Endothelial function and dysfunction in the cardiovascular system: the long non-coding road

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Abstract

Present throughout the vasculature, endothelial cells (ECs) are essential for blood vessel function and play a central role in the pathogenesis of diverse cardiovascular diseases. Understanding the intricate molecular determinants governing endothelial function and dysfunction is essential to develop novel clinical breakthroughs and improve knowledge. An increasing body of evidence demonstrates that long non-coding RNAs (lncRNAs) are active regulators of the endothelial transcriptome and function, providing emerging insights into core questions surrounding EC contributions to pathology, and perhaps the emergence of novel therapeutic opportunities. In this review, we discuss this class of non-coding transcripts and their role in endothelial biology during cardiovascular development, homeostasis, and disease, highlighting challenges during discovery and characterization and how these have been overcome to date. We further discuss the translational therapeutic implications and the challenges within the field, highlighting lncRNA that support endothelial phenotypes prevalent in cardiovascular disease.

Keywords

Long non-coding RNA • Endothelial function • Endothelial heterogeneity • RNA-sequencing • LncRNA mechanism

1. Introduction

Lining the totality of the vascular system, the endothelium is a continuous barrier, the surface of which directly interacts with nearly every system in the body to regulate vascular development, homeostasis and pathogenesis. The single layer of endothelial cells (ECs) that constitutes this barrier is in itself uniquely versatile, showing remarkable physiological and morphological heterogeneity across the vasculature. These differences reflect the variety of functions they perform and the shifts in the priority of these roles across different anatomical locations in the cardiovascular system. For instance, the angiogenic capacity of ECs plays a vital role during embryological growth, tissue development, and wound healing in damaged tissues. Maintenance of vessel function, and therefore cardiovascular homeostasis, is highly dependent on the ability of the endothelium to react to external stimuli, mediating not only vasodilation and constriction but also thrombogenic, immune and inflammatory responses. Dysregulated, these mechanisms can lead to, among others, the unrestrained vessel formation often seen in cancerous tumours and the pathological remodelling of mature vessels associated with the development of pervasive conditions such as hypertension and atherosclerosis. Unsurprisingly, endothelial dysfunction is often an early pathophysiological feature in most forms of cardiovascular disease (CVD) and an independent predictor of future cardiovascular outcomes. Understanding the finer molecular determinants governing endothelial function and dysfunction is therefore essential when addressing vascular disease.

Apparent during both health and disease, the unique versatility of ECs indicates complex control of the underlying transcriptional programmes and this is becoming more apparent with advances in our understanding of the human transcriptome. This is particularly true with the emergence of non-coding RNAs (ncRNA) as regulators of gene expression both at the transcriptional and post-transcriptional level. With only an estimated
1–2% of the human genome encoding for proteins,\textsuperscript{10} there have been increased efforts in recent years to uncover novel regulatory mechanisms within the uncharacterized portion of the transcriptome. While the extent of their function is still debated\textsuperscript{11} ncRNA transcripts are believed to comprise approximately 70–90% of our genome and encompass thousands of operationally significant RNAs associated with all manner of biological processes.\textsuperscript{12,13} Whilst examples of small non-coding RNA-mediated regulation are now well-established, the concept of widespread control of cell function by long non-coding RNA (lncRNA) has only been advocated within the last decade.\textsuperscript{14} This class of genes, initially thought to only contain non-functional transcriptional by-products, has sparked great interest as some have been found to be critical in development and dysregulated in disease.\textsuperscript{15}

Widespread transcription of lncRNA across the genome became more apparent with the increased use of RNAseq technologies revealing previously undetected transcriptional activity. Defined simply as non-coding transcripts longer than 200 bp in length, these genes are generally less abundant and far less conserved compared with protein coding genes. Indeed, in a survey of 17 species, over 70% of all lncRNA in each species originated within the last 50 million years, indicating a high rate of evolutionary turnover within the class.\textsuperscript{15} Recent estimates describe approximately 27,000 lncRNA transcripts produced in human, and ~1000 lncRNA are conserved in other mammals.\textsuperscript{16,17}

LncRNAs collectively evade exact definition, with a variety of intersecting subclasses described based on traits such as their genomic proximity relative to surrounding genes (antisense, intergenic, bidirectional, intron-contained), the chromatin signatures of their transcriptional start sites (promoter, enhancer), and their mode of regulation (transcriptional vs. post-transcriptional).\textsuperscript{18} Relatively few have been characterized compared with the tens of thousands of genes annotated, but those that have demonstrate a wide range of mechanisms with epigenetic, transcriptional, and post-transcriptional effects, able to activate or suppress gene expression and translation\textsuperscript{19,20} (Figure 1). Such diversity leads to challenges during the study of lncRNA, but their prevalence in the transcriptome provides an attractive opportunity for discovery of new mechanisms that control cell behaviour and the possibility of developing novel clinical targets.

Discovery of new clinical targets is a current priority for pathologies where endothelial dysfunction plays a significant role and treatment options are limited. Aside from providing an opportunity to find novel regulatory mechanisms to manipulate therapeutically, lncRNAs often show restricted expression patterns that could be clinically advantageous.\textsuperscript{21} Using in situ hybridization data, leading studies by Mercer et al.\textsuperscript{22} found lncRNA to have expression patterns associated with particular anatomical regions, cell types, and subcellular compartments. Tissue-specificity is high for lncRNAs, often surpassing that of protein-coding genes.\textsuperscript{23} Additionally, they often have stage-specific expression patterns during development and disease.\textsuperscript{24,25} Whether such tendencies for localized expression could potentially explain some degree of endothelial heterogeneity through regulation of transcriptional programmes in certain vessel types or tissues is currently an open question.

Herein, we will discuss the role of lncRNA in endothelial biology during cardiovascular development, homeostasis and disease and how this is yet to be fully defined. We will highlight challenges during lncRNA discovery and characterization and how these have been overcome so far, using as examples those lncRNA that support endothelial phenotypes prevalent in cardiovascular disease (CVD).

2. LncRNA discovery in endothelial cells: current state of the art

As interest in lncRNA function grows, a wealth of established in vitro and in vivo models are being used as a basis to study their expression patterns. Such models are yet to be thoroughly examined from an lncRNA perspective and a full representation of endothelial lncRNA expression throughout the cardiovascular system is yet to be realized, although clearly a wealth of data will emerge in the next months and years. To date, a number of studies on EC function have identified lncRNAs with clear functional impact on the EC (Table 1). For instance, hypoxic conditions are commonly observed in myocardial infarction, peripheral ischaemia, and stroke, these often trigger a variety of distinct endothelial responses to prevent further tissue damage and restore blood supply. Several hundred genes with hypoxia-sensitive expression have already been identified and later validated\textsuperscript{in vitro} using human umbilical vein endothelial cells (HUVECs), including MALAT1, H19, MIR503HG, and LINC00323. Many of these have been shown to regulate hypoxia-induced EC functions such as proliferation, migration and angiogenesis after further in vitro and in vivo characterization.\textsuperscript{28,30,31} Additionally, lncRNAs previously characterized in other cell types, such as MEG3, MIAT, and RNRCP3, have been tied to EC-mediated angiogenesis via hyperglycaemic induction in renal EC and are now associated with microvascular visual impairment.\textsuperscript{39–41} (Figure 2).

LncRNA involved in EC inflammatory responses have also been explored. Lipopolysaccharide-stimulation of ECs can cause apoptosis, endothelial dysfunction and propagation of sepsis leading to elevated CVD risk. Hundreds of so far uncharacterized lncRNA have been found to be differentially expressed during the process, several with notably high fold changes.\textsuperscript{42} A key feature of an innate EC response are the chemotactic intermediaries produced from the CXCL locus involved in neutrophil recruitment. These were recently found to be primed for activation in TNFα-stimulated HUVECs by UMLIL0, a proximal enhancer-transcribed RNA.\textsuperscript{38} Such innate-responsive lncRNAs are likely to directly impact on endothelial function through pro-apoptotic or pro-migratory effects on ECs.

Models of endothelial development from human embryonic stem cells (hESCs) have also been used to identify lncRNA expressed at specific stages in cell fate determination. Such differentiation models have identified genes such as SENCR\textsuperscript{25} and PUNISHER (AGAP2-AS1)\textsuperscript{25} which are both up-regulated during endothelial commitment. While differentiation models allow for identification of genes involved in determining cell fate, many may also be important in maintaining endothelial homeostasis. SENCR expression, for example, was shown to be altered in the vascular tissue of patients with critical limb ischaemia and premature coronary artery disease (CAD).\textsuperscript{35} Later studies have also found perturbations in mature EC membrane integrity induced upon SENCR knockdown.\textsuperscript{36}

However, publications often do not acknowledge endothelial phenotype heterogeneity and several EC-dependent mechanisms have yet to receive similar attention as those supporting angiogenesis and homeostasis. For example, the well-established endothelial–mesenchymal transition has so far only been associated with a single lncRNA, GATA6-AS\textsuperscript{25,63} with no published data of transcriptome-wide shifts in lncRNA expression during this transition.

A bias towards HUVEC-based models is also apparent with only a single lncRNA-screening study including an EC subpopulation from outside the umbilical vein published so far.\textsuperscript{27} This is of particular importance as studies highlight distinct lncRNA functions across vessel types;
LncRNA classification and function

Transcription start site

Promoter-derived

Pol II

Enhancer-derived

Pol II

Surrounding coding genes

Sense-overlapping

Intronic

Antisense

Bidirectional

Intergenic (lincRNA)

Regulatory function

Molecular scaffold

Chromatin modifier

miRNA sponge

RNA interacting protein

IncRNA

Transcriptional regulator

miRNA host

mRNA processing

Translation

Degradation

miRNA

Protein

Figure 1 LncRNA classification and function. LncRNAs can be categorized based on their transcription start site, surrounding coding genes and regulatory function. Promoter-derived transcripts are more likely to be spliced, poly-adenylated, lengthy and stable when compared to enhancer-derived which, though separately categorized as eRNAs, are often included in lncRNA studies if >200 bp. The position of a lncRNA relative to surrounding coding genes as a categorization method provides indication of potential lncRNA function, e.g., bidirectional transcripts likely impact their partner gene. LncRNAs whose function has been characterized fall into distinct groups based on the its molecular interactions and the mechanism of action used to impact gene transcription or translation. As components of RNP complexes, lncRNAs can regulate the activity or localization of a particular protein, or play a structural role within a larger protein complex. LncRNAs can also control gene transcription by modulating the activity of transcription factors, or through the recruitment of chromatin modifying complexes. In addition to acting as miRNA host genes, lncRNAs can function as miRNA sponges, titrating specific miRNAs away from their mRNA targets. Post-transcriptionally, lncRNAs have been shown to modulate both mRNA translation and degradation.
| Gene name | LncRNA type | Sequence/synteny conservation (GENCODE aligned to PLAR annotation) | Cell/tissue type | Study design | ID Tech. | Selection strategy | Characterization of LncRNA in Endothelial Context | Phenotypic effect | Key effectors + interactions | Proposed mechanism | References |
|-----------|-------------|---------------------------------------------------------------|----------------|-------------|--------|----------------|-------------------------------------------------|----------------|--------------------------------|------------------|-----------|
| AGAP2-AS1 (PUNISHER) | Antisense | Eutheria (Synteny: Ray-finned Fish) | Differentiated ECs | Differentiation from hESCs to vascular EC | RNAsq | Enriched in final stage of differentiation | Zebrafish/mouse embryo, HUVECs | Early vessel branching in zebrafish embryonic development, maintenance of endothelial differentiation | TAL1, FOXC1 | Unknown | 25 |
| GATA6-AS | Antisense | Mammalia (Synteny: Ray-finned Fish) | HUVEC | Normoxia to hypoxia (12 + 24 h) | RNAsq | High abundance and up-regulation relative to other LncRNA | Hela/HUVECs | EndMT/hp cell formation/migration | LOXL2 | Directs nuclear portion of LOXL2 to remove H3K4me3 | 26 |
| HAGLR (STEEL, HOXD-AS1) | Antisense | Ray-finned fish (Synteny: Ray-finned fish) | HUVEC/HMVEC | Profiling of primary vessel cell types | LncRNA custom microarray | Enriched expression vs. four non-EC types, proximity to Hox locus | HUVEC | Migration/proliferation/apoptosis/angiogenesis | KLF2, eNOS PARP1 | Recruits epigenetic regulator PARP1 to target promoters | 27 |
| H19 (ASM) | IncRNA | Eutheria (Synteny: Eutheria) | HUVEC | Normoxia to hypoxia (24 + 48 h) | RNAsq | Hypoxia-sensitive mouse ortholog, sensitive to vascular injury | HAOEC | Supports hypoxia-induced angiogenesis | Not examined here | Not examined here | 28 |
| LINC00520 (LEEENE) | eRNA | No sequence ortholog (Synteny: Ray-finned fish) | HUVEC | Physiological (Pulsatile) vs. pathological (Oscillatory) shear stress | RNAsq | High up-regulation relative to other LncRNA, correlation with eNOS | HUVEC | eNOS expression | PolII, KLF4, Med1 | Recruitment of Pol II to eNOS promoter | 29 |
| LINC00332 (C21orf130) | Antisense | Catarrhini (Synteny: Eutheria) | HUVEC | Normoxia to hypoxia (12 + 24 h) | RNAsq + non-coding microarray | Strongest up-regulation | HUVEC/HCAEC | Supports hypoxia-induced angiogenesis | eIF4A3 | Scaffold, indirect binding to GATA2 | 30 |
| MALAT1 (HCN, LINC00047) | IncRNA | Vertebrates (Synteny: Ray-finned fish) | HUVEC | Profiling of HUVEC | RNAsq | Presence in other EC types | HUVEC | Supports hypoxia-induced angiogenesis | S-phase cyclins, p21 | Not examined in ECs | 31 |
| MANTIS (AK125871, ANXA4-AS) | Antisense | Absent from GENCODE | HUVEC | siRNA targeting histone demethylase JARID1B | Exon-array | Upregulated after histone demethylase depletion | HUVEC | Supports endothelial angiogenic function | BRG1, BAF155 | Nucleosome remodeling via BRG1 interaction | 32 |
| MEG3 (GTL2, LINC00023) | IncRNA | Eutheria (Synteny: Ray-finned Fish) | HUVEC | Profiling of HUVEC during hypoxia + senescence | RNAsq+RT-qPCR | Up-regulated in high HUVEC passage number | RRP6A (Primate retinal EC) | Supports proliferation, migration, glucose-induced apoptosis | Akt, EZH2/JARID2 (documented in ESCs) | Recruitment of EC-enriched histone demethylase JARID2 | 31334 |
| MIR503HG (H19X) | mIR host | Eutheria (Synteny: Lobe-finned fish) | HUVEC | Normoxia to hypoxia (12 + 24 h) | RNAsq + non-coding microarray | Strong up-regulation | HUVEC/EaHy926 | Supports proliferation and migration but no angiogenic effect | Not examined here | Host for mIR-503 | 30 |
Table 1

| Gene name | LncRNA | Sequence/synteny | Identification of LncRNA in endothelial context | Characterization of LncRNA in Endothelial Context | Cell/tissue type | Study design | ID Tech. | Proposed mechanism | Key effects + interactions | References |
|-----------|--------|-----------------|------------------------------------------------|-------------------------------------------------|-----------------|-------------|---------|------------------|-----------------------------|-----------|
| CCL5, CXCL3L1, | Binds CKAP4, freeing (GENCODE aligned interactions) | | | | | | | | | |
| | | | | | | | | | | |
| SENCR (FLI1-AS1) | Antisense Eutheria (Synteny: Mammalia) | | | | | | | | | |
| | | | | | | | | | | |
| UMILO | (ACT12193) | | | | | | | | | |

List of lncRNAs reported to have endothelial regulatory functions in cardiovascular disease. LncRNAs are presented together with their type and evolutionary conservation, followed by details regarding their identification and characterization.

3. Strategies for detection and selection of functional endothelial IncRNA

In the last decade the advent of relatively affordable sequencing technology has created a boom in transcriptomic techniques, resulting in sophisticated RNAseq-based methods becoming available to scientists and routinely utilized as a discovery tool. In tandem, the methodology to quantify gene expression has been refined, providing an ever-more accurate account of transcriptional fluctuations within models, including for endothelial pathology and differentiation. This work has helped to expand and validate IncRNA annotations where sequencing depth is effective, as well as increase our understanding of their origins, structure and expression. However, the specific spatiotemporal expression of IncRNAs poses a challenge, and the annotation of the human transcriptome is still incomplete and likely missing transcripts, including IncRNAs, which are well-expressed in EC types and behaviours that have not been profiled yet. Detecting novel endothelial IncRNA is therefore a high priority. This is in addition to evaluation of the thousands of already annotated IncRNA for endothelial association. Here, we provide an overview of the process of identifying IncRNA coupled to the subsequent selection of high priority candidates that might be functionally relevant in ECs (Figure 3).

Microarrays, though now superseded in sensitivity and accuracy by RNAseq, have provided the basis of several important screens for knockdown of the IncRNA MIR503HG, for example, was shown to have anti-proliferative and migratory effects on venous EC but not on arterial EC. Further, given the wide variety of tissue microenvironments to which EC are exposed is pivotal to guiding their fundamental function, it is important to acknowledge the extracellular cues that may dictate some of these differences in phenotype. In vitro, the use of 3D multicellular co-culture models allow for a physiologically relevant cellular arrangement and the exchange of intracellular components such as protein, RNA and DNA. The release of extracellular vesicles (EVs) by neighbouring cells is one such cellular exchange system shown to be a key regulator of endothelial function and dysfunction. Some emerging evidence now indicates that IncRNAs can be selectively packaged into EVs to induce a variety of phenotypic changes under both physiological and pathological conditions. For instance, exosomes released from tumour cells containing high quantities of the IncRNA H19 promote EC network formation, stimulating vascular endothelial growth factor (VEGF) and VEGFR1 production. Exosomal release of the atherosclerosis-associated IncRNA GASS by monocytes was also found to regulate apoptosis of vascular ECs. Conversely, communication between ECs and vascular smooth muscle cell (VSMC) has been shown to be facilitated by EVs carrying the IncRNA RNR3, and that these EV-derived exosomes can induce VSMC proliferation and migration.

Ultimately, research addressing EC heterogeneity and the physiological relevant cues that surround these subpopulations has the potential to reveal an unexplored and therapeutically attractive subset of IncRNA. As novel sequencing data and protocols become available to tackle these cellular mechanisms and typically hard-to-culture cell populations, annotation of EC functional diversity in the literature is likely to improve over the next years. It is, therefore, important to acknowledge transcriptomewide discovery as a prerequisite for understanding EC function and to consider the available emerging tools and techniques.
endothelial lncRNAs. However, the necessity to decide on which annotation set the probe population will be based on eliminates the chance to find novel transcripts, even if using arrays specifically designed for lncRNAs. This is coupled with increased background noise from non-specific probe binding, which limits sensitivity particularly in regard to those lncRNA that are expressed at low levels. However, arrays can provide a relatively cheap alternative to deeper RNAseq methods in studies with high sample number, such as those screening multiple vascular cell types, or where many replicates are required to obtain a signal of co-expression with genes of interest.

The gold standard technique for lncRNA identification is RNAseq. It is sensitive, increasingly cost-effective and presents a largely unbiased, whole-transcriptome view of shifts in gene expression. RNAseq of ECs has been used to identify lncRNAs responding to hypoxia, pathological shear stress, and those expressed in developmental models. It has also allowed profiling of transcriptional activity at loci containing notable endothelial-expressed genes such as eNOS or SR1P. However, only one of these studies capitalizes on the ability to detect expression of completely novel transcripts outside of current annotation sets and this led to identification of PUNISHER. Other such novel lncRNA are rare in the literature at present though the previously unannotated SENC, has been characterized with an endothelial function despite being initially identified in smooth muscle cells. Interestingly, both these functional lncRNA are expressed in unstimulated HUVECs, which have a high amount of sequencing data readily available, yet both were found without the use of publicly available annotation sets. This demonstrates that even well-studied cell types can yield previously unseen transcripts with high phenotypic impact.

Figure 2 Known function of endothelial lncRNAs. List of lncRNAs reported to have endothelial regulatory functions with impact on cell differentiation, EndMT, angiogenesis, inflammation, EHT, and vessel homeostasis. EHT, endothelial-to-haematopoietic transition; EndMT, endothelial-to-mesenchymal transition.
A key caveat for use of RNAseq is that sufficient read depth must be used to be able to reliably detect and annotate lowly expressed lncRNAs. This problem is even more acute when considering use of single cell RNA-seq to identify lncRNA expression on a cell-specific level. An important recent study showed how lncRNA expressed at a low level in a given tissue can actually be highly abundant within certain populations of the constituent cells. This study used 200 million reads per sample—a prohibitively expensive amount of sequencing until recently, but increasingly affordable with the introduction of NovaSeq machines. The use of single cell RNA-seq to examine lncRNAs directing endothelial heterogeneity, transitions or development remains an area of high interest and opportunity.

The use of RNAseq data for prediction of new lncRNAs is typically based on algorithmic reconstruction of transcript models from short RNAseq reads (these algorithms are usually ‘seeded’ with existing annotations), followed by filtering to determine which transcripts are non-coding with high confidence. Several computational pipelines address these issues. Typical filtering steps include the use of several algorithms to evaluate coding potential and combination of their scores, exclusion of short or very lowly expressed transcripts, and exclusion of transcripts found in close proximity to annotated genes, as these often correspond to unannotated extensions of UTRs.

For example, transcripts containing long ORFs (i.e. possessing long stretches of uninterrupted sequence between in-frame start and stop codons) with characteristic codon frequencies and/or with high homology to existing proteins can be identified with the widely-used coding prediction calculator (CPC) scoring method. Others exclude candidates with ORFs predicted to produce proteins with structural homology to known Pfam protein domains (HMMR), the detection of sequence composition characteristic of coding sequences, or candidates containing ORFs with codons that are maintained (with the same or similar codons and without frameshifting mutations) over large evolutionary distances (RNAcode and PhyloCSF). The codon-conservation tools are particularly powerful for detecting short conserved ORFs but also can have some false positives in regions of extremely high conservation and limited variation between species. Concepts relevant to all these tools are reviewed elsewhere, there remains an opportunity for such approaches to expand the endothelial lncRNA repertoire and aid our understanding of EC function.

Analysis of high-throughput data typically identifies tens to hundreds of potentially relevant lncRNAs and selection of candidates for functional follow-up can be challenging. There is no silver bullet available for homing in on a prospective lncRNA on which to focus wet-lab resources. There are, however, general trends emerging from the accumulated
knowledge of lncRNA which provide good starting points. LncRNAs with substantial transcript abundance and differential expression are most likely to be associated with the phenotype in question. Expression levels also correlate with evolutionary conservation, indicating that more abundant genes are more likely to be maintained for functional importance across species. On the other hand, lncRNAs that have cis-acting scaffold functions do not necessarily need to be abundant for carrying out their function(s), as exemplified by the involvement of UMILO in regulation of the CXCL locus in HUVECs.

Sequence conservation also offers a route to prioritize functional lncRNA. LncRNAs are in many cases poorly conserved, but ~1000 lncRNA genes are conserved among mammals, and ~100 between human and fish. The regions conserved in sequence in these lncRNAs are typically short, in many cases restricted in just a single exon with some bias towards the 5’ of the RNA. These short patches of conservation may correspond to functional domains with autonomous functions such as a binding sites for other RNAs or proteins. BLAST or whole genome alignments can be used to find regions of significant sequence similarity between potentially orthologous transcripts. Some lncRNA are conserved only through synteny, where only the relative position and the orientation of the transcribed locus of transcription is constrained whilst sequence diverges to a point where significant similarity is no longer detectable. Such ‘positional’ orthologs are harder to call with confidence, as multiple transcripts can be present in the same locus in distantly related species. Discovery of all such relationships can be automated using a relatively easily implemented tool, stickY, which can be used to annotate lncRNA in sparsely-annotated cardiovascular animal models and then predict their orthologous relationships to human transcripts.

The presence of deeply conserved orthologs can imply a significant contribution of a lncRNA to endothelial homeostasis or development. Such genes are therefore strong candidates for targeting in functional studies. Conversely, human- or mouse-specific transcripts may very well also be functional, and many of these could also potentially add to our understanding of differences between pre-clinical animal models and an eventual clinical context. Prioritization of such transcripts is typically based on their expression levels and/or proximity to functionally-relevant genes.

The selection process will become better informed as the list of functionally characterized lncRNA grows; a greater number of validated genes will allow for clearer guidelines for effective selection to emerge. Until then potential key drivers of endothelial heterogeneity or pathology could be waiting to be unearthed.

4. Approaches for characterizing the molecular interactions of lncRNAs

Being highly diverse, lncRNAs carry out their functions through a wide range of mechanisms. At the transcriptional level, they have been shown to bind and guide chromatin-modifying complexes to specific DNA sequences, either activating or repressing their target gene expression. Additionally, they can also act as decoys for DNA-binding proteins and prevent their association to a target gene. At the post-transcriptional level, a growing number of studies have implicated lncRNAs at various stages of control, regulating mRNA stability, enhancing mRNA translation, and even acting as miRNA sponges. Recent publications also point towards the existence of widespread cross-regulatory interactions between non-coding RNAs classes, adding a further functional role for lncRNAs.

Some of these regulatory networks are represented in large-scale databases, such as StarBase v2.0, a repository of thousands of experimentally validated RNA–RNA and protein–RNA interactions that offer supporting information for mechanistic studies. Nevertheless, the use of appropriate RNA-focused tools to elucidate such complex interactions is essential given the variety of different interactions across not only between different tissues and cell types but also within same-cell subpopulations.

4.1 Cellular localization

In line with their diverse functions, lncRNAs show a variety of subcellular distributions: accumulating predominantly either in the cytoplasm, nucleus, or distributed between both compartments. Our understanding of how the localization is encoded in lncRNA sequences is still relatively rudimentary, but several recent studies have identified specific sequence elements other features that are associated with enrichment in the nucleus in lncRNAs and mRNAs. Understanding the localization of a transcript may thus give an initial insight into putative functions and serve to guide future experiments.

Isolation of nuclear and cytoplasmic extracts has proven to be a simple, yet effective strategy. For example, different subpopulations of EC express high levels of the nuclear enriched lncRNAs TUG1, MEG3, and MALAT1, whereas SENCR transcripts show both cytoplasmic and nuclear accumulation. Unsurprisingly, all of these have now been found to regulate different aspects of EC function. Such fractionation methods, however, give a crude resolution quantification of subcellular localization that should be accompanied by more detailed localization through the use of single-molecular FISH methodologies.

4.2 RNA:protein interaction

The past decade has seen a growing appreciation for the role of RNA:protein interactions in regulating gene expression. These interactions can be studied either through protein-focused and RNA-focused perspectives. Well-established immunoprecipitation assays include RNA Immunoprecipitation (RIP), which purifies full RNA molecules associated with the precipitated protein, and Cross-Linking Immunoprecipitation (CLIP), which is typically used to identify higher-resolution footprints of RNA binding proteins. Conversely, RNA-centric approaches such as RNA chromatography will require the in vitro generation of a labelled RNA of interest to identify binding partners. Other hybridization-based methods such as RNA antisense purification (RAP) will instead use labelled antisense oligos to purify the endogenous RNA instead. While these techniques have now expanded and become quite varied in their methodology, in general they allow for the purification a specific RNA complex to identify directly interacting proteins using quantitative mass spectrometry or western blot (Figure 4). Nonetheless, while there has been progress in understanding the interactomes of individual lncRNAs, such as HOTAIR, MALAT-1 and Xist, the majority are still not well understood, particularly within an endothelial-specific context.

In ECs, RNA chromatography-based approaches have been extensively used. For example, in order to uncover the interacting partners of the nuclear enriched endothelial lncRNA MANTIS Leisegang et al. exposed 3’end biotinylated transcripts to EC nuclear extracts, allowing for RNA:protein complexes to be formed which were then be captured and isolated. This study identified an interaction of MANTIS with Brahma-like gene 1 (BRG1), a subunit for the chromatin-remodelling complex SWI/
SNF. This interaction was shown to regulate SMAD6, SOX18, and COUP-TFII expression, leading to the increased angiogenic function associated with the lncRNA. A similar in vitro strategy was used to identify a direct interaction between SENCR and the cytoskeletal-associated protein 4 (CKAP4), via a non-canonical RNA-binding domain. This CKAP4:SENCR association was found to indirectly stabilize CDH5 at the adherens junction and thus maintain normal EC membrane homeostasis. Nonetheless, despite its success, this system relies on the in vitro transcription of the lncRNA rather than targeting endogenously expressed transcripts present in the cell, which is prone to the formation of non-physiological interactions.

More recently, biotin-labelled RNA antisense probes were used to investigate endogenous GATA6-AS:protein complexes in HUVEC. The study demonstrated that this lncRNA exerted its effects on EC function by binding the nuclear enzyme LOXL2 and impairing its deamination activity on H3K4me3, which is accompanied by transcriptional silencing of a variety of endothelial genes.

4.3 RNA:RNA interaction
Much like miRNAs, snoRNAs, and tRNAs, lncRNAs can directly interact with other RNA transcripts through direct base pairing. Several strategies to uncover these RNA:RNA interactions have started to emerge, many of which have successfully been used to understand the mechanistic action of ribosomal RNA and small nuclear RNAs.

Similarly to RNA:protein detection approaches, modified versions of RAP can be used to detect lncRNA:RNA interactions. These techniques rely on RNA capture using one or several antisense probes.
oligonucleotides followed by RNA sequencing. Various cross-linking methods (i.e. 4′-aminomethyltri-oxalene, formaldehyde, disuccinimidyl glutarate, or ultra-violet irradiation) can be used depending on the interactions of interest, be it only direct RNA:RNA interaction or indirectly via a protein intermediates. Techniques such as CLASH (cross-linking, ligation and sequencing of hybrids) for example, take advantage of UV cross-linking to induce the formation of covalent RNA bonds to identify RNA:RNA interactions occurring in close physical proximity. This method has led to the experimental identification of more than 18 000 miRNA:RNA interactions. Highly expressed lncRNAs can potentially act as competing endogenous RNAs (ceRNAs) or sponges to regulate the expression of other RNAs, be it non- or protein coding. Large bioinformatic databases can assist in the discovery of such interactions. For example, based on StarBase v2.0 predictions, Shan et al. found that the EC-associated lncRNA RNCR3 could regulate the expression of the atheroprotective Kruppel-like factor 2 (KLF2) by binding to miR-185-5p, a post-transcriptional regulator of KLF2.

4.4 RNA:DNA interaction
LncRNAs are key regulators of chromatin states in a variety of biological processes, both in cis, via the regulation of neighbouring genes, or in trans to regulate distantly located genes. While IncRNA:DNA co-localization can be validated using fluorescent probes, FISH-based strategies have limited ability to identify DNA regions bound by IncRNAs and higher resolution methods are needed. RNA-based methods for high-throughput identification of chromatin regions bound by IncRNAs have recently emerged. As with RNA:protein and RNA:RNA interactions, RNA capturing techniques can be modified to target chromatin interactions, these include chromatin isolation by RNA purification (ChiRP), capture hybridization analysis of RNA targets (CHART) and RAP-DNA.

First introduced in 2011, ChiRP is now widely used to identify associations between a lncRNA of interest and chromatin. As with some of the previous methodologies described, the samples are crosslinked and biotin labelled oligonucleotides targeting a lncRNA of interest. The IncRNA:DNA complexes can then be purified using biotin-binding, magnetic streptavidin beads and then sequenced to identify any associated genomic regions. In its original study, ChiRP was used to isolate DNA regions associated with the IncRNA HOTAIR, showing that the IncRNA preferentially associates with GA-rich DNA motifs. A similar approach was recently used to fine-map genome-wide MEG3 binding sites. Using 15 biotin-labelled antisense DNA oligonucleotides (oligos) spanning across lncRNA, the pulldown found that the genomic regions of 5622 genes can be associated with MEG3, including several TGF-β pathway genes. MEG3 expression has since been consistently linked to EC migration, proliferation and angiogenesis.

5. LncRNA discovery, function and translation: challenges and future directions
Whilst the therapeutic potential of IncRNAs is mentioned in most studies, real-world examples of tissue-specific clinical applications based on IncRNAs remain limited, with many emerging pre-clinical studies focusing on their utility as markers of disease. This is particularly true in cancer research, where MALAT1 overexpression has been linked to tumour development and progression in a variety of tissues. A recent meta-analysis of 14 independent studies comprising data from 1373 patients found a significant association between MALAT1 expression and survival rates, independent of cancer type or country of residence, making it a powerful prognostic marker for cancer patients and an attractive target for anti-metastatic therapy. Similarly, the IncRNA HOTAIR has also been put forward by multiple studies as a potential biomarker for various cancers involving breast, liver, gastric, lung, and oesophagus. Throughout the various aetiologies of cardiovascular disease, some IncRNAs markers, whilst not endothelial-specific, have been reported. A study comparing the expression of IncRNAs in peripheral blood cells of healthy volunteers and myocardial infarction patients, demonstrated that the IncRNA HIF1αAS2, KCNQ1OT1, MALAT1 were significantly up-regulated in myocardial infarction patients. In a recent clinical study of CAD, the IncRNA CoroMarker was used to successfully identify 78% of CAD patients out of 221 CAD patients and 187 control individuals. Importantly, CoroMarker is mainly present in circulating EVs, which are stable in plasma and easy to use as a biomarkers. The IncRNA LIPCAR is consistently upregulated in the plasma of ischaemic and non-ischaemic heart failure patients and has been consistently reported to be an independent predictor of cardiovascular-related death.

Expressed in vascular ECs, macrophages, and coronary smooth muscle cells, higher plasma levels of the IncRNA ANRIL have been found to be associated with the incidence of in-stent restenosis (ISR). Considering the importance of inhibiting neointimal proliferation, while promoting re-endothelialization after vascular stenting, along with the IncRNAs reported regulation VEGF expression and function in primary EC, ANRIL may ultimately be an optimal prognostic factor for ISR. Additionally, a meta-analysis of 14 genome-wide association studies highlighted ANRIL as a crucial locus of genetic sensitivity for CAD. Several single-nucleotide polymorphisms in this locus, influencing ANRIL function and levels of expression, have since been found to be associated with increased susceptibility to CAD and diabetes. Lastly, ANRIL has also been consistently found to be up-regulated in plaque and plasma of atherosclerosis patients, making it a potential biomarker for atherosclerosis.

The introduction of IncRNA targeting strategies into the clinical setting comes with many challenges. Due to the pleiotropic nature of some IncRNAs, tissue-specific delivery is imperative to guarantee treatment efficiency and minimal off-target effects. While certain transcripts may be involved in particular pathologies, their desired function may be tissue-specific and even cell-type–specific. For example, while ANRIL expression may be a prognostic factor for ISR and atherosclerosis, systemic modulation of this lncRNA may prove to be harmful as it is one of the most commonly altered IncRNAs during cancer development and progression, including ovarian cancer, breast cancer, and lymphoblastic leukaemia. Additionally, with studies showing an average of 4 different isoforms per IncRNA, the transcriptional complexity of a particular IncRNA locus must be thoroughly characterized before treatment strategies can translated into the clinical setting. As such, effective therapies targeting or using IncRNAs in the clinical setting must take into account not only possible off-target effects, the route of delivery used, drug immunogenicity, treatment dosage, and duration but also sub-cellular transcript location, transcript size and sequence.

Further, the lack of sequence conservation across different species makes the translation of pre-clinical animal studies extremely challenging. Take for example the IncRNAs myocardial infarction-associated transcript 1 (MIRI71) and 2 (MIRI72), which while found to be associated with left ventricular remodelling after myocardial infarction in mice, have no corresponding human homologs. Conversely, smooth muscle...
enriched lncRNA (SMiLR) seems to be conserved only in humans, signifi-
cantly limiting future preclinical studies using animal models and possible
clinical translation.\textsuperscript{113} However, promoter regions of lncRNAs, have in
fact been shown to harbour substantial conservation throughout differ-
ent organisms, comparable to that of protein-coding genes.\textsuperscript{114} Further, it
is possible that in some cases, despite divergent sequences, lncRNA sub-
structures may be conserved between human and model organisms\textsuperscript{115,116} and so small molecules targeting these structures might have similar effects across species.

Finally, given their high spatiotemporal expression specificity, certain
lncRNA may allow to circumvent the need for endothelial-targeting
tools with minimal off target effects. Take for example the Wisp2 super-
enhancer-associated lncRNA (WISPER), whose expression and function
are highly specific to cardiac fibroblasts, making it an attractive candidate
for targeted antifibrotic therapies.\textsuperscript{117} With continued implementation,
new lncRNA discovery and characterization techniques have the potential
to reveal previously unknown subsets of EC-specific lncRNAs.

6. Conclusions

An increasing body of evidence demonstrates that lncRNAs are active
regulators of endothelial function. It is necessary to further define both
the key lncRNA candidates and the molecular partners involved at a
mechanistic level. Greater variety in lncRNA profiling in diverse ECs is
clearly required. Increased lncRNA annotation in animal EC models is
possible an even greater challenge and it is crucial to expand in vivo
evidence of causality. The continued emergence of high-throughput data-
sets has identified several attractive candidates, yet these are often far
from fully characterized mechanistically. Meeting these challenges is only
possible with continued screening efforts using cutting-edge RNAseq
techniques paired with robust RNA capturing tools, this is particularly
important with the emergence of single-cell RNA sequencing offering
further insights into cell transcriptome heterogeneity in ECs. As more in-
dividual lncRNA are characterized, and as the class as a whole is further
investigated, their general categorization, characteristics and quirks be-
come ever more clear. The field is now poised to answer whether
lncRNA are intrinsically linked to broad questions surrounding endothel-
ial heterogeneity and fate. For instance, the spatiotemporal expression
of lncRNA could fit well with fundamental differences between ECs de-
derived from various vessel types or other vascular cell types. With the
potential to contribute answers to such pertinent questions, alongside their
potential as precise modulators of ECs via gene therapy, it is only a mat-
ter of time until a more fully-fledged and representative landscape of EC
lncRNA emerges.

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