated cardiomyopathy, hypertrophic cardiomyopathy, and arrhythmogenic right ventricular cardiomyopathy, were highly enriched in both ParoAF_Control and PersAF_Control, including host genes solute carrier family 8 (sodium/calcium exchanger) member 1 (SLC8A1), ryanodine receptor 2 (cardiac) (RYR2), integrin alpha 7 (ITGA7), among others. The calcium signaling pathway was only enriched in ParoAF . The top ten KEGG pathways and number of their input mRNAs of ParoAF_Control and PersAF_Control are shown in Figure 5a, 5c.

The network consisting of pathways and host genes were constructed (Fig. 5b, 5d). We found that TTN, epidermal growth factor (EGF), ITGA7, RYR2, and SLC8A1 were hub genes in the network associated with ParoAF and PersAF. Moreover, ITGA7, RYR2, and SLC8A1 were involved in more than five pathways in both ParoAF and PersAF. Among the host genes involved in more than four pathways, host genes adenylate cyclase 9 (ADCY9), phosphatidylinositol-4,5-bisphosphate 3-kinase, and catalytic subunits alpha (PIK3CA) were only involved in ParoAF, while CACNA1C was only related to PersAF.

### Interaction and co-expression network analysis

We studied the interactions between DE mRNAs of ParoAF_Control, which are shown in Figure 6a, 6b. The up-regulated genes include DCN, COL3A1, COL1A1, secreted protein acidic cysteine-rich (SPARC), COL6A1, COL1A2, dynein cytoplasmic 1 heavy chain 1 (DYN1H1), and cyclin B2 (CCNB2). The down-regulated genes, including breast cancer 1 early onset (BRCA1) and COL2A1, are the key genes that interacted with many other DE mRNAs in ParoAF_Control network (Fig. 6a). In PersAF patients, up-regulated genes, including protein tyrosine phosphatase, non-receptor type 11 (PTPN11), major histocompatibility complex class II DQ alpha 1 (HLA-DQA1), cell division cycle 25A (CDC25A), beta-2-microglobulin (B2M), COL6A1, COL3A1, SPARC, COL1A1, and COL1A2, and down-regulated DE mRNAs, including cyclin-dependent kinase 2 (CDK2), kelch repeat and BTB (POZ) domain containing 13 (KBTBD13), histone deacetylase 1 (HDAC1), split hand/foot malformation (ectrodactyly) type 1 (SHFM1), F-box and leucine-rich repeat protein 19 (FBXL19), and ring finger protein 19A RBR E3 ubiquitin-protein ligase (RNF19A), are essential genes that interacted with other DE mRNAs (Fig. 6b).

Furthermore, we assessed the possible target genes of the DE IncRNAs (Trans prediction). A total of 709 and 1275 mRNAs were detected in ParoAF_Control and PersAF_Control, respec-
tively, with the threshold of $r > 0.99$. We selected DE mRNAs, which were also the target genes of DE IncRNAs, as shown in Figure 6c, 6d. There were 12 and 31 DE IncRNA and DE mRNA were co-expressed in ParoAF and PersAF patients, respectively, when compared to control.

The selected mRNAs were used for mRNA-IncRNA network analysis. The mRNA-IncRNA co-expression network of ParoAF_Control revealed that anoctamin 3 (ANO3) had the co-down-expression treeed with XLOC_002352, XLOC_110321, XLOC_098657, and XLOC_110333. Huntingtin interacting protein 1 related (HIP1R), fibrinogen C domain containing 1 (FIBCD1), tensin 4 (TNS4), and transcription factor Dp-2 (TFDP2) have a complex co-down-expression relationship with DE IncRNAs as XLOC_027189, XLOC_082023, XLOC_095062, and XLOC_077085. Translocated promoter region, nuclear basket protein, and contactin associated protein-like 2 (CNTNAP2) have co-up-expression with XLOC_127021 (Fig. 6e). The mRNA-IncRNA co-expression network of PersAF_Control also showed that ANO3 co-expressed with XLOC_002352, XLOC_110321, XLOC_098657, and XLOC_110333. XLOC_130822 targeted both coiled-coil domain containing 63 (CCDC63) and solute carrier family 6 (neutral amino acid transporter) member 19 (SLC6A19, Fig. 6f).

CircRNA-miRNA interaction network

We constructed the ceRNA network consisting of 14 common circRNAs DE between ParoAF_Control and PersAF_Control. A total of 3019 circRNA-miRNA interactions were predicted. Through the circRNA-miRNA interaction network, we found that hsa_circ_0124903, chr1:237890387|237951435, hsa_circ_0002142, and hsa_circ_0141424 acted as sponges of more than 300 miRNAs. These circRNAs have the host genes of mannosidase beta A (MANBA), lysosomal RYR2, DENN/MADD domain containing 2A (DENND2A), and zinc finger protein 709 (ZNF709), respectively. Conversely, there were 12 miRNAs (hsa_miR-6735-5p, hsa_miR-4739, hsa_miR-4763-3p, hsa_miR-3154, hsa_miR-3916, hsa_miR-4689, hsa_miR-6511a-5p, hsa_miR-665, hsa_miR-671-5p, hsa_miR-6797-5p, hsa_miR-6847-5p, hsa_miR-8089) that were sponged by not less than seven circRNAs (Fig. 7). We made
the network with predicted miRNAs to have a less binding free energy (< −50 kcal/mol) and found that hsa_miR-671-5p, hsa_miR-328-5p, and hsa_miR-6782-5p sponged more circRNAs.

Validation of differentially expressed lncRNAs and mRNAs with qRT-PCR

A total of four mRNAs and lncRNAs (COL1A1, COL1A2, FKBP5, and RP11-442H21.2) were validated by qRT-PCR in ParoAF and control samples (Fig. 8). On the other hand, a total of four mRNAs and lncRNAs (COL1A1, COL1A2, CCL5, and CTA134P22.2) were validated by qRT-PCR in PersAF and control samples. The expression profiles of mRNAs and lncRNAs were consistent using either RNA-Seq or qRT-PCR, except COL1A2 in PersAF_Control, although deviation of exact fold change existed between the two techniques.

**Discussion**

AF is the most prevalent heart disease worldwide, causing tremendous physical and psychological pain in individuals and a heavy burden to countries. In recent years, several researches have been channeled toward the mechanisms of AF. RNAs, such as mRNA, IncRNAs, and circRNAs, all play their various roles in regulating AF. In the present study, DE mRNAs, DE IncRNAs, and DE circRNAs in PersAF and ParoAF samples were clearly distinguished from control samples.

We focused on the relationship between circRNA isoforms and their host gene to examine whether circRNA isoforms originating from the same genes were dysregulated in AF. The circRNA isoforms of CLNS1A and MYPN were found to have opposite expression patterns in PersAF when compared with control, indicating that these expression-switched circRNA isoforms may have opposite functions in PersAF patients. We identified the two circRNA isoforms of MYPN (chr10:69881195|69882097 and chr10:69902697|69948883), which were significantly down-regulated and up-regulated, respectively, in PersAF patients when compared with control. In addition, logistics regression analysis showed that expression of chr10:69902697|69948883 was a protective factor for PersAF. Hu et al. (21) reported the significant up-regulation of circRNA02637 and down-regulation of circRNA11156 in patients with PersAF when compared with control and MYPN and TTN was the host gene of circRNA02637 and circRNA11156, respectively. Hence, in our study, we found an obviously up-regulated circRNAs chr10:69902697|69948883...
Figure 6. Interaction and co-expression network analysis of ParoAF and PersAF as compared to control. (a, b) represent the protein interaction network of ParoAF_Control and PersAF_Control, respectively. The red color represents the up-regulated DE mRNAs, while the blue color represents the down-regulated DE mRNAs. The Venn map in (c, d) showed the number of target genes of DE lncRNA and DE mRNAs of ParoAF_Control and PersAF_Control, respectively. (e, f) the co-expression network of DE lncRNA and DE mRNAs of ParoAF_Control and PersAF_Control, respectively. The “diamond nodes” represent DE lncRNAs, while the “circles nodes” represent mRNAs. The rose-red and green colors represent up-regulated and down-regulated DE lncRNAs, respectively. The red and blue color represent the up-regulated and down-regulated DE mRNAs, respectively. The size of the node in A, B, E, and F represent the DE IncRNAs or DE mRNAs they connect. DE - differentially expressed; lncRNA - long non-coding RNA; ParoAF - paroxysmal atrial fibrillation; PersAF - persistent atrial fibrillation.
and down-regulated circRNAs chr10:69881195|69882097 in patients with PersAF and ParoAF, respectively. Both of them were isoforms of MYPN, which play crucial roles in differentiation and development of muscle (22, 23). These results showed that their dysregulation might be of great value in the pathogenesis of AF.

In the present study, COL1A2 and COL1A1 were involved in platelet-derived growth factor binding in both ParoAF and PersAF samples. Moreover, COL1A1, COL1A2, and COL2A1 also participated in most enriched KEGG pathways in ParoAF patients. In a study by Dawson et al. (6), it was revealed that COL1A1 and COL1A2 were target genes of miR-29, which might play a vital role in atrial fibrotic remodeling and considered as biomarkers or therapeutic targets. Gambini et al. (24) demonstrated that TGF-β1 could induce the up-regulation of COL1A1 and COL1A2 in human cardiac mesenchymal progenitor cells of AF. In one RNA-Seq analysis of ParoAF, the authors also found dysregulated COL1A1 and COL1A2 as in our study, which was not only validated by our present study, but also demonstrated that these two genes participated in electrical and structural remodeling process of extracellular matrix/cardiac fibrosis (10). We then confirmed the expression of COL1A1 and COL1A2 through qRT-PCR. The expression level of COL1A1 through qRT-PCR was consistent with that of RNA-Seq and was up-regulated in both ParoAF and PersAF samples. Moreover, in the present study, COL1A1 and COL1A2 act as essential genes that correlate with more DE mRNAs in the protein-protein network. These researches might suggest the crucial roles of these two genes on ParoAF and PersAF.

We focused on KEGG analysis of DE mRNAs, nearby mRNAs of DE IncRNAs, and host genes of DE circRNAs. Also, the pathways of TGF-β signaling, calcium signaling, MAPK signaling, and cAMP signaling were significantly enriched. The TGF-β signaling pathway was significantly enriched in ParoAF_Control, with the involvement of DCN. The calcium signaling pathway was only enriched in PersAF samples, with the involvement of PLN enriched in it. For the DE IncRNA upstream and down-
stream mRNAs, KEGG functional analysis revealed that FGF14 and CACNA1C were enriched in the MAPK signaling pathway in the upstream mRNAs and CACNA1C and HCN4 were enriched in the cAMP signaling pathway in the downstream mRNAs.

In a previous study of TGF-β signal pathway of AF, it was revealed that the TGF-β signal pathway might be involved in the course of atrial structural remodeling on AF and is related to the occurrence and maintenance of AF (25). In the study by Shen et al. (26), it was revealed that the activation of Gal-3 in AF could subsequently activate the TGF-β1/α-SMA/Col I pathway in cardiac fibroblasts, which may strengthen atrial fibrosis. Suppressing the TGF-β overexpression can prevent atrial remodeling (27-29). TGF-β is also a promising therapeutic target for decreasing cardiac fibrosis (30). In the present study, the TGF-β signaling pathway was differentially significant in ParoAF_Control and the genes SMURF2 and DCN were involved in it. SMURF2 induces proteasomal degradation of Smad7, which promotes the TGF-β signal pathway (29, 31), and was up-regulated in ParoAF_Control in our study. DCN is a proteoglycan that binds to collagen fibrils in the ECM (extracellular matrix). DCN interacts with many growth factors, inhibiting the activity of TGF-β (32), which is up-regulated in both ParoAF_Control and PersAF_Control in our study. Moreover, DCN was connected mostly in protein-protein networks with other DE mRNAs in the present study. Combined with these researches, the TGF-β signal pathway and its involved gene DCN might play an essential role in the occurrence and maintenance of AF. Also, suppressing the overexpression of TGF-β may prevent the occurrence of AF.

The calcium signaling pathway was DE in PersAF_Control, including the gene PLN involved in it. Moreover, the host genes of DE circRNAs also participated in the calcium signaling pathway. The other research showed that calcium signaling pathway plays a vital role in the electrical remodeling of AF and might promote the recurrence of AF (12). Tan et al. (33) demonstrated that IncRNA HOTAIR is involved in the modulation of calcium homeostasis in human cardiomyocytes. They further confirmed that HOTAIR inhibited intracellular Ca^2+ contents via regulation of L-type calcium channels. In a study regarding ParoAF and PersAF (34), it was revealed that PersAF mice had the phenomenon of enhanced diastolic Ca^{−ΔΔCt} release, marked conduction abnormalities, and atrial enlargement. PLN absence can increase Ca^{−ΔΔCt} transient amplitude and cause faster Ca^{−ΔΔCt} decay rate (35). Combining these findings with those of our study, we suggest that calcium signaling pathway may play an essential role in the processing of ParoAF to PersAF.

In the study of Zhang et al. (36), it was revealed that MAPKs/TGF-β1/TRAF6 signaling pathways participates in atrial fibrosis in patients with rheumatic heart disease, resulting to the occurrence of AF after cardiac surgery. MAPK is an important signal pathway that prevents atrial parasympathetic remodeling and

**Figure 8.** qRT-PCR validation of DE mRNAs and DE lncRNAs. CCL5 - chemokine (C-C motif) ligand 5; COL1A1 - collagen type I alpha 1; COL1A2 - collagen type I alpha 2; DE - differentially expressed; lncRNAs - long non-coding RNAs; ParoAF - paroxysmal atrial fibrillation; PersAF - persistent atrial fibrillation; qRT-PCR - quantitative real-time PCR.
occurrence of AF via inhibiting MAPK pathway (37). The induction of AF and structural remodeling was related to MAPK expression and reduction of collagenase activity (12). CACNA1C was enriched in MAPK signal pathway, which is the direct target gene of miR-29a-3p. Combined with these results, we suggest that miR-29a-3p may be a potential therapeutic target in AF (38). Combining these findings with those of our study, MAPK signal pathway can be regarded as an important pathway that participates in AF occurrence by preventing atrial parasympathetic remodeling. The co-expression network revealed the correlation between lncRNAs and mRNAs, including transforming growth factor, calmodulin, and zinc finger protein. The co-expression results could broaden the understanding of the role of lncRNAs and mRNAs in AF.

Through KEGG pathway analysis, we found that DE circRNAs in PersAF and ParoAF were significantly associated with dilated cardiomyopathy, hypertrophic cardiomyopathy, and arrhythmogenic right ventricular cardiomyopathy, which suggest the crucial roles of these circRNAs in AF pathogenesis and development.

The network between pathways and host genes of DE circRNAs revealed that ITGA7, RYR2, EGF, ADCY9, CACNA1C, PIN3CA, and SLC8A1 play an essential role in both ParoAF and PersAF. EGF and that RYR2 host genes participate in most pathways in the two groups. In the study by Tang et al. (39), it was revealed that RYR2 was down-regulated in AF, which is consistent with our study. In the study by Donald et al. (40), RYR2 was identified as a potential therapeutic target in heart failure and AF. In another study on circRNAs of AF, RYR2 acted as a host gene of some important circRNAs that were DE in AF when compared with control (41). Host genes, such as ADCY9 and PIK3CA, only participate in ParoAF, while CACNA1C only participates in PersAF. These genes might play essential roles in the pathogenesis and development. Combined with the related studies, we boldly suggest that RYR2, CACNA1C, and other genes could serve as essential biomarkers for AF.

An interesting finding was the type of sample used for NGS. In the present study, GO enrichment analysis of host genes of common DE circRNAs between PersAF and ParoAF revealed that the main functions were correlated with muscle stretch and contractile fiber, as reported in Hu et al. (21). However, in a study, using lymphocytes from patients with AF (19), the host genes of circRNAs revealed that PIN3CA, only participate in PersAF, while CACNA1C was the vital circRNA that participates in AF.

Through this study, we found some pathways and genes, such as those related to TGF-β signal pathway, calcium signaling pathway, COL1A1, COL1A2, among others, that might play essential roles in AF. Moreover, we also identified some circRNAs that could play an essential role in AF. CircRNAs, including chr1:237890387|237951435 and chr10:69902697|69948883, the host gene of RYR2 and MYPN, respectively, might play essential roles in AF pathogenesis and development in ParoAF and PersAF via KEGG pathways associated with cardiomyopathy diseases. The expression of chr10:69902697|69948883 was identified to be a protective factor against PersAF. The host gene CACNA1C was only DE in PersAF and involved in most of the KEGG pathways associated with cardiomyopathy diseases, which might be crucial for the development from ParoAF to PersAF. Moreover, chr12: 2666117|2721179, with the host gene of CACNA1C, was the sponge of miRNA-384/miRNA-328/miR-29a-3p, which might be a vital circRNA that participates in AF.

Data availability: The raw data were deposited on the NCBI Sequence Read Archive (SRA), with the SRA accession number of PRJNA531935.

Conflict of interest: None declared.

Peer-review: Externally peer-reviewed.

Author contributions: Concept – H.S., J.Z., Y.S.; Design – H.S., Y.S.; Supervision – H.S., Y.S.; Fundings – None; Materials – H.S., J.Z.; Data collection &/or processing – J.Z.; Analysis &/or interpretation – H.S., J.Z., Y.S.; Literature search – H.S., J.Z., Y.S.; Writing – H.S.; Critical review – Y.S.

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