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The Function and Therapeutic Potential of Long Non-coding RNAs in Cardiovascular Development and Disease

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The popularization of genome-wide analyses and RNA sequencing led to the discovery that a large part of the human genome, while effectively transcribed, does not encode proteins. Long non-coding RNAs have emerged as critical regulators of gene expression in both normal and disease states. Studies of long non-coding RNAs expressed in the heart, in combination with gene association studies, revealed that these molecules are regulated during cardiovascular development and disease. Some long non-coding RNAs have been functionally implicated in cardiac pathophysiology and constitute potential therapeutic targets. Here, we review the current knowledge of the function of long non-coding RNAs in the cardiovascular system, with an emphasis on cardiovascular development and biology, focusing on hypertension, coronary artery disease, myocardial infarction, ischemia, and heart failure. We discuss potential therapeutic implications and the challenges of long non-coding RNA research, with directions for future research and translational focus.

New sequencing technologies, combined with bioinformatics and computational tools, have allowed the scientific community to appreciate the great complexity of the transcriptome. In particular, the discovery of various types of non-protein coding RNAs (ncRNAs) and their different functions in regulating developmental and disease processes is expanding our knowledge of molecular biology and could significantly advance therapeutic options for many patients, including those suffering from cardiovascular disease. Thousands of ncRNAs have been described and classified into two large groups: small ncRNAs, which are up to 200 nucleotides long, and long non-coding RNAs (IncRNAs), which are longer than 200 nucleotides.

IncRNAs are a heterogeneous group of transcripts exerting major regulatory roles in gene expression, and their importance in cardiovascular disease has been reinforced. The dynamic expression and specific profiles of IncRNAs in different pathophysiological states suggest their functional relevance and potential to be used as non-invasive markers of disease and therapeutic targets. However, establishing the biological actions of each IncRNA is proving more complex than investigating microRNAs (miRNAs, the most popular class of small ncRNAs within the biomedical community). This is due to IncRNAs’ multiple modalities of action and their low conservation among vertebrates. Therefore, a large gap remains between the number of IncRNAs identified, and then listed in databases, and their functional characterization and implications in pathophysiological situations. A list of databases and their major characteristics, such as number of IncRNAs, species, and association with function and other genes, is given in Table 1.

So far, it has been demonstrated that IncRNAs can regulate gene expression through functional mechanisms including epigenetic, transcriptional, and post-transcriptional, either activating or suppressing gene expression. IncRNAs can also mediate signaling, such as phosphorylation, and trafficking of proteins. One way to classify IncRNAs is according to their mechanism of action: signal, decoy, guide, scaffold, enhancer, or sponge IncRNAs (particularly circular IncRNAs [circRNAs]) (Figure 1). In this review, we do not address in detail the IncRNAs mechanisms of action but instead refer to reviews on the subject.

A growing number of IncRNAs are implicated in cardiovascular development and disease, although it is not clearly understood how they participate in pathological processes. Their potential as therapeutic targets has often been raised, and there are a few examples of in vivo modulation of IncRNAs. However, modulating IncRNAs has been a challenging task to date. Here, we summarize the current understanding of IncRNA function in cardiovascular pathophysiology and discuss its potential for therapy.

Function of IncRNAs in the Cardiovascular System

Cardiac Development and Biology

Transcriptomics profiling and loss-of-function approaches in progenitor and embryonic stem cells (ESCs) have demonstrated the...
importance of lncRNAs for cardiac development and cell differentiation. More than 1,000 lncRNAs were reported as being dynamically regulated during differentiation, and further transcriptome analyses of embryonic and adult-stage murine hearts identified several lncRNAs specific to tissue and developmental stage. Among biologically validated lncRNAs, several have been associated with cardiac development (Table 2). For example, Braveheart (Bvht) has a critical role in cardiac lineage commitment in mouse. It is abundantly expressed in embryonic stem cells and regulates the transition from nascent mesoderm to cardiac progenitor. Bvht, by modulating the core cardiovascular gene network and mediating the epigenetic regulation of cardiac fate, is necessary to maintain cardiac commitment. Conversely, the lateral mesoderm-specific lncRNA Fendrr (fetal-lethal non-coding developmental regulatory RNA) controls mesodermal differentiation, as well as heart and body wall development, by binding to the histone-remodeling polycomb repressive complex PRC2 and TrxG/MLL to modulate chromatin status.

Numerous enhancer-associated lncRNAs have been implicated in cardiogenic differentiation, among which the enhancer lncRNA Novlnc6 modulates expression of MKX2.5, a transcription factor critical for cardiac differentiation and maturation. CARMEN (cardiac mesoderm enhancer-associated non-coding RNA) is also responsible for cardiogenic specification and differentiation in precursor cells, possibly by regulating PRC2. Furthermore, several lncRNAs regulate specific mRNA abundance during heart development, although as yet there is no clear understanding of their role during cardiogenic differentiation. For example, n411949 regulates Mccc1 mRNA, which metabolizes leucine, and n413445 modulates ReIb, which is involved in the nuclear factor κB (NF-κB) pathway. Overall, fetal gene program reactivation constitutes a hallmark in multiple cardiovascular diseases. Although a moderate number of dynamically regulated lncRNAs in embryonic cells are equally regulated in the hypertrophic heart, some lncRNAs associated with cardiac pathologies may also be implicated in cardiac development. As for cell proliferation, a study identified eight lncRNAs putatively implicated in the proliferative capacity of cardiac cells in fetal heart that require further investigation.

Cardiomyocyte repolarization during the final stage of the action potential needs potassium fluxes mediated by the K_{v}7.1 channels. In late embryogenesis, lncRNA Kcnq1ot1 (potassium voltage-gated channel, KQT-like subfamily, member 1 opposite strand/antisense transcript 1) regulates the expression of the transcript Kcnq1, which encodes the potassium channel K_{v}7.1. Such regulation fulfills the requirement for increased cardiac contractile activity in this late developmental stage. Dysregulation of KCNQ1OT1 expression has

| Database     | What                                                                 | Species                  | No. of lncRNAs | Last Update | Association with Function | Association with Protein-Coding RNAs | Association with miRNAs | Reference |
|--------------|----------------------------------------------------------------------|--------------------------|----------------|-------------|---------------------------|--------------------------------------|------------------------|-----------|
| ANGIOGENES   | in silico screening of protein-coding genes and lncRNAs in ECs       | human, mouse, zebrafish  | 24,382 (15,149 in human) | 2016        | X                         |                                      |                        | 164       |
| ChIPBase     | transcriptional regulation of lncRNA from ChIP-seq data              | 10                       | 10,200 ChIP-seq datasets | 2016        | X                         |                                      |                        | 165,166   |
| deepBase     | identification, annotation, and function prediction of lncRNAs from RNA-seq data | 14                       | 191,547 | 2016        | X                         |                                      |                        | 167,168   |
| GENCODE      | manually curated human and mouse IncRNA reference based on ENCODE project | human, mouse             | 42,302 | 2016        |                            |                                      |                        | 169,170   |
| LincSNP      | annotated disease-associated SNPs in human lncRNAs                  | human                    | 244,545 | 2016        | X                         | X                                    |                        | 171       |
| LNCipedia    | annotated lncRNA sequences, structures, protein coding potential, and miRNA binding sites | human                    | 118,777 | 2016        | X                         | X                                    | X                      | 172,173   |
| IncRNAdb     | curated reference database of functionally annotated eukaryotic lncRNAs | 71                       | 295 (183 in human) | 2015        | X                         |                                      |                        | 174,175   |
| LncRNADisease| experimentally supported and predicted associations between lncRNAs and diseases | human                    | 1,564   | 2015        | X                         |                                      |                        | 176       |
| lncRNome     | annotated human lncRNAs                                            | human                    | 17,547   | 2013        | X                         | X                                    | X                      | 177       |
| NONCODE      | integrated annotation of ncRNAs, especially lncRNAs                | human                    | 487,164 (167,150 in human) | 2016        | X                         | X                                    |                        | 178       |

ChIP-seq, chromatin immunoprecipitation sequencing.
been associated with left ventricular (LV) dysfunction after myocardial infarction (MI), thereby potentially linking this lncRNA to cardiac contractility and arrhythmia in a clinical setting.

A switch in myosin heavy chain (MHC) isoforms accompanies the acquisition of the adult cardiac contractile phenotype. The expression of α-MHC in adult left and right ventricles is associated with higher filament sliding velocity, while the slower β-MHC confers higher force at lower energy cost. In rodent models (which mainly express the α-MHC isoform in the normal adult stage), the intergenic region between the two genes has been shown to regulate the transition from β- to α-MHC during cardiac development through co-transcription of an antisense RNA, called β-RNA, targeting and inhibiting the myosin heavy chain 7 (MYH7) transcript (encoding the β-MHC isoform). This mechanism is responsive to thyroid status and further implicated in the response to pressure overload.

Vascular Development and Biology

Growing evidence describes lncRNAs as key molecular players of vascular and endothelial cell (EC) biology. SENCR (smooth muscle and EC-enriched migration/differentiation-associated lncRNA) was among the first lncRNAs to be identified in human vascular smooth muscle cells (VSMCs) and ECs, being involved in their differentiation. The lncRNA SMILR (smooth muscle-induced lncRNA) appears to promote VSMC proliferation and may achieve this by regulating expression of adjacent transcripts, HAS2 (hyaluronan synthase 2). HAS2 plays a role in proliferation in saphenous vein-derived VSMCs, in which small interfering RNA (siRNA) targeting of HAS2 resulted in reduced proliferation ability.

SMILR could be a target for therapy of atherosclerosis because VSMC aberrant function is one of the defining features of atherosclerotic plaques (see Coronary Artery Disease and Atherosclerosis). MALAT1 (metastasis-associated lung adenocarcinoma transcript 1) is one of the most abundant lncRNAs in mammalian cells, and it was observed in ECs. Due to its increased expression in hypoxia, MALAT1 is proposed to have a role in vascularization, although knockout mice did not present severe developmental abnormalities. MALAT1 is involved in alternative splicing and possibly regulates gene expression during vascular development and disease.

In vitro differentiation of embryonic stem cells can recapitulate the development process, with transcriptome studies being employed to identify novel lncRNAs whose role is important for either commitment of cardiovascular progenitors or endothelial commitment. A study that identified hundreds of novel ncRNA transcripts in the vascular setting functionally characterized the lncRNA PUNISHER,
which is expressed in mature ECs. Morpholino targeting of PUNISHER in zebrafish culminated in extensive vascular defects, including abnormal branching and vessel formation. PUNISHER silencing in human umbilical vein ECs (HUVECs) using short hairpin RNA (shRNA) revealed similar defects. Overall, PUNISHER compromises EC function, but its mechanism of action or its involvement in vascular pathologies have not yet been elucidated.

### lncRNAs in Cardiovascular Disease

The association between lncRNAs and cardiovascular disease is just coming to light with several reports about their specific expression in different cardiac diseases. Dysregulation of certain lncRNAs has been shown in both human and rodent models (Figure 2), in which some studies present encouraging results for disease prognosis and therapy. The biological context of lncRNAs discussed in this section is illustrated in Figure 3. However, because of their poor conservation across species, translation of animal findings to human applications should be approached with caution. Here we overview the role of lncRNAs in hypertension, coronary artery disease (CAD), MI, ischemia, and heart failure.

Some lncRNAs differentially expressed during cardiovascular development also participate in a pathological setting, while others are involved in more than one cardiovascular disease. SENCR and H19, for example, are widely implicated in cardiovascular disease. SENCR, besides playing a role in VSMC and EC differentiation during development, has also been suggested to affect CAD. This lncRNA was found to be downregulated in VSMCs from a type 2 diabetes mellitus mouse model, promoting proliferation and migration. In addition, SENCoverexpression protected against the effects of high glucose stress on mouse VSMCs, and its reduced expression has been associated with premature CAD in humans. H19 is an important regulator of mammalian development and disease in that it inhibits cell proliferation. It is normally highly expressed during in utero development and downregulated at birth; however, studies reveal a re-expression of lncRNA H19 in cardiovascular disease settings, although not all mechanisms and involved players have been described. Human genome-wide association studies (GWASs) have demonstrated significant associations between H19 locus and systolic or mean arterial blood pressure. High H19 expression has been linked to hyperhomocysteinemia, a known risk factor for CAD, and polymorphisms correlate with CAD risk. Methylation at the IGF2/H19 locus have been implicated in regulation of glucose metabolism and development of diabetes, renal development, pre-eclampsia, and aortic stenosis, indicating possible links. Furthermore, H19 was reported to sponge let-7 family miRNAs, which are believed to have atheroprotective or proatherosclerotic roles and are downregulated in CAD patients. In addition, H19 was identified as differentially expressed in normoxic versus hypoxic ECs. Finally, it is a precursor of miR-675, which inhibits cardiomyocyte hypertrophy and contributes to cardiac

### Table 2. lncRNAs Associated with Cardiovascular Biology

| lncRNA   | Expression          | Biological Context                        | Action | Genomic Localization | Organism      | Reference |
|----------|---------------------|------------------------------------------|--------|----------------------|---------------|-----------|
| **Biht** | embryonic stem cells| cardiomyocyte differentiation            | signal | intergenic           | mouse         | 24,25     |
| **Fendrr** | lateral plate mesoderm | development of heart and body wall | signal | intergenic           | human, mouse, rat | 26       |
| **Novlinc6** | embryonic stem cells (particular left ventricle), cardiomyocytes | cardiac differentiation and maturation | decoy  | unknown              | human, mouse | 27       |
| **CARMEN** | cardiac precursor cell | cardiomyocyte differentiation of cardiac precursor cells | enhancer | intergenic           | human, mouse, rat | 28       |
| **n411949** | embryonic heart | cardiac development | unknown | antisense           | mouse         | 22       |
| **n413445** | embryonic heart | cardiac development | unknown | intronic            | mouse         | 22       |
| **KCNQ1OT1** | smooth muscle cells | maintenance of smooth muscle cells' differentiated state | signal | antisense           | human         | 29       |
| **β-RNA** | unknown | contractile phenotype, pressure overload | unknown | antisense           | rat           | 30       |
| **Vascular Development** | smooth muscle cells | maintenance of smooth muscle cells' differentiated state | decoy  | antisense           | human         | 37,38     |
| **SMILR** | smooth muscle cells | proliferation of smooth muscle cells | proposed scaffold or enhancer | intergenic           | human         | 39       |
| **MALAT1** | ECs | proliferation of ECs and vascularization | decoy  | intergenic           | human, mouse | 40       |
| **PUNISHER** | ECs | identity of ECs | guide    | antisense           | human, mouse, zebrafish | 42       |

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fibroblast proliferation and fibrosis, acting through repression of DUSP5/ERK1/2 (Figure 4).67

**Hypertension**

Hypertension has a complex etiology, involving an interplay of environmental and genetic components, and is a major risk factor for other cardiovascular diseases. Although many miRNAs have been shown to act in the pathogenesis of hypertension,68 reports on lncRNAs that relate to hypertension are scarce. However, studies based on animal and cell models in this area are emerging. One lncRNA involved in hypertension and vascular remodeling is GAS5 (growth arrest-specific 5).69 GAS5 was found to be downregulated in the plasma of human hypertensive patients and in the arteries and retina of a rat model, the spontaneously hypertensive rat. In these rats, GAS5 knockdown exacerbated the hypertensive phenotype, arterial remodeling, and microvascular dysfunction.69 In HUVECs and VSMCs, proliferation, migration, and resistance to oxidative stress were altered by GAS5 siRNAs. Co-culture experiments suggested that GAS5 participates in extracellular vesicle-mediated cross-talk between ECs and VSMCs.

A screening approach using angiotensin II (Ang II)-treated rat VSMCs identified differentially expressed lncRNAs, one of which, lnc-Ang362, is proximal to miR-221 and miR-222.70 These two miRNAs, which regulate the proliferation of rat VSMCs71 and the migration of HUVECs,72 were also upregulated in response to Ang II and appeared to be co-transcribed with the lncRNA. Consistently, lnc-Ang362 siRNA knockdown decreased miR-221/222 expression and reduced VSMCs proliferation.70 Thus, together with miR-221/222, lnc-Ang362 may represent an interesting therapeutic target that deserves further investigation, because it is conserved in human.

Given the poor evolutionary conservation of many lncRNAs, any approach based solely on animal models may limit discovery. In a cohort of patients with acute MI, expression of four lncRNAs—ANRIL (antisense non-coding RNA in the INK4 locus), aHIF (hypoxia-inducible factor 1A antisense RNA 2), MIAT (MI-associated transcript), and MALAT1—was found to be significantly associated with hypertension.73 Although their mechanisms of action in hypertension are not yet described, ANRIL affects cell adhesion, proliferation, and apoptosis,73 and MALAT1 modulates EC migration, sprouting, and proliferation.17 A novel bioinformatics tool, LncDisease, has been used to predict four human lncRNAs associated with hypertension, three of which were validated as dysregulated in Ang II-treated human VSMCs.74 Further investigation is required to firmly establish their validity in human hypertension.

**CAD and Atherosclerosis**

Atherosclerosis is typified by the formation of a fibro-fatty plaque in the arterial vessel wall and involves the molecular and functional
dysregulation of ECs, VSMCs, macrophages and other leukocytes, and platelets.\textsuperscript{75} When atherosclerosis occurs in the epicardial vessels of the heart, it is referred to as CAD, which is a leading cause of death worldwide. Dysregulated expression of specific lncRNAs has been reported to contribute to CAD. The lncRNA \textit{RNCR3} (retinal non-coding RNA 3) expression is altered during atherosclerosis, being overexpressed in atherosclerotic VSMCs and ECs compared with non-atherosclerotic tissue in mouse and human.\textsuperscript{76} Compared with control mice, downregulation of \textit{RNCR3} with shRNA aggravated atherosclerosis in thoracic aorta tissue and increased inflammatory factors in plasma. In vitro treatment with oxidized low-density lipoprotein (ox-LDL) increased \textit{RNCR3} levels in HUVECs and VSMCs, reducing proliferation and viability and increasing apoptosis. These data suggest that \textit{RNCR3} is atheroprotective. Moreover, the same study demonstrated in vitro that exosomes derived from ECs are rich in \textit{RNCR3}, which is transferred to VSMCs and induces their proliferation and migration. The proposed mechanism of action in ECs is that \textit{RNCR3} regulates the transcription factor KLF2 by sponging miR-185-5p, which targets KLF2. Thus because of the atheroprotective role of \textit{RNCR3} in atherosclerosis, its induced upregulation potentially represents a therapeutic intervention.\textsuperscript{76}

\textit{LincRNA-p21} was identified as a transcriptional target of p53.\textsuperscript{77} In VSMCs, this lncRNA disrupted the binding between p53 and its inhibitor, mouse double minute 2 (MDM2), with consequent effects on cell proliferation and apoptosis.\textsuperscript{78} \textit{LincRNA-p21} protected against neointimal hyperplasia in the carotid artery injury mouse model and was downregulated in aortic atherosclerotic plaques and in coronary artery tissues from CAD patients.\textsuperscript{79} Furthermore, polymorphisms in \textit{lincRNA-p21} have been associated with CAD risk.\textsuperscript{79} The therapeutic potential of \textit{LincRNA-p21} in acute vascular injury is suggested by its regulatory role of cell proliferation and apoptosis in CAD.

Remodeling of the extracellular matrix and neointimal formation are additional key features of CAD. Deposition of hyaluronan, synthesized by \textit{HAS2}, contributes to this process. Two lncRNAs independently regulate \textit{HAS2}: HAS2-AS1 (HAS2 antisense RNA 1) and \textit{SMILR}. The antisense transcript \textit{HAS2-AS1} was increased in atherec- tomy samples collected from severely diseased carotid arteries and appears to promote \textit{HAS2} transcription in VSMCs in the presence of O-GlcNAcylation by altering chromatin configuration.\textsuperscript{80} This may be particularly relevant to neointimal formation in diabetic patients. \textit{SMILR}, which promotes VSMC proliferation, was significantly upregulated in VSMCs stimulated with interleukin 1\(\alpha\) and platelet-derived growth factor compared to unstimulated cells. In addition, its levels in plasma correlated with the inflammatory marker C-reactive protein and were upregulated in human carotid artery atherosclerotic plaques compared with adjacent healthy tissue.\textsuperscript{89}

Several other lncRNAs have been associated with inflammation,\textsuperscript{81–88} including in the context of diabetes,\textsuperscript{89–91} although direct links to CAD remain to be established. Downregulation of the lncRNA termed \textit{CoroMarker}, originally identified as a biomarker of CAD,\textsuperscript{92} has been shown to decrease pro-inflammatory cytokine secretion from...
Coronary Artery Heart Failure Ischemia

| Hypertension | Coronary Artery Disease | Ischemia | Heart Failure |
|--------------|-------------------------|----------|--------------|
| Polymorphisms, methylation | Polymorphisms, methylation | Sponge (miR-let-7 family) | Sponge (miR-let-7 family) | Protein interaction (DUSP5/ERK1, 2) |
| - Blood pressure | - Glucose metabolism | - Insulin resistance | - Vascular injury | - Cardiac fibrosis |
| - Pre-eclampsia | - Diabetes | - Hypoxia | - Inhibition of cardiomyocyte hypertrophy |
| - Aortic stenosis | | | |

Figure 4. H19 Is Associated with Hypertension, CAD, Atherosclerosis, Ischemia, and Heart Failure

Although mechanistic insights into the role of H19 in cardiovascular disease are lacking, methylation regulation and sponging of miRNAs have been suggested and may overlap among diseases. Polymorphisms have been correlated with blood pressure and CAD. H19 action as a sponge for the miRNA-let-7 family has been linked to CAD and could be a possible mechanism in hypoxia. In heart failure, it acts by interacting with protein to regulate cardiac fibrosis and is a precursor of miR-675, which targets an inducer of hypertrophy.

M1 and Ischemia

Although advances in treatment and diagnosis of MI have increased patient survival and quality of life, MI is still a major cause of mortality and morbidity worldwide. Several lncRNAs have been uncovered as being dysregulated in MI, and some may play roles in pathological angiogenesis and ischemic cardiac injury. Several GWASs have revealed an association between the INK4 locus and the risk of CAD, including MI. This locus is important for cell-cycle progression and revealed as being dysregulated in MI, and some may play roles in pathophysiology.

In a mouse model of MI induced by coronary ligation, several lncRNAs were dysregulated in the heart, among which the two most strongly upregulated were named Mirt1 and Mirt2 (myocardial infarction-associated transcript 1 and 2). Their levels peaked 24 hr after MI and returned to baseline after 2 days, indicating that lncRNAs may be dynamically regulated in pathological processes. Mirt1 and Mirt2 levels correlated with expression of genes involved in reversing LV remodeling and preserved ejection fraction, suggesting a protective role in LV function. This study evidenced a therapeutic potential of these two lncRNAs. However, no human homologs of Mirt1 and Mirt2 have been described so far.

In addition to their potential as therapeutic targets, lncRNAs could serve as clinical biomarkers. One of the first studies to provide evidence of the feasibility of using lncRNAs as biomarkers for cardiovascular disease identified and validated LIPCAR (long intergenic non-coding RNA predicting cardiac remodeling) in a large number of patients. LIPCAR levels were increased in plasma samples from patients with LV remodeling after acute MI and in patients with type 2 diabetes mellitus. Circulating LIPCAR may also have prognostic value because its levels correlated with higher mortality risk in patients with heart failure. LIPCAR's therapeutic potential remains to be investigated.

Myocardial infarction-associated circular RNA (MICRA) was the first circRNA to be identified as a potential biomarker of LV dysfunction after MI, with its predictive value confirmed in two independent cohorts. Therapeutic applications for this circRNA are yet to be discovered. A few circRNAs with relevance to cardiovascular disease have been unveiled and reviewed. For example, Cdr1as (cerebellar degeneration-related protein 1 antisense transcript) was uncovered as a miR-7a sponge in cardiomyocytes, showing upregulation in MI mice and cardiomyocytes under hypoxia.

The lncRNA UCA1 (urothelial carcinoma-associated 1), proposed as a biomarker as well, presented altered expression in MI patients. In rats with ischemia and reperfusion (I/R)-induced heart injury, another study found that UCA1 contributes to cardiac injury by enhancing apoptosis of cardiomyocytes. However, its application as a biomarker seems limited, because it performed worse than classical markers of MI (e.g., creatine kinase). Nonetheless, because it has a role in I/R injury, future studies could reveal a therapeutic
potential to UCA1. Another lncRNA playing a role in the heart response to ischemia is HIF1A-AS2, also known as aHIF. It destabilizes the mRNA producing the hypoxia-inducible factor 1-α (HIF1α), which is considered the master transcriptional regulator of cellular response to hypoxia, including post-ischemic angiogenesis.121 Besides being overexpressed in the failing heart,122 aHIF was found to be dysregulated in the blood of patients after MI.123

Although a certain level of autophagy has been shown to be cardioprotective in ischemia,122 reports suggest that the accumulation of autophagosomes can trigger cardiomyocyte death, particularly during post-ischemic reperfusion.123,124 The IncRNA APF (autophagy-promoting factor) participates in the regulation of autophagy and MI in mice.125 APF is increased during I/R injury and sequesters miR-188-3p, resulting in an upregulation of the miR-188-3p target gene ATG7, a promoter of autophagy. APF is important in determining myocardial I/R injury. Because inhibition of autophagy can be protective in the setting of MI, both APF and miR-188-3p represent potential targets for therapy.125

Several studies have identified IncRNAs involved in limb ischemia. Inhibition of MALAT1 using GapmeRs led to worse outcomes following experimental hindlimb ischemia. This suggested the possibility that MALAT1 plays a reparative, proangiogenic role.126 Moreover, SENCR was found to be reduced in human critical limb ischemia muscles.127 Several additional IncRNAs, including H19, were identified as differentially expressed in normoxic versus hypoxic ECs, followed by expressionional and functional validation in the mouse limb ischemia model.126

Heart Failure
Heart failure is a complex condition of declined cardiac function in response to various pathophysiological stresses that cause cardiac remodeling, characterized by maladaptive hypertrophy. Maladaptive remodeling in the failing heart is considered an important target for therapy, and several IncRNAs are implicated in this process.126,127

CHRF (cardiac hypertrophy-related factor), which is conserved between humans and mice, stimulates cardiac hypertrophy and was the first IncRNA reported to have implications in heart failure.126 It acts as a sponge to miR-489, hence upregulating its downstream target, MYD88, which is a key gene in activating cardiac hypertrophy.126 This was observed in cardiomyocytes of mice with pressure overload-induced cardiac hypertrophy, but the authors also reported a natural overexpression of CHRF in human heart failure tissue, emphasizing that this transcript may have a similar function in human.126

The heart-enriched IncRNA Chaer (cardiac hypertrophy-associated epigenetic regulator) is also required for cardiac hypertrophy and is functionally conserved between mouse and human.126 By interacting with PRC2, Chaer inhibits histone lysine methylation at the promoter regions of pro-hypertrophic genes, thus allowing their expression.128 Similarly, CHAST (cardiac hypertrophy-associated transcript) plays a role in promoting hypertrophy and is functionally conserved.15 CHAST levels were endogenously increased during cardiac hypertrophy in mice and in hypertrophic heart tissue from patients with aortic stenosis, a cause of cardiac hypertrophy and fibrosis. Induced overexpression of CHAST in mice led to cardiomyocyte hypertrophy, while its suppression attenuated remodeling and hypertrophy without signs of toxicity.15 This is one of the most prominent examples of the strong therapeutic potential of lncRNAs for cardiac remodeling, showing that manipulation of a specific IncRNA can improve cardiac function.

A study identified in mice a cluster of cardiac-specific IncRNAs termed Mhrt (myosin heavy-chain-associated RNA transcripts) that are transcribed from the Myh7 locus, which is critical for cardiac contraction.129 Besides being transcribed from the same locus as β-RNA (antisense IncRNA involved in cardiac development), the transcripts have different sequences. Although highly expressed in adult hearts, Mhrt transcripts were suppressed during pathological stress. Induced restoration of Mhrt levels prevented cardiac hypertrophy and failure, revealing their cardio-protective role. Mhrt acts as a decoy to inhibit the aberrant expression of pathogenic genes involved in cardiac contractility, thus maintaining cardiac function. Finally, the authors found that the human version of MHRt was repressed in different cardiomyopathies (hypertrophic, ischemic, or idiopathic), indicating a conserved mechanism.129 This study provides further evidence in support of IncRNAs as potential therapeutic targets, for which development of a related therapy is facilitated by the conserved epigenetic regulation in human and mouse.

It has been uncovered that the IncRNA ROR (regulator of reprogramming) plays a role in cardiac hypertrophy. This transcript was naturally overexpressed in murine hypertrophic heart and cardiomyocytes, and its knockdown with siRNA attenuated hypertrophy. ROR enhanced cardiac hypertrophy by interacting with miR-133, a muscle-enriched miRNA that plays a role in hypertrophy.130 Both RNA molecules could be investigated as anti-hypertrophic therapeutic targets.

The circRNA Hrcr (heart-related circular RNA) has a protective role in cardiac hypertrophy and heart failure in mice. It acts as an endogenous sponge for miR-223, thus upregulating the expression of ARC (apoptosis repressor with caspase recruitment domain).127 ARC protein is normally highly expressed in the heart and is involved in cardiomyocyte hypertrophy and apoptosis.131 Overexpression of miR-223 in mice using adenovirus-induced cardiac hypertrophy, and levels of Hrcr were downregulated in failing mouse hearts, indicating that Hrcr might constitute another target to treat heart failure if the mechanism is conserved in humans.117

Therapeutic Applications of IncRNAs
Although IncRNAs offer a multitude of prospective targets due to the diversity of actions and cellular processes implicated, few practical examples of therapeutic applications of IncRNAs have been reported so far. The up- or downregulation of specific IncRNA abundance have
been the most thoroughly investigated approaches. Strategies for up-regulation of lncRNAs include the use of recombinant adenoviral or lentiviruses. Adeno-associated viral (AAV) vectors may represent a more promising approach due to their low pathogenicity.133-136 This strategy used for targeting miRNAs in preclinical models showed promising results157-159 and reached successful clinical trials to deliver protein coding genes,135,140,141 but its use to deliver lncRNAs remains to be determined.

lncRNA downregulation can be obtained using shRNA or siRNA, more suitable for cytoplasmic lncRNAs,142 antisense oligonucleotides (ASOs)-mediated knockdown using aptamers,143 or GapmeRs forming heteroduplexes with their target lncRNAs that are then recognized and cleaved by the RNase H.144 The latter approach, more suitable for nuclear lncRNAs and with fewer off-target effects than shRNA,145 is already undergoing testing in cell and animal models,15,17,18 while ASO and siRNA have been used to deplete MALAT1 in human cancer cells and animal models, reducing metastasis.146-148 Hopefully, it will be possible to transfer some findings in other diseases to help accelerate the development of therapies for cardiovascular disease. Ribozymes or deoxyribozymes, catalyzing the cleavage of the flanked region of the RNA target, represent an additional tool to knock down lncRNAs.149,150 Finally, small molecules that compete with ligands to bind lncRNAs or induce conformational change in lncRNAs are being identified through large screening efforts.151

The most promising lncRNA targets for therapeutic applications in cardiovascular disease are those for which mechanism of action and effect are well described and preferably cell specific. One example is CHAST, for which the GapmeR-mediated silencing attenuated transverse aortic constriction-induced cardiac remodeling in mice.15 No apparent side effects were observed due to treatment with GapmeRs. Future experiments will determine whether cardiac hypertrophic remodeling may similarly be targeted through the downregulation of CHRF, which regulates Myd88, a factor associated with hypertrophy development,126 or by restoring expression levels of MIHRT, thus preventing cardiomyopathy by restricting stress-associated aberrant gene expression mediated by the chromatin-remodeling factor, Brg1.129 Other approaches to decrease cardiac cell death following MI could target apoptotic or autophagic processes by downregulating APP.123 In vascular disease, prevention of MALAT1 upregulation could be used as anti-angiogenic therapy to prevent diabetes-associated microvascular complications.17,90,91

Several limitations and challenges remain to be resolved before lncRNAs can reach clinical application. Foremost is target specificity, given the pleiotropic implications of a single lncRNA in pathophysiological processes throughout the human body. Although lncRNAs may show dysregulation specific to certain diseases, they exhibit various functions in the organism and some lncRNAs may act through more than one mechanism. As an example, modulation of ANRIL, for which SNPs are associated with CAD,106,172 is probably hazardous given its implication in cancer development and progression.154,155

Second, the low conservation of lncRNAs across evolution156 makes both the identification of human lncRNAs and their clinical testing real challenges, because rodents may not be an adequate model. The hurdles to translate animal findings to human are illustrated by Mirt1 and Mirt2, which may have a protective role in LV function, but no homologs in human have been described so far.157 However, it has been suggested that it is the secondary structure of lncRNAs that is conserved and functional, rather than the primary sequence. For example, GAS5 acting as decoy or signal may depend on its secondary structures and their affinities for different ligands.177,158 This may explain why some lncRNAs with important mechanistic roles have not been observed in other species. If structure is more critical to function than sequence, then lncRNAs previously considered non-conserved may have structural homologs in other species, which would enable the use of existing animal models.

Third, before therapeutic application, the structure-function relationship of each lncRNA must be further elucidated, using newly developed methods to resolve secondary and tertiary structures.27,66,83,152,161 Few have been sufficiently characterized, either in terms of regulation of the disease or in the ability to be externally regulated. Therefore, much remains to be done to retrieve the most promising candidates for therapeutic development from the huge amount of sequencing data available.

Future work is required for a thorough functional characterization of lncRNAs in cardiovascular pathology, both at the molecular and at the cellular level. The role of lncRNAs as epigenetic regulators is critical for gene regulation and disease pathogenesis, yet the fine molecular mechanisms involved remain to be fully elucidated. Although several RNA-seq experiments have been conducted and many potential candidates have been identified,27,66,83,152,161 few have been sufficiently characterized, either in terms of regulation of the disease or in the ability to be externally regulated. Therefore, much remains to be done to retrieve the most promising candidates for therapeutic development from the huge amount of sequencing data available.

The involvement of circRNAs in cardiovascular pathologies has emerged.113,117,162 Although appealing due to their resistance to degradation by exoribonucleases, their use as therapeutic targets requires further investigation. Considering the number of previously
characterized circRNAs and the plethora of circRNAs that remain to be characterized, this new branch of the ncRNA family constitutes an invaluable reservoir of therapeutic targets and may be useful to move theranostics a step forward, because they may be used for both diagnostics (biomarkers) and therapeutic purposes. Finally, gene editing with the CRISPR system appeared as an appealing approach for therapy, and a study reported an efficient downregulation of MALAT1 with this system, representing a potential tool for therapeutic applications in cardiac disease through modulation of the expression of IncRNAs.

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