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Functionally conserved non-coding regulators of cardiomyocyte proliferation and regeneration in mouse and human.

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Transcriptomic regulation of cardiac regeneration.

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Heart Failure and Cardiac Disease

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Abstract

Background

The adult mammalian heart has little regenerative capacity after myocardial infarction (MI) while neonatal mouse heart regenerates without scarring or dysfunction. However, the underlying pathways are poorly defined. We sought to derive insights into the pathways regulating neonatal development of the mouse heart and cardiac regeneration post-MI.

Methods and Results

Total RNA-seq of mouse heart through the first 10 days of postnatal life (referred to as P3, P5, P10) revealed a previously unobserved transition in microRNA expression between P3 and P5 associated specifically with altered expression of protein-coding genes on the focal adhesion pathway and cessation of cardiomyocyte cell division. We found profound changes in the coding and non-coding transcriptome after neonatal MI, with evidence of essentially complete healing by P10. Over two thirds of each of the mRNAs, lncRNAs and microRNAs that were differentially expressed in the post-MI heart were differentially expressed during normal postnatal development, suggesting a common regulatory pathway for normal cardiac development and post-MI cardiac regeneration. We selected exemplars of miRNAs implicated in our data set as regulators of cardiomyocyte proliferation. Several of these showed evidence of a functional influence on mouse cardiomyocyte cell division. In addition, a subset of these microRNAs, miR-144-3p, miR-195a-5p, miR-451a and miR-6240 showed evidence of functional conservation in human cardiomyocytes.

Conclusions

The sets of mRNAs, miRNAs and lncRNAs that we report here merit further investigation as gatekeepers of cell division in the postnatal heart and as targets for extension of the period of cardiac regeneration beyond the neonatal period.
Background

Heart disease is amongst the commonest causes of death worldwide. Whilst planarians, teleost fish and some amphibians have the ability to regrow limbs or organs including the heart, mammals are limited in their regenerative abilities. Following myocardial infarction (MI), damaged myocardium is replaced by scar tissue triggering cardiac remodelling and impaired cardiac function.

A major barrier to cardiac regeneration in adult mammals is the withdrawal of the cardiomyocyte from the cell cycle in early postnatal life. In the mouse, although DNA replication continues in the first week of postnatal life, cytokinesis ceases. By the second week of life, mouse cardiomyocytes withdraw from the cell cycle, 90% of cardiomyocytes are binucleated and, aside from a recent report of a proliferative burst at P15, recently contested, heart growth after the first week of life occurs mainly through cardiomyocyte hypertrophy rather than proliferation. This programme of cell cycle arrest is hypothesised to result from metabolic, physiological and anatomical changes in the first week of life including a shift to oxidative metabolism with relative hyperoxia compared to foetal life, increasing ventricular pressure and accumulation of extracellular matrix. These considerations raised the possibility that regeneration of the mouse heart could follow cardiac injury in the immediate neonatal period and indeed complete cardiac regeneration has recently been demonstrated following apex resection and infarction of the mouse left ventricle (LV) on the first day of postnatal life.

Transcriptome analyses in planarians and amphibians have yielded significant insights into the regulatory mechanisms underlying tissue and organ regeneration in these species but morphological, physiological and genetic differences between these species and mammals...
limit the translational potential for application to human disease. They do, however provide the basis of the molecular investigations in mammals\textsuperscript{19}. In mice, the role of individual microRNAs (miRNAs) and protein-coding messenger RNAs (mRNAs) have been defined by genetic analyses and gene targeting of specified mRNAs and miRNAs\textsuperscript{16,20,21}. More recently with recognition of the functions of other RNA species, certain long non-coding RNAs (lncRNAs) have been implicated in cardiac biology\textsuperscript{22}, for example, in protection from cardiac hypertrophy, foetal heart development, and autophagic cell death in myocardial infarction\textsuperscript{23-26}. Although previous genome-wide studies have examined the coding transcriptome in neonatal and regenerating heart following apical resection\textsuperscript{27}, genome-wide changes in the non-coding transcriptome have not been reported.

Here we have performed an in-depth analysis of the coding and non-coding mouse LV transcriptome by RNA sequencing at key time points in early postnatal mouse heart development and in the LV during the period of regeneration following neonatal ligation of the left anterior descending coronary artery (LAD). The study defines the major sets of coding and non-coding RNAs associated with normal postnatal cardiac development and with regeneration of the neonatal heart following MI. We perform functional studies on a key set of exemplar miRNAs in mouse and human cardiomyocytes and identify conserved roles for these miRNAs in mammalian cardiomyocyte proliferation and mitosis. Our study provides new insights into the transcriptional regulation of neonatal cardiac development and regeneration in mammals that will be of value in future comparative and human intervention studies of cardiac regeneration.

**Materials and Methods**

The data, analytic methods, and study materials have been made available to other researchers for purposes of reproducing the results or replicating the procedure. They have been made publicly available at the Annotare, accession number E-MTAB-6272. All animal experiments
were performed in accordance with the Austrian Ethical Board, the Imperial College and the UK Home Office guidelines.

Left anterior descending artery (LAD) ligation was performed in P0.5 neonatal C57BL6J mice, as previously described [15]. Left ventricle (LV) was harvested from three C57BL6J mice from sham-operated and LAD-ligated animals at three, five, seven and 10-days post ligation. Left ventricle (LV) was also harvested from three C57BL6J mice at P1, P3, P5, P7, P10 (referred to as physiological time points) in which no surgical procedures had been performed. Coding and non-coding RNA-Seq libraries were prepared using Illumina TruSeq stranded RNA library preparation and TruSeq small RNA library preparation kits following manufacturers’ protocols. Mouse genome assembly GCRm38/mm10 and the Ensembl transcript annotations (version GRCm38.87) were used as the reference sequence in all the analyses. RNA-Seq reads were quantified using Salmon (v.0.8.2)\textsuperscript{28}. Differential expression (DE) analysis was performed using DESeq2 Bioconductor package. Raw p values were adjusted for multiple testing with the Benjamini-Hochberg procedure. Weighted gene co-expression cluster analysis (WGCNA) and a short timer series expression miner (STEM) analysis were performed to identify clusters of co-expressed mRNAs. Enrichment of KEGG Pathways for DE mRNAs was calculated using DAVID (v6.8) across all pairwise comparisons. MiRNA-Seq reads were aligned with Bowtie and MirDeep2 was used to determine the presence and quantity of miRNAs based on mouse precursor sequences and mature sequences from mouse and rat with miRBase release 19. MiRNA binding sites were predicted in-silico across each gene using the union of five separate prediction methods. Correlation matrices were generated between mRNAs and miRNAs and between mRNAs and IncRNAs. Potential functional relationships were identified by Spearman correlation, adjusted for multiple testing correction at FDR < 0.05. P5 mouse cardiomyocytes were treated with mmu-miR-22-5p, mmu-miR-144, mmu-miR-148a-3p, mmu-miR-193a-3p, mmu-miR-193b-3p, mmu-miR-221-3p, mmu-miR-331-3p, mmu-miR-451a inhibitors and
mmu-miR-6240 mimic and iCell® Cardiomyocytes were treated with human analogues of these miRs. Cells were incubated 10 µM EdU 4 h after seeding and subsequently fixed with 4% paraformaldehyde and permeabilized in 0.2% (v/v) Triton X-100 before incubation with Click-iT reaction. Hoechst was used for nuclear staining and pH3 to mark mitotic cells. The analysis was then performed with conventional epifluorescence microscopy.

Results

To define the transcriptional changes occurring during physiological postnatal cardiac development and after neonatal MI, we generated RNA-Seq expression data of the coding and non-coding transcriptome from triplicate LV tissue harvested from C57BL/6 mice on postnatal day 0.5, 3.5, 5.5, 7.5 and 10.5, referred to as P1, P3, P5, P7 and P10, and from LV at 3 to 10 days following LAD ligation (Figure 1).

Transcriptional changes in coding RNA

During the time course of physiological postnatal growth from P1 to P10, we identified 9,450 unique differentially expressed (DE) mRNAs across all possible pairwise comparisons (Supplemental Table 1).

We identified an increase in gene expression of 11 cardiomyocyte markers at different time points and an increase in cardiac fibroblast marker (Ddr2) after P5, reflecting the change in cellular composition within the LV (Supplemental Figure 1). WGCNA and STEM analyses of these genes identified clusters enriched for focal adhesion (p-adj = 1.22E-13), DNA replication (5.47E-16), ribosome (1.64E-50) and OXPHOS (p-adj = 0.013) pathways of KEGG analysis (Supplemental Figure 2A, B). These results were affirmed in pairwise comparisons between time points, with enrichment for DNA replication genes between P1 and P5, oxidative phosphorylation, focal adhesion genes between P3 and P10, and ribosomal transcripts throughout a 10-day period (Figure 2A, Supplemental Table 2). Investigation of pairwise comparisons between adjacent time points revealed a sharp increase in the number of
differentially expressed genes (DEG) from between P3 to P5 (494) to P5 to P7 (3,545), with
the largest number identified between P7 and P10 (4,375) (Figure 2B, Supplemental Figure
3A). Of the 40 most DEG between P5 and P7, 10 genes (Ube2c, Kif20a, Top2a, Racgap1,
Cdca3, Cenpf, Ccna2, Iqgap3, Anln, Ccnb1 and CenpE) had GO terms associated with mitotic
cell cycle process all of which were downregulated between P5 and P7 (Figure 2C,
Supplemental Figure 2B).

Following sham operation and LAD ligation, transcriptome analysis showed a large number of
DEG between sham-operated and LAD-ligated mice three days after injury (shamvLAD (P3)
= 2,741). The number of DEG declined very sharply three days post ligation, with 499 genes
found to be DE between sham and LAD at P5, 112 between sham and LAD at P7, and 61
between sham and LAD-ligated at P10 (Figure 2D, Supplemental Figure 3B). Upregulation of
sarcomere expressed Mypn and cardiac fibroblast marker Ddr2 was observed following LAD
ligation at P3 with restoration of physiological expression profile of cardiomyocyte markers
from P7 (Supplemental Figure 1B).

STEM analysis of the post-LAD ligation data showed 15 statistically significant profiles of
changing gene expression, which had generally decreasing gene expression related to immune
processes such as phagosome (p-adj = 5.9E-9) and cytokine-cytokine receptor interaction (p-
adj=8.77E-8) (Supplemental Figure 2C). Four profiles (40, 42, 48 and 49) showed increasing
gene expression pattern and were significantly enriched for OXPHOS which was also observed
in the WGCNA analysis (Supplemental Figure 2C, D). STEM analysis of mRNA expression
in the sham-operated mice (P3-P10) showed pathway enrichment for 13 profiles, mirroring
enrichments observed in the physiological samples.

Consistent with the STEM annotation analysis, pairwise comparisons of the sham and LAD
data at P3 showed that the major classes of DEG between P3 sham and LAD were within
OXPHOS and lysosome pathways (Figure 2E, Supplementary Table 4). Of the top 40 most
significant DE mRNAs, we identified five genes (Fn1, Col1a1, Tnc, Thbs1 and Col1a2) with an increase in expression between sham and LAD at P3 that are implicated in focal adhesion pathways and three genes (Cd68, Laptm5 and Atp6v0d2) representing lysosome pathways (Figure 2E, F). Strikingly, 74% of the 3,210 genes that were DE between sham and LAD were also DE in the pairwise comparisons in the normal physiological data (Figure 2G). Of the 10,284 DEG, 20 were validated and further characterised by qPCR across all conditions used in the study using an independent set of triplicate samples (Supplementary Figure 4A).

**Changes in non-coding RNA transcriptome**

Next, we analysed changes in the expression of non-coding RNAs including lncRNAs and miRNAs in the normal developing heart. Between all pairwise time point comparisons from P1 to P10, we identified 545 unique DE lncRNAs (Supplementary Table 1). A fourfold increase in the number of DE lncRNAs was observed between P3 and P5 (n=24) and between P5 and P7 (n=107) comparisons (Figure 3A). Only 59 of 545 DE lncRNAs have assigned names, for the remainder, there has been limited, functional characterisation. Four DE lncRNAs between P5vP7, within the top 40 DE, that have names and functions associated with them include: Nespas, Sorbs2os, H19 and Lockd (Figure 3B, Supplementary Table 1). This is the first report showing DE of any of these lncRNAs in the postnatal mammalian heart.

To explore potential interactions between lncRNAs and mRNAs in the developing heart, we tested for correlation between lncRNA and mRNA expression across P1 to P10 time points. Of the 545 DE lncRNAs, 491 correlated significantly (p-adjSpearman < 0.05) with between 1 and 2,604 mRNAs either in cis or trans. Overall, we found that there were slightly more (median = 26) lncRNAs significantly correlating in trans compared to in cis (median = 15), implying that their regulatory potential is not limited by chromosomal location (Figure 3C).

To determine possible functional regulatory roles of DE lncRNAs, we performed a KEGG analysis on the sets of genes correlating in cis or trans with DE lncRNAs. We identified 86
IncRNAs that correlated significantly with gene sets enriched for the ribosome pathway, 113 for oxidative phosphorylation, and 103 with enrichment for the focal adhesion pathway (Supplementary Table 3).

Between sham-operated and LAD-ligated LV at P3 we identified 51 DE IncRNAs, 55 DE IncRNA at P5 and eight DE IncRNAs at P7. No DE IncRNAs were identified at P10 (Figure 3E, Supplementary Table 1), in keeping with the marked reduction in DE mRNAs and miRNAs at later time points. The 51 DE IncRNAs between sham and LAD comparisons at P3 include the known IncRNAs H19, Dnm3os, Lockd, Malat1, Meg3, Mhrt, Mirt1, Neat1, Slmapos2, Zfp469 and 41 IncRNAs with unknown function (Figure 3E). A selection of these IncRNAs was significantly correlated with gene sets enriched in ribosome, OXPHOS, focal adhesion, lysosome and phagosome KEGG pathways (Supplementary Table 3). Seventy three of the 109 DE IncRNAs (67%) between sham and LAD were also DE between time points in the physiological samples (Figure 3F, Supplementary Table 3).

Analysis of small RNAs identified 413 DE miRNAs across all pairwise comparisons of physiological time points (Supplementary Table 4). Expression of 22 of 413 DE miRNAs was tested in separate samples from different animals, in all time points by qPCR and these were all validated (Supplementary Figure 4B). The changes were also validated in sorted cells’ subpopulations, showing that the change of expression occurred both in cardiomyocytes and endothelial cells (data not shown). Of the 413 DE miRNAs, 240 were DE between the P3vP5 time points, 197 were unique (Figure 4A, Supplementary Table 4). The marked transition in expression of these miRNAs, between P3 and P5, has not previously been observed.

To identify the potential roles of DE miRNAs during the P1 to P10 time period, we examined the correlation between the 413 miRNAs that were DE between all the time points and all mRNAs expressed in these samples, and intersected these data with the *in silico* predicted binding partners of the DE miRNAs to give a set of RNAs that correlate with and may be
targeted by these miRNAs (Supplementary Figure 5). We identified 65 unique miRNAs where their significantly correlated gene targets are enriched for specific KEGG pathways, 34 of which target a total of 67 genes associated with the focal adhesion pathway (Supplementary Table 5). Interestingly, orthologues of 49 of these 65 miRNAs were also identified in the human genome and these showed conservation of gene targets for a median of 84% of the orthologous genes within the human pathways (Supplementary Table 5).

We also investigated the temporal relationship between miRNAs and mRNAs. The 240 DE miRNAs, identified between P3 and P5, are predicted to target 2,731 mRNAs. Of these mRNAs, we observed a significant overlap with 222 of 494 of DE mRNAs between P3 and P5 (OR=2.09, p=7.51e-15) and 1,091 of the 3,545 DE mRNAs between P5 and P7 (OR=1.18, p=3.79e-4).

Small RNA-seq analysis showed 153 DE miRNAs between sham and LAD three days post ligation, followed by a marked decline in the number of DE miRNAs between sham and LAD at later time points (Figure 4D). The top 40 significantly DE miRNAs between sham and LAD at P3 have not been previously reported as DE following LAD ligation (Figure 4E). The 153 DE miRNAs identified between sham and LAD at P3 are predicted to target 2,231 mRNAs. Of these 2,231 mRNAs, 1,090 overlap with the 2,741 DE mRNAs identified between sham and LAD at P3 (OR=2.06, p<2.2e-16).

Of the 39 DE miRNAs that correlated with and have predicted targets amongst the DE mRNAs, 14 miRNAs target gene sets of between 9 and 314 genes in pathways for cancer, and 14 miRNAs target between 13 and 23 mRNAs in focal adhesion (Figure 4E, Supplementary Table 5). Interestingly, 31 of 39 miRNAs were conserved in humans and targeted a median of 75.7% of the orthologous genes in corresponding human pathways. Mirroring the mRNA data, 83% of the miRNAs that were DE between sham and LAD were also DE in the pairwise comparisons between the physiological time points (Figure 4F).
Functional analysis of miR inhibition and overexpression in P5 mouse cardiomyocytes

To test the functional effects of miRNAs on cardiomyocyte proliferation we performed inhibition and overexpression studies in mouse and human cardiomyocytes, on a set of miRNAs that exhibited significant changes in physiological and pathological conditions and correlated with changes in mRNA in focal adhesion pathway. We obtained over 80% reduction of the expression of nine miRNAs in primary mouse cardiomyocytes and a subset of four of their human orthologues in iCell® cardiomyocytes, and over 50% overexpression of miR-6240 (data not shown). qRT-PCR analysis of the expression of cell cycle-regulating cyclins revealed that the levels of CcnA2, CcnD2, and CcnE2 increased significantly (> 2-fold) following treatment with miR-22-5p, miR-451a, and miR-195a inhibitors, and with miR-6240 mimic, in comparison to cells treated with scramble (p < 0.05) (Figure 5A). Treatment with seven other miR inhibitors did not result in any significant changes (p > 0.05) of tested cyclins expression (Figure 5A). Expression of CcnA1, CcnD1, CcnD3, and CcnE1 did not change in response to inhibition or overexpression of any of the miRNAs.

To determine whether inhibition or overexpression of these miRs plays a direct role in promoting cardiomyocyte proliferation we measured the nuclear incorporation of EdU (S-phase marker) and pH3 staining (mitosis marker) in P5 mouse cardiomyocytes. A marked increase in proliferating (EdU positive) cells (up to 5-fold) was observed for cardiomyocytes treated with miR-22-5p, miR-143-3p, miR-148a-3p, miR-193a-3p, miR-193b-3p, miR-195a-5p, miR-221-3p, miR-331-3p, miR-451a inhibitors and miR-6240 mimic (Figure 5B). Likewise, an increase of mitotic (pH3 positive) cells was seen (up to 3-fold), following treatment with miR-22-5p, miR-195a-5p and miR-451a inhibitors and miR-6240 mimic (Figure 5C, Supplementary Figure 6A). Scramble-treated mouse cells served as the negative control for both assays.

Functional analysis of selected miRs in human cardiomyocytes
Given our data showing that several miRNAs regulate aspects of proliferation in P5 mouse cardiomyocytes, we tested whether the human orthologues of these miRNAs can functionally regulate cardiomyocyte proliferation in iCell® cardiomyocytes. We transfected iCell® cardiomyocytes with a subset of human miR inhibitor and mimic orthologues that we had previously tested in mouse cardiomyocytes. qRT-PCR analysis of cyclins expression revealed elevated levels of Ccna2, CcnD2 and CcnE2 in miR-22-5p, miR-451a and miR-6240 treated cells in comparison with scramble treatment (p < 0.05) (Figure 5D). As with the mouse miR interventions, levels of Ccna1, CcnD1, CcnD3 and CcnE1 were unchanged (Figure 5D). iCell® cardiomyocytes treatment with miR-6240 mimic showed an increase in number of proliferating cells and treatment with miR-144-3p, miR-195a-5p, miR-451a and miR-6240 showed up to a 2–fold increase in the number of mitotic cells (Figure 5E, F, Supplementary Figure 6B).

**Discussion**

We set out to define the programme of the coding and non-coding transcriptome in the healthy neonatal heart during the period of loss of regenerative capacity and to relate this to the transcriptional changes associated with cardiac regeneration following neonatal MI. We found a sharp transition in microRNA expression in the developing heart between P3 and P5 associated with subsequent changes in expression of genes on the focal adhesion pathway and cardiomyocyte division arrest. We mapped profound changes in the transcriptome that returned to normal within 10 days following neonatal MI, indicating essentially complete healing of the myocardium by this time point, confirming our previous findings\(^1\). We showed that two thirds of all RNA species that were DE in the post-MI heart were also DE during normal postnatal development, suggesting a common regulatory pathway for normal post-natal cardiac development and post-MI regeneration. Finally, we demonstrated that miR-144-3p, miR-195a-5p and miR-451a inhibition and miR-6240 activation have functionally conserved roles in cell proliferation and mitosis in mouse and human cardiomyocytes.
We found that the first 10 days of postnatal life were associated with alterations in gene expression of thousands of genes, particularly those encoding proteins involved in cell cycle progression at early time points, oxidative phosphorylation at later time points and protein translation throughout. These enriched pathways are likely reflective of changes in ventricular pressure, transition from hypoxic to the oxygen rich postnatal environment with increased reliance on oxidative metabolism, and changes in cellular architecture and the extracellular matrix between P3 and P7\textsuperscript{13,29}. During the P5 and P7 time window, one quarter of the most DEG correspond to GO terms associated with M-phase mitosis and mitotic cell cycle checkpoint, including Cdk1\textsuperscript{30}, Ccna2\textsuperscript{31}, Cdc13\textsuperscript{32} and Bub1\textsuperscript{33}, in keeping with the withdrawal of cardiomyocytes from DNA replication and cell division at this time point. While the relative abundance of myocytes, cardiac fibroblasts, endothelial cells and vascular smooth muscle cells change in the LV during the first ten postnatal days\textsuperscript{34} and ontologies and pathways identified through our transcriptomic study are in part reflective of this, we were able to identify putative drivers of cardiomyocyte proliferation and functionally validate them in mouse primary cells and human cardiomyocyte cell line.

We found major differences in mRNA, miRNA and lncRNA expression between LAD-ligated and sham-operated mice three days following MI, but these differences had almost completely resolved within seven days of LAD ligation and increased gene expression of cardiomyocyte markers is restored to mirror closely the physiological gene expression changes. At the transcriptional level, therefore, the regenerative process was essentially complete by P10, although certain developmental and cardiac failure markers, like Nppa\textsuperscript{35}, remained elevated. The most profoundly DEG three days post LAD were those involved in immune processes, similarly shown in the contrasting model of heart regeneration following apex removal together with cell cycle progression and RNA synthesis\textsuperscript{27} and oxidative phosphorylation, in keeping
with previous observations of the importance of an active immune response in physiological regulation of cardiac regeneration in mice\(^{36,37}\).

Similar changes in expression were observed with lncRNAs, where of the 107 DE lncRNAs between P5 and P7, only seven, including \(H19\) and \(Neat1\), have proposed functions, in cell proliferation\(^{38-40}\), and none have been previously associated with postnatal heart development or regeneration. We also found evidence for \textit{trans}-regulation of expression by lncRNAs with enrichment amongst correlating gene sets on OXPHOS, ribosomes and focal adhesion pathways, and show significant enrichment for imprinting amongst DE lncRNAs. While previously described in other tissues\(^{41}\), enrichment for imprinted loci has rarely been observed previously in the postnatal heart or following MI\(^{42}\).

We observed a profound shift in microRNA expression in the developing heart between P3 and P5 associated with an altered expression of genes on the focal adhesion pathway between P5 and P7. Since genes and proteins on the focal adhesion pathway mediate the transduction of external stimuli such as increasing blood pressure or hypoxia\(^{29,43,44}\) into processes such as DNA replication and cell division\(^{45}\), we hypothesise that the set of miRNAs that were DE in the P3 to P5 time window are key to the regulation of molecular events leading to withdrawal of the cardiomyocyte from cell division in the first week of life. To test this hypothesis, we performed \textit{in vitro} inhibition and over-expression studies on 10 miRNAs which exhibited significant changes in physiological and pathological conditions. They include two miRNAs (miR-195a-5p and miR-22-5p) for which previous evidence has been presented\(^{20,46}\). Our results demonstrate that the inhibition of miR-22-5p and miR-451a and miR-6240 up-regulation individually elevate the expression of \(CcnA2\), \(CcnD2\) and \(CcnE2\) in P5 mouse and human cardiomyocytes leading to increased proliferation and cell division. We did not observe changes in expression of \(CcnA1\) (expressed in germ cells), \(CcnE1\) (lowly expressed in heart), \(CcnD1\) or \(CcnD3\) (low expression in tested cardiomyocytes) in comparison to scramble-treated
cells. Targets of miR-22 include Map2k1, Map3k9, Rock2 representing the focal adhesion
pathway, regulation of cell proliferation, and Aurkb participating in the regulation of alignment
and segregation of chromosomes during cell division. miR-451a targets Tbx1 and Ybx1
transcription factors regulating proliferation and differentiation of multipotent heart
progenitors and is implicated in translational control of foetal myocardial gene expression
after cardiac transplant. There is limited knowledge on the functional role of miR-6240, and
here we show for the first time, its function in cardiomyocyte proliferation and heart
regeneration in mouse and human cardiomyocytes. Interestingly, miR-22 has been previously
found to be highly expressed in cardiac muscle, upregulated during myocyte differentiation
which alone has been found to be sufficient to induce cardiomyocyte hypertrophy.

Our study reports the transcriptional changes in the developing and post-MI postnatal heart and
defines sets of mRNAs, miRNAs and lncRNAs that we propose to be the key regulators, at the
level of the transcriptome, of withdrawal of the postnatal mouse heart from DNA replication
and cell division. We also identify miR-144-3p, miR-195a, miR-451a and miR-6240 as
functionally conserved, non-coding regulators of cardiomyocyte division in neonatal mouse
and humans. Whilst we have not studied all the downstream consequences of our findings,
including more detailed impact on protein, cell cycle, and in vivo validation, our work provides
a platform for future studies.

Recent progress in research in developmental cardiology has significantly advanced our
understanding of heart development and regeneration. Insights from zebrafish models of heart
regeneration, following apex removal or cryosurgery, show that they are capable of myocardial
regeneration mediated mainly through the proliferation of pre-existing gata4+ cardiomyocytes
with miR-133 and miR-101, playing regulatory roles in this process, as also shown in our
neonatal mouse data set. More recently, the attempt to pinpoint the regulatory hubs in zebrafish
heart regeneration revealed a function of il6st, adam8, and cd63, also shown to be DE
expressed in our post-ligation data sets. Studies of heart regeneration in neonatal mice reported
*Myh7* and *Igf1r* as key drivers of gene interaction networks and pointing to *C1orf61, Aif1, Rock1* as potential inhibitors of cardiomyocyte proliferation and G1/S phase transition, genes that were also DE between physiological time points in our set. In addition, miRNAs from the miR-15 family, miR-503-5p, miR-199a, miR-99/100 and Let7a/c were also reported as critical regulators of the regeneration process, which were also found as DE in our physiological and sham/LAD comparisions in our data set. Interleukin 13, DE in the regenerating neonatal heart in our data set, has also been identified as a regulator of cardiomyocyte cell cycle entry mediated by STAT3/periostin and STAT6. Whilst our data show considerable overlap with previous observations in mice and zebrafish, we provide a systematic and comprehensive analysis of coding and non-coding transcriptome changes over multiple time points of the first 10 days of postnatal life and after neonatal LAD ligation, which has not been available hitherto.

In summary, we present a finely grained time course for mRNA, miRNA and IncRNA in the normal developing heart from postnatal day 1 (P1) to P10, and in the 3 to 10 days following neonatal MI. We found profound changes in the coding and non-coding transcriptome after neonatal MI, with evidence of essentially complete transcriptional healing by P10. We find a sharp transition in miRNA expression in physiological cardiac samples between P3 and P5, with differentially expressed miRNAs associated specifically with altered expression of genes on the focal adhesion pathway and cessation of cardiomyocyte division. Two thirds of each of the mRNAs, IncRNAs and microRNAs that were differentially expressed in the post-MI heart were also differentially expressed during normal postnatal development, suggesting a common regulatory pathway for normal cardiac development and post-MI cardiac regeneration. Of the miRNAs that we implicate in regulation of cardiomyocyte development and regeneration, 67% had targets that were conserved between mice and humans. We present a subset of miRNAs:
miR-451a, miR-6240, miR-195a-5p and miR-144-3p that showed functional evidence in vitro as regulators of cell division in mouse and/or human cardiomyocytes.

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Disclosures

None

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**Figure legends**

**Figure 1.** Experimental design.

Overview of experimental design showing time points at which LV tissue was harvested (A) during physiological time points, and following LAD or sham operation. P1-10, postnatal days 1-10; MI myocardial infarction, (B) sequencing pipeline and (C) functional investigation. All the experiments were performed in three individual animals for each time point and condition.

**Figure 2.** Changes of mRNA expression in physiological LV and following MI.
All mRNA sequencing experiments and data analyses were performed in individual animals for each time point and condition.

(A) KEGG pathway analysis between adjacent pairwise comparisons in physiological LV. (B) Venn diagram showing numbers of DE mRNAs between physiological pairwise comparison (C) Top 40 DE mRNAs between P5 and P7, (D) DE transcripts between LAD and sham samples-pairwise comparison, (E) KEGG pathway analysis between LAD and sham samples is pairwise comparison, (F) Top 40 DE mRNAs between LAD and sham 3 days post-surgery, (G) Overlap between DE coding transcripts in physiological and MI LVs.
Figure 3. Changes of lncRNA expression in physiological LV and following MI.

All lncRNA sequencing experiments and data analyses were performed in individual animals for each time point and condition.

(A) Venn diagram showing numbers of DE lncRNAs between adjacent pairwise comparisons in physiological time points. (B) Top 40 most DE transcripts between P5 and P7. (C) The number of correlating DE mRNAs with DE lncRNAs in the increasing distance from transcription start site (TSS). (D) Numbers of DE lncRNAs following sham and LAD operations in pairwise comparisons. (E) Identities of the most DE lncRNAs between sham and LAD-operated LVs three days post-surgery. (F) Overlap between DE lncRNAs between physiological LVs and following surgery.
Figure 4. Changes of miRNA expression in physiological LV and following MI.

All miRNA sequencing experiments and data analyses were performed in individual animals for each time point and condition.

(A) Venn diagram showing numbers of DE miRNAs between adjacent pairwise comparisons in physiological time points. (B) Heat map showing 40 most DE expressed miRNAs. (C) Focal adhesion and growth factor pathways diagram showing the genes targeted by DE miRNAs. (D) Numbers of DE miRNAs following MI. (E) Heat map of the most DE miRNAs three days post MI. (F) Overlap between DE miRNAs between physiological LVs and following surgery.
Figure 5. Functional analysis of miR inhibition and overexpression in P5 mouse and human cardiomyocytes.

Functional analysis experiments were performed in triplicates for each cell type and each transfection miRNA.

(A) Changes in mRNA expression of cell cycle regulating cyclins in P5 mouse primary cardiomyocytes following treatment with miRNA inhibitors and mimic. A significance indicated by star. EdU and pH3 staining revealing number of proliferating (B) and dividing cells (C) following treatment with miRNAs. (D) Changes in mRNA expression of cell cycle regulating cyclins in human iPSC derived cardiomyocytes following treatment with miRNA inhibitors and mimic. EdU and pH3 staining revealing number of proliferating (E) and dividing cells (F) iPSC derived cardiomyocytes following treatment with miRNAs.

A significance vs. scramble control indicated by stars as follows: *** $p \leq 0.001$, ** $p \leq 0.01$, * $p \leq 0.05$. 
References


