

MOLECULAR MECHANISM OF CARDIAC REGENERATION

by

Galip Servet Aslan

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APPROVED BY:

Assist. Prof. Dr. Fatih Kocabaş
(Thesis Supervisor)
.....

Assist. Prof. Dr. Esra Çağavi


.....

Assist. Prof. Dr. Hüseyin Çimen


.....

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ABSTRACT

MOLECULAR MECHANISM OF CARDIAC REGENERATION

Neonatal mammalian heart has recently been shown to possess the capacity to regenerate completely after injury. This remarkable regenerative capacity is lost after postnatal day 7. This transition has been marked with cardiomyocyte cell cycle arrest and induction of fibrotic response similar to what occurs after myocardial infarction in adults. We have recently outlined the function of Meis1 as a new cardiogenic factor that plays a pivotal role in neonatal cardiac regeneration. However, underlying molecular mechanisms of neonatal cardiac regeneration and other cardiogenic factors remained elusive. Here, we investigated the involvement of novel putative cardiogenic factors in neonatal cardiac regeneration and cardiomyocyte cell cycle withdrawal. We have confirmed their expression in the heart and cardiomyocytes. We have shown that expressions of Inpp5d, Dnmt3a, c-Myc and Cbl are significantly downregulated during neonatal cardiac regeneration process. Intriguingly, these four factors are upregulated in non-regenerative period of 7-day old mice after injury. Taken together, our findings suggest that Inpp5d, Dnmt3a, c-Myc and Cbl may be involved in the regulation of cardiomyocyte cell cycle progression and represent new targets for induction of cardiac regeneration.

ÖZET

KALP REJENERASYONUN MOLEKÜLER MEKANİZMALARI

Yeni doğan memeli kalbinin oluşturulan hasar sonrası rejeneratif özelliğe sahip olduğu yakın zamanda gösterildi. Öne çıkan bu çalışmada, rejeneratif kapasitenin doğumdan sonraki 7. günden itibaren kaybolmaktadır. Bu geçiş evresinin, miyokardiyal infraksüyona benzer şekilde kardiyomiyosit hücre siklus aresti ve fibrotik doku oluşumu ile tespit edilmektedir. Yakın zamanda yapılan çalışmalarda yeni doğan kardiyak rejenerasyonunda öncül bir rol oynayan Meis1'in fonksiyonunu vurgulanmıştır. Fakat, yenidoğan faredeki kardiyak rejenerasyonunun altında yatan diğer moleküler mekanizmaların ve diğer kardiyojenik faktörler hala bilinmemektedir. Burada, farklı olarak kardiyojenik faktörlerin yeni doğanda kardiyak rejenerasyonuna etkisini ve hücre döngüsündeki gerilemesini araştırdık ve bu faktörlerin kalpteki ve kardiyomiyositlerdeki ekspresyonunu doğruladık. Lnp5d, Dnmt3a, c-Myc ve Cbl faktörlerinin ekspresyonunun yeni doğanda kardiyak rejenerasyon sürecinde önemli ölçüde baskılandığını gösterdik. İlginç bir şekilde, rejeneratif olmayan zaman diliminde (doğumdan sonra 7. gün) yapılan cerrahi müdahaleden sonra, bu dört faktöründe arttığı gözlemlenmiştir. Hepsi birlikte ele alındığında, bulgularımız Lnp5d, Dnmt3a, c-Myc ve Cbl faktörlerinin kardiyomiyosit hücre döngüsü regülasyonunda etkili olabileceğine işaret etmekte ve kardiyak rejenerasyonun indüksiyonu için yeni hedefler sunmaktadır.

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LIST OF SYMBOLS/ABBREVIATIONS

BrdU	Bromo deoxyuridine
CDKI	Cyclin dependent kinase inhibitor protein
CSCs	Cardiac stem cells
ESC	Embryonic stem cells
FGF	Fibroblast growth factor
GATA	Globin transcription factor
GFP	Green fluorescent protein
HF	Heart failure
iCMs	Induced cardiomyocytes
LAD	Left anterior descending artery
μ L	Microliter
μ g	Microgram
mL	Microliter
Ph3	Phospho histone protein 3
RT-PCR	Real time polymerase chain reaction
siRNA	small interfering RNA

1. INTRODUCTION

1.1. HEART FAILURE

Heart Failure (HF) is a complex clinical syndrome associated with decreased function of ventricle to fill or eject blood and affecting more than 23 million people in worldwide [1]. Unfortunately heart transplantation in the presence of appropriate donor remains only definitive treatment against HF [2].

Cardiac regeneration is multidisciplinary research area comprising physiology, stem cell, developmental biology and tissue engineering, and has ultimate goal of achieving to reverse heart failure in the context of regenerative medicine (Figure 1.1). Over the past decade, there have been mounting evidences demonstrating that the heart is certainly not a terminally differentiated organ. There is a constant cardiomyocyte turnover within the mammalian, and the human heart throughout life [3-6]. Evidence for role of cardiac resident stem cell, cardiomyocyte proliferation and contribution of exogenous stem cells were identified in back to back reports [7-10].

However revealing cardiac regenerative capacity of human heart and designing robust therapeutical strategies requires learning more about molecular mechanism of cardiac regeneration. Due to the complexity of heart organ, different populations and regulators within the heart have been recently identified and indicated a complex system involving in regenerative capacity of heart. Moreover, studies on model organism including zebrafish, newt and murine heart giving great opportunity to enlighten underlying mechanism and recipe for cardiac regeneration. In the ligh of findings from those organism human based cardiovascular therapies are currently being developed and utilized in clinical trials to be used.

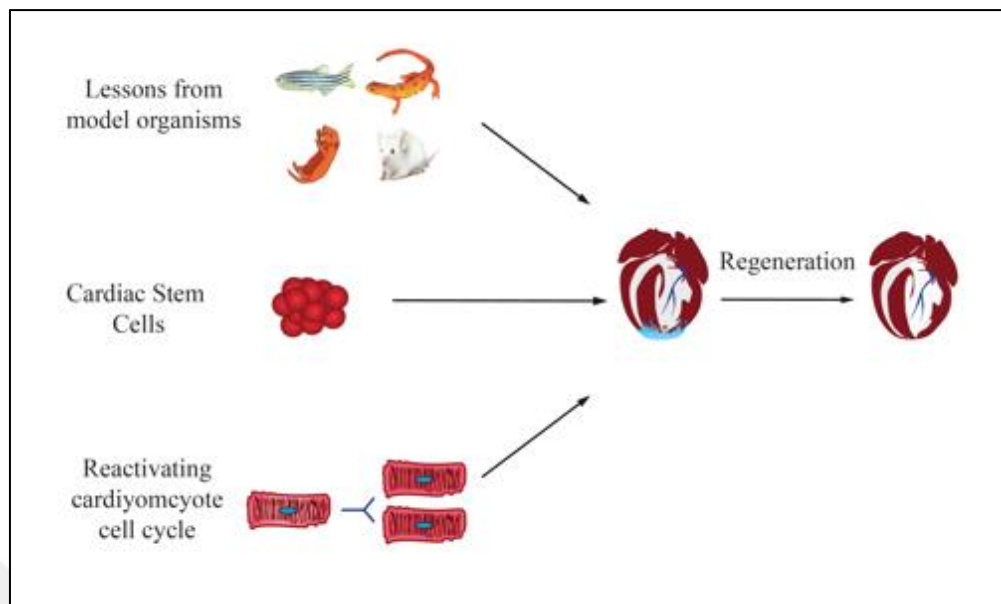


Figure 1.1. Different strategies to achieve cardiac regeneration in adults

1.2. HEART REGENERATION

Heart regeneration in lower vertebrates has been intensively studied. The regenerative potential of vertebrate hearts including amphibian, axolotls and newts was identified in early reports [11-13]. Using electron microscopy in 1974, Oberpriller et al. (1974) demonstrated the prospect of cardiac regeneration in newt. Later, Witman et al. (2011) reported that adult newt is able to completely regenerate its heart after a basal resection [14]. Zebrafish (*Danio rerio*) is a tropical fresh water fish that has been widely used in many different regenerative studies including heart [7, 8, 15], kidney [16], central nervous system [17] and others. The complete regeneration of zebrafish heart after amputation of the ventricular apex has already been reported [15] and led to new studies to understand the mechanisms of cardiac regeneration [7, 8, 18, 19]. On the other hand, the utilization of a recently developed cardiac injury model in 1-day old neonatal mice revealed that the neonatal mouse heart is also capable of regeneration after apical resection of 15% of the ventricular apex [20, 21]. Many different studies regarding the mechanism of cardiac regeneration in mammals were reported to enlighten underlying mechanisms of heart regeneration. Here, we review studies regarding cardiac regeneration in zebrafish, newt and neonatal mice (Table 1.1).

Table 1.1. Various cardiac injury methods in different organisms and their regenerative

Organism	Zebrafish	Newt	Neonatal Mice	Adult mice	Human
Injury model	Apical Resection	Apical Resection	Apical Resection	Apical Resection	-
	Cryoinjury	Basal Resection	Cryoinjury	Cryoinjury	LVAD
	Genetic ablation	-	Ischemic MI	Ischemic MI	Ischemic MI
Response and time.	Regeneration in 60 days	Incomplete regeneration	Regeneration-21 days	No regeneration	-
	Regeneration > 130 days	Regeneration 60 days	Regeneration 21 days	No regeneration	No regeneration
	Regeneration in 30-45 days	-	Regeneration in 21 days	Fibrosis & No regeneration	Fibrosis & No regeneration

1.3. HEART REGENERATION IN ZEBRAFISH

Heart regeneration has been observed in non-mammalian vertebrates' hearts such as in salamanders and zebrafish [15, 22-25]. Zebrafish have become one of the major model organisms to study cardiac regeneration over a last decade. This is largely due to the visibility of structures during development, easy access to the heart to perform surgical operations, large number of offspring and low cost of maintenance. In addition, an intact cardiovascular system in a zebrafish embryo is not required, which allowed the investigation of cardiac regeneration studies without causing the death of zebrafish embryos [26]. Poss et al. (2002) demonstrated zebrafish cardiac regeneration following an amputation of up to 20% of the ventricle by surgical resection [15]. This operation initially led to fibrosis, followed by the complete regeneration of lost tissue in 60 days. In addition to the resection of the heart, other means of injury in zebrafish have been shown to provide tools to study different aspects of heart regeneration with different degrees of regenerative response [27, 28].

The cryoinjury method, for instance, depends on the induction of injury by a liquid nitrogen probe on the heart. When this procedure was performed in zebrafish, it led to heart regeneration over a longer time period (more than 130 days) [28, 29]. Wang et al. (2011)

applied a genetic ablation injury to extrapolate the regenerative response of zebrafish hearts. They have selectively expressed diphtheria toxin gene A (DTA) in cardiomyocytes by Cre-loxp mediated recombination, which is under control of a cardiac myosin light chain 2 promoter (*cmclc2*). This led to the genetic ablation and death of cardiomyocytes, albeit it resulted in complete regeneration of the heart in 45 days [27]. These findings prompted studies regarding the identification of the origin of newly formed cardiomyocytes.

The source of newly grown cardiomyocytes following myocardial injury in zebrafish has been a subject of debate. Many researchers used to think that new cardiomyocytes following cardiac injury in zebrafish were originated from progenitor cells instead of pre-existing cardiomyocytes [30]. However, two landmark studies provided evidence that newly formed cardiomyocytes in the cardiac regeneration process were largely derived from pre-existing cardiomyocytes [7, 8]. Integration of the Cre recombinase system as well as the GFP inducible genetic lineage tracing method in zebrafish led to tracking the origin of newly formed cardiomyocytes in the apical injury model following the removal of 20 % of the ventricular apex [7, 8]. Expression of GFP in newly formed cardiomyocytes provided that they arise from pre-existing ones. Furthermore, this study suggested a dedifferentiation mechanism, which has been measured by the disassembly of sarcomeric organization of cardiomyocytes, and initiates cardiomyocyte cell cycle progression and proliferation. Besides, this cell cycle progression has been regulated by polo like kinase1 (*plk1*), an important cell cycle modulator [7].

Kikuchi *et al.* (2010) has provided further evidence on the origin of newly formed cardiomyocytes, which has relied on GATA4 expression. GATA4 has been expressed in cardiomyocytes of the subepicardial ventricular layer and proliferating cells near the site of injury [31-33]. Kikuchi *et al.* (2010) utilized *gata4*-EGFP and demonstrated that myocyte marker carrying cells expressed GFP. On the other hand, cells with epicardium marker did not express GFP two weeks post-injury. These results suggested that cardiomyocytes existing near the injury site are triggered to express GATA and reactivated the cardiomyocyte cell cycle and proliferation [8].

1.4. HEART REGENERATION IN NEWT

Notophthalmus viridescens, a kind of red-spotted newt, is classified in the urodele amphibians and is commonly accepted as the champion of regeneration. Regenerative biology studies in newt have established the extraordinary regenerative ability of various organs and tissues including limbs, tail, lenses, spinal cord and heart [14]. The newt heart is located close to the skin and made of three chambers (two atria and one ventricle). Trabeculae form the cardiac ventricle of newt, where a single layer of epicardial cells surrounds myocytes, fibroblasts and nerve fibers [34]. Initial reports on newt cardiac regeneration date back to the 1970s. In 1974, Oberpriller and colleagues showed the mitotic response of the newt heart and the possibility of newt cardiac regeneration. Although underlying studies did not report the complete regeneration of the newt heart after amputation of one-eighth of the ventricular apex, they led to increased mitosis in the heart [35, 36]. Thus, studies were rather performed with a modified apical resection model, in which the ventricular cavity was left intact and investigated for a longer period to assess regenerative response. In this case, complete cardiac ventricular regeneration has been observed in 60 days along with an increased expression of cardiac specific transcription factors such as GATA4, Nkx-2.5, GATA5, Islet1, and HAND2 at the peak of proliferation. This indicates that a proliferative response is achieved by a coordinated expression of transcription factors [14]. In addition, newt change the expression of extra cellular matrix (ECM) related genes instead of metabolic or inflammation related ones following cardiac injuries. The expression of ECM genes, such as collagen III and tenascin-C, increases just after amputation or injury of the ventricular apex. This suggested that reorganization of the ECM was involved in the replenishment of the lost cardiomyocytes [37, 38]. Moreover, Mercer et al. (2013) reported that tenascin-C significantly increases the reentry of cardiomyocytes into the cell cycle *in vitro* [37].

1.5. HEART REGENERATION IN MAMMALS

It was believed that the total number of cardiomyocytes in a mammalian heart is set at birth and does not change through life. However, it has been demonstrated over the past decade that the heart is certainly not a terminally differentiated organ [3-6]. A number of recent

studies provided strong evidence for the fact of cardiomyocyte renewal in human heart (Bergmann et al., 2012b; Laflamme et al., 2002; Quaini et al., 2002; Kajstura et al., 2010). Bergmann et al. (2009) utilized an elegant approach to determine the age of cardiomyocytes, thus determining if any cardiomyocyte turnover occurs in the human heart. Pulse-chase conditions of ^{14}C level in the atmosphere due to the testing of nuclear weapons during cold war enabled to measure the age of cardiomyocytes in human subjects (older than 20 years). Analysis of the ^{14}C content and turnover in cardiomyocytes indicated that cardiomyocytes were younger than expected, which suggested that they are not set at birth. Further analysis and mathematical modeling indicated that about 1% of cardiomyocytes are renewed per year at the age of 20, and 0.4% at the age of 75. This provided an estimation of 40-50% cardiomyocyte renewal in an average human lifespan [3].

Kajstura and colleagues (2010) have provided further evidence of cardiomyocyte renewal by utilizing samples from post-mortem hearts of thymidine analogue iododeoxyuridine (IdU) treated cancer patients. Analysis of IdU incorporation and turnover in the heart indicated the presence of 22 % cardiomyocyte turnover per year, which is higher than the estimations of Bergmann and colleagues [5]. Discrepancy between these two studies has been thought to be due to the age and distribution of human subjects. Mollova et al. (2013) recently outlined that there are distinct, age-dependent cardiomyocyte division rates (0.016% in 0-1 year old, 0.01% in 2-10 year old and 0.005% in 10-20 year old) [39]. In another study, male patients who received heart from female donor were subjected for chimerism of transplanted heart. Depending on Y chromosome analysis and immunolabeling of recipient primitive cells, contribution of primitive cells migration from recipient to graft area thus chimerism of heart was reported [40].

Moreover, Shiba et al. (2012) reported that integrated cardiomyocytes, which derived from human embryonic stem cells, could be used against arrhythmias in Guiana pig model. Beside previous findings suggested that transplantation of fetal cardiomyocytes can improve the function of infarcted hearts this was a landmark study regarding cell replacement therapies for cardiovascular disease [41-44]

Studies showed that the DNA damage response due to a high oxygen environment during postnatal mice exposure has been shown to be an important mechanism in cardiomyocyte cell cycle arrest [45]. A recent study investigated the effect of the left ventricular assist device (LVAD) on mitochondrial content and cardiomyocyte proliferation [46]. By

comparing pre-LVAD and post-LVAD patients, they have demonstrated that prolonged mechanical unloading causes to % 60 decreased mitochondrial mass and ROS as well as about three fold increased cardiomyocyte proliferation [46].

Examination of the regenerative capacity of the mouse heart took cardiac regeneration studies a step further. Mouse cardiomyocytes are highly proliferative during embryogenesis. After 4 days from birth (postnatal day 4), cardiomyocytes dramatically lose this proliferative capacity. Cardiomyocytes undergo karyokinesis without the cytokinesis step thus resulting in binucleation of 90% of adult cardiomyocytes [47-49]. Mammals differ from other vertebrates in terms of cardiac regeneration capacity by possessing mostly binucleated cardiomyocytes, greater heart volume, four chambered hearts, and high pressure containing blood flow and an associated complex genome [50]. Similar to zebrafish, one of the debated issues was the source of newly formed cardiomyocyte in mammals that was recently enlightened by rodent and human studies [21, 51]. Mice possess a low rate of cardiomyocyte turnover confirmed by various studies and different approaches. BrdU incorporation and quantification by an anti-BrdU antibody were utilized to assess cell proliferation in the mouse heart. Similarly, a thymidine analog (thymidine [³H]) was incorporated into newly formed DNA strands as the cell cycle progress and used as a marker for cardiomyocyte proliferation. Another approach utilized the incorporation of ¹⁵N, and coupled to multi-isotope imaging mass spectrometry (MIMS) to assess proliferating cells in the heart. These studies indicated that an adult mouse shows 0.74 - 4.5 % of an unstimulated rate of cardiomyocyte renewal (Table 1.2) [48, 52-54].

Table 1.2. Unstimulated rate of cardiomyocyte renewal in different species

Species	Estimated cardiomyocyte renewal/year	Methods	Sources of newly formed cardiomyocytes	References
Zebra fish	ND	Not determined	Largely cardiomyocytes but it doesn't not exclude the involvement of cardiac progenitors	[7, 8]
Mouse	0.74-4.5%	BrdU, ¹⁵ N, imaging mass spectrometry,	Largely cardiomyocytes but it doesn't exclude the	[52, 53, 55]

		[³ H] thymidine	cardiac progenitors	
Human	0.04-40%	¹⁴ C, accelerator mass spectrometry, Ki67, phospho-H3, Aurora B, and IdU	Largely cardiomyocytes but it doesn't exclude the cardiac progenitors	[5, 39, 56]

The source of newly formed cardiomyocytes in mammals have been the subject of debate for years [57]. Recent studies demonstrated that proliferation of pre-existing cardiomyocytes occurs in mice after myocardial infarction and reported that cardiac progenitor cells have a modest effect as suggested in previous studies [51, 52, 58]. However, the possibility of a progenitor or stem cell population to involve in cardiac regeneration following injury through differentiation has not been excluded. Along with the resident capacity to replenish cardiomyocytes, recent studies especially in neonatal animals suggest that mammalian hearts possess a hidden regeneration potential.

1.6. HEART REGENERATION IN NEONATAL MOUSE

Compared to zebrafish and newt, the adult mammalian heart has a limited capacity for cardiomyocyte renewal following injury and responds to cardiac tissue damage by scar formation. As we have explained earlier, mouse cardiomyocytes undergo dramatic changes during the first week of life as marked with the expression of adult isoforms of contractile proteins, and the induction of DNA synthesis without cytokinesis resulting in binucleation and cell cycle arrest at G₀/G₁ [48]. A recent landmark study accomplished a similar injury model of zebrafish in mouse and demonstrated that 1-day old neonatal mouse is capable of heart regeneration [21]. One study reported the complete regeneration of neonatal mouse heart without a visible scar and fibrosis following amputation of 15 % of the ventricle [21]. Another study permanently ligated the left anterior descending (LAD) coronary artery of 1-day-old mice, thus it induced an ischemic myocardial infarction [59]. This study further provided that a neonatal mouse following LAD ligation could regenerate the heart in as short as 21 days without obvious fibrosis and scar formation [59]. In addition, a Cre-lox inducible genetic fate mapping approach has been utilized to address the source of regenerated cardiomyocytes, and showed newly formed cardiomyocytes arise from the pre-existing

cardiomyocytes after the apical resection of the neonatal myocardium [59]. Moreover, a cryoinjury model was used to study the regenerative response of neonatal mice hearts. One study indicated that cardiac function was not recovered after a transmural (severe) cryoinjury [60]. In contrast, although cardiomyocyte proliferation was not robust, non-transmural (mild) cryoinjury allowed for complete recovery of cardiac function [60]. These cardiac regeneration models (Figure 1) allowed identification of the cardiomyocyte cell cycle modulators as well as prospective targets to induce heart regeneration.

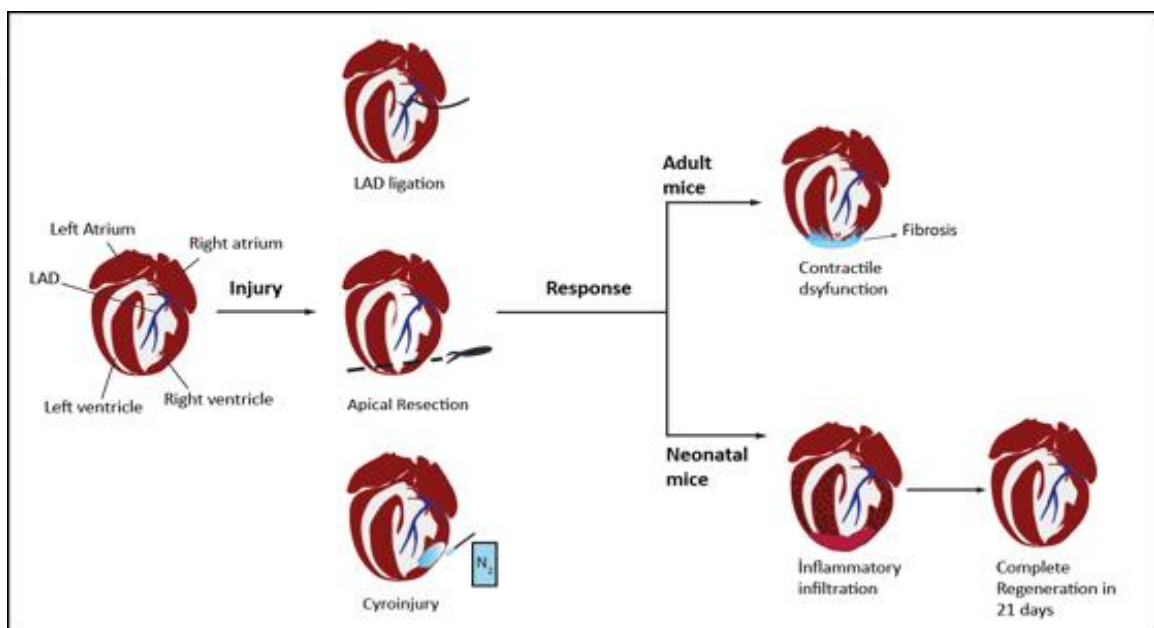


Figure 1.2. Response to various types of injuries in the mammalian heart. Different injury models utilized to measure regenerative response of the mammalian heart. Left anterior descending artery (blue) has been permanently ligated in the LAD ligation model. The apical resection injury model leads to an amputation of up to 15% of the ventricular apex. On the other hand, the cryoinjury model induces cardiac damage on the ventricular apex by a pre-cooled probe (cooled by liquid nitrogen).

1.7. MODULATORS OF CARDIOMYOCYTE RENEWAL

Myocardial infarction leads to loss of substantial amount of cardiomyocytes, which negatively influence cardiac function. This urges therapeutic approaches that either preserve

existing cardiomyocytes or increase the number of functional cardiomyocytes following myocardial injuries.

In this frontier, studies to uncover the mechanism of functional cardiomyocytes renewal became a major point of focus in the context of cardiac therapies. Development of an injury model in zebrafish [15] and neonatal mouse [21] provided a great opportunity to investigate these mechanisms and factors involved in heart regeneration. Over the last decade, contribution of different mechanisms including transdifferentiation [61, 62], dedifferentiation [7, 8], proliferation of pre-existing cardiomyocytes [7], the contribution of both cardiac resident stem cells [10], and bone marrow derived stem cells [5] were suggested to be plausible in treatment of cardiovascular disorders (Figure 2). These studies revealed some of the important factors that modulate cardiac progenitors or the cardiomyocyte cell cycle.

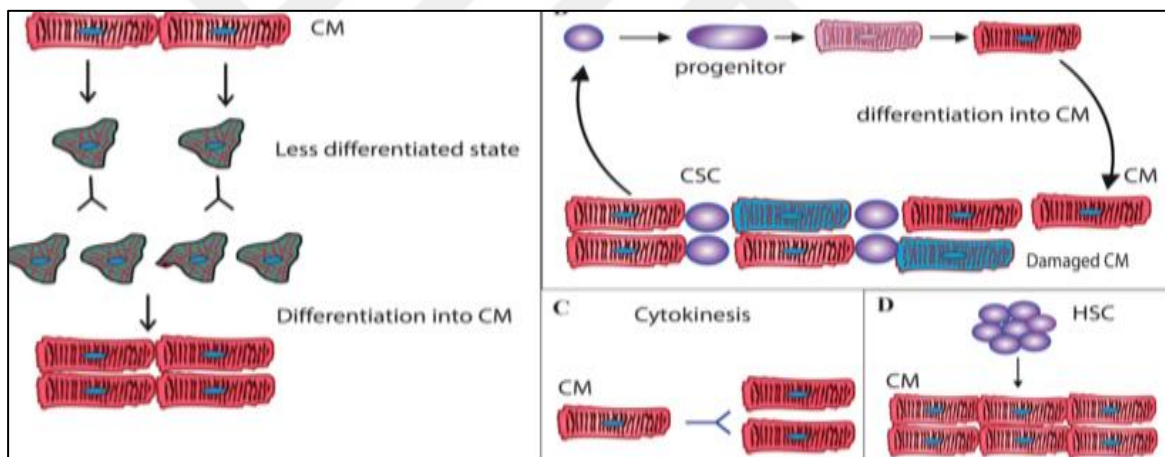


Figure 1.3. Mechanisms of cardiomyocyte renewal. a) Dedifferentiation initiated by detachment of cardiomyocytes followed by differentiation back into cardiomyocytes. b) Cardiac resident stem cells give rise to new cardiomyocytes through differentiation. c) Proliferation of pre-existing cardiomyocytes. d) Transdifferentiation of bone-derived hematopoietic stem cells into cardiomyocytes

1.8. CARIOGENIC FACTORS OF CARDIOMYOCYTES

Various molecular intervention approaches have been utilized to manipulate cardiomyocyte proliferation (Table 3) [55, 63-66]. Jackson et al. (1990) overexpressed c-myc during

embryogenesis of mice and demonstrated both increased cardiomyocyte number (almost 2 fold) and heart weight [65]. In another study, adenoviral overexpression of oncogene E1A in cardiomyocytes resulted in induced cardiomyocyte cycling followed by apoptosis [67]. Overexpression of cell cycle regulatory proteins has been also tested to see if they enhance cardiomyocyte proliferation. Pasumarthi et al. (2005) overexpressed cyclin D1, cyclin D2 and cyclin D3, which are considered as positive regulators of G2/M transition state. They reported that neither cyclin D1 nor cyclin D3 increased proliferation of cardiomyocyte after myocardial infraction; however, cyclin D2 overexpression resulted in promoted cardiomyocyte proliferation in adult transgenic mice [66]. Successive studies including forced expression of cyclin B1-CDC2 and transgenic expression of cyclin A2 have resulted in an increased percentage of cardiomyocytes in G2/M *in vitro*, increased cardiomyocyte proliferation and induced myocardial regeneration in adult mice [63, 68]. Other studies investigated the downregulation of cell cycle inhibitors such as cyclin-dependent kinase inhibitors (CDKIs) (p21^{Waf1}, p27^{Kip1}, and p57^{Kip2}) due to their high expression in neonatal and adult heart and reported an increased cardiomyocyte number [69].

Over the past decade, a number of transcription and growth factors involved in the modulation of the cardiomyocyte cycle were identified [70-74]. Development of the neonatal mouse cardiac regeneration model gave an opportunity to investigate inhibitors of mammalian cardiac regeneration being activated after the neonatal period [20, 21, 59, 75]. Thus, we successfully used this model to identify Meis1, one of the key regulators of neonatal cardiac regeneration and reported that Meis1 inhibits cardiomyocyte proliferation through transcriptional activation of CDKIs p15, p16 and p21 [75].

Signaling pathways have been intensively studied to understand and overcome the limited regenerative capacity of the heart [76]. In this frontier, Neuregulin, a ligand for neuregulin/ErbB2/ErbB4 signaling cascade, was revealed as a positive regulator of cardiomyocyte proliferation [77] both in overexpression [18] and recombinant protein administration studies [78-81]. In addition, administration of recombinant oncostatin M, TWEAK, FGF10, periostin and co-administration of FGF1 with p38 inhibitor resulted in cardiomyocyte proliferation after myocardial infraction [72, 73, 82-84]. Several studies on the Hippo signaling pathway demonstrated its prospect in cardiac regeneration [85]. Overexpression of one of the key component of The Hippo pathway, yes-associated

protein [85] and knockdown of an upstream effector element of the Hippo pathway resulted in an increased cardiomyocyte number and a thickening of the myocardial wall [86-90].

Nerves have been known to guide to organ regeneration. However, their function in cardiac regeneration was not determined until recently [91]. In this frontier, Mahmoud et al. (2015) reported that pharmacological inhibition of cholinergic nerve formation in zebrafish and newborn mice reduce cardiomyocyte proliferation following injury thus suggesting that innervation is crucial for heart regeneration [92]. Moreover, mechanical inhibition of innervation (left vagotomy surgical operation) decreases cardiac regenerative response in newborn mice that could be rescued by recombinant neuregulin 1 (NRG1) and nerve growth factor (NGF) administration. In addition, they reported that immune response and inflammatory associated genes are downregulated following denervation, which shows denervation impairs heart regeneration through down regulating immune response mechanism [92].

1.9. CARIOGENIC MODULATION OF STEM AND PROGENITOR CELLS

A number of studies attempted to modulate resident or non-resident progenitor and stem cells to induce new cardiomyocyte formation following myocardial infarctions. Embryonic stem cells (ESCs) demonstrate a capacity to differentiate into beating cardiomyocytes *in vitro*. Thus, ESCs are considered to be an option to use towards regenerative cardiology. However, several drawbacks regarding teratoma formation following transplantation, immune reactions and ethical concerns made them unsuitable for use in clinical studies [93]. The recent discovery of induced pluripotent stem cells (iPSCs) provided new angles to overcome these issues and eliminated major ethical concerns [94, 95], iPSCs have been shown to share many characteristics of ESCs and they have been successfully generated from various somatic cells [96, 97]. In addition, differentiation of iPSCs into specific cells including cardiomyocytes were reported [98-101]. Although there are no clinical trials yet using iPSCs cells for myocardial regeneration, intense research is currently focused on the discovery of new methods for safer cellular reprogramming methods and induction of lineage specific differentiation of iPSCs to prevent teratoma formation.

Skeletal myoblasts (satellite cells) are also thought to be a potential source for cardiac therapies. *In vitro* expansion of skeletal muscle cells derived from skeletal muscle biopsies

avored them for autologous transplantation and their ischemia-resistant property made them among the first cells tried in cellular therapies in the treatment of cardiac failure. Engraftment of skeletal myoblasts into damaged myocardium resulted with improved cardiac function [102, 103] and prevented progressive ventricular dilatation [104]. Although several studies suggest that engrafted skeletal myoblast cells do not transdifferentiate into functional cardiomyocytes [105] and electrophysiologically differ from resident cardiomyocytes [106, 107], clinical trials are still proceeding to test the potential of these cells in cardiac regenerative therapy.

1.9.1. Cardiac stem cells and induced cardiomyocytes

Cardiac stem cells (CSCs) are widely investigated in the treatment of cardiovascular disorders (reviewed in [108]). The discovery of c-kit⁺ CSCs followed the identification of other CSCs including epicardial progenitors, Is11⁺ cardiovascular progenitors, side population progenitors, Sca1⁺ progenitors, heterogeneous progenitors containing cardiospheres and cardiac mesenchymal stem cells [10, 109-113]. Following identification of these progenitors, factors involved in differentiation into cardiomyocytes started to emerge. Oxytocin treatment on Sca-1⁺-CD45⁻ cells has been shown to induce differentiation into spontaneously-beating cardiomyocytes [114]. Furthermore, transplantation of these cells into necrotic myocardium increased cardiac function [112]. In another study, intramyocardial injection of HGF-cMet and IGF-1 factors after induction of myocardial injury resulted in an increased number of cardiac resident stem cells [115]. Qyan et al. (2007) reported that cardiac mesenchymal cells regulate the renewal and differentiation of cardiac Is11⁺ cardiovascular progenitors via the Wnt/ β -catenin pathway [116]. In addition, chemical inhibition of glycogen synthase kinase-3 (GSK-3) resulted in a 2 fold-increased number of cardiac Is11⁺ cardiovascular progenitors. Cardiospheres, which were derived from endomyocardial biopsy specimens, also have a potential use in cardiac stem cell therapy. The existence of different progenitors and differentiated cells within cardiospheres mimic the stem cell niche existing in the heart thus it can take a step further in cardiac stem cell studies [117].

A recent study reported the direct reprogramming of cardiac fibroblasts into cardiomyocytes, which has provided an alternative source of cells to trigger heart regeneration [99]. Stable integration of cardiac specific markers Gata4, Tbx5 and Mef2x led to transform 20% of

cardiac fibroblast into induced cardiomyocytes (iCMs), which have similar epigenetic states and gene expression as in normal cardiomyocytes [118, 119]. Integration of different factors (Oct4, Sox2, Klf4 and c-Myc) by Efe et al. (2011) supported the reprogramming of mouse embryonic fibroblast into beating cardiomyocytes in 11-12 days, which was shorter when compared to the study by Ieda et al. (2010) [120]. A decreased trend towards tumor formation and the ability to reprogram a large number of a patient's fibroblast into cardiomyocytes made iCMs an alternative for cardiac therapies. Even though there are many advantages of iCMs, it requires further investigations to effectively use endogenous fibroblast cells in the repair of damaged myocardium before proceeding into clinical trials.

1.9.2. Bone marrow derived stem cells in myocardial regeneration

The bone marrow contains heterogenous cell populations. Investigations on bone marrow cells (BMC) and hematopoietic stem cells (HSCs) in the induction of myocardial regeneration date back to the early 2000s. Orlic and colleagues (2001) showed that bone marrow derived cells acquire a cardiomyocyte-like phenotype and provide a functional recovery following myocardial infarction [9]. Further clinical studies with BMCs demonstrated the prospect of human heart regeneration [121-123]. Studies based on bone marrow derived mesenchymal stem cells (MSC) indicated the ability of MSCs to induce proliferation and differentiation of resident cardiac stem cells [124, 125]. Many different mechanisms have been proposed to explain the effect of BMC cells in myocardial regeneration [126, 127]. A recent study showed that bone marrow c-kit⁺ cells but not MSCs stimulate an endogenous pool of cardiac progenitors that dilute the pool of cardiomyocyte specific GFP expression thus they improve cardiac function [128]. In addition, induction of a number of growth factors including hepatocyte growth factor (HGF), insulin-like growth factor (IGF-1), vascular endothelial growth factor (VEGF) and basic fibroblast growth factor (bFGF) were reported just after treatment with MSCs or multipotent human BM stem cells (hBMSCs) (Yoon et al., 2005). In another study, TGF- β and bone morphogenetic protein (BMP)-2 increased the expression of cardiac transcription factors in a paracrine manner. In addition, it was reported that periostin and neuroglin administration induce cardiomyocyte proliferation. However, the source of these ligand receptor interactions (existing in both cardiomyocytes and HSCs) remain undetermined. The paracrine effect could be the

underlying mechanism giving rise to a modest improved diastolic function following BMC derived stem cell treatment.

Table 1.3. Major factors involved in cardiomyocyte proliferation

Cardiogenic factors and manipulations	Fold change in proliferating cardiomyocytes	Reference
Meis1 knockout	9 (pH3 + CMs, Aurora B + CMs)	[75]
GSK-3 inhibition	5 (pH3 + CMs)	[129]
Foxo1 dominant negative	2.5 (pH3 + CMs)	[130]
miR-133a knockout	2.5 (pH3 + CMs)	[131]
Jumonji knockout	2.2 (pH3 + CMs)	[132]
p27^{KIP1} knockout	2-3 (troponin I + CMs)	[133]
Constitutively active ERBB2	>12 (Ki67 + CMs, pH3 + CMs, Aurora B+ CMs)	[77]
Nrg1 (or FGF1, periostin) treatment	>4 (BrdU + CMs, Aurora B + CMs, pH3 + CMs,)	[71] [18]
Activated Yap1	>7 (Ki67 + CMs, pH3 + CMs, Aurora B+ CMs)	[89]
Salv knockout	>4 (pH3 + CMs)	[88]
IL13 (or IL3, CTGF, Nrg1) treatment	>1.5 (3H Thymidine CMs, Ki67 + CMs, BrdU + CMs)	[134]
Oncostatin M treatment	>2 (EdU + CMs)	[83]
TWEAK treatment	6.2 (BrdU + CMs)	[84]

C3orf58 treatment	>2 (Ki67 + CMs, BrdU + CMs, Aurora B + CMs)	[135]
Periostin treatment	>5 (BrdU + CMs, pH3 + CMs, Aurora B+ CMs)	[72]
FGF10 treatment	2 (Ki67 + CMs, pH3 + CMs,)	[73]
Cyclin D2 overexpression	>5 (MHC-nLAC + CMs)	[66]
Cyclin B1-CDC2 or cyclin a2 overexpression	>1.4 (CMs)	[63] [64]
Activated Notch	>7 (Ki67 + CMs, BrdU + CMs, Aurora B + CMs)	[136]
c-myc or E1A overexpression	2 (CMs)	[65-67]

1.9.3 Putative regulators of cardiac regeneration

Recent findings in the last decade led to identify major factors involved in cardiomyocyte proliferation (Table 1.3). Different effect of those regulators changed dogma that heart is terminally differentiated organ. Moreover, recent studies in different quiescent cell type also enabled scientist to monitor their effect on other quiescent cells including but not limited to cardiomyocyte. To this end, one of the important regulator, meis1, which is a homeodomain transcription factor, was reported to be important for HSCs development, and recently identified as major regulator of HSCs quiescence [142]. Moreover, recent study also revealed Meis1 in cardiac regeneration, and suggested that Meis1 also negatively regulates cardiomyocyte proliferation similar its effect on shifting HSCs quiescence [75]. This finding led to identify another meis1 like regulators to be screened in cardiac regeneration. To this end, carefully investigation of literature indicated six different regulator to be important for cardiac regeneration (APPENDIX C).

The role of different transcription factors have been suggested to be important for HSCs differentiation. The Growth factor independence 1 (Gfi1), a member of zinc finger proteins, reported to be major regulator of transcriptional network of hematopoiesis required for

HSCs maintenance. Moreover, in a recent study, role of Gfi1b for erythroid and megakaryocytic development, thus HSCs. The effect of Gfi1b in HSCs was suggested to depend on increased level of ROS due to activation of those developmental pathways and ultimately resulted with expansion of HSCs [143].

Another putative regulator of cardiac regeneration, SHIP1 (inositol-5-phosphatase) belongs SH2 domain containing protein family, suggested to be a negative regulator of hematopoiesis. This action of mechanism in HSCs expansion was reported to be formation of tyrosine residues which lead to a novel signalling complex with DOK1 (p62) and CRK (p38) [144].

ITCH, E3 ubiquitin ligase, transcriptional corepressor of p45/NF-E2 and another negative regulator of HSCs expansion. In a recent study, *Itch*^{-/-} mice lead to increased number of HSCs and increased long term repopulating activity of HSCs which indicate multiple effect of Itch on HSCs. Moreover, *Itch*^{-/-} mice resulted with increased proliferation of HSCs with decrease in progenitor characteristics. Moreover, notch signalling pathway was suggested to reverse this increased number of HSCs proliferation which explained the mechanism of action of Itch on HSCs biology through regulating notch pathway [145, 141].

Dnmt3a, NA (cytosine-5)-methyltransferase 3A, enzyme responsible to transfer methyl groups to specific CpG regions in DNA, which is defined as DNA methylation. Depending on study using conditional ablation strategy, it was reported abnormality in HSCs differentiation and impaired HSCs over serial transplantation while expanding HSCs numbers in bone marrow. Moreover, *Dnmt3a*^{-/-} mice resulted with substantial CpG hypermethylation and altered HSCs multipotency genes while downregulate differentiation factors. These findings established Dnmt3a as a critical regulator of epigenetic mechanism of HSCs which enabling efficient differentiation and expand HSCs [146].

Study regarding to another putative regulator, Depending on conditional elimination of c-Myc protein in HSCs, its unexpected function on HSCs homeostasis was revealed. Moreover, conditional knock out of cmyc transcriptional activity in bone marrow lead to cytopenia and accumulation of HSCs in situ. Furthermore, observed abnormality in differentiation capacity of c-myc knock out mice HSCs was correlated with up-regulation of several adhesion receptors, suggesting that release of HSCs from the stem cell niche requires c-Myc activity. Collectively, these findings revealed that c-Myc controls the balance

between stem cell self-renewal and differentiation, through controlling HSCs and their niche in transcriptional manner [147].

The final putative regulator of cardiac regeneration, Cbl, is proto-oncogene encoding RING finger E3 ubiquitin ligase which is required to target substrates to be degraded by proteasome. Cbl is ubiquitinating conjugating enzyme (E2) to substrates. Moreover, N-terminal phosphotyrosine binding domain led to Cbl enzyme to interact with several tyrosine-phosphorylated substrates. Moreover, Cbl reported to regulator of cellular activation pathways. Cbl mutations, for instance, are associated with myeloproliferative disorders (MPD). Moreover, in a recent study, link between HSC expansion and MPD development upon combined Cbl and Cbl-b deletion were reported. Depending on cell cycle analysis, Cbl^{-/-} mice HSCs showed reduced quiescence. Moreover, Cbl^{-/-} mice showed a sustained c-Kit and FLT3 signalling which promoted loss of colony forming potential [138].

2. MATERIAL AND METHODS

2.1 ANIMAL INFORMATION

Balb/c mice have been used in this study, and animal studies were used under decision number 417 which approved by the Institutional Clinical Studies Ethical and the Institutional Animal Care and Use Committee of Yeditepe University (YUDHEK, decision number 417).

2.2 NEONATAL MICE SURGERY OPERATION

Apical resection and LAD surgeries were performed on neonatal mice (Balbc) at on post-natal day 3 (P1) and day 7 (P7). Considering that neonates up to one 1 week can endure and survive in hypothermic conditions, mice were anesthetized on ice bath approximately for 5 minutes. Additionally, this anesthesia method prevent extreme bleeding by decreasing blood flow during injury. Lateral thoracotomy was performed in order to heart take out. Left anterior descending artery was ligated using 7-0 non absorbable silk suture. Skin sore closed up by suturing and using skin adhesive. For sham group, only chest cavity was opened mice and skin sore closed up immediately. Hearts were harvested 4 days after surgery. Harvested hearts were washed in PBS solution for a short time and stored at -80 until use.

2.3 IMMUNOFLUORSCENCE DETECTION OF PUTATIVE REGULATORS

After antigen retrieval step using EDTA Buffer (1mM EDTA, 0.05% Tween 20, pH 8.0) in boiling water for approximately 40 min, paraffin sections were permeabilized with 0.25% triton X/PBS for 10 minutes and then blocked with 1% BSA for 30 minutes at incubator. Primary antibodies against (Gfi1b (Sigma, HPA007012), Inpp5d (SCBT, sc-8425), ITCH (Sigma, HPA021126), Dnmt3a (Sigma, HPA026588), c-myc (SCBT, sc-789), CBL (Sigma, HPA027956) were incubated for overnight at 4 Celsius and secondary antibodies for detection (Life technologies, Alexa Fluor 488 anti mouse; Anti-Mouse anti rabbit) were done incubatin for 45 minuts at incubator. Afterwards, sections were washed with PBS for three

times and detection under immunofluorescence microscope under 40X magnification was performed.

2.4 IN VITRO siRNA KNOCKDOWN

In vitro siRNA knockdown approach was utilized on cultured rat neonatal cardiomyocytes. To this end, cardiomyocytes were cultured on 48-well plates at 70-75% confluency in the presence of fibroblast inhibitor factor (BrdU), and triplicates per group was done. Diluted lipofectamine (invitrogen) and siRNA (20 μ M) in OPTIMEM media was given to culture and incubated for 6- hours. Afterwards, cells were either fixed or used for RNA or protein isolation.

2.5 IMMUNOFLUORSCENCE DETECTION OF CARDIOMYOCYTES PROLIFERATION

Immunostaining of siRNA treated neonatal cardiomyocytes were performed after fixation step using paraformaldehyde. To this end, cells were incubated in paraformaldehyde for 10 minutes at incubator. Coming after, to provide cell membrane permeability 0.1% Triton-X in 1X PBS for 10 minutes at incubator. Than blocking step was done by %1 BSA-tween 20 solution for 30 minutes at incubator. Fixed cells were incubated with TnnT (1:200) overnight at +4⁰C. The day after cells were incubated with PH3(1:200) for 2 hours at incubator. Following, cells are treated with suitable secondary antibodies containing Alexa Fluor® 488 Donkey Anti-Mouse IgG (H+L) Antibody and Alexa Fluor® 555 Donkey Anti-Rabbit IgG (H+L) Antibody, Hoechst 33342 staining and fluorescent imaging. Each PH3 positive cardiomyocyte cells were counted by 40X objective.

2.6 RT-PCR ANALYSIS OF cDNA SAMPLES

Total RNA was isolated using TRIzol reagent according to manufacturer's instructions. Briefly, 1ml TRIzol reagent was used for 1 million cells and RNA was precipitated using % 100 propanol, and washed out using %75 alcohol. cDNA synthesis was performed using 5 μ g of RNA using NEB cDNA synthesis kit (NEB, protoscript). Indicated primers (Table

2.1) were ordered from Sentegen Technologies. RT-PCR was performed using BioRad Fx96 system and using SyberGreen (Thermoscientifi). Results were normalized according to the either GAPDH or actin gene expression by using $\Delta\Delta C_t$ method.

Table 2.1. Primers used to detect putative regulators

Primer Oligo ID	Primer 5' to 3'
mGfi1b-F	CTAGAAAGGACCGTGGCATT
mGfi1b-R	CAGGGACAGTGTGGAGGTTTC
mInpp5d-F	GTGAAGAACCTCATGGGGAC
mInpp5d-R	GCTGTTCCGGAATTGTGTTT
mItch-F	CCTTATGTAGAAGTCACAGTAG
mItch-R	TCACCTACAAGCTGCAAAGTCA
mDnmt3a-F	TACATCAGCAAACGGAAACG
mDnmt3a-R	CCTCCTCCACCTTCTGAGACT
mCbl-F	TTCCAGCACTTCTCCACCAT
mCbl-R	GATCGGGCTCATGAAGGAC
mMyc-F	TGAAGTTCACGTTGAGGGG
mMyc-R	AGAGCTCCTCGAGCTGTTTG

2.7 ISOLATION OF ADULT MOUSE CARDIOMYOCYTES

Isolation of adult mouse cardiomyocytes were performed by previously defined protocol [140]. Briefly; buffer and media were prepared according to Table 2.2. Perfusion system was set on to 37°C and pump was started on lowest setting (15 RPM, 6 ml/min). Perfusion system was sterilized by flushing with %70 ethanol then remove ethanol traces by flushing with distilled water. The digestion buffer was loaded into perfusion system and was let to circulate

until all air bubbles are removed. Secondly, Heart cannulation step was performed. To this end, ice cold perfusion buffer circulated for several times to heart from aorta by using 18G blunt needle. Heart was fixed into system using 18G blunt needle by catgut, then strap the two ends of the catgut to ensure stability of the heart during perfusion and was let the system running until the heart begin slouching as the collagen is degraded and it loses mechanical support. For Mechanical Dissociation and Purification step, 7.5 ml of digestion buffer was collected from the heat jacket of the perfusion system and was placed back to a petri dish then add 2.8 μ l 1M CaCl₂ was added. Heart was removed from system was triturated in digestion buffer added petri dish. Petri dish was placed in to incubator 37°C with 5% CO₂ was agitated every two 2min until collecting sufficient number of cardiomyocytes. For the termination of isolation step, 7.5 mL of stop buffer was added to digestion buffer. Following that, digested tissues was filtered using sterile gauze bandage. It was added 7.5 mL of digestion buffer and procedure was applied to for remaining tissue again. Collected supernatants were let to settle the cells by gravity for 15 minutes. This step was repeated for 4-5 times. Afterwards, collected cells were resuspended in media and 7,500 cells/well were cultured on gelatine coated well plates. Cells were characterized using immunofluorescence staining method against to Troponin T.

Table 2.2. Reagents for isolation of adult mouse cardiomyocytes

Cardiomyocyte isolation buffer (CIB)	
Component	1X (g/L)
NaCl (M _w : 58.44 g/mole)	7.013
KCl (M _w : 74.55 g/mole)	0.403
Na ₂ HPO ₄ .2H ₂ O (M _w : 177.99 g/mole)	0.058
MgSO ₄ .7H ₂ O (M _w : 246.48 g/mole)	0.123
Taurine (M _w : 125.1 g/mole)	3.753
BDM (M _w : 101.1 g/mole)	1.011
HEPES (M _w : 238.3 g/mole)	5.958

Glucose (M_w : 180.16 g/mole)	3.964
Adjust the pH to 7.1 with NaOH.	
Adjust the volume to 1L with ultrapure water.	
0.088 g of $\text{Na}_2\text{HPO}_4 \cdot 2\text{H}_2\text{O}$ (M_w : 268.07 g/mole) can be used instead of $\text{Na}_2\text{HPO}_4 \cdot 2\text{H}_2\text{O}$.	
Perfusion Buffer (for 200ml)	
CIB	200 ml
EGTA (0.4M)	200 μl
Digestion Buffer (for 15ml)	
CIB	15ml
CaCl_2 (1M)	4.5 μl
Collagenase II	36 mg
Stop Buffer (for 15ml)	
Perfusion buffer	14.25 ml
FBS	750 μl
CaCl_2 (1M)	22.5 μl
Culture media (for 100ml)	
MEM media	90ml
FBS	10ml
Penicillin Streptomycin	0.2 ml

2.8 WESTERN BLOT ANALYSIS OF TISSUE SAMPLES

All the western blot equipment's and glasses were sterilized using %70 alcohol. %10 APS solution was prepared by dissolving 0.05 g of APS in 500 μ l. Separating gel was prepared according to Table 2.3. Prepared gels were poured into cassette and was incubated for gel solidification. Afterwards, stacking gel was prepared by adding 0.65 ml %30 acrylamide, 1.25 ml 4x Tris-Cl/SDS pH 6.8, 3.05 ml distilled water, 0.05 ml %10 APS and 0.02 ml TEMED. The comb was placed and it was waited again for solidification of gel. Running buffer was prepared by diluting 10x running buffer into 1x. To prepare 10x running buffer, 15.14 g of Tris BASE and 72.06 g of Glycine and add 400 ml of distilled water were mixed. Samples diluted with Laemmli buffer were prepared with addition β -mercaptoethanol. Samples were heated at 95°C for 5 minutes. After loading samples into the wells, gel was run at 70V for 10 minutes and voltage was increased to 110 V. Gel was run until staining was completely disappear. For transfer step, gel was stacked into whatman paper and nitrocellulose membrane. Afterwards, gel was transferred into nitrocellulose membrane on 350 mA currency for an hour in 1x transfer buffer. Blocking step was accomplished using %5 non-fat milk with 50 ml of 1X TBS-T and was incubated in this solution for 1.5 hour by shaking at 35 rpm. Primary antibody against putative regulators were incubated for over weekend at 4 °C. Then, primary antibody was removed ant was kept at -20°C for further use and membrane was washed for three times (15 minutes) with 1X TBS-T on the shaker. Second antibody against to primary antibody (Cell signaling, Cat No: 7074S) was incubated for 2 hours in 35 rpm shaker. After washing the membrane with 1X TBS-T for 3 times for 10 minutes in the shaker imaging step was performed using imaging solution kit according to manufacturer instructions (Cell signaling, Cat No:6883S).

Table 2.3. Reagents for preparation of western blot gels

Concentration (%)	6	7	7,5	8	9	10	12
%30 acrylamide	3	3,5	3,75	4	4,5	5	6
Tris-Cl/SDS pH 8.8	3,75	3,75	3,75	3,75	3,75	3,75	3,75
H2O	8,25	7,75	7,5	7,25	6,75	6,25	5,25

%10 APS	0,05	0,05	0,05	0,05	0,05	0,05	0,05
TEMED	0,02	0,02	0,02	0,02	0,02	0,02	0,02

2.9 STATISTICAL ANALYSIS

Results are expressed as mean \pm SEM and a 2-tailed Student *t* test was used to determine the level of significance. $p < 0.05$ was considered statistically different.



3. RESULTS

3.1. IMMUNOFLUORESCENCE DETECTION OF PUTATIVE REGULATORS CONFIRMED PROTEIN LEVEL IN ADULT HEART MYOCARDIUM

Immunofluorescence detection of putative regulators of cardiac regeneration using primary antibodies against Gfi1b (Growth factor independent 1B), Inpp5d (Inositol polyphosphate), ITCH (E3 ubiquitin ligase), Dnmt3a (DNA (cytosine-5)-methyltransferase 3A), c-myc (Myc protooncogene), Cbl (E3 protein ubiquitin ligase) and secondary antibodies for detection (Life technologies, Alexa Fluor 488 anti mouse; Anti-Mouse anti rabbit) were performed.

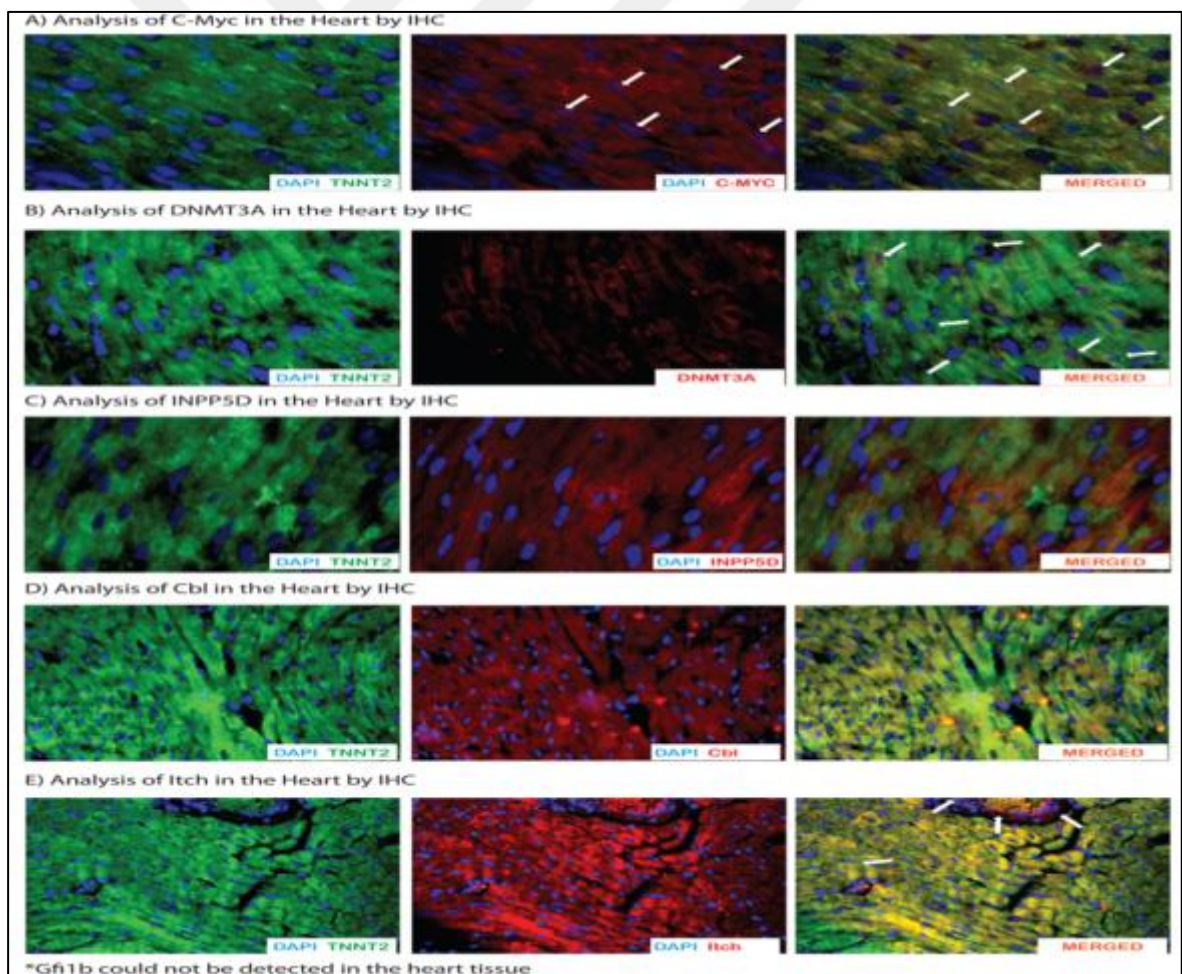


Figure 3.1. Detection of putative regulators of cardiomyocyte cell cycle modulators using immunofluorescence method. a) C-myc, b) Dnmt3a, c) INPP5D, d) Cbl, e) Itch immunostainings were shown.

The considerable level of protein of each putative regulators were observed in almost all samples expect in GFi1b. The findings indicated that these regulators could be important repressor regenerative capacity in adult myocardium (Figure 3.1).

3.2. PROFILE OF mRNA EXPRESSION IN CARDIOMYOCYTES AND FIBROBLAST REVEALED CARDIOMYOCYTE SPECIFIC REGULATORS

To identify cardiomyocyte specific putative regulator, relative mRNA expressions were measured and expression of putative regulators were analyzed. To this end, landgerdorf apparatus was utilized digest adult heart tissue which enabled to collect cells within heart (Figure A.1). Afterwards, RNA isolation and RT-PCR analysis were performed to identify mRNA expression level. Results indicated that Itch, Dnmt3a, C-myc and Cbl were mostly expressed in cardiomyocotes rather than fibroblast which also suggested that these regulators could have more important role in cardiomyocyte proliferation and could be cardiomyocyte specific genes.

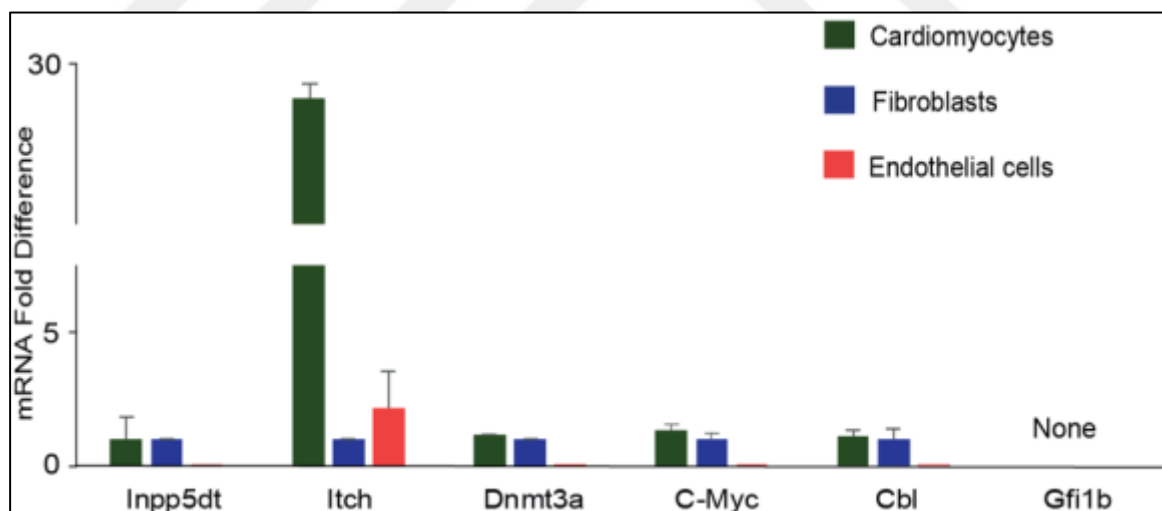


Figure 3.2. Differential expression of putative regulators in cardiomyocytes and fibroblast. Separated cells utilized for RT-PCR to measure mRNA fold difference. ITCH, Dnmt3a, C-myc and CBL were mostly expressed in cardiomyocotes.

Next, relative mRNA expression profile of putative regulators of cardiac regeneration were detected in whole adult mouse heart. To this end, RNA extraction and RT-PCR was utilized from homogenized adult heart myocardium and relative mRNA expression profile was detected using $\Delta\Delta CT$ method. (Figure 3.3). CBL was detected to have the highest mRNA expression in heart among the others. Since higher expression of CBL in cardiomyocyte was already detected in previous data (Figure 3.2), the highest global expression in heart tissue indicated its important role within the heart tissue.

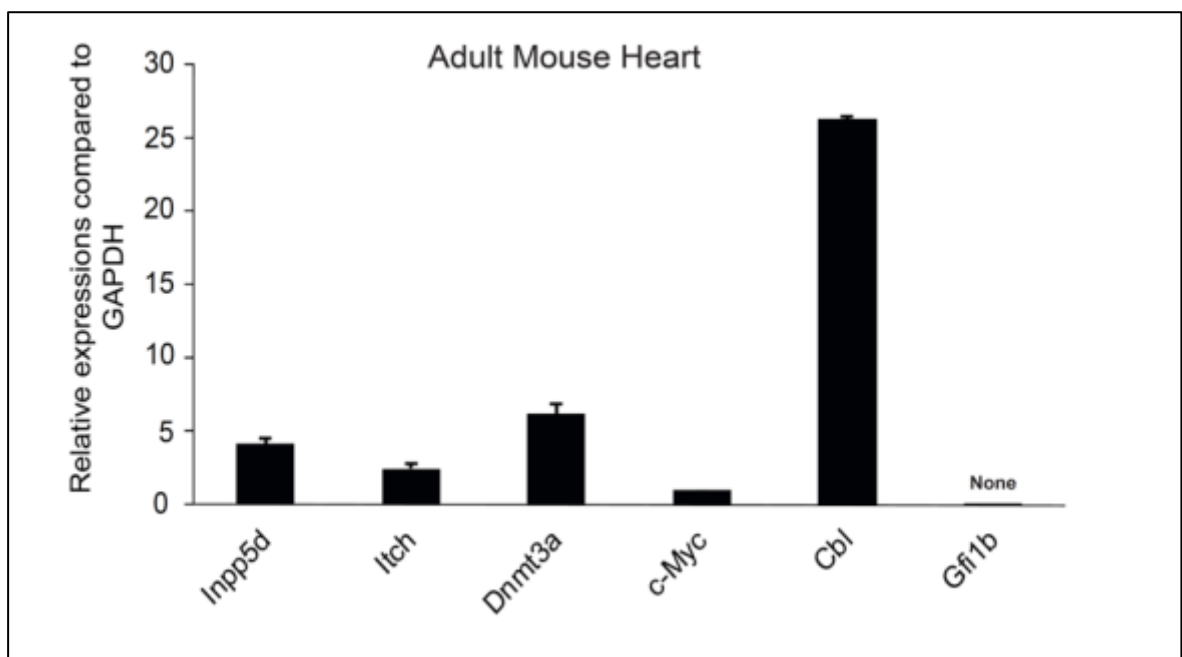


Figure 3.3. Relative mRNA expression of putative regulators in Adult mouse heart. CBL is mostly expressed among the other regulators in adult mouse heart.

Findings in RT-PCR utilized for cardiomyocytes and fibroblast, and adult mouse heart indicated potential role of CBL in heart tissue (Figure 3.2 and Figure 3.3). The reveal the role of CBL in heart tissue in more deeply different strategies and experiments were designed to be utilized.

3.3. WESTERN BLOT ANALYSIS CORRELATED WITH RT-PCR AND INDICATED HIGH EXPRESSION OF CBL IN HEART

To identify protein level of putative regulators in different organs western blot method was utilised and detection of relative protein level of each regulators were identified (Figure 3.4.). Western blot analysis indicated that high expression of CBL, Dnmt3a and relatively high level of of c-myc in heart tissue.

Moreover, protein level of CBL in heart tissue was highest among the others which also correlates with previous RT-PCR data and enabled to confirm its expression both in RNA and protein level.

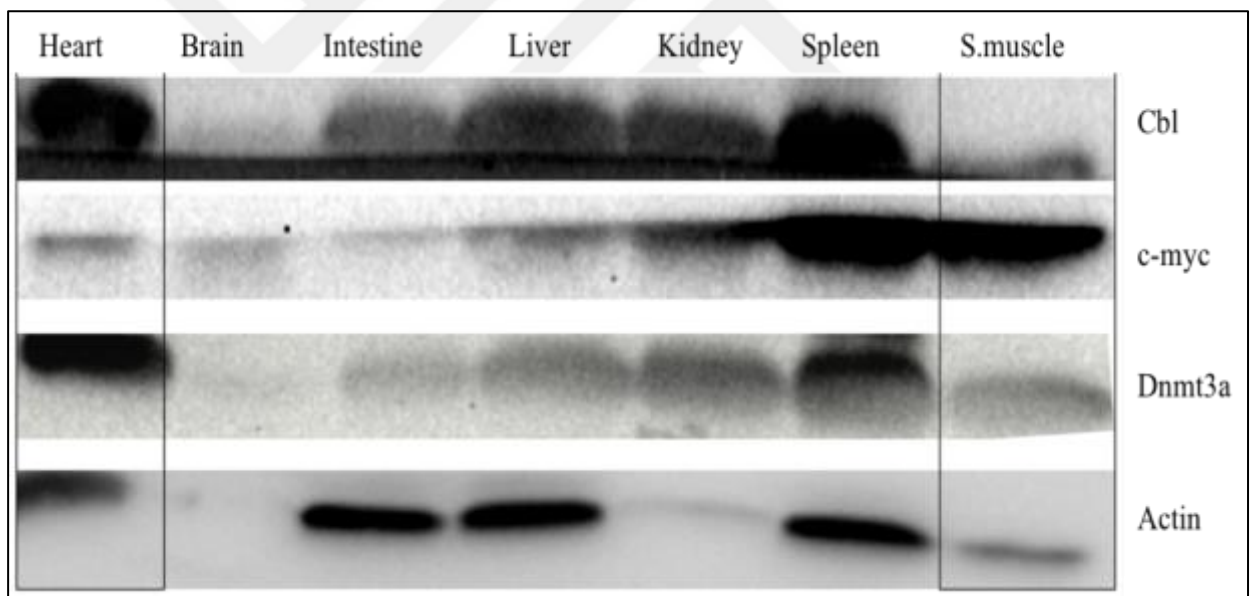


Figure 3.4. Western blot image of putative regulators in different tissue. High expression of Cbl, Dnmt3a and relatively highg expression of c-myc was shown

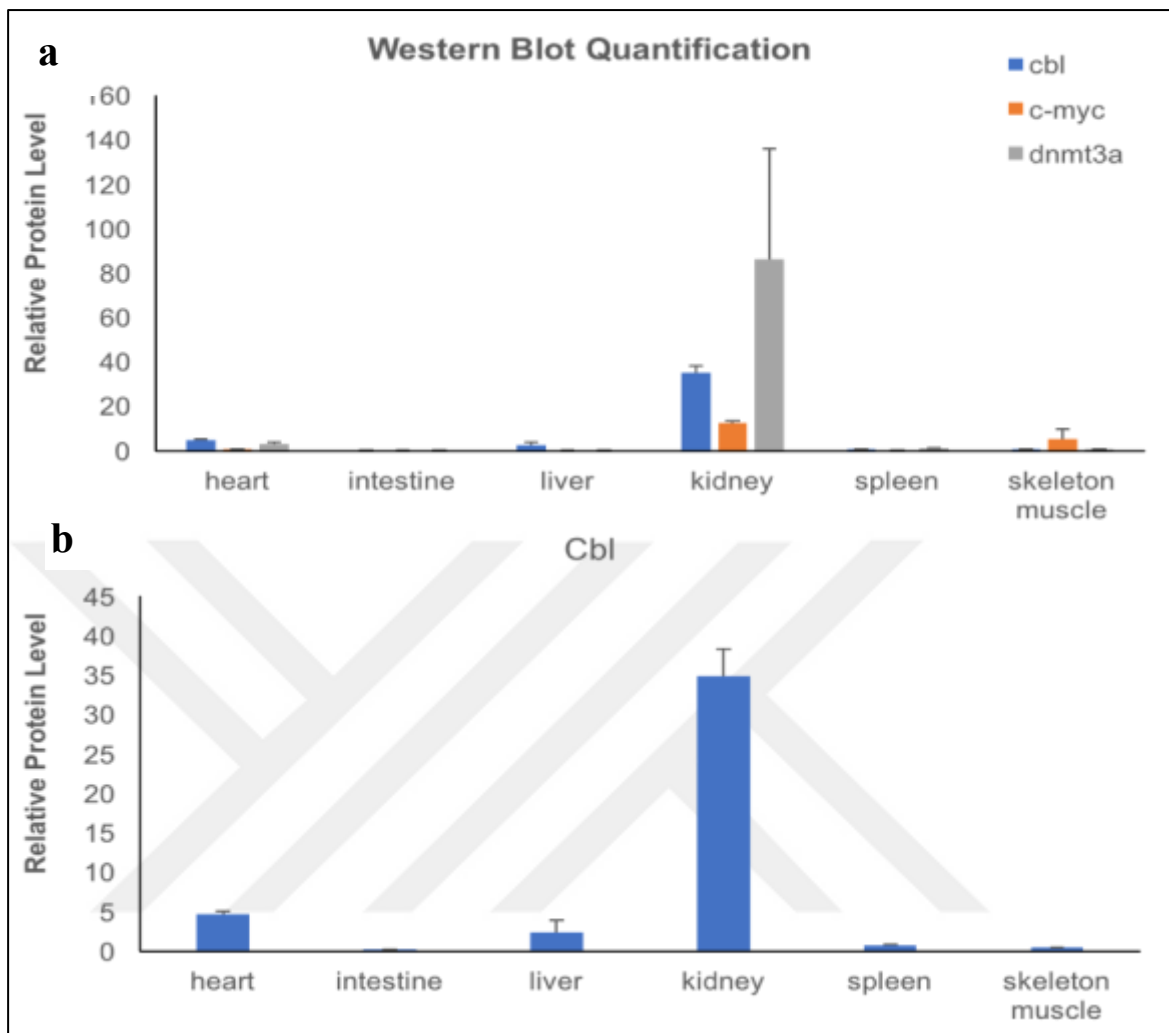


Figure 3.5. Quantification of Western Blot data. Indicating relative protein level in different tissue of adult mouse.

3.4. NEONATAL SURGERY MODEL ON NEONATAL MOUSE SHOWED NEGATIVE REGULATOR OF REGENERATIVE RESPONSE IN MOUSE

To test whether these regulators of neonatal mouse heart regeneration are negatively or positively affecting regenerative response of myocardium upon a injury, we performed apical resection and ligation LAD surgery model on neonatal mouse (Figure A.2). To this end, new born mice were anaesthiad on ice bath and followed by lateral thoracotomy was

applied to open chest cavity which enabled to perform indicated surgery model.

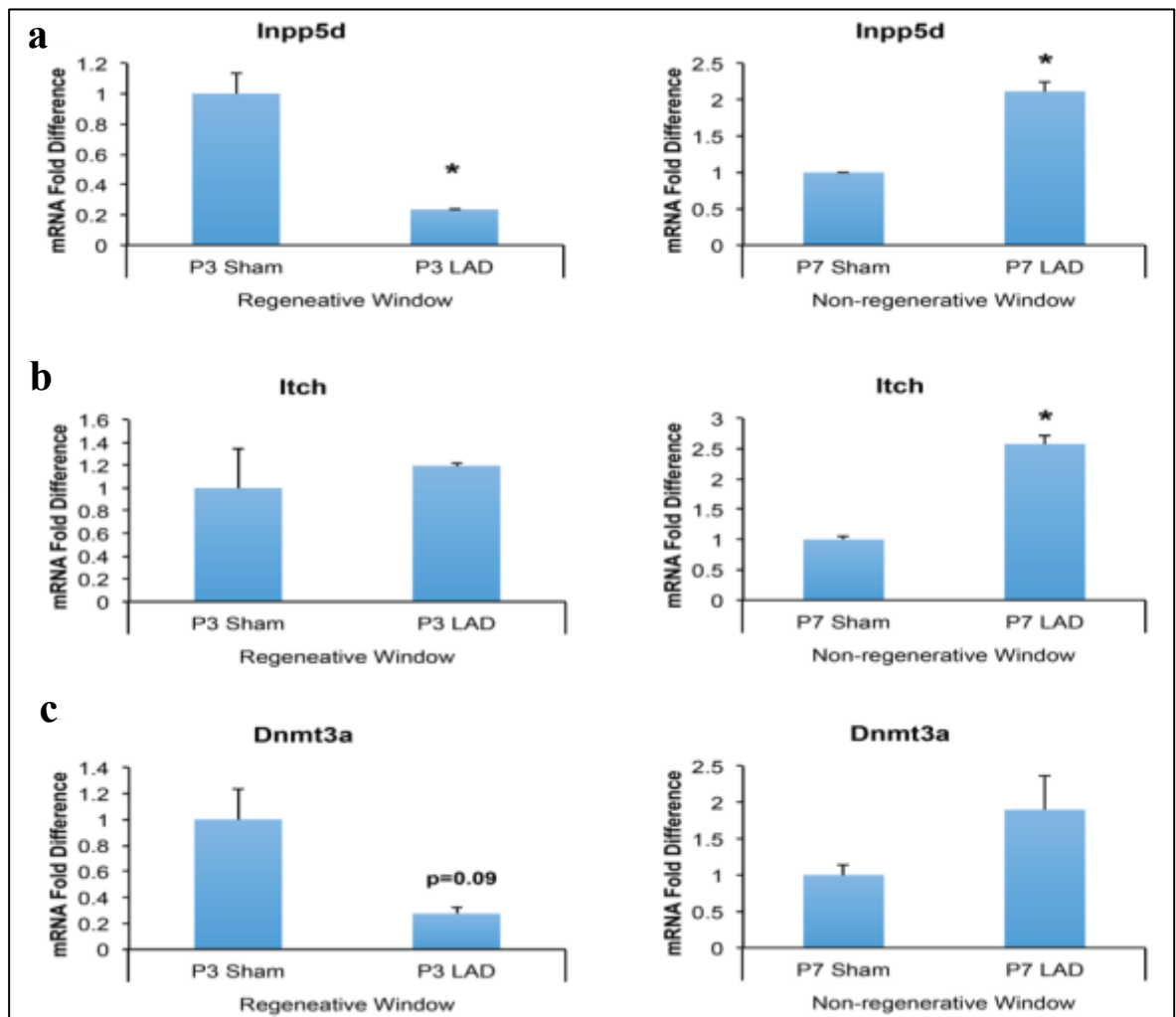


Figure 3.6. RT-PCR analysis of operated mouse at P3 and P7. Sham refers to control group. a) Expression profile of Inpp5d, b) Itch and c) Dnmt3a, * $p < 0.05$. $n=3$

All the surgery operation was carried on day 3 (p3) after birth and day7 (p7) in which myocardium is regenerative and non regenerative, respectively. Samples were collect after 4 days of neonatal surgery operation in order to analyse RNA and protein change in heart tissue. The surgery model enabled us to have regenerative myocardium between P3-P7 and non regenerative myocardium between P7-P11 which was used to identify negative and positive effect of these putative regulators (Figure 3.4 and Figure 3.5).

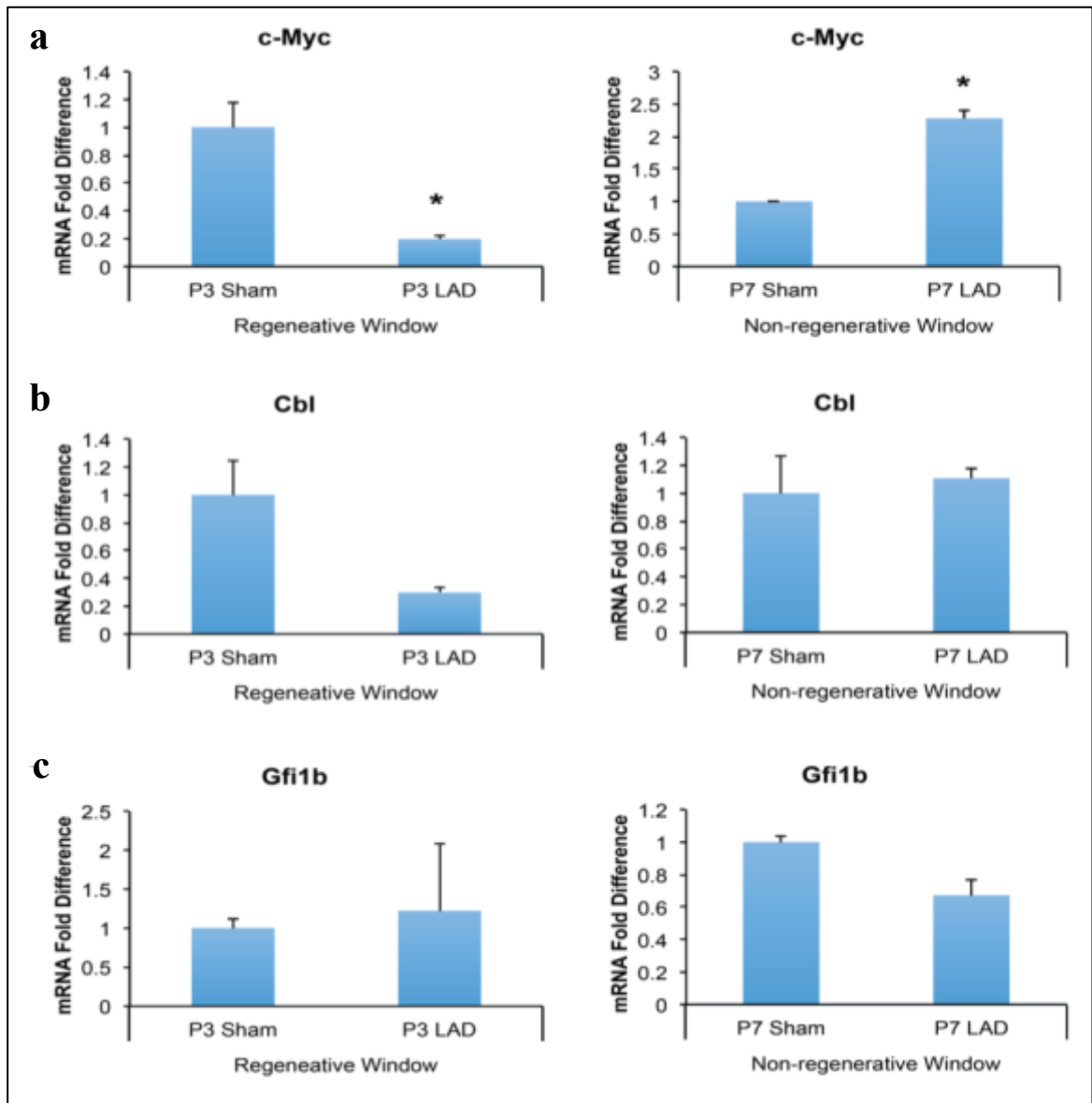


Figure 3.7. RT-PCR analysis of operated mouse at P3 and P7. Sham refers to control group. A) Expression profile of c-Myc, B) Cbl and C) Gfi1b, * $p < 0.05$. $n=3$

Depending on RT-PCR data, downregulation and upregulation of putative regulators were shown (Figure 3.6 and Figure 3.7) and summarized (Figure 3.10). Since operated mice at P3 have regenerative myocardium, downregulation in this sample suggested to increase this capacity through negatively regulating proliferation of cells in heart. Moreover, upregulation of these putative regulators in operated mice at P7 confirms their negative effect of

regenerative response and cell proliferation since it was observed significant decrease in their mRNA expression (Figure 3.7.).

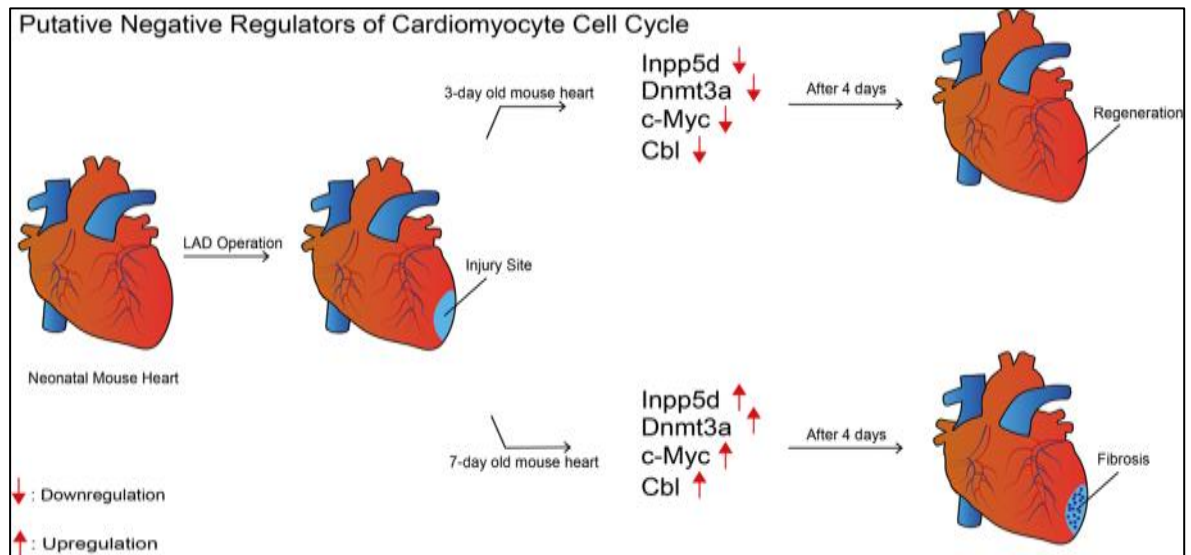


Figure 3.8. RT-PCR analysis summary for upregulation and downregulation of regulators. Inpp5d, Dnmt3a, c-Myc and Cbl down regulated in regenerative myocardium (operated at P3) and upregulated in non regenerative myocardium (operated at P7).

3.5. SIRNA KNOCKDOWN OF PUTATIVE REGULATORS INDICATED NEGATIVE EFFECT ON CARDIOMYOCYTE PROLIFERATION

To test effect of putative regulators on cardiomyocyte proliferation siRNA knockdown study was performed. To this end, cells were incubated with siRNAs according protocol mentioned. Following this, cells were fixed and immunofluorescence detection of proliferating cardiomyocytes and fibroblast were done using Anti Tnnt and Anti-pH3 (mitosis marker) primary antibodies conjugated with Alexa Fluor 488 and Alexa Fluor 555 secondary antibodies (Figure 3.10). Cbl siRNA group showed a significant increase in cardiomyocyte proliferation. Moreover, ITCH and Dnmt3a also showed an increase in cardiomyocyte proliferation (Figure 3.9A). In order to check effect of these knockdown on fibroblast, we also count proliferating fibroblast and observed that CBL also increased

proliferating fibroblasts, but not as much as in cardiomyocyte (Figure 3.9B). In the light of findings above and here, we confirmed a negative role of CBL, ITCH, and c-Myc in cardiomyocyte proliferation, thus neonatal mouse cardiac regeneration.

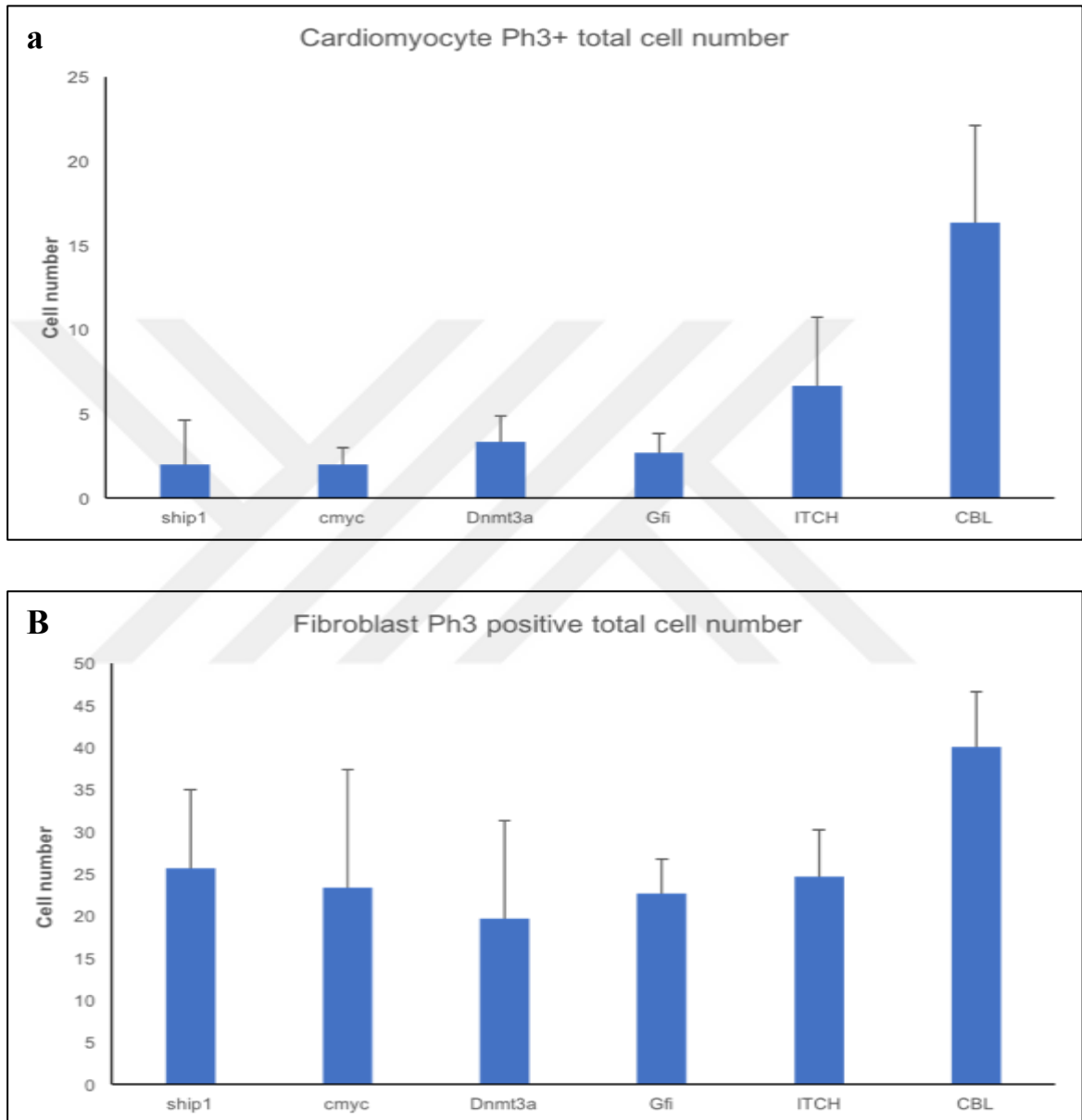


Figure 3. 9. Cell count after siRNA treatment. siRNA against to putative regulators of cardiac regeneration. A) Cardiomyocyte and Ph3 positive cells. B) Fibroblast and Ph3 positive cells.

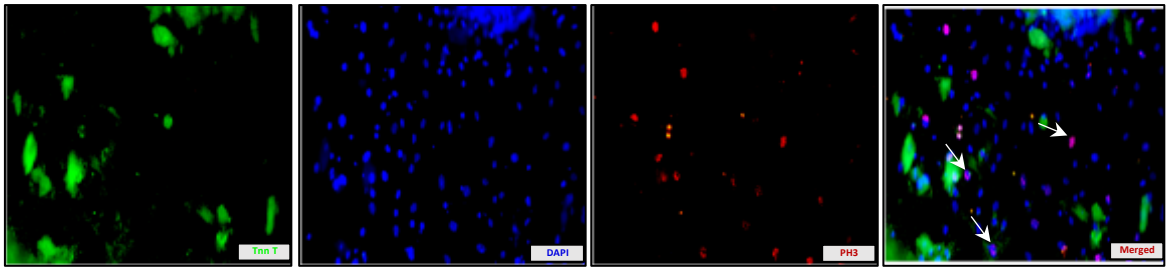


Figure 3.10. Representative image of immunofluorescence of neonatal rat cardiomyocytes under 40x magnification. Stained against TnnT (cardiomyocyte marker) and pH3 (mitosis marker). a) Cardiomyocyte and pH3 positive cells. b) Fibroblast and pH3 positive cells

4. DISCUSSION

Recent studies in different animal models of cardiac injury shed light on the underlying mechanisms and prospects of heart regeneration. The presence of barriers to rejuvenate lost cardiomyocytes such as high levels of cell cycle inhibitors and fibrosis, and the lack of factors to stimulate cardiomyocyte proliferation and stem cell differentiation into cardiac cells following myocardial injuries are among the major issues. De novo CM proliferation and differentiation are thought to be a prospect for cardiac regeneration. Manipulations used for CM cell cycle modulation have yielded DNA synthesis, karyokinesis and cytokinesis in the heart to some extent [51, 56]

Inducible knockout systems used in adult mouse models further demonstrated that CM cell cycle re-entry may be achieved in adult mammalian heart. Discovery of small molecules that trigger and promote differentiation of stem cells into CMs and induce CM cell cycle re-entry brought further excitement for development of therapies targeting MI and HF [75, 137]. Overall, studies have proven feasibility of resident CMs and stem cell recruitment following therapeutic stimulation in heart regeneration.

CM renewal, for instance, has been documented in adult mammalian heart, albeit inadequate for restoration of cardiac function following cardiac injury [51, 52]. Cardiac regeneration in zebrafish, newt, and neonatal mouse is associated with reactivation of CM cell cycle. Discovery of CM cell cycle modulators provided a new platform for development of cardiovascular therapeutics targeting CM cell cycle. Use of different approaches including miRNA, small molecules or other factors to stimulate cardiac cell proliferation brings up questions regarding their utilization. More studies are needed to identify suitable strategies and targets to achieve neonatal mouse cardiac regeneration.

Cardiac regeneration in human have been reported in many different reports which enabled to this field to develop different strategies in order to find out novel factors important for human cardiac regeneration field [4, 57, 108]. To this end, role of many different regulators were suggested to be important in cardiac regeneration field [18, 75, 77, 87, 135]. The negative or positive effect of those regulators on cardiomyocyte proliferation were reported in back to back report and enabled to develop robust therapeutical strategies against to heart failure. To this end, neonatal mouse surgery model was established which facilitate to

identify negative or positive effect of factors in mouse cardiac regeneration [20, 21]. Different surgery model were reported in last years and enabled to screen regulators using different model to reveal robust results[60]. One of the negative regulator of this response, Meis1, was identified using this model in the last year and promised for future therapeutical agent [75]. Mahmoud et al. (2013) identified role of Meis1, in that study, the negative role of Meis1 on cardiomyocyte proliferation was identified using LAD ligation surgery model and many different strategies. The work presented here also utilize similar approach to identify the role of six different putative regulators of neonatal mouse cardiac regeneration. The differential role of these candidates and suggested role cell proliferation (summarized in Table A.1) were collected and included in this study in order to reveal their effect. Moreover, their mRNA expression and protein level was confirmed using different databases (BIOGPS, Human Protein Atlas) prior to research. The initial detection of these putative regulators were analyzed using immunofluorescence method on paraffin embedded sections derived from adult mouse heart organ. This enabled us to confirm databases and observe their expression in non regenerative myocardium (Figure 3.1). Following that, their mRNA expression in cardiomyocyte and fibroblast indicated that they could be important for both of cell type residing in the heart. Higher mRNA expression of ITCH, c-Myc, Cbl, and Dnmt3a in cardiomyocytes rather than fibroblast suggested that they could be cardiomyocyte specific gene and could specifically induce their proliferation.

To test, which one of those regulators are expressed in adult heart organ in mRNA level, we also utilized another RT-PCR analysis, and reported that Cbl is expressed highest among the others (Figure 3.3). These findings enabled us to analysis to measure relative mRNA level of those regulators and decide which one could be more important for neonatal mouse cardiac regeneration. In order to confirm their protein level as alternative to immunofluorescence method, western blot analysis was utilized to measure relative protein content of those regulators in different tissues of adult mouse. Similar to RT-PCR result, Cbl was expressed greater than other regulators in adult mouse heart tissue and confirmed by other experiments.

Next, neonatal mouse surgery model was utilized to identify downregulation or upregulation of those candidates upon an injury (Figure A.2). The method enabled us to observe change of mRNA level in regenerative (P3) and nonregenerative myocardium (P7) similar to conducted by Mahmoud et al. (2015) [75]. It was observed downregulation of Inpp5d,

Dnmt3a, c-Myc and Cbl after operation on P3 neonates, but upregulation on P7 neonates (Figure 3.8). This enabled us to suggest that, downregulation of these regulators on P3 neonates which have regenerative myocardium enabled heart to increase regenerative response, and their upregulation on P7 neonates which have non regenerative myocardium enabled heart to decrease regenerative response upon an injury.). To test whether this suggestion also works in vitro, siRNA knockdown method was applied to cultured neonatal rat cardiomyocytes. After successful isolation of neonatal rat cardiomyocytes, siRNA treatment was applied to culture and cells were fixed at the day of 4 after culture (Figure 3.10.). Immunostaining against Tnnt and Ph3 (mitosis marker) was utilized and used to detect proliferating cardiomyocytes (Figure 3.10). Results indicated that Cbl, ITCH, and Dnmt3a siRNA treatment significantly increased proliferating cardiomyocytes. Moreover, this increase was highest in Cbl group, which was also highly expressed regulator both in RNA and protein level.

Similar findings regarding Cbl and c-myc resulted with increase in cell proliferation was reported in another reports [138, 139]. The similarity of Hematopoietic Stem Cells (HSCs) quiescence with cardiomyocyte cell cycle arrest could be directed into similar results in terms of cell cycle stimulation for Cbl [138]. In that study, knock out profile of Cbl in HSCs triggered cell cycle and increased population of HSCs existing in bone marrow [138]. Moreover, in another study, the knock out of cmyc resulted with decreased heart fibrosis which also correlates finding in this study [139]. Since decreased heart fibrosis could directly contribute to cardiac regeneration, the results obtained from neonatal heart surgery (Figure 3.7.) could be reason why decrease in cmyc expression enabled to heart to regenerate [139]. Similar to cmyc and cbl, ITCH showed a negative effect on neonatal mouse cardiac regeneration and its siRNA knockdown showed a considerable increase in proliferating cardiomyocytes. Moreover, ITCH, E3 ubiquitin ligase, was suggested to be important negative regulator of homeostasis and function of HSCs in a recent study which also correlates with our findings and indicate dual effect of ITCH on two different quiescent cells [141].

Taking all findings into consideration, cmyc, ITCH, and Cbl indicate a potential role in the mouse cardiac regeneration and promise as future therapeutic agents. In this study indicated role of putative regulators on neonatal mouse cardiac regeneration. Previous reports regarding their role and importance in many different pathways also affect cardiac

regeneration in neonatal mouse. Their negative effect on cardiomyocyte proliferation and cardiac regenerative response could be a valuable targeting strategy to develop therapies against cardiovascular diseases.



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APPENDIX A: LANGERDORF APPARATUS

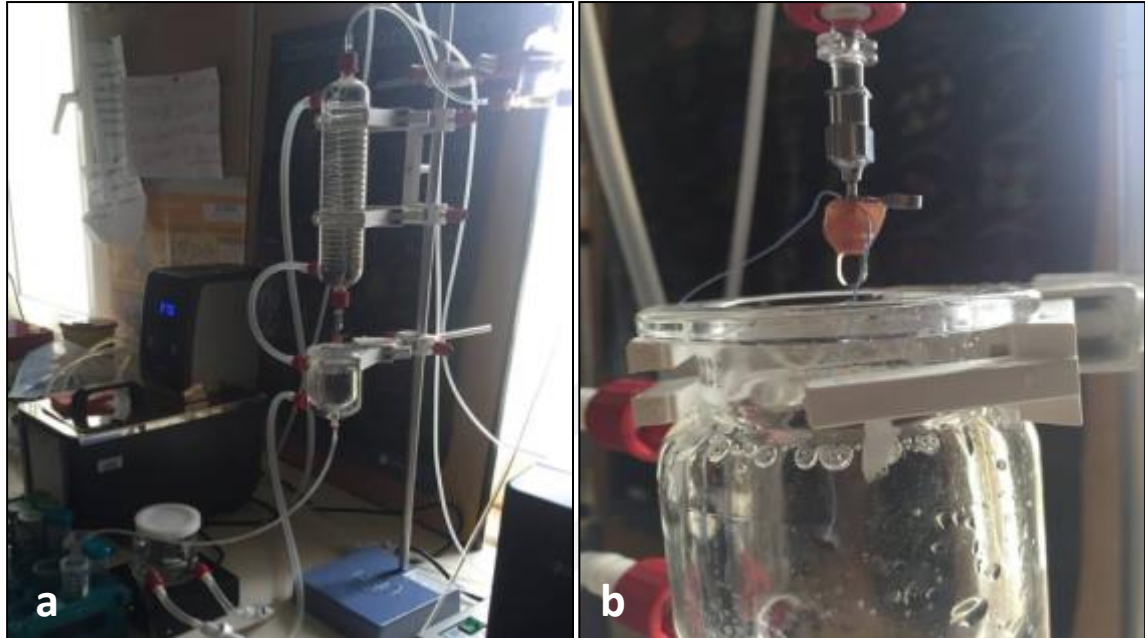


Figure A.1. Langendorff apparatus to digest heart tissue. A) Complete picture of langendorff system which include heated jacket, isolation unit and enzyme container. B) Heart at the tip of langendorff apparatus.

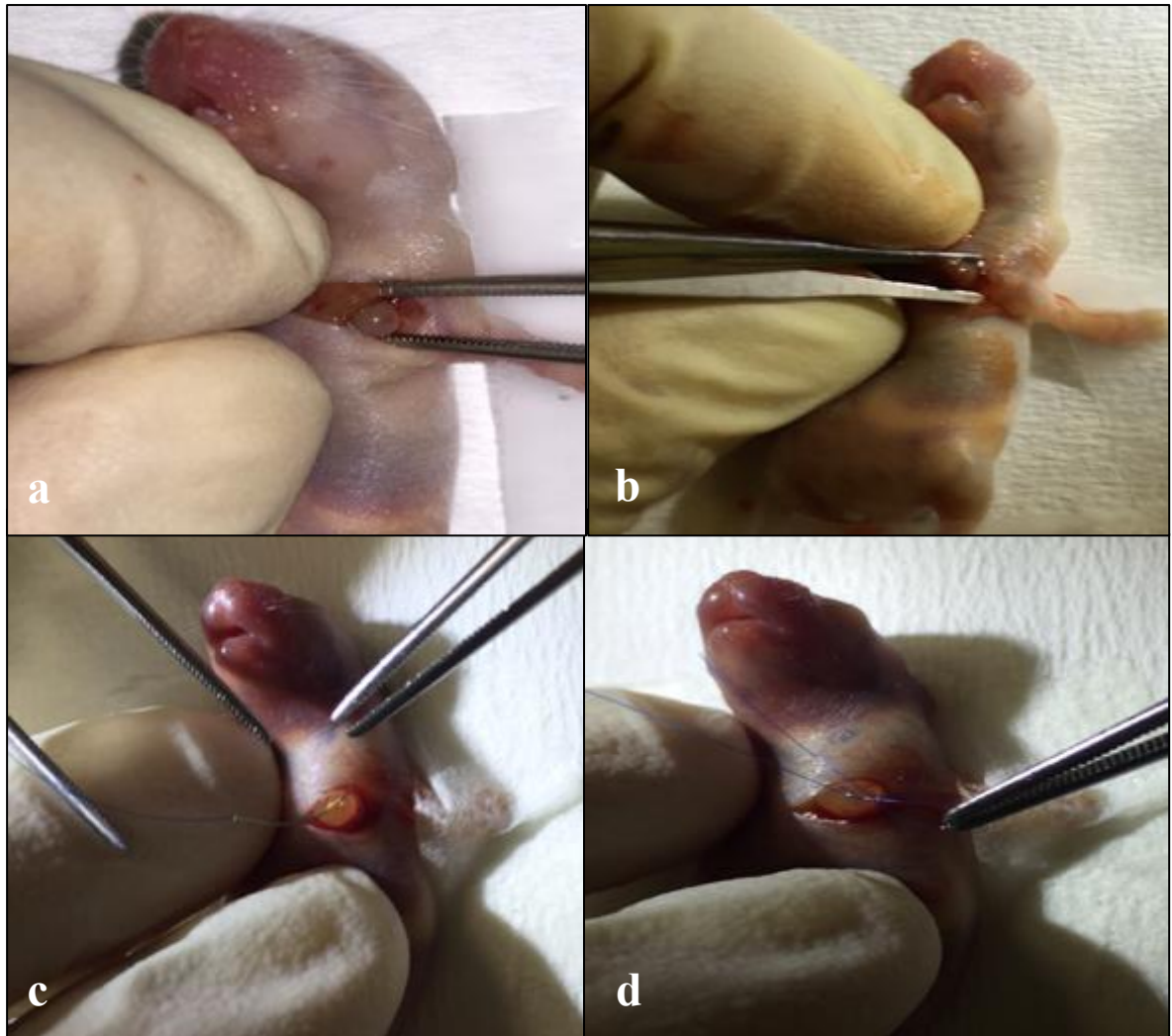
APPENDIX B: NEONATAL MOUSE SURGERY

Figure B.1. Lateral throcatmoy and heart surgery operation on neonatal mouse. a-b) Apical Resection surgery model. c-d) Ligation of LAD surgery model on neonatal mouse

APPENDIX C: SUMMARY FOR PUTATIVE REGULATORS

Table C.1. Summary of previous reports regarding role of putative regulators of cardiac regeneration.

Putative Regulators	Protein Type	Type of mouse (deleter)	Change in HSc number	Criteria used for HSC phenotype definition	Fold Difference in HSC :%	IHC Results (HPA)
Gfi1b	Transcription repressor	cKO	+	LSK CD150+CD48-	39	Moderate
Inpp5d	DNA methyltransferase	cKO	+	LSK Thy1-lo	5.7	Weak
Itch	DNA methyltransferase	KO	+	LSK CD150+CD48-	5	Moderate
Dnmt3a	RNA binding protein	KO	+	LSK CD34-Flk2-	4.5	Moderate
Meis1	Transcription factor	cKO (Scl-Cre)	+	LSK Flk2-CD34-	4.5	Weak
c-Myc	TPO receptor	KO	+	LSK Flk2-	3.6	Moderate
Cbl	Transcription factor	KO	+	LSK CD150+CD48-	3.1	Moderate
hoxa9	Transcription factor	cKO	+	LSK CD150+	2.75	No info