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SAN DIEGO STATE UNIVERSITY

Gene Therapy and Cell Fusion Enhances Stem Cell Mediated Cardiac Repair

A dissertation submitted in partial satisfaction of the requirements for the degree

Doctor of Philosophy

in

Biology

by

Pearl Jennine Quijada

Committee in charge:

University of California, San Diego

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Professor Deborah L. Yelon

San Diego State University

Professor Mark A. Sussman, Chair
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Professor Greg L. Harris

2015

The Dissertation of Pearl Jennine Quijada is approved, and it is acceptable in quality and form for publication on microfilm and electronically:

Chair

University of California, San Diego

San Diego State University

2015

DEDICATION

I want to dedicate this to my family. My father, Jaime, for his kindness and patience, your calm is a perfect balance for our eclectic family. My brother Thomas for teaching me how far you can go when you stop caring about what other people think. My sister Becky, your strength amazes me, mentally and physically. My sister Jessica, your drive and motivation are inspiring. And of course my mother Laura for her unyielding support and unconditional love, you instilled in me drive and an amazing work ethic. But most of all, you guided me towards what I love and I thank you for that. Of course, I would like to dedicate this to Benjamin Knowles, my biggest fan and cheerleader. You carefully challenge as well as support me. Your optimism depletes my pessimistic attitude, and no day is boring when I'm with you. Thank you for being in my life.

EPIGRAPH

“Every day you play with the light of the universe.”

–Pablo Neruda

“Be less curious about people and more curious about ideas.”

-Marie Curie

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LIST OF ABBREVIATIONS

2N	diploid, euploid DNA content
4N	tetraploid, aneuploid DNA content
α -SMA	α -smooth muscle actin
ANOVA	analysis of variance
AWT	anterior wall thickness
B1-AR	B1-adrenergic receptor
B2-AR	B2-adrenergic receptor
BMC	bone marrow cell
BMP4	bone morphogenic factor 4
Ca ²⁺	calcium
CAD	coronary artery disease
CaMKII	calcium/calmodulin kinase II
CC	CardioChimera
CC1	CardioChimera 1
CC2	CardioChimera 2
CPC	cardiac progenitor cell
CPC + MSC	cardiac progenitor cells and mesenchymal stem cells
CPCe	cardiac progenitor cells overexpressing eGFP
CPCe δ B	cardiac progenitor cells overexpressing CaMKII δ B
CSC	cardiac stem cell
cTNT	cardiac troponin T
CVD	cardiovascular disease

DAPI	4',6-diamidino-2-phenylindole
Dex	dexamethasone
dP/dT	developed pressure over time
EF	ejection fraction
eGFP	enhanced green fluorescent protein
ESC	embryonic stem cell
FACS	fluorescence activated cell sorting
FBS	fetal bovine serum
FVB/NJ	friend virus B, common mouse strain
GAPDH	glyceraldehyde 3-phosphate dehydrogenase
GATA4	GATA binding protein 4
HDAC4	histone deacetylase 4
HDAC5	histone deacetylase 5
HW/BW	heart weight to body weight ratio
HSC	hematopoietic stem cell
IL-6	interleukin-6
IP3R	inositol 1,4,5-trisphosphate receptor
iPSC	induced pluripotent stem cell
LAD	left anterior descending artery
LVAD	left ventricular assisted device
MEF2	myocyte-specific enhancer factor 2
MH-CC	mouse-human CardioChimera
MI	myocardial infarction

MLHF	Minnesota Living with Heart Failure Questionnaire
MSC	mesenchymal stem cell
Myh6	myosin heavy chain α
Myh7	myosin heavy chain β
NRCM	neonatal rat cardiomyocyte
NS	nucleostemin
NYHA	New York Heart Association
P ₂ YR	purinergic receptor P ₂ Y
PBS	phosphate buffered saline, vehicle control group
PECAM (CD31)	platelet endothelial cell adhesion molecule
PGK	phosphoglycerate kinase
pHDAC4	phosphorylated histone deacetylase 4 on serine 632
PKA	phospho-kinase A
PKD	phospho-kinase D
RNA-seq	RNA-sequencing
RyR	ryanodine receptor
SCPIO	Stem Cell Infusion in Patients with Ischemic cardiomyopathy
SDF-1	stromal derived factor-1
SERCA	sarco/endoplasmic reticulum Ca ²⁺ -ATPase
sh-Ctrl	lentivirus expressing small hairpin control
sh- δ B	lentivirus small hairpin targeting CaMKII δ B
SM22	smooth muscle 22
TOPRO	TO-PRO-3 iodide

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Chapter 1, in full, is prepared for submission. Nuclear Calcium/Calmodulin-Dependent Protein Kinase II Signaling Enhances Cardiac Progenitor Cell Survival and Cardiac Lineage Commitment. Pearl Quijada, Nirmala Hariharan, Jonathan Cubillo, Kristin M. Bala, Lucia Ormachea, Donald M. Bers, Mark Sussman and Coralie Poizat. The dissertation author was the primary author and investigator of this manuscript.

Chapter 2, in full, is prepared for submission. Cardiac Stem Cell Hybrids Enhance Myocardial Repair. Pearl Quijada, Hazel T. Salunga, Nirmala Hariharan, Jonathan Cubillo, Farid El-Sayed, Maryam Moshref, Kristin M. Bala, Jaqueline M. Emathinger, Andrea De La Torre, Lucia Ormachea, Roberto Alvarez Jr., Natalie A. Gude, and Mark A. Sussman. The dissertation author was the primary author and investigator of this manuscript.

Chapter 3 is presented in this dissertation as an extension of Chapter 2 to support the creation CardioChimeras with human derived stem cell lines. I would like to acknowledge Megan Monsanto for the isolation of fetal adult stem cells, Sarmistha Ganguly for her part in creating CardioChimeras between mouse and human adult stem cells and Michael McGregor for his initial contribution in identifying senescence markers in stem cells.

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2011-2015	ARCS Scholarship
2011	Provost Award, SRS, San Diego State University
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Scientific Presentations

June 2015	International Society of Heart Research, Seattle, WA
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November 2014 American Heart Association Scientific Sessions, Cardiac Regeneration/Cellular Therapy: Experimental. Chicago, IL

June 2014 Gordon Research Conference: Cardiac Regulatory Mechanisms, New Concepts/Emerging Themes in Cardiovascular Biology, New London, NH

June 2014 Gordon Research Seminar: Cardiac Regulatory Mechanisms, iPS Cells: A Window on Human Myocardial Biology and Disease, New London, NH

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ABSTRACT OF THE DISSERTATION

Gene Therapy and Cell Fusion Enhances Stem Cell Mediated Cardiac Repair

by

Pearl Jennine Quijada

University of California, San Diego, 2015

San Diego State University, 2015

Professor Mark A. Sussman, Chair

Cardiovascular disease is the leading cause of mortality in the United States. Myocardial infarction (MI) induces massive cellular death and leads to a decline in cardiac function. Cardiomyocytes have limited proliferative capacity sparking interests in molecular and cellular strategies to promote stem cell conversion into new cardiomyocytes.

Cardiac progenitor cells (CPCs) are tissue resident stem cells that give rise to cardiomyogenic structures. Although, CPCs introduced into the heart confer improvements in cardiac function after MI, these effects are not sufficient to support complete heart regeneration and prevent heart failure. Studying molecular pathways that contribute to CPC survival and commitment is essential in advancing CPC based therapeutic approaches. Ca^{2+} /Calmodulin-dependent protein kinase II δ B (CaMKII δ B) regulates survival and growth in cardiomyocytes. However, the role of CaMKII δ in CPCs has not been previously explored. CPCs increase nuclear CaMKII after MI and *in vitro* differentiation suggesting that CaMKII δ B contributes to the regulation of CPC commitment. Overexpression of CaMKII δ B in CPCs reduces proliferation, enhances resistance to death and increases cardiac specific differentiation. CaMKII δ B may serve as a novel modulatory kinase to promote CPC survival and commitment.

Despite increasing use of stem cells for regenerative-based cardiac therapy, the optimal stem cell population(s) remains uncertain. In the past decade there has been increasing interest and characterization of stem cell populations reported to directly and/or indirectly contribute to cardiac regeneration through processes of cardiomyogenic commitment and / or release of cardioprotective paracrine factors. Future therapies require development of unprecedented concepts to enhance myocardial healing. Combinatorial cell therapy utilizing CPCs and bone marrow derived mesenchymal stem cells (MSCs) promote enhanced reparative functions *in vivo*. However, identifying cell specific mechanisms of cardiac repair are difficult using dual cell systems. Here,

we performed cell fusion between CPCs and MSCs to obtain hybrids with combined cell characteristics called CardioChimeras. Our ideal cell therapy is to combine the beneficial properties of CPCs to undergo cardiac specific commitment as well as MSCs that foster an improved microenvironment with protective paracrine secretion.

INTRODUCTION OF THE DISSERTATION

Cardiovascular Disease

Cardiovascular disease (CVD) is the most common cause of morbidity and mortality in westernized countries due in part to genetics and poor lifestyle behaviors. According to the American Heart Association, preventative measures include the maintenance of healthy eating habits and regular exercise to ward off symptoms of CVD. In general, healthy lifestyle practices need to be extended to the youth as 50% of children from 12-19 years of age are obese and have increased chances of developing CVD in early adult years¹. The socioeconomic burden of CVD estimates in to the billions of dollars making this disease a biomedical priority for millions of Americans currently and into the future¹.

Pharmaceutical and technological advances have led to improved detection, treatment and prevention of CVD in the past 20 years². Coronary artery disease (CAD), caused by atherosclerosis of the major arteries promotes symptoms of angina pectoris, leads to myocardial infarction (MI) and/or stroke³. Implantation of vascular stents and administration of drugs reduces the impact of ischemic events after MI and during chronic remodeling of the heart². Inevitably, global heart remodeling will lead to decreased cardiac function and heart failure³. Heart transplantation or left ventricular assisted device (LVAD) implantations are end-stage cardiovascular interventions that modestly extend life span³. Unfortunately, early and late stage treatments of CVD do not support regeneration of the heart by direct cardiomyocyte replacement or prevention of collagen deposition. Cardiomyocytes are post-mitotic cells leading to the inability

of the heart to heal. Therefore, the development of novel molecular and cellular strategies to induce regeneration is of strong interest in the biomedical research field.

Cardiomyocyte-based Regeneration

DNA synthesis in cardiomyocytes is highest during the embryonic stage, which drops dramatically in adulthood. The potential for cardiomyocyte division decreases by 20 times in ventricular cardiomyocytes one-day post birth and 4000 times in adult rodent models (0.0005% of total cardiomyocytes) measured by ³H-thymidine incorporation⁴⁻⁶. Interestingly, complete heart regeneration is observed after apical resection of the left ventricle or after MI if the damage occurs before 7 days post-birth in the mouse model^{7, 8}. Cardiomyocyte cell-cycle withdrawal limits essential regeneration of the heart after damage, yet this discovery has supplied researchers an invaluable tool to investigate novel signaling pathways and microRNAs that regulate cardiomyocyte turnover during this short regenerative window^{8, 9}. In contrast, MI induces cardiomyocyte cell-cycle entry observed in 0.0055% to 0.0083% of total myocytes bordering the infarct zone or 11 to 16 fold relative to basal proliferative indices⁴⁻⁶.

In the adult heart, mature cardiomyocytes respond to damage by undergoing hypertrophy, which impairs cardiac function as early as a few days after MI¹⁰. Transgenic mouse models over expressing proto-oncogenes c-Myc or nuclear-targeted Akt have been shown to increase cardiomyocyte cell-cycle entry¹¹⁻¹³. Nuclear Akt accumulation in cardiomyocytes increases the presence of

small myocytes, which corresponds to improved contractility and cardiac performance¹¹. Generation of transgenic murine models is important for the elucidation of mechanisms to promote cardiomyocyte-based regeneration, but there remain limitations in applying mouse genetic models towards clinical use.

Stem Cell Therapies: Pluripotent Stem Cells

Not surprisingly given the controversies and inefficiencies of endogenous cardiomyocyte repair, researchers and clinicians have turned their attention towards the isolation and expansion of primary stem cell populations from both embryonic and adult tissue to promote regeneration after adoptive cell transplantation. Pluripotent embryonic stem cells (ESCs) derived from the inner cell mass have been observed to differentiate into cells of the cardiovascular system¹⁴. The next generation counterpart “induced pluripotent stem cells” (iPSCs) do not cause adverse immune responses after transplantation and differentiation *in vivo*^{15, 16}. Cell culture protocols involving the addition of growth factors (BMP4 and activin A), DNA modifiers such as 5-azacytidine and trichostatin A and thyroid hormones enrich for ES/iPSC derived cardiomyocytes (70%-90%) with accumulation of differentiated cell properties reminiscent of young cardiomyocytes including mono-nucleation with the potential to divide¹⁷⁻²¹. Cardiomyocyte purity and efficiency of ESC differentiation is of critical importance as undifferentiated ESCs form teratomas and prevent ESC-cardiomyocyte maturation *in vivo*^{19, 22}. Unfortunately, purified ESC derived myocytes are unable to electrically couple with the existing myocardium in both pig and non-human

primates despite suppression of arrhythmias in small animal models^{19, 23}. These studies indicate that protocols for the derivation of ESC-cardiomyocytes need to be improved before proceeding to human clinical trials²⁴.

Stem Cell Therapies: Bone Marrow Derived Cells

Cellular therapy using stem cells derived from the bone marrow and cardiac origin are validated to treat damage after MI in both animal models and human clinical trials^{10, 25-29}. Bone marrow derived stem cells are historically the most widely used for clinical therapy¹⁴. Popularity of bone marrow derived therapy arises from the relative ease and efficiency of isolation, straightforward enrichment of mononuclear bone marrow cells and mesenchymal stem cells (MSCs) from the patient, as well as delivery by both autologous and allogeneic means³⁰⁻³². MSCs are of interest because of ability to secrete an assortment of paracrine factors although they lack marked ability to transdifferentiate into functional cardiac muscle³³⁻³⁵. Additionally, MSCs may also provide for immunomodulatory effects *in vivo*, reducing inflammatory responses and stimulating ECM turnover³⁶. Reports have highlighted the inconsistencies in clinical trial design, randomization, and statistics to support the efficacy of bone marrow derived cells for use in the United States despite common clinical practice across Europe. These results cast doubts over the value of bone marrow derived cells, which admittedly provide for modest myocardial recovery even under the best of circumstances³⁷.

Stem Cell Therapies: Cardiac Stem Cells

The coveted cardiac-derived stem cell (CSC) has been traced as early as the developmental stage that defines the mesoderm. Analysis of the early embryonic heart reveals distinct first and second heart fields, housing regulatory niches for multipotent CPCs (Mef2c⁺ and Nkx2.5⁺)³⁸. In the past decade researchers have come to recognize differential CPCs due to the heterogenic nature of the heart, such as LIM homeodomain transcription factor Islet1 cells, sca-1⁺ cells and side population cells³⁹. The receptor tyrosine kinase kit is highly expressed in the bone marrow, a marker of hematopoietic stem and progenitor cells and was subsequently used to discover stem and progenitor cell populations in the heart. C-kit lineage transgenic mice, which express the green fluorescent protein under the regulatory control of the c-kit promoter, facilitated the identification of cells of myocardial and vascular lineage⁴⁰⁻⁴³. Use of c-kit cells in the clinical trial Stem Cell Infusion in Patients with Ischemic cardiomyopathy (SCIPIO) increased ejection fraction by 12% and reduced fibrotic scar by 30% based on a one year follow up¹⁰. Additionally, CSC treatment improved quality of life based on New York Heart Association (NYHA) functional parameters and the Minnesota Living with Heart Failure (MLHF) Questionnaire score, which was downgraded in most patients to NYHA Class I and MLHF score between 20-30 one year following treatment¹⁰. These studies mediate the validation and future use of CPCs for cardiac therapy.

Genetic Engineering Strategies

Optimal cell proliferation and enhanced survival are indispensable traits in an adult stem cell population tailored for cellular therapy. Cardiac ischemia results in cardiomyocyte death, increased inflammation and impaired proteolysis creating a challenging environment for transplanted stem cells^{44, 45}. Stem cell populations efficient in DNA replication but susceptible to oxidative stress and inflammatory insults can be augmented by increasing the number of delivered cells to challenge cell death during acute damage. However, limited persistence of stem cells 24-hours after intramyocardial injection reduces the initial population to less than 10% of cells as quantified by sensitive PCR methods^{46, 47}. Increased quantity of cells during delivery creates higher rates of competition between injected stem cells and the microenvironment depleting cell resourcefulness. Molecular approaches to enhance stem cell ability to thrive in the damaged myocardium should provide for enhanced proliferation and survival characteristics *ex vivo* and prior to delivery.

Exogenous expansion of adult stem cells is necessary to deliver adequate numbers of cells and support regeneration after damage especially in view of the inevitable losses of cells following adoptive transfer. Methodologies to invigorate stem cells by improving proliferation and survival capabilities for transplantation studies have employed genetic engineering with viral vectors (adeno-, retro- and lentiviruses). Boosting stem cell properties has been accomplished with genetic overexpression of serine threonine kinases Akt and a downstream activator Pim-1. Pim-1 is a constitutively active protein implicated in cardioprotection after

pathological stimulus and promotes CPC cycling and cardiomyogenic differentiation in mouse and human systems⁴⁸⁻⁵¹. Bone marrow cells (BMCs) migrate to the heart after myocardial damage, yet do very little to maintain cardiac integrity with limited evidence of transdifferentiation⁵². In a study completed by our laboratory, delivery of Pim-1 over expressing BMCs enhanced structural integrity of the heart after damage compared to non-genetically modified stem cells possibly through increased persistence and secretion of paracrine factors from BMCs well into the third month after delivery⁵³. Similarly, mouse and human CPCs support cardiac regeneration directly up to 8 months after delivery through means of increased engraftment and differentiation into mature cardiogenic cells^{49, 53}. Pim-1 overexpression increases growth kinetics and provides for transient lengthening of telomeres in mouse CPCs⁵⁴. Routine protocols in our laboratory allow for isolation of c-kit⁺ CPCs from patients exhibiting symptoms of severe heart failure before LVAD implantation⁵⁵. Isolated human CPCs with slow proliferative indices correlate with shorter telomeres and increased susceptibility to oxidative stress^{55, 56}. Genetic enhancement of human CPCs with Pim-1 increases telomerase activity, stabilizes telomere lengths and prevents premature cell cycle arrest in culture⁵⁵. Senescent properties of CPCs can be reversed using Pim-1 and can further broaden the use of CPCs from patients regardless of suboptimal stem cell traits. Additionally, our group has identified nucleostemin (NS) as a downstream target of Pim-1⁵⁷. NS is known to play a role in regulation of ribosomal biogenesis, proliferation and growth in proliferative stem cells making NS an ideal biomarker to identify youthful CPCs

derived from the heart^{56, 58}. Stem cell therapy would benefit by isolation of proliferative and survival competent cells, but also cells that are receptive to molecular strategies to supplement inherent limitations in the reparative potential of the heart.

Stem Cell Fusion

Cell fusion for reprogramming of somatic cells has undergone a form of renaissance in the regenerative medicine era, sparking new interest in defining the optimal genetic factors to activate dormant cell types⁵⁹⁻⁶¹. Fusion of slow growing MSCs with an immortal cell line produces hybrids that escape replicative senescence^{60, 61}. Hematopoietic stem cells (HSCs)-hepatocyte hybrids observed *in vivo* results in silencing of transcription factors associated with HSC maintenance, increased acquisition of hepatocyte chromatin regulators and overexpression of growth factor genes in the bone marrow nuclei overall leading to liver specific commitment in combination with enhanced bone marrow derived features⁶². In the cardiac context, proliferative stem cells fused with cardiomyocytes results in hybrids with constitutive expression of DNA synthesis markers and maintenance of well-defined sarcomeres⁵⁹. These studies validate that cell fusion conducted between a proliferative parent cell and a slow growing, committed or senescent cell population can facilitate in the creation of hybrids with more youthful phenotypes, pre-committed cells with an ability to proliferate and optimal properties to overcome an aging cardiac environment. Fortunately, cell fusion is being discussed at a critical time for improving cellular based

approaches, as stem cell transplantation to support cardiomyocyte replacement occurs through a process of uncontrolled fusion of stem cells with the myocardial milieu in order to salvage damaged tissue^{41, 63, 64}. However, there has been a dearth of studies to delineate the most favorable stem cell types to be used in a cell fusion based protocol *ex vivo* and to support repair of the myocardium.

Defining the Optimal Stem Cell Properties

Efforts to publicize widespread application of cellular therapy are hindered by reports of little to no improvement in cardiac function after long-term follow up studies using a variety of stem cell strategies. This is further complicated by the fact that isolation of stem cells from aged organs display senescent phenotypes⁶⁵. Improvement of stem cell engraftment and survival has been attempted with co-injection of stem cells with biomaterials^{66, 67}, cytokines and growth factors⁶⁸, or genetically engineering cells with pro-survival and anti-apoptotic genes^{48, 69}. Despite recent advances in gene therapy, the discovery of the optimal protein(s) and/or activated signaling pathways, which tailor stem cells for paracrine secretion in combination with cardiomyogenic commitment is needed. Furthermore, it is imperative that genetic strategies promote enhancement of pro-survival pathways in stem cells without initiating extreme proliferative phenotypes. Collectively, the field continues to struggle with uncertainties regarding the potency of adult stem cells to mediate meaningful cardiac repair during development or after myocardial damage.

Despite established isolation techniques, there appears to be a lack of understanding of the native stem cell biology in culture. Optimal properties that encompass a composite stem cell would include enhanced survival and proliferation, commitment, and ability to communicate with the endogenous cardiac environment. Ultimately, a picture of the ideal stem cell population emerges from our assessment and overview, but predictably the collective characteristics needed indicate that such a population might not exist under natural conditions to mediate cardiac repair. Therefore, we posit that a combination of stem cells or a single stem population created by *ex vivo* engineering will be required to advance the next generation of cell-based therapy. Our goal is to point toward new avenues and novel transformative therapeutic angles that embrace the ideal properties of adult stem cells.

CHAPTER 1

Nuclear Calcium/Calmodulin-Dependent Protein Kinase II Signaling Enhances Cardiac Progenitor Cell Survival and Cardiac Lineage Commitment

INTRODUCTION

Cardiac regeneration, homeostatic or after acute myocardial damage, is in part supported by the migration of stem and progenitor cells from the bone marrow and endogenous cardiac niches^{70, 71}. Stem cells with cardiomyogenic potential were identified based on expression of the receptor tyrosine kinase c-kit and termed as cardiac stem cells or CSCs present in early cardiac development and in the adult heart^{40, 72}. Importantly, c-kit⁺ cells are up regulated temporally after myocardial damage by undergoing proliferation and commitment towards the cardiomyogenic lineage confirmed by genetic lineage tracing^{43, 73}. CSCs isolated and expanded *ex vivo* acquire cardiac specific transcription factors and are referred to as cardiac progenitor cells (CPCs)⁷⁴. CPCs exhibit properties of self-renewal and multipotency and give rise to cardiomyocytes, endothelial and smooth muscle lineages *in vitro*⁴⁸. The clinical relevance of CPCs has been further validated by isolation of stem cells from human cardiac tissue used in the **Stem Cell Infusion in Patients with Ischemic Cardiomyopathy (SCIPIO) Phase I** clinical trial¹⁰. However, the intrinsic mechanisms involved in the regulation of CPC survival, proliferation and direct cardiomyogenic commitment have not been elucidated.

Calcium (Ca²⁺) is an integral second messenger, regulating cellular processes such as cellular survival, proliferation, growth and differentiation⁷⁵. Increases in intracellular Ca²⁺ bind to calmodulin which then activates Ca²⁺/calmodulin-dependent serine/threonine kinase, a class of enzymes known

as CaMKs⁷⁶. CaMKII is the predominant enzyme expressed in cardiac tissue and can be activated with oxidative stress following cardiac injury⁷⁷. Chronic up regulation of the kinase results in cardiomyocyte hypertrophy leading to cardiac failure in mouse models^{78, 79}. CaMKII δ , the main isoform expressed in the heart, is elevated in heart failure samples implicating CaMKII in the regulation of proper cardiomyocyte contractility^{80, 81}. However, the distinct role of CaMKII and the main cardiac δ isoforms in resident CPCs has not been previously addressed.

CaMKII δ B and CaMKII δ C are the predominant splice variants described in the adult myocardium. CaMKII δ B localization remains differentiated from CaMKII δ C due to a nuclear localized sequence. Yet CaMKII δ B expression is not exclusive to the nucleus as the CaMKII holoenzyme is formed by a majority of δ subunits^{82, 83}. Nuclear CaMKII δ (B isoform) regulates cellular growth through indirect de-repression of myocyte enhancer factor 2 (MEF2) after phosphorylation and inactivation of the histone deacetylase 4 (HDAC4)⁸³⁻⁸⁵. Furthermore, CaMKII δ B has been shown to promote cellular protection by binding to the transcription factor GATA4 and indirectly inhibiting the expression of inflammatory genes⁸⁶⁻⁸⁸.

CaMKII δ B regulates vascular smooth muscle cell migration, proliferation and growth suggesting kinase activity is not limited to cardiomyocytes^{89, 90}. CaMKII is linked to the regulation of proliferation and differentiation of embryonic stem cells after inhibition of Class II HDACs⁹¹. CaMKII δ B phosphorylation of HDAC4 induces translocation to the cytosol, thereby relieving its inhibitory action and allowing transcription of genes involved in cell cycle arrest and lineage

specific differentiation in a variety of stem cells^{83-85, 92-94}. Currently the use of HDAC inhibitors such as Trichostatin A and 5-aza cytidine are used to increase the efficiency of reprogramming and differentiation of stem cells, supporting the role of HDACs in maintaining pluripotency and proliferation⁹². Therefore, this study aims to characterize a CaMKII δ B-dependent mechanism of cardiac progenitor survival and cardiogenic commitment through class IIa HDAC inhibition.

METHODS

Cardiac progenitor cell isolation

Adult CPCs were isolated from 12 week-old FVB male mice. After anesthetizing mice with ketamine-xylazine solution, the chest was opened and the aortic arch was isolated and curved forceps were used to slip a 4-0 suture (Ethicon) underneath. A small incision was on the aortic arch to insert a 22-gauge cannula (Radnoti LLC). Basic buffer, which consists of J-MEM (Sigma) supplemented with HEPES, Taurine, Insulin, Penicillin, Streptomycin, Glutamine, Amphotericin and Gentamycin and collagenase II (30Units/mL Worthington Biochemical) was slowly perfused through the heart after suspending from a Radnoti EZ Myocyte/Langendorff Isolated Heart System while being submerged in a 100mL reservoir for no more than 15 minutes. The heart was then removed from the cannula and placed in a sterile 15-mL conical tube in basic buffer supplemented with 0.5% bovine serum albumin. In a sterile hood, the heart was passed through a 100- μ m filter followed by a 40- μ m filter and collected in a 15 mL conical tube in basic buffer with BSA. Large cells and cardiomyocytes were separated by quick centrifugation (1 minute, 100g, at 4°C). The supernatant was then passed through a 30- μ m filter (Miltenyi Biotec Inc.). Cells were counted and centrifuged (10 minutes, 600g, 4°C). The second supernatant was aspirated, and the pellet was resuspended in 80 μ L per 10^7 cells in washing buffer (phosphate buffered saline supplemented with 0.5% BSA) and 20 μ L of CD117-conjugated microbeads (Miltenyi Biotec Inc.). Cells were passed over Miltenyi Biotec

MiniMACS sorting columns to select for c-kit⁺ cells. Cells were resuspended in 10% embryonic stem cells fetal bovine serum supplemented cardiac stem cell medium (Dulbecco's modified Eagle's medium and Ham's F-12 medium (ratio, 1:1), insulin-transferrin-selenium (0.1%), leukemia inhibitory factor (10 ng/mL), basic fibroblast growth factor (10 ng/mL), epidermal growth factor (20 ng/mL), 10% embryonic stem cells grade FBS, and 1% penicillin-streptomycin-glutamine), plated on a 35-mm cell culture-grade dish, and placed in an incubator at 37°C. Media was changed 5–7 days later, and the resulting adherent cultures were passaged using Cell Stripper (Cellgro) combined with TryLE Express Enzyme (Life Technologies).

Differentiation media conditions

CPCs in growth media (GM) were cultured in full medium and used as a control. Differentiation was induced by culturing CPCs in α -minimal essential media alone or with the addition of 10nM dexamethasone for 6 days.

Lentiviral constructs and cell transduction

Bicistronic lentiviral constructs were created to over-express a HA tagged CAMKII δ gene under control of a myeloproliferative sarcoma virus LTR-negative control region deleted promoter and enhanced green fluorescence protein (eGFP) driven off a vIRES. The control lentivirus drives expression of eGFP alone. Transduction of CPCs with bicistronic lentivirus expressing eGFP or HA-CaMKII δ -eGFP was performed with a multiplicity of infection of 10. Cells were allowed 48 hours to express the eGFP (CPCe) and HA-CaMKII δ -eGFP

(CPCe δ B), then purified after fluorescence activated cell sorting (FACS) by placing one-cell per well of a 96-micro plate to allow for clonal expansion. Three CPCe clones were derived and five CPCe δ B. Silencing lentiviral constructs utilized the U6 promoter to drive expression of small hairpin targeted RNA. Two shRNAs were created, a scrambled control and sh towards CaMKII δ B. Both constructs had an inserted cytomegalovirus (CMV) eGFP cassette to label transduced cells. Transduction with sh- scrambled control (sh-Ctrl) or sh to CaMKII δ B (sh- δ B) was performed with a MOI of 10 and allowed 48 hours for knockdown before performing population sorts using FACS based on eGFP expression.

Evaluation of cell morphology

Images of cultured CPCs were obtained on a Leica DMIL microscope and outlines were traced using ImageJ software. Parameters such as area, “shape descriptors” and “Feret’s diameter” were measured, based on which the cross sectional area and roundness were determined. Feret/MinFeret was used to evaluate length to width ratio of each cell.

Proliferation assay and cell doubling time

Cell proliferation was determined using the CyQuant Direct Cell Proliferation Assay (Life Technologies) according the manufacturer’s instruction. CPCs were plated at a density of 500 cells in 100 μ L of full growth media per well of a 96-well flat bottom microplate. Assay was started on day of plating, day 2 and day 4 and day 6 by adding of 100 μ L of CyQuant direct green fluorescent

nucleic acid stain in each well and incubated for 60 minutes. Green fluorescence intensity was measured at 495 nm using a plate reader and represented as a fold change relative to fluorescence intensity measured on the day of plating (day 0). Population doubling times were calculated using the readings from CyQuant Direct Proliferation Assay and use of a population doubling time online calculator (<http://www.doubling-time.com/compute.php>).

Cell cycle analysis

Cells were fixed in 70% ethanol and stored overnight at -20°C. Cell cycle distribution was analyzed by staining with propidium iodide (PI) plus RNase staining buffer (BD Biosciences) at 37°C for 15 minutes. Cell cycle was analyzed using a BD FACSCanto and FlowJo software to determine relative distributions of cells in G1 and G2/M phases of the cell cycle.

Metabolic activity assay (MTT-based assay)

CPCe and CPCeδB were subjected to a MTT colorimetric reducing assay which analyzes (3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide), a yellow tetrazole being reduced to a purple formazan in living cells. This assay was used in order to determine relative rates of metabolic activity between cell lines. In this assay 500 cells were plated per well in a 96-well flat bottom plate incubated with 10µL of 5mg/mL MTT reagent for four hours. Reaction was stopped with 100µL of diluted HCL for lysis overnight. The MTT assay was performed on the day of plating, 3 or 7 days after plating and incubation with CPC growth media, Minimum essential media- α modification (α-MEM) with 10%

fetal bovine serum (FBS) or 10% FBS α -MEM supplemented with Dex. Absorbance was measured at 595nm in order to determine relative concentrations of cells at given days.

Cell death assay

CPCs were plated in a 6-well dish (80,000 cells per well) and incubated in starvation media (growth factor and FBS depleted media) with 1% PSG for 18 hours. Cells were treated with either 40 or 80 μ M hydrogen peroxide for 4 hours. Analysis of cell death was initiated by collecting cells from suspension and adherent cells and pelleting at 1600rpm for 5 minutes. The pellet was resuspended in Annexin V binding buffer and incubated with Annexin V (1:40) from BD Biosciences combined with 7-amino-actinomycin D (7-AAD) staining to label apoptotic and necrotic cells collectively. Data was acquired using a FACS Canto from BD Biosciences and analyzed with FACS Diva software from BD Biosciences. Cell death was quantitated by co-labeling of Annexin V and 7-AAD and represented as a fold change or percentage of cell death relative to cells in starvation media alone.

Immunoblot

Protein lysates from whole hearts and cultured cells were prepared in sample buffer (containing 150mM Tris (pH 6.8), 150mg/ml sucrose, 2mM ethylene diamine tetraaceticacid (EDTA) (pH 7.5-8), 480mg/ml urea, 8mg/ml dithiothreitol, 0.2% sodium dodecyl sulfate, 0.2 mg/ml bromophenol blue at a final pH of 6.8, supplemented with protease and phosphatase inhibitor cocktails

(Sigma-Aldrich). Whole hearts from mice were prepared by homogenizing tissue in isolation buffer (containing 70 mM sucrose, 190 mM mannitol, 20mM HEPES solution, and 0.2 mM EDTA in de-ionized water) using a Next Advance bullet blender. Protein lysates from homogenized tissue were incubated 1:1 with sample buffer. CPCs were either lysed directly with sample buffer or were fractionated into nuclear and cytosolic compartments according to manufacturer's protocol prior to incubating in sample buffer (PARIS Kit, Life Technologies). All protein samples for western blot analysis were separated on a 4%–12% Bis-Tris mini-gel (Life Technologies) and transferred to a polyvinylidene difluoride membrane. Membranes were blocked for 1 hour with 10% milk in TBST (1% Tris-buffered saline/0.1% Tween) and then probed with primary antibody overnight in milk. Next day blots were washed with TBST buffer and incubated in secondary antibodies in milk for 1.5 hours. Primary antibodies for western blot are as follows: rabbit anti-CaMKII δ (1:15000; UC Davis, Dr. Donald Bers), mouse anti-HDAC4 (1:1,000; Cell Signaling) rabbit anti-Phospho-HDAC4 (Ser632)/HDAC5 (Ser661)/HDAC7 (Ser486) (1:1000; Cell Signaling) goat anti-GFP (1:1000; Rockland), mouse anti-HA tag (1:200; Santa Cruz Biotechnology, Inc.), mouse anti-p16 (1:200, Santa Cruz Biotechnology), rabbit anti-p53 (1:500, Abcam), rabbit anti- α -sarcomeric actinin (1:500; Abcam), mouse anti- α -smooth muscle actin (1:1000; Sigma Aldrich), rabbit anti-Tie2 (1:100; Santa Cruz Biotechnology), mouse anti-mouse β -actin (1:500; Sigma Aldrich), mouse anti-GAPDH (1:3000; Chemicon), and rabbit anti-Lamin A (c-terminal) (1:1000; Sigma Aldrich).

Immunocytochemistry

CPCs were plated at a density of 15,000 per well of a two-chamber permanox slide. Cells were then fixed in 4% paraformaldehyde for 60 minutes then washed in phosphate buffered saline. Cells were permeabilized in 0.1% Triton X in PBS for two minutes and washed twice with PBS. Cells were then blocked in 10% horse serum in PBS for one hour and then incubated with primary antibody overnight. Next day, cells were washed in PBS and incubated with secondary antibody for 1.5 hours. Cells were imaged on a Leica TCS SP2. Primary antibodies are as follows: rabbit anti-CaMKII δ (1:1500; UC Davis, Dr. Donald Bers) and rat-anti Tubulin (1:50, Harlan).

Immunohistochemistry

Heart sections were deparaffinized, and antigen was retrieved in 1 mmol/L citrate (pH 6.0), followed by a one-hour block in TNB. Primary antibodies were incubated overnight. Slides were washed in 1% Tris/NaCl (TN buffer) followed by secondary antibody incubation for two hours. Cells were washed after secondary antibodies in TN followed by a final wash containing DAPI (1:10,000 in TN for 10 minutes to stain for nuclei). Primary antibodies are as follows: goat anti-CD117 (c-kit) (1:100, R&D Systems) and GFP anti-rabbit (Life Technologies 1:500), mouse anti-cardiac troponin T (1:100, Abcam). CD117 required tyramide amplification.

Quantitation of CaMKII δ expression in CPCs in vivo

C-kit cells were identified in paraffin heart sections after

immunohistochemical staining and by using a Leica TCS SP8 confocal microscope. In the Leica software, a measuring tool was used to create a region of interest around the border of c-kit⁺ cells and the nucleus separately. The mean fluorescence value was measured and used to represent the relative expression levels of CaMKII δ in the whole cell and the nuclear compartment of c-kit⁺ cells.

RNA extraction and quantitative real time PCR

Reverse transcriptase was performed using protocol described for iScript cDNA Synthesis Kit (BIORAD). cDNA was diluted 1:100 in nuclease free molecular grade water before performing qRT-PCR. cDNA was incubated with primers at 100nM concentration. Real time PCR was performed on all samples in triplicate using iQ SYBR Green (Bio-Rad) following the manufacturer's protocol. The fold change in gene expression was determined using the ddCt method. CaMKII δ B and CaMKII δ C forward and reverse primers were used as previously described⁸⁷. Primer sequences are as follows: cardiac troponin t, forward 5'-ACCCTCAGGCTCAGGTTCA-3' and reverse 5'-GTGTGCAGTCCCTGTTCAGA-3'; α -smooth muscle actin mouse forward 5'-GTTTCAGTGGTGCCTCTGTCA-3' and reverse 5'-ACTGGGACGACATGGAAAAG-3'; 18s forward CGAGCCGCCTGGATACC and reverse CATGGCCTCAGTTCCGAAAA.

Experimental animals

The review board of the Institutional Animal Care and Use Committee at San Diego State University approved all animal protocols and studies.

Statistical analysis

All data are expressed as mean \pm SEM. Statistical analyses were done using paired or unpaired Student's t-test, one way-ANOVA with Tukey post-tests or using two way ANOVA with Bonferroni post-tests on Graph Pad Prism v5.0. A value of $p < 0.05$ was considered statistically significant.

RESULTS

CaMKII δ is expressed in CPCs during post-natal growth and is upregulated after pathological stress

In order to validate levels of CaMKII δ isoforms during different post-natal stages, immunoblot and immunohistochemical analysis was performed using whole heart lysates and heart tissue sections from mouse origin. CaMKII δ B protein expression is elevated in hearts from post-natal day 2 through 30 and decreases with progression into adulthood (Figure 1.1A and 1.1B). CaMKII δ C protein levels steadily increase with hypertrophic growth maintaining protein expression in mouse adulthood (Figure 1.1A and 1.1C). Since both CaMKII δ B and CaMKII δ C are known to inhibit HDAC4 activity by phosphorylation on the serine 632, we assessed total and phosphorylated HDAC4 in the developing heart. HDAC4 and phosphorylated HDAC4 on the serine 632 (pHDAC4) decrease with aging consistent with the role of HDAC4 to suppress growth in cardiomyocytes (Figure 1.1D-1.1G). The increased presence of c-kit⁺ CPCs during development coincides with a burst in cardiomyocyte proliferation and hypertrophic growth⁴². In order to determine if endogenous c-kit⁺ CPCs express CaMKII δ isoforms *in vivo*, CPCs were co-labeled with a pan CaMKII δ antibody. CaMKII δ protein is detected in cardiomyocytes during an early postnatal day heart (Figure 1.1H) and is down regulated in a 30-day-old heart based on immunohistochemical analysis (Figure 1.1I). At the same post-natal time points, CaMKII δ protein was detected in c-kit labeled CPCs at low levels (Figure 1.1H

and 1.1I). CPCs up regulate both cytoplasmic and nuclear CaMKII δ B 7 days after myocardial infarction (MI) relative to c-kit cells discovered in 3-month-old sham surgery controls (Figure 1.1J-1.1L). Overall, differential expression of CaMKII δ in CPCs *in vivo* suggests relevance of the kinase in stem cells after pathological stress and possibly differentiation

CaMKII δ B localizes to the nucleus and inhibits HDAC4 in CPCs undergoing cardiogenic commitment

In order to investigate CaMKII δ expression and localization in CPCs during basal and differentiation conditions, CPCs were isolated from the adult myocardium based on established protocols⁴². CPC commitment is characterized by decreased proliferation and increased cellular size concomitant with increased expression of proteins of the cardiomyogenic lineage following dexamethasone (Dex) treatment⁹⁵. Relative to basal levels, CaMKII δ B mRNA levels are up regulated in CPCs treated with Dex (Figure 1.2A), whereas CaMKII δ C mRNA levels remain unchanged when comparing cells treated without and with Dex (Figure 1.2B). Following Dex stimulation CPCs have increases in both CaMKII δ isoforms in whole cell lysates visualized after immunoblotting (Figure 1.2C and 1.2D). CaMKII δ is primarily localized in the cytosol of CPCs during regular growth media conditions (Figure 1.2E), and is upregulated after differentiation along with a marked presence of CaMKII δ B in the nucleus of CPCs (Figure 1.2F). Fractionated CPCs were analyzed for CaMKII δ in the cytoplasmic and nuclear

compartments of the cells, confirming that CaMKII δ B localizes in the nucleus during commitment of CPCs (Figure 1.2G-1.2I).

CaMKII δ B dependent regulation of HDAC4 has been previously reported^{84, 85}, therefore we attempted to investigate if this also occurs in our isolated CPCs. Inactivated HDAC4 (pHDAC4) protein trended towards an increase in the cytoplasmic fraction of CPCs treated with differentiation media without and with Dex compared to growth media conditions (Figure 1.3C and 1.3D), indicating a correlative role during differentiation to increase CaMKII δ B in the nucleus and de-repress genes necessary for growth and differentiation. However, total HDAC levels were not significantly changed in CPCs without and with Dex treatment (Figure 1.3A and 1.3B). In order to validate that HDAC4 is a target of CaMKII δ in CPCs, we used a lentivirus to overexpress CaMKII δ B (CPCe δ B), as confirmed by immunoblot by the presence of an HA tag and green fluorescent protein (Figure 1.3E and 1.3F). Lentivirus expressing GFP alone was used as a control (CPCe) (Figure 1.3E and 1.3F). Although total HDAC4 levels were unchanged in CPCe relative to CPCe δ B (Figure 1.3G and 1.3H), CPCe δ B have increased cytosolic pHDAC4 relative to CPCe, correlating with a decreased level of pHDAC4 in the nuclear compartment (Figure 1.3I and 1.3J). These results suggest that CaMKII δ B overexpression facilitates the inactivation of HDAC4.

Nuclear CaMKII δ overexpression in CPCs increases cellular size and decreases cell proliferation

Overexpression of CaMKII δ B in CPCs presented phenotypic characteristics that are relevant to increased cardiomyogenic differentiation⁵⁵. In support of this, CPCe δ B show decreased proliferative potential (Figure 1.4A) and increased doubling time (Figure 1.4B) compared to CPCe. CPCe δ B are less present in the G2/M phase of the cell cycle compared to CPCe (Figure 1.4C). Interestingly, CPCe δ B exhibits increases in cellular size based on measurement of cell surface area (Figure 1.4F) and cell length to width ratio (Figure 1.4G) during basal growth conditions relative to CPCe (Figure 1.4D-1.4G). Cellular senescence was not evident in CPCe δ B based on p53 or p16 protein levels relative to CPCe (Figure 1.4H-1.4J). Therefore, the decreased proliferative rate and larger cell morphology exhibited by CPCe δ B is not due to increased senescence or irreversible cell cycle arrest.

CaMKII δ B overexpression in CPCs increases cell commitment towards the cardiomyogenic lineage

CPCe δ B treated with Dex for six days shows a strong up regulation of cardiac and smooth muscle markers such as *cardiac troponin T (tnnt3, cTNT)* and *α -smooth muscle actin (α -SMA)* based on mRNA levels relative to CPCe (Figure 1.5A and 1.5B). Consistent with increased differentiation phenotype, CPCe δ B have increased metabolic activity during growth conditions and during differentiation, where CPCe has increased metabolic activity only with the

addition of Dex (Figure 1.5C). Cardiac marker α -sarcomeric actinin was upregulated in Dex treated CPCe δ B based on protein expression (Figure 1.5D and 1.5E). CPCe δ B commitment to the vascular endothelial and smooth muscle differentiation is increased relative to CPCe based on immunoblot analysis of endothelial marker Tie2 (Figure 1.5F and 1.5G) and smooth muscle marker α -SMA (Figure 1.5F and 1.5H). This data indicates that CaMKII δ B can drive the differentiation of CPCs and enhance the transition to mature cells of the cardiac, endothelial and smooth muscle lineages.

CaMKII δ B expression in CPCs antagonizes apoptotic cell death after oxidative stress stimuli

Expression of CaMKII δ B prevents apoptosis in cardiomyocytes following doxorubicin or hydrogen peroxide (H₂O₂) stimulation^{86, 87}. Overexpression of CaMKII δ B in CPCs similarly improves survival after 40 μ M and 80 μ M H₂O₂ induced death compared to CPCe (Figure 1.6A and 1.6B). In order to establish a pro-survival role of CaMKII δ B in CPCs, a small hairpin RNA to CaMKII δ B (sh- δ B) was used to decrease the expression of the kinase before stimulation with oxidative stress (Figure 1.6C and 1.6D). CPCs with reduced levels of CaMKII δ B had increased susceptibility to cell death at increasing concentrations of H₂O₂ (Fig. 1.6E and 1.6F). Collectively, CaMKII δ B plays an integral role in early commitment of CPCs while enhancing cell survival during oxidative stress.

DISCUSSION

There is debate as to the stem cell type that is needed to treat myocardial damage. CPCs, although limited, have been validated as a cell type to treat heart disease due to their cardiomyogenic potential^{10, 73}. In this study, we present a canonical calcium-signaling cascade implicated in growth and survival of CPCs by CaMKII. CaMKII δ isoforms are studied in the context of maladaptive hypertrophy in transgenic mice⁷⁸. However, recent studies have implicated CaMKII δ B to reduce expression of inflammatory factors in a global CaMKII δ knockout model, indicating a protective role of the δ B kinase in the cardiac context after pathological damage⁸⁸. Until now, it remained unknown whether CaMKII δ isoforms are present in resident CPCs although expression is reported in smooth muscle cells in the heart^{89, 90}. Our study is the first to identify nuclear translocation of the CaMKII δ B isoform during lineage commitment of CPCs (Figure 1.1 and Figure 1.2). Furthermore, overexpression of CaMKII δ supports distinct morphological changes and increases differentiation accompanied by decreased cell cycle progression (Figure 1.3 and Figure 1.4). Consistent with cardiomyocyte data, CaMKII δ B confers survival in CPCs, which is abrogated when δ B expression is reduced and subjected to oxidative stress stimuli (Figure 1.6). Collectively, this data supports the ability of CPCs to acquire growth and differentiation phenotypes regulated by CaMKII δ signaling to the nucleus.

Currently, there is interest in identifying proteins and signaling cascades in CPCs related to mature cardiomyocytes. During basal conditions, CPCs express the B2-adrenergic receptor (B2-AR) regulating stem cell proliferation but acquire

the mature B1-AR after co-culture with cardiomyocytes⁹⁶. Ca^{2+} in fetal CSCs supports cellular growth, proliferation and commitment⁹⁷. Inositol-1,4,5-triphosphate (IP3) receptors on the sarcoplasmic reticulum induce spontaneous Ca^{2+} oscillations in mouse and human CPCs^{97,98}. CPCs are validated to not only express IP3 receptors, but also purinergic G protein-coupled receptors (P2Y) and SERCA2, which are functionally stimulated and activated after introduction of Ca^{2+} and/or ATP^{98,99}. Furthermore, IP3 receptors promote an influx of Ca^{2+} in the nucleus activating CaMKII/MEF2 and cellular growth¹⁰⁰. In Figure 1.1, expression levels of CaMKII δ are increased and localized to the nucleus during acute stress, indicating that a short-term stimulus is sufficient to prime cardiac commitment of stem cells. This was further validated in isolated CPCs, as our differentiation protocol induced nuclear accumulation of CaMKII δ B (Figure 1.2), correlating with inactivated p-HDAC4 in the cytosolic fraction (Figure 1.3). These studies suggest that the transitory fate of CPCs during cell division and differentiation can be defined by a complex interplay of calcium-regulated molecules prior to acquiring cardiomyogenic fate.

CPCs under genetic modification with mature cardiomyocyte genes increase our knowledge as to the potential of stem cells to promote cardiac repair after adoptive transfer in the heart. CPCs express Ca^{2+} receptors and pumps, however, expression of the Ryanodine receptors and B1-AR are not present in CPCs indicating that these cells hold a primitive molecular cardiac signature⁹⁹. Related to our study, CPCs transfected with a siRNA targeting HDAC4, and therefore inhibiting the repression of growth genes, increased differentiation of

CPCs *in vivo* supporting myocardial regeneration⁹⁴. In cardiomyocytes, HDAC4 and HDAC5 form a complex to inhibit MEF2 and serum response factor elements^{83, 84}. Inactivation of Class IIa HDACs by CaMKII and protein kinase D promotes shuttling of HDAC4 from the nuclear compartment by the chaperone 14-3-3^{101, 102}. Our data shows a decrease of nuclear p-HDAC4 in our non-modified CPCs (Figure 1.3). Conversely, p-HDAC was increased in the cytosol of Dex treated CPCs or CPCe δ B (Figure 1.3). However, the results were modest indicating that additional factors affect the kinase activity of CaMKII and/or inhibition of Class IIa HDACs. In contrast, HDAC inhibition, including inhibition of Class I HDACs, has been shown to decrease the proliferative and differentiation potential of mesenchymal stem cells indicating that HDACs are essential for maintenance of proper stem cell function¹⁰³.

We evaluated if overexpression of CaMKII δ B can enhance the differentiation patterns of CPCs. Here a lentiviral protocol was employed and characteristics such as increased cellular size and decreased proliferation were immediately apparent after overexpression of CaMKII δ B (Figure 1.4). In order to delineate a CaMKII δ B dependent role to enhance stem cell survival relative to the CaMKII δ C isoform, we subjected CPCs to oxidative stress and observed a decrease in late apoptotic cells (6-fold reduction) relative to control CPCs (Figure 1.6). In contrast, knockdown of CaMKII δ B increases cell susceptibility to apoptosis (Figure 1.6). This data confirms that CaMKII δ B is essential in CPC survival consistent with other reported cell types. Interestingly, we observed an increase in mRNA expression of CaMKII δ C following the knockdown of

CaMKII δ B. Models of CaMKII δ C overexpression exaggerates maladaptive cardiac remodeling during development and after trans aortic constriction surgery relative to overexpression of CaMKII δ B⁷⁸. At the cellular level, cardiomyocyte apoptosis and sensitivity to stress stimuli are increased by overexpression of CaMKII δ C¹⁰⁴. Furthermore, proliferation and differentiation was not significantly altered relative to control cells after transfection of CPCs with shRNA to CaMKII δ B. This data may indicate that CaMKII δ B is not required for growth and commitment of CPCs and there are alternative compensatory mechanisms that sustain CPC self-renewal capabilities. This brings into question the diverse forms of CaMKII, the differential isoforms and interplay in the entire cell. Currently, identification of calcium-associated proteins brings validation to CPC origin and potency status and supports the potential of CPCs as a cardiac regenerative population.

SUMMARY POINTS

- CaMKII δ isoforms are expressed in endogenous CPCs during post-natal growth and is induced after injury.
- Isolated CPCs upregulate CaMKII δ in the cytosol concurrent with CaMKII δ B localization in the nuclear compartment during commitment.
- CaMKII δ B overexpression in CPCs inactivates HDAC4.
- CaMKII δ B overexpression in CPCs reduces proliferation, improves survival and increases cardiomyogenic commitment.
- Knockdown of CaMKII δ B in CPCs increases susceptibility to death stimuli but does not impair differentiation capacity.
- CaMKII δ expression in CPCs may serve as a regulatory kinase to enhance therapeutic properties.

FIGURES

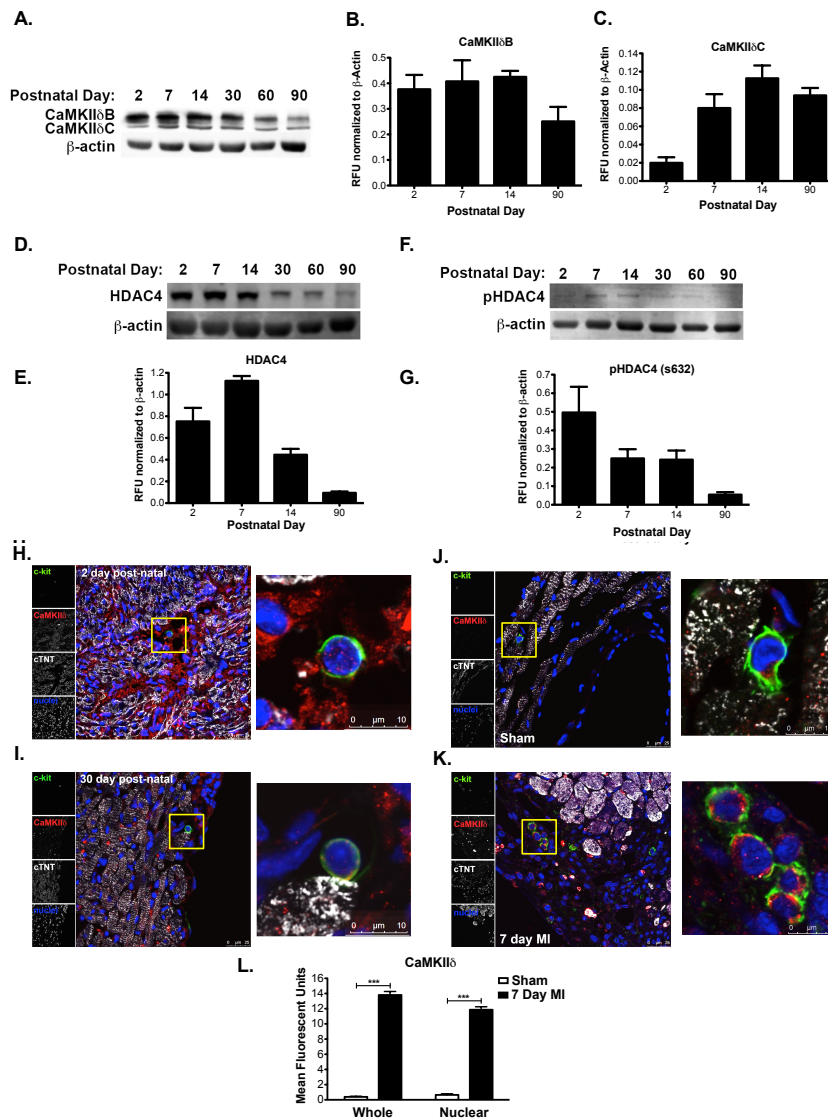


Figure 1.1: CaMKIIδ is expressed in CPCs during post-natal growth and is upregulated after pathological stress.

(A) CaMKIIδB (top band) and CaMKIIδC (bottom band) protein expression in whole heart lysates at increasing postnatal days. (B) Quantitation of CaMKIIδB and (C) CaMKIIδC expression levels represented as relative fluorescent units (RFU) normalized to β-actin. (D) Total HDAC4 levels at different postnatal days in the mouse heart. (E) Quantitation of HDAC4 expression normalized to β-actin represented as RFU. (F) Phosphorylated HDAC4 on the serine 632 in the developing mouse heart. (G) Quantitation of pHDAC4 expression normalized to β-actin represented as RFU. (H) 2 day and (I) 30-day-old hearts visualized for expression and localization of CaMKIIδ in myocytes and c-kit⁺ CPCs. (J) CaMKIIδ labeling in CPCs after sham or (K) Following MI surgery for 7 days. (L) Quantitation of CaMKIIδ expression and localization (whole or nuclear) in endogenous CPCs in sham and 7 day MI treated mice. Mice are 3 months of age prior to MI surgery. Cardiac troponin T (cTNT) and TO-PRO-3 iodide were used to label myocardium and nuclei respectively. *** p < 0.0001 Sham vs. 7 Day MI.

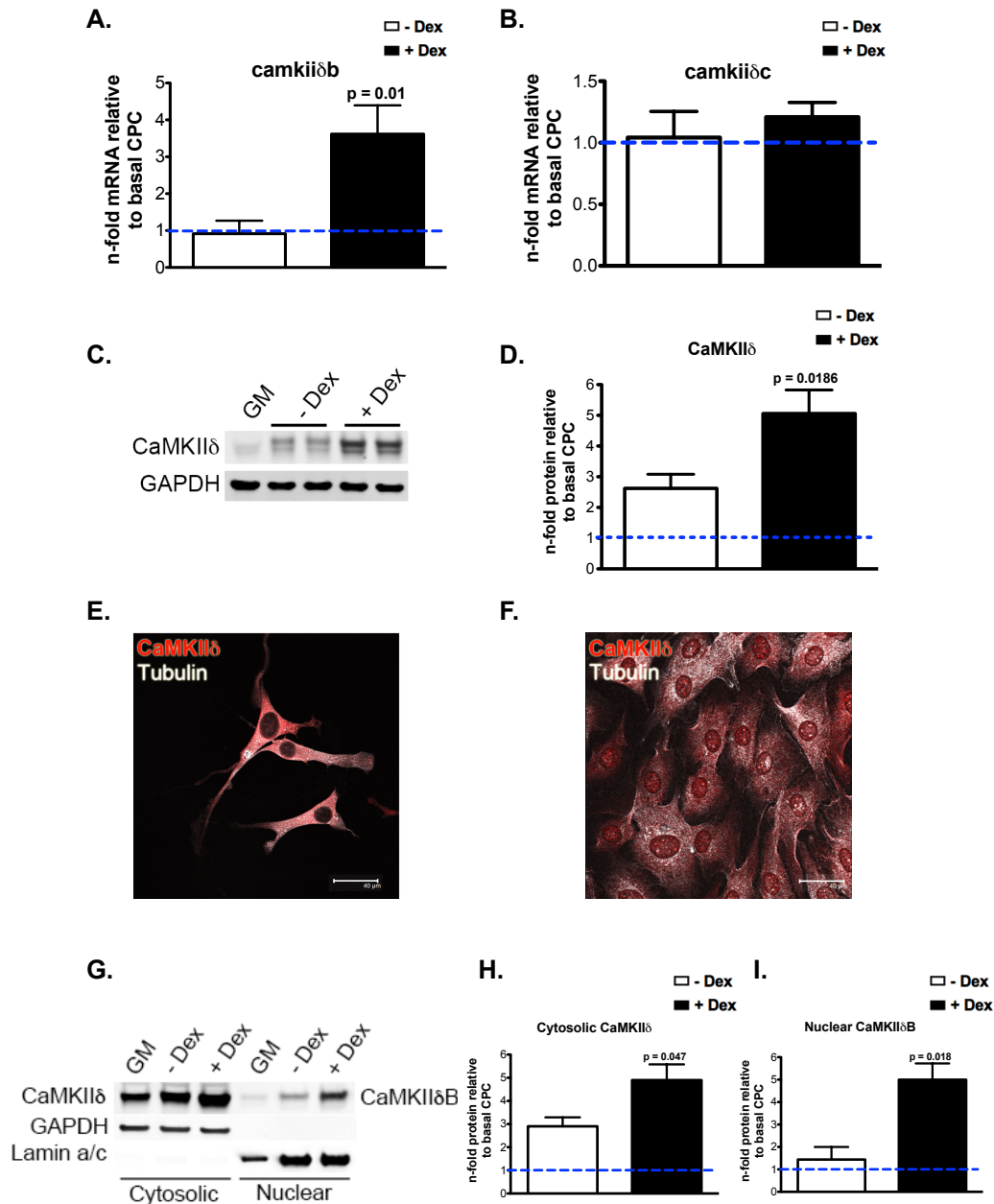


Figure 1.2: CaMKIIδB localization to the nucleus is increased in CPCs during commitment.

(A) CaMKIIδB and (B) CaMKIIδC mRNA in CPCs with and without Dexamethasone (Dex) stimulation for seven days represented as a fold change relative to CPCs maintained in growth media (GM). (C) CaMKIIδ protein levels in whole cell lysates with and without Dex stimulation. (D) Quantitation of total CaMKIIδ levels relative to GM treated CPCs. (E) CaMKIIδ protein is primarily cytosolic in CPCs without differentiation stimulus. (F) CaMKIIδ increases in expression and localizes to the nuclear compartment of CPCs after six days of Dex treatment. (G) CaMKIIδ expression in the cytosolic and nuclear fractions of CPCs after induction with differentiation media. (H) Quantitation of cytosolic CaMKIIδ and (I) nuclear CaMKIIδB. Graphs are represented as a fold change relative to basal CPCs in cytosolic and nuclear fractions. GAPDH is probed as a loading control for immunoblots. P values compare CPCs in 10% FBS α-MEM without Dex to CPCs treated with Dex.

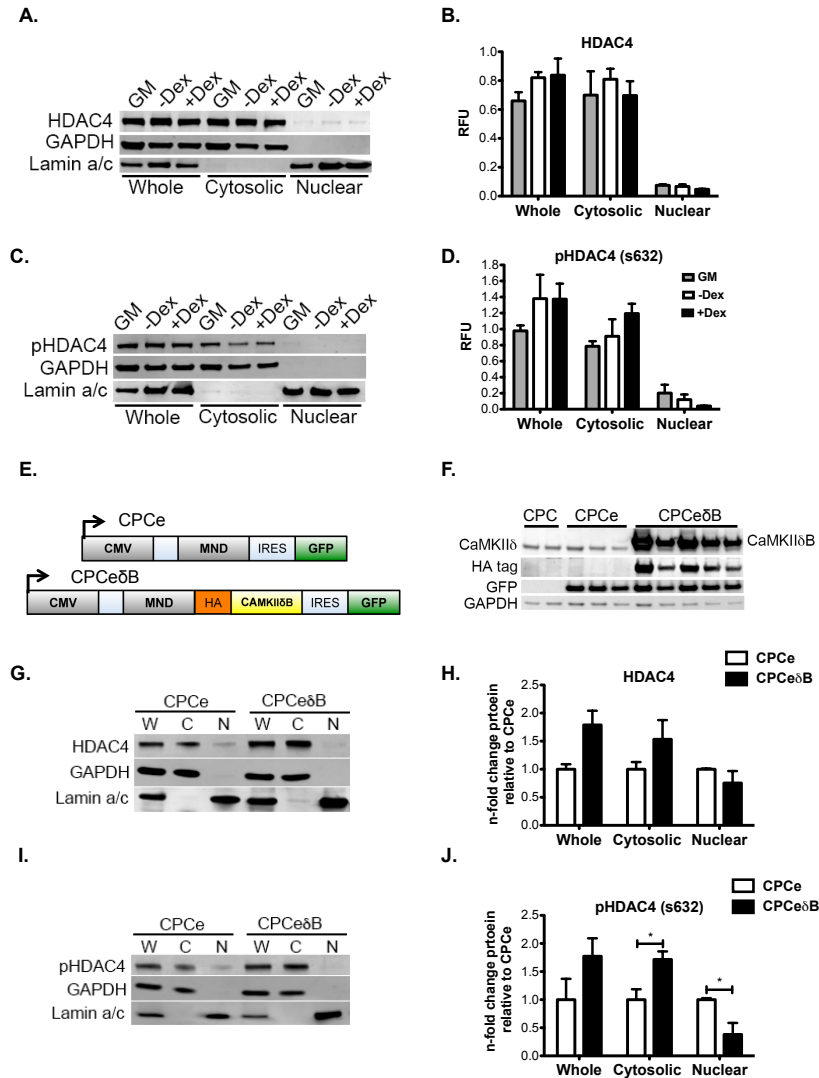


Figure 1.3: CaMKIIδB localizes to the nucleus and inhibits HDAC4 in CPCs undergoing cardiogenic commitment.

(A) Immunoblot of total HDAC4 protein levels in whole, cytosolic and nuclear fractions of CPCs treated with GM, -Dex or +Dex supplemented media. (B) Quantitation of total HDAC4. (C) Immunoblot pHDAC4 (s632) protein levels in whole, cytosolic and nuclear fractions of CPCs treated with GM, -Dex or +Dex supplemented media. (D) Quantitation of pHDAC4 (s632) Immunoblots are presented as a fold change relative to CPCs in GM and normalized to GAPDH or Lamin A (C-terminus) ** $p < 0.01$ -Dex vs. +Dex. (E) Lentiviral constructs to establish CPCe and CPCeδB lines. (F) CPCeδB lines overexpress CaMKIIδB as well as the HA tag. CPCe overexpress eGFP. GAPDH was probed as a loading control. (G) CPCe and CPCeδB lines probed for total HDAC4 levels by immunoblot and (H) Quantitation in whole cell lysates, cytosolic and nuclear fractions. (I) Phosphorylated HDAC4 on the serine 632 protein levels in CPCe or CPCeδB by immunoblot and (J) Quantitated from whole cell lysates, cytosolic and nuclear fractions. Immunoblots are probed with GAPDH to normalize for protein loading of the whole and cytosolic lysates. Lamin A (C-terminus) antibody was utilized to normalize for loading of the nuclear fraction. Total and phosphorylated HDAC4 are represented as a fold change relative to CPCe. * $p < 0.05$ CPCe vs. CPCeδB. W=Whole cell, C=cytosolic fraction and N=nuclear fraction

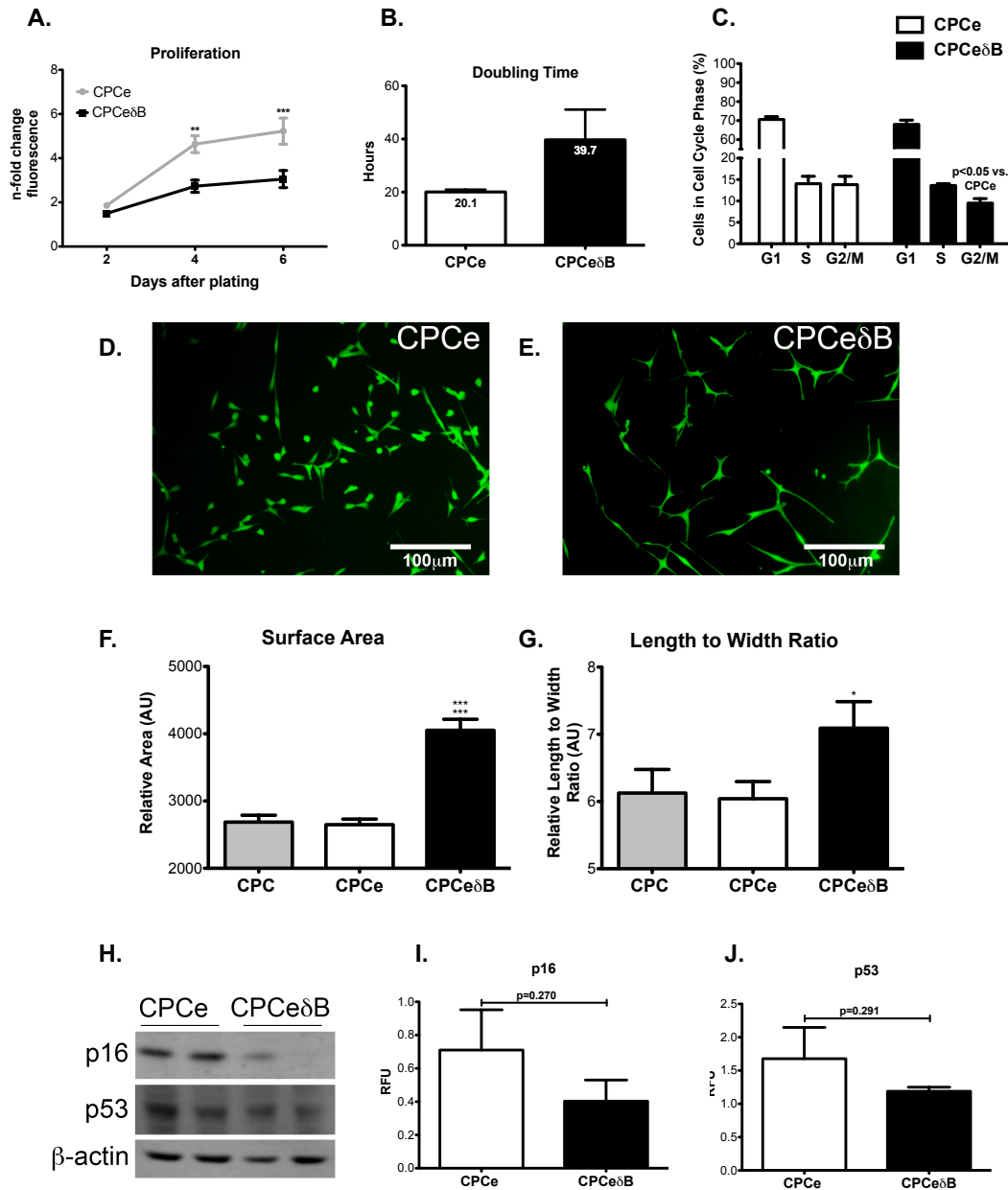


Figure 1.4: Nuclear CaMKII δ overexpression in CPCs increases cellular size and decreases cell proliferation.

(A) CPCe δ B has decreased proliferative capacity relative to CPCe based on a fluorescent nucleic acid stain measured at 2, 4 and 6 days after seeding equal cell numbers. ** and *** $p < 0.01$ and $p < 0.0001$ CPCe δ B relative to CPCe. (B) CPCe δ B populations shows an increased doubling time relative to CPCe. (C) Cell cycle analysis using flow cytometry in CPCe and CPCe δ B. (D) Fluorescent images of CPCe and (E) CPCe δ B populations in growth media. (F) CPCe δ B shows an increase in relative cell surface area. *** $p < 0.0001$ CPCe δ B relative to CPC and CPCe. (G) CPCe δ B shows an increase in length to width ratio relative to non-modified CPCs and CPCe. * $p < 0.01$ CPCe δ B relative to CPCe. (H) Expression of senescence markers p16 and p53 by immunoblot. β -actin was probed as a loading control. (I) Quantitation of p16 and (J) p53 in CPCe and CPCe δ B populations.

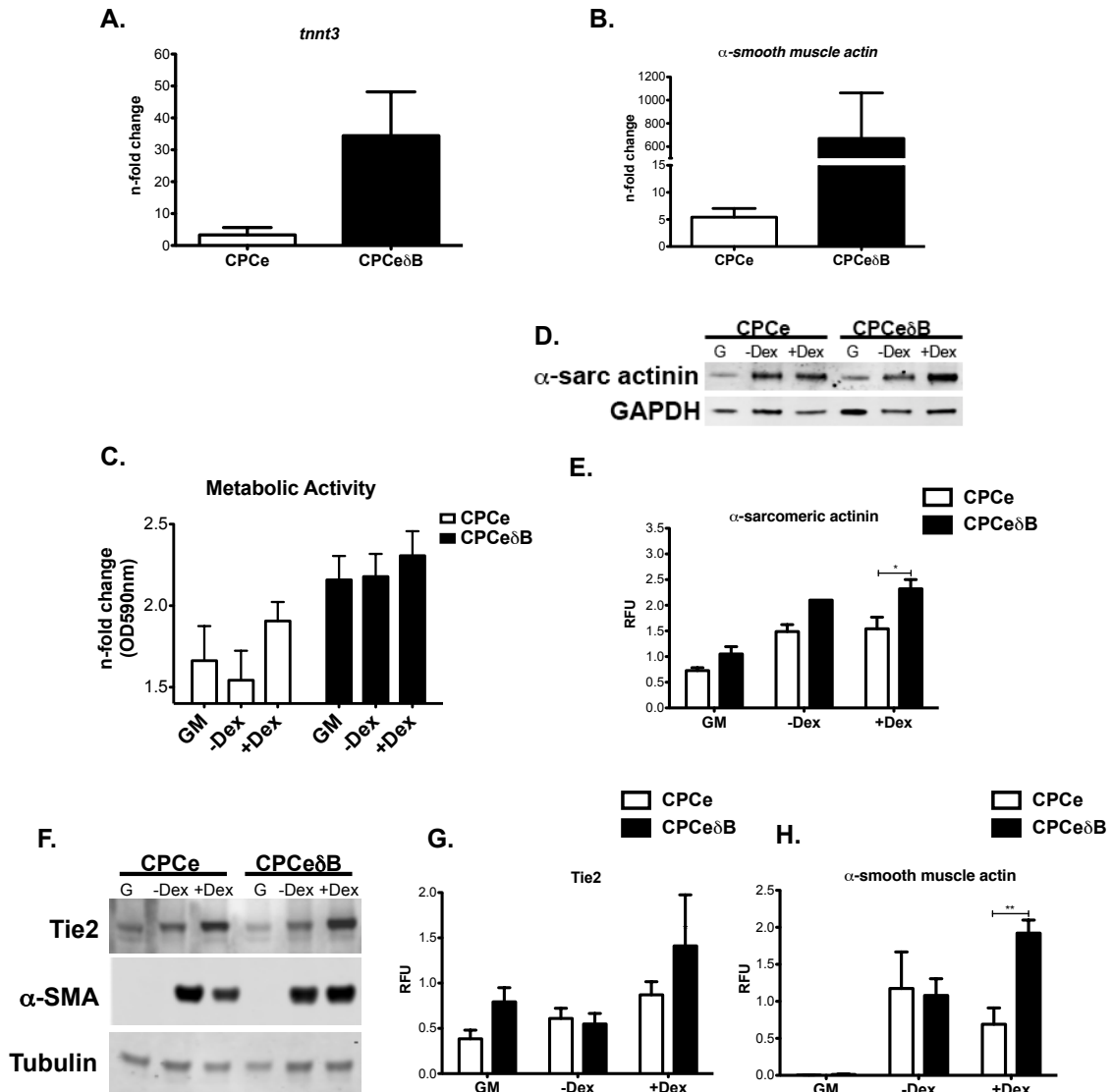


Figure 1.5: *CaMKII δ B* overexpression in CPCs increases cell commitment towards the cardiomyogenic lineage.

(A) CPCe δ B stimulated with Dex for six days show increased expression of cardiogenic marker cardiac troponin T (*tnnt3*) and (B) α -smooth muscle actin based on mRNA expression. (C) Cardiac marker α -sarcomeric expression and (D) Quantitation in CPCe and CPCe δ B in normal growth conditions, -Dex and + Dex. (E) Metabolic activity under GM, -Dex or + Dex growth conditions. (F) Endothelial (Tie2) and smooth muscle (α -SMA) were probed in CPCe and CPCe δ B grown in normal growth conditions, -Dex or + Dex. (G) Quantitation of Tie2 and (H) α -SMA, which is upregulated in Dex treated CPCe δ B. Values are represented as relative fluorescent units (RFU) normalized to GAPDH or tubulin. * $p < 0.05$ and ** $p < 0.01$ CPCe vs. CPCe δ B.

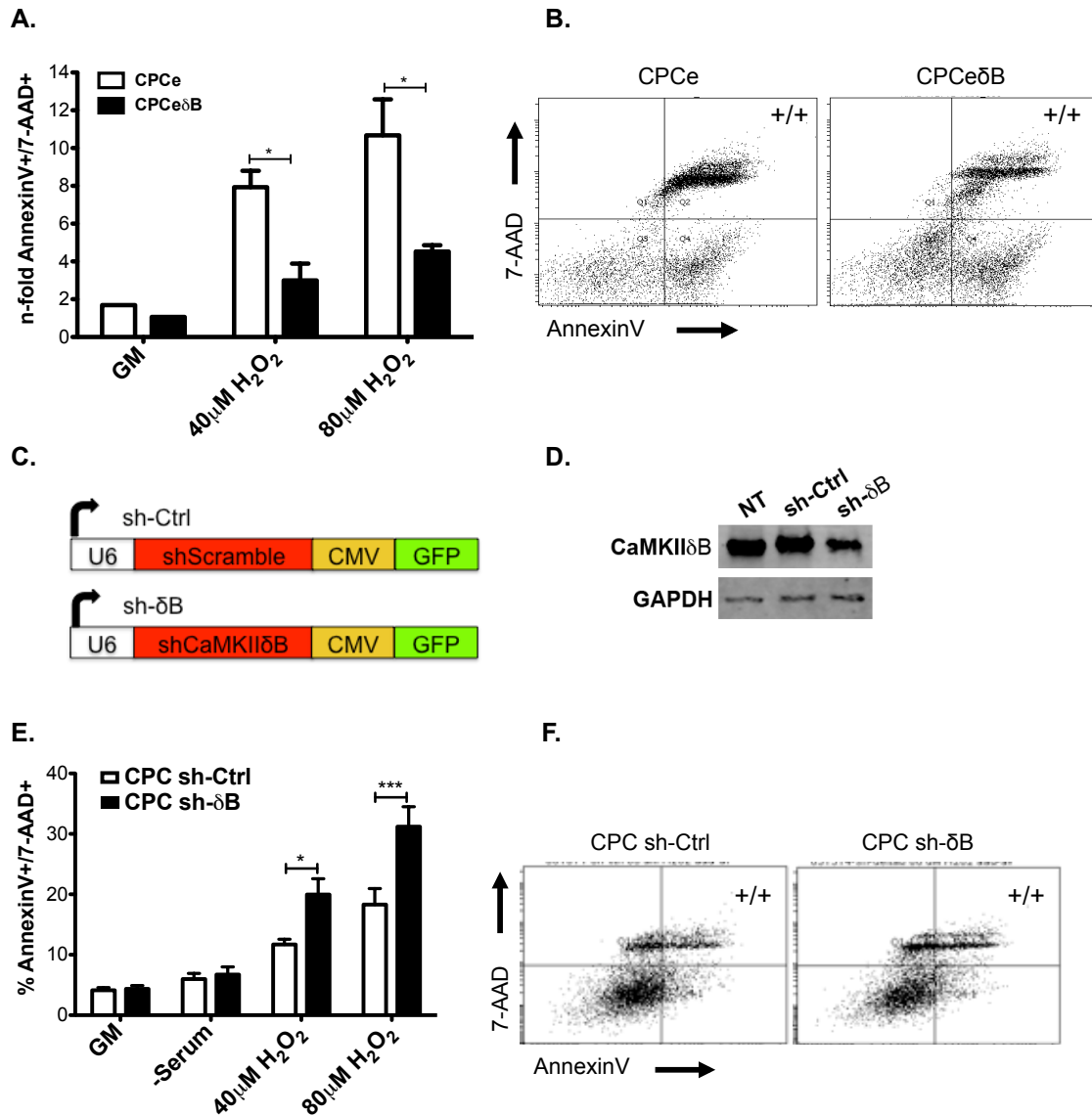


Figure 1.6: CaMKII δ B expression in CPCs antagonizes apoptotic cell death after oxidative stress stimuli.

(A) Quantitation of Annexin V and 7-AAD double positive cells (to label for cells in late apoptosis) in (B) CPCe and CPCe δ B after incubation in growth media GM, 40 or 80 μ M H₂O₂. Values are represented as a fold change relative to GM treated cells. (C) Schematic of constructs (top) and (D) confirmation of knockdown of CaMKII δ B in CPCs relative to controls (NT: non-treated and sh-Ctrl). (E) Quantitation of late apoptosis in CPCs transfected with (F) small hairpin (sh) control or Sh to knockdown CaMKII δ B and subjected to growth media, serum starvation, 40 or 80 μ M H₂O₂. Values are represented as a percentage based on flow cytometric analysis.

Chapter 1, in full, is prepared for submission. Nuclear Calcium/Calmodulin-Dependent Protein Kinase II Signaling Enhances Cardiac Progenitor Cell Survival and Cardiac Lineage Commitment. Pearl Quijada, Nirmala Hariharan, Jonathan Cubillo, Kristin M. Bala, Lucia Ormachea, Donald M. Bers, Mark Sussman and Coralie Poizat. The dissertation author was the primary author and investigator on this publication.

CHAPTER 2

Cardiac Stem Cell Hybrids Enhance Myocardial Repair

INTRODUCTION

Cell therapy for regeneration of the myocardium after myocardial infarction (MI) involves two concurrent processes: 1) stimulation of endogenous repair, and 2) exogenous cellular commitment. Regenerative medicine would benefit tremendously from identification of optimal stem cell population(s) that exert both direct and indirect mechanisms to mediate survival of existing cardiomyocytes, support proliferation and differentiation of endogenous stem cells, reduce inflammation and prevent scar formation. Coupling intrinsic mechanisms of myocardial repair with the propensity of stem cells to undergo cardiomyogenesis should be carefully balanced and integrated with the existing heart scaffold. Delivery of single stem cell types promote relatively modest functional and structural recovery of the heart owing to limited reparative capacity of donated cell populations derived from cardiac and bone marrow origin. Increasing cell numbers can enhance beneficial cellular properties, but excess reactive oxidative species and inflammation after acute damage contribute to elimination of more than 90% of delivered cells after one-week^{46, 47}. While the genetic engineering of stem cells prior to delivery remains a promising alternative to enhance persistence and regeneration^{48, 49}, potential additional benefits of combinatorial cell therapy remain largely unexplored.

Resident c-kit⁺ cardiac progenitor cells (CPCs) are a desirable cell choice due to enhanced proliferative capacity and ability to form cardiomyocytes, vascular smooth muscle and endothelial cells *ex vivo*¹⁰⁵. Endogenous c-kit⁺ cells

have limited capacity towards cardiomyogenic commitment during development and after myocardial injury⁷³. Despite limited regenerative capability, clinical application of CPCs confers improvements in myocardial structure and function as highlighted in the Cardiac Stem Cell Infusion in Patients With Ischemic Cardiomyopathy (SCIPIO) patient trial¹⁰. Bone marrow is the most popular source of adult-derived stem cells because of proven safety and efficacy after transplantation¹⁴. In particular, mesenchymal stem cells (MSCs) are commonly used for autologous and allogeneic clinical therapies³². MSCs are valued for paracrine-mediated effects such as reducing inflammation and promoting pro-survival and growth cascades to surrounding cells¹⁰⁶. MSC injection after infarction promotes robust recruitment of c-kit⁺ CPCs, induces cardiomyocyte cycling and facilitates the outgrowth of stem cells from myocardial biopsies *ex vivo*¹⁰⁷. Recently, combining these two distinct stem cells types, CPCs and MSCs, was investigated in a porcine model of myocardial damage¹⁰⁸. Functional recovery and detection of human derived cells in the myocardium was improved over injection of single cells alone, indicating synergism of combining two cell types¹⁰⁸. However, cellular mechanisms of myocardial recovery were not addressed and cell numbers were skewed towards increased MSCs in order to confer protective effects *in vivo*¹⁰⁸.

Cell fusion to create syncytia is an endogenous and homeostatic process coupled with differentiation and organ development⁶³. Although low at basal levels, fusion increases in acute and chronic settings of inflammation, DNA damage and apoptotic events after bone marrow cell (BMC) transplantation¹⁰⁹,

¹¹⁰. Artificial cell fusion between the same or different cell types to produce heterokaryons can be accomplished with addition of polyethylene glycol, electric pulses or viral fusogens¹¹¹. In rare events, mononucleated hybrids (synkaryons) from bi-nucleated cell states occur, which is largely dependent on the ability of one cell type to undergo DNA synthesis after fusion¹¹². BMCs and MSCs have been observed to readily fuse to more mature cells, allowing successful transfer of mitochondria and phenotypic traits such as increased survival and proliferation^{59, 64, 113}. Spontaneous *in vivo* cell fusion as a mechanism to support regenerative therapy have been underwhelming leading to the conclusion that cell fusion alone is not a major contributor to heart regeneration.

In this manuscript, we present the creation and characterization of CPC and MSC hybrids, referred to as CardioChimeras (CCs), generated by *ex vivo* viral cell fusion. CCs exhibit enhanced molecular and phenotypic traits relative to individual stem cells and these distinct hybrids were evaluated for *in vivo* therapeutic effects after myocardial damage in a mouse model. Recovery of anterior wall thickness (AWT) and ejection fraction (EF) were markedly improved, concomitant with increased engraftment and expression of early cardiomyogenic lineage markers in CC treated hearts. CardioChimeras represent a novel therapy that complements the paracrine effects of MSCs to orchestrate endogenous repair with direct cell contributions from CPCs in promotion of *de novo* cellular regeneration.

METHODS

Study design

These studies were designed to test the reparative capacity of CPCs, MSCs, CPC + MSC and CCs in a mouse model of MI. Initially, we expanded 18 CCs and chose two phenotypically distinct hybrids, CC1 and CC2. Inclusion of CCs was contingent on pro-proliferative and pro-survival capabilities. Furthermore, co-culturing CCs with NRCMs mediated the identification of CCs that facilitate survival and growth of cardiomyocytes as compared to parent MSCs. Overall, all 18 CCs were analyzed for optimal profiles in proliferation, survival and stem cell properties and/or differentiation before an *in vivo* mouse trial. We required approximately 16 animals per cell group to allow for analysis of at 3-5 mice per time point (4, 12 and 18 WPI) without impacting statistical significance obtained during longitudinal assessment by echocardiography. This number was chosen based on an average of 65-75% survival rate immediately after injury. Mice with a measured EF between 35-50% one-week post infarction were included in the experiment. EF >50% or <35% were excluded from the experiment. Throughout the time course, mice were not subjected to echocardiography if mice were perceived to be in distress. The study was concluded after determining statistical significance in wall thickness recovery and EF at 18 WPI. The study was not randomized, but was blinded to the operator during echocardiographic acquisition and analysis.

CPC and MSC isolation

CPCs were isolated and maintained as previously described¹¹⁴. CPCs were used during passages 10-20. Mesenchymal stem cells were isolated from 12 week old female FVB mice by flushing the femur and tibiae with 5% Fetal Bovine Serum in PBS through a 40- μ m filter and centrifuged (10 minutes, 600g, 4°C). Cells were resuspended in media consisting of α modified minimum essential media and 15% FBS. Cells were plated in 150mm dish and media was changed every two days to remove non-adherent cells. Adherent cells created colonies in approximately two weeks. MSCs were passaged using 0.25% Trypsin and used during passages 2-4 for experiments.

Lentiviral constructs

A third generation enhanced green fluorescent protein (eGFP) lentivirus with a phosphoglycerate kinase (PGK) and puromycin (puro) selection marker was purchased from Addgene (pLenti PGK GFP Puro (w509-5) was a gift from Eric Campeau, plasmid # 19070). pLenti PGK GFP Puro was used as a backbone to sub clone mcherry in the place of eGFP and bleomycin (bleo) to replace the puro gene in order to create pLenti PGK mcherry Bleo.

Stem cell transduction with lentivirus

MSCs at passage 1 were lentivirally transduced with pLenti PGK GFP Puro at a multiplicity of infection (MOI) of 50 and maintained in puromycin supplemented MSC media for one week starting at 48 hours post-infection. CPCs at passage 10 were lentivirally transduced with pLenti PGK mcherry Bleo

at a MOI of 10 and subjected to fluorescent activated cell sorting (FACS) to purify mcherry positive CPCs. Fluorescent protein expression in MSCs (MSC-GFP) and CPCs (CPC-mcherry) was confirmed by fluorescent light microscopy and flow cytometric analysis.

Cell fusion and creation of CardioChimeras

Cell fusion was conducted using the GenomONE™ - CF EX Sendai virus (Hemagglutinating Virus of Japan or HVJ) Envelope Cell Fusion Kit (Cosmo Bio. USA). According to the manufacturer's protocol, we subjected MSCs and CPCs to the plating method for cell fusion. Here, 100,000 MSC-GFP in a 100mm dish were incubated in CPC media for 24 hours. Next day, 100,000 CPC-mcherry cells were suspended in 20 μ L of cell fusion buffer and 10 μ L of Sendai virus and placed on ice for 5 minutes for absorption of the virus on the cell membrane. Media from MSC-GFP plate was removed and washed once with cell fusion buffer, and CPC-mcherry + Sendai virus was added. The plate was then centrifuged (10 minutes, 1200rpm at 4°C) to force cell-to-cell contact. To induce cell fusion, cells were placed at 37°C for a total of 15 minutes. Non-fused CPC-mcherry cells were removed by aspiration and CPC media was added back to the plate. The next day, media was changed, and within 48 hours cells were trypsinized and subjected to FACS to place one-cell per well of a 96-micro plate and allow for clonal expansion of double positive cell populations expressing GFP and mcherry. 18 double positive clones expanded from single cell sorted

were confirmed by secondary flow cytometric analysis. Two representative clones were chosen for experiments outlined in this paper.

Light microscopy and measurement of cell morphology

Images of stem cells were obtained on a Leica DMIL microscope and cell outlines were traced using ImageJ software. Relative surface area was determined as previously described¹¹⁵.

Neonatal rat cardiomyocyte (NRCM) co-culture with stem cells

NRCMs were isolated and plated as previously described¹¹⁶. After enzymatic digestion, cells were plated in M199 media (Life Technologies) with 15% FBS (Omega Scientific Inc.) at a density of 260,000 cells per well of a 6-well culture dish pretreated with 1% gelatin (Sigma-Aldrich). Within 18 hours, myocyte cultures were washed with PBS and incubated with M199 with 10% fetal bovine serum for 24 hours. The next morning, the cells were subjected to serum starvation (0.5% FBS in M199) for 24 hours. After low serum conditions, stem cells were added to the plate at a ratio of 1:10 (CPCs, MSCs, CPC + MSC combined, CC1 and CC2) and allowed to incubate with NRCMs for an additional 24 hours in low serum conditions. Controls for NRCMs included leaving cells in 0.5% alone, adding back 10% M199 or maintaining NRCMS in 10% M199 for the duration of the experiment. NRCM size was measured after staining cardiomyocytes with sarcomeric actinin (1:100, Sigma-Aldrich) and nuclei with TO-PRO-3 iodide and as previously described¹¹⁷. Separation of NRCM and stem cells was accomplished with fluorescent activated cell sorting (FACS) of

negative cells (NRCMs) versus GFP⁺, mcherry⁺ or GFP⁺/ mcherry⁺ stem cells. After sorting, cells were centrifuged and suspended in RNase buffer for isolation and quantitation of mRNA from NRCMs or stem cells.

Immunocytochemistry

Stem cells were placed at a density of 15,000 per well of a two-chamber permanox slide and stained according to previous studies⁵³. Before scanning, cells were washed in PBS containing TO-PRO-3 iodide (1:10,000, Life Technologies) to stain for nuclei. Slides were visualized using a Leica TCS SP2 confocal microscope. Primary antibodies are as follows: rat anti-mcherry (1:100, Life Technologies); rabbit anti-GFP (1:100, Life Technologies).

Flow cytometric analysis

Cells in suspension were counted (2.0×10^5 per sample) and stained with primary and secondary antibodies according to previous studies⁵³. Samples were analyzed using a FACS Canto (BD Biosciences). Primary antibodies are as follows: goat anti-CD117 (1:40, R&D Systems); or goat anti IgG as a control (1:40, Santa Cruz Biotechnology, Inc.). Secondary antibody: donkey anti-goat 647 (1:400, Jackson Immunoresearch).

Centromere labeling

Cells were fixed on glass two chamber slides in 3:1 ethanol: acetic acid for 30 minutes and then passed through graded alcohol series 70, 90, 100% (2 minutes each step). Slides were baked at 65°C for 15 minutes and then transferred to acetone for 10 minutes. Slides were then incubated for 1h at 37°C

in 2X SSC (NaCl/NA Citrate) plus RNase (100µg/ml). Cells were treated with pepsin, 10mM HCl mixed with 0.5µl of stock pepsin solution (1mg/ml) at room temperature for 2-3 minutes and then dehydrated through ethanol series. Denaturing cellular DNA was done by immersing slides in 70% formamide in 2X SSC at 70°C for 2 minutes and then placed in ice cold 70% ethanol for 2 minutes followed by passing through an ethanol series. Prior to hybridization the centromere probe, CENPB-Cy3 (PNA Bio; ATTCGTTGGAAACGGGA), was warmed to 37°C for 5 minutes. The probe was denatured for 10 minutes at 85°C then immediately chilled on ice before applying probe to the slides. The hybridization protocol required 16 hours at 37°C. Post hybridization washes for 5 minutes at 37°C in 2X SSC were followed by two washes in 50% formamide/2X SSC 37°C, for 5 min each time and final wash in 2X SSC, twice for 5 min each time. DAPI (Sigma-Aldrich) was added to the final wash. Cell nuclei were visualized using a Leica TCS SP8 confocal microscope and the Z-stacking feature. Measurements of nuclear size and centromere intensity were determined after outlining the nucleus and getting the area (µm²) and mean gray values (fluorescent intensity/µm²) after creating a projection of Z-Stack scans.

Proliferation assay and cell doubling time

Cell proliferation was determined using the CyQuant Direct Cell Proliferation Assay (Life Technologies) according to the manufacturer's instruction and as previously described¹¹⁵. Population doubling times were calculated using

the readings from CyQuant Direct Proliferation Assay and use of a population doubling time online calculator (<http://www.doubling-time.com/compute.php>).

Cell death assay

Stem cells were plated in a 6-well dish (80,000 cells per well) and incubated in starvation media (growth factor and FBS depleted media) with 1% PSG for 18 hours. The cells were then treated with either 40 μ M or 80 μ M hydrogen peroxide for 4 hours. Cells were resuspended with Sytox Blue (1:2,000, Life Technologies) to label necrotic cells. Data was acquired on a FACS Aria (BD Biosciences) and analyzed with FACS Diva software (BD Biosciences). Cell death was quantitated by measurement of Sytox Blue positive cells and represented as a fold change relative to cells in starvation media alone.

In co-culture conditions of stem cells with NRCMs, whole populations were analyzed and stained with Annexin V (1:40, BD Biosciences) and Sytox Blue and only the negative (non-fluorescent NRCM) population was analyzed for cell death. Cell death of NRCMs was represented as a fold change relative to cells in growth media (10% M199). NRCMs in 0.5% M199 and 0.5% plus add back of 10% M199 at the time of stem cell addition were maintained as positive and negative controls for cell death.

mRNA isolation, cDNA synthesis and quantitative RT-PCR

RNA was enriched using the Quick RNA Mini Prep kit from ZymoResearch according to the manufacturers instructions. Reverse transcriptase was performed using protocol for the iScript cDNA Synthesis Kit (BIORAD). qRT-PCR

was read after incubation of cDNA, primers (100nM) and IQ SYBR Green Supermix (BIORAD) as previously described¹¹⁵. Data was analyzed using the $\Delta\Delta C(t)$. Primers are as follows: cardiac troponin t, forward 5'-ACCCTCAGGCTCAGGTTCA-3' and reverse 5'-GTGTGCAGTCCCTGTTTCAGA-3'; connexin 43 forward 5'-GGACCTTGTCCAGCAGCTT-3' and reverse 5'-TCCAAGGAGTTCCACCACTT-3'; smooth muscle 22 forward 5'-GACTGCACTTCTCGGCTCAT-3' and reverse 5'-CCGAAGCTACTCTCCTTCCA-3'; platelet endothelial cell adhesion molecule forward 5'-TGCTCTCGAAGCCCAGTATT-3' and reverse 5'-TGTGAATGTTGCTGGGTCAT-3'; p53 forward 5'-GCAGGGCTCACTCCAGCTACCT-3' and reverse 5'-GTCAGTCTGAGTCAGGCCCACT-3'; p16 forward 5'-CGTACCCCGATTTCAGGTGATG-3' and reverse 5'-CGGGCGGGAGAAGGTAGT-3'; interleukin-6 forward 5'-ATCCAGTTGCCTTCTTGGGACTGA-3' and reverse 5'-TAAGCCTCCGACTTGTGAAGTGGT-3'; 18s forward CGAGCCGCCTGGATACC and reverse CATGGCCTCAGTTCCGAAAA.

Enzyme-Linked Immuno Assay (ELISA)

The ELISA assay was performed in NRCMs alone (0.5%, 0.5% + 10% rescue, and 10% M199 treated cells), NRCMs incubated with stem cell groups and stem cells alone in normal growth media. Briefly, after 24 hour incubation with serum or stem cells, the 96-well microplate was centrifuged for 5 minutes at 1200rpm and 100 μ L of media supernatant was removed and used for IL-6 Mouse ELISA Kit (Life Technologies) performed according the company's instructions.

Myocardial infarction and intramyocardial injection

Myocardial infarctions were carried out in eleven-week old female FVB mice under 2-3% isoflurane anesthesia and by tying off the left anterior descending artery (LAD) using a modified protocol¹¹⁸. After ligation, injections with either PBS (5 μ L per injection, 5 injections total per mouse), parents (CPCs or MSCs), parents combined (CPC + MSC) CC1 or CC2 (20,000 cells per 5 μ L injection, 5 injections making a total of 100,000 cells injected per mouse) were introduced to the pre-ischemic border along the infarcted region. Placing the heart out of the chest and placing it back in the chest without ligation of the LAD was considered a sham surgery.

Echocardiography and hemodynamics

Echocardiography was used to evaluate cardiac function after MI and injections using the Vevo 2100 (Visual Sonics) and as previously described⁵³. Closed-chest hemodynamic assessment was performed after insertion of a microtip pressure transducer (FT111B, Scisense) and as previously described⁵³. Cardiac function assessed by echocardiography 2 days post-infarction was not statistically different between infarcted/injected groups. The review board of the Institutional Animal Care and Use Committee at San Diego State University approved all animal protocols and studies.

Retroperfusion

Mice were sacrificed under chloral hydrate sedation before removing hearts from mice and as previously described⁵³. After retroperfusion, hearts were processed for paraffin embedding.

Immunohistochemistry

Heart sections were deparaffinized, and incubated with primary and secondary antibodies as previously described⁵³. Subsequent tyramide amplification was performed as necessary. Slides were incubated in DAPI (Sigma-Aldrich) for 10 minutes to stain for nuclei. Primary antibodies are as follows: goat anti-CD117 (c-kit) (1:100, R&D Systems); rabbit anti-GFP (1:500, Life Technologies); rat anti-mcherry (1:200, Life Technologies); mouse anti-cardiac troponin T (1:100, Abcam); CD117, GFP and mcherry required subsequent tyramide amplification.

Quantitation of c-kit cells, infarct size and cellular engraftment

Paraffin sections were probed with primary antibodies for proteins cardiac troponin T (cTNT), c-kit, GFP and mcherry and visualized on a Leica TCS SP8 Confocal Microscope. Nuclei were visualized after DAPI staining. For infarct size, cTNT was probed to visualize live myocardium and DAPI to determine nuclei distribution and area of infarction. Area of live versus dead myocardium was measured using the drawing tool in the Leica Software and normalized to the total area of the left ventricular free wall and converted to percentage. In this area, c-kit⁺ cells were counted. For engraftment, area of mcherry⁺ (CPCs, CPCs

in CPC⁺ MSC group, CC1 and CC2) or GFP⁺ (MSCs alone and MSCs in CPC⁺ MSC group) was measured and normalized to total area. 4 and 12 week sections had an n=3-4 per group.

Masson's Trichrome

Trichrome (Masson) kit was used to stain for collagen deposition in infarcted hearts according to manufacturer's protocol and based on previous reports¹¹⁴. Staining was visualized using a Leica DMIL microscope.

Statistical analysis

All data are expressed as mean \pm SEM. Statistical analyses was done using paired or unpaired Student's t-test, one-way ANOVA with a Tukey post-test or using two-way ANOVA with Bonferroni post-tests on Graph Pad Prism v5.0. A value of $p < 0.05$ was considered statistically significant.

RESULTS

Phenotypic characterization of CardioChimeras

CardioChimeras (CCs) were created after fusion of fluorescently labeled CPCs (mcherry) and MSCs (eGFP) with an inactivated RNA Sendai virus (Figure 2.1A). After fusion, dual fluorescent hybrids were purified by fluorescent activated cell sorting and allowed to undergo clonal expansion (Figure 2.2A). 18 mononucleated hybrids were successfully expanded one-month after initial sorting, and two unique CCs (CC1 and CC2) were maintained for this study based upon comparable proliferative and survival properties to the parental cells. CC2 exhibits a proliferative rate similar to CPC parent while CC1 shows modest proliferation, and all cells had increased proliferation over the MSC parent based on a fluorescent dependent cell proliferation assay and cell doubling time (Figure 2.1B and 2.1C). CCs are not increasingly susceptible to cell death compared to parent cells (Figure 2.1D) and did not exhibit elevated expression of cell cycle arrest or senescence markers based on mRNA for p16 or p53 (Figure 2.1E and 2.1F). CC1 has increased cell size and is morphologically similar to MSCs (Figure 2.1G, 2.1I and 2.1J). CC2 displays a slight increase in cell size but is not significantly different from CPCs (Figure 2.1G, 2.1H, and 2.1K). Mononucleated CC1 and CC2 exhibit increased nuclear size and centromere intensity relative to parent cells after nuclear hybridization (Figure 2.2B-2.2F). Collectively, CCs represent a novel stem cell population where increased DNA content does not negatively impact on survival or proliferation after induced cell fusion.

CardioChimeras exhibit increased basal expression of cardiomyogenic commitment markers

MSCs and CC1 populations have little to undetectable c-kit⁺ cells, while CC1 and CPCs maintain 20% and 50% c-kit positivity (Figure 2.3A). Gap junction marker *connexin43* and *platelet endothelial cell adhesion molecule (pecam or cd31)* mRNA are modestly upregulated in CC2 at basal levels (Figure 2.3B and 2.3C). MSCs express high levels of endothelial and smooth muscle markers as indicated by *cd31* and *smooth muscle 22 (sm22)* gene expression (Figure 2.3C and 2.3D)¹¹⁹. Although *sm22* was not upregulated in CCs, co-incubation of CPCs with MSCs at a 1:1 ratio increased mRNA expression of *sm22* (Figure 2.3D). Interestingly, CC1 has increased mRNA for *cardiac troponin T (cTNT or tnnt3)* (Figure 2.3E). This data supports CCs potential for increased cardiomyogenic activity making them an attractive cellular source for cardiac therapy.

CardioChimeras promote cardiomyocyte growth after co-culture

In order to test the beneficial effects mediated by CCs and parental cells before *in vivo* cell transfer, neonatal rat cardiomyocytes (NRCMs) were co-incubated with stem cell groups (CPC, MSCs, CPC + MSC, CC1 and CC2) at a ratio of 1:10 in serum depleted conditions. NRCMs maintained in low serum conditions (0.5%) resulted in smaller cardiomyocytes relative to NRCMs maintained in high serum conditions (10%) (Figure 2.4A, 2.4B and 2.4G). Addition of MSCs, CPC + MSC, CC1 or CC2 to low serum treated NRCMs significantly increased cardiomyocyte size within 24 hours (Figure 2.4C-E and

2.4G), but CPCs could not induce significant growth of NRCMs (Figure 2.4F and 2.4G). Slow twitch β -myosin heavy chain (*mhy7*) over fast twitch α -myosin heavy chain (*mhy6*) gene expression was not significantly elevated in cardiomyocytes after 24 hours co-incubation with stem cell groups but is highly expressed in low serum conditions indicating the stem cells do not induce a maladaptive hypertrophic responses in cardiomyocytes (Figure 2.4H). Regardless of the stem cell population added to cardiomyocytes, NRCMs were protected from cell death based on flow cytometric analysis of apoptotic and necrotic markers (Figure 2.4I). With the addition of CC1 and CC2, NRCMs had increased mRNA for *stromal derived factor-1 (sdf-1)* (Figure 2.4J) a cardioprotective cytokine and homing ligand for C-X-C chemokine receptor type 4 (CXCR-4) positive stem cells¹²⁰.

CardioChimeras have increased gene expression of commitment and paracrine markers after co-culture with cardiomyocytes

After co-culture with cardiomyocytes, *sm22* was not significantly upregulated in CC groups (Figure 2.5A). However, CPC + MSC and CC2 displayed the largest induction of endothelial marker expression of *pecam*, whereas CC2 induced *cTNT* gene expression after 7 days of co-culture with NRCMs (Figure 2.5B and 2.5C). Paracrine factors are routinely touted as a mechanism for cardioprotection¹²¹, therefore we analyzed stem cells for expression of growth and immunomodulatory factors. Gene expression for *interleukin-6 (Il-6)* and protein expression is upregulated in CC2 after 24-hour incubation with serum starved NRCMs (Figure 2.5D and 2.5E). Early release of

immunomodulatory factors such as IL-6 after acute cardiac damage is anti-apoptotic¹²².

CardioChimeras improve left ventricular structure and cardiac function after myocardial injury

To establish therapeutic efficacy of CCs relative to parent cells or parent cells combined, we injected a total of 100,000 cells within the border zone region of an acutely damaged mouse heart (left anterior descending artery ligation). At 1-week post injury (WPI), all groups had similar reductions in AWT and EF (Figure 2.6A and 2.6D and Table 2.1). CC1 and CC2 exhibited increased AWT at 4 WPI, but only CC1 treated hearts preserved AWT up to 18 WPI (Figure 2.6A). Heart weight to body weight ratios (HW/BW) at 12 and 18 weeks did not increase in CC treated hearts indicating that hypertrophy was not a contributing phenotype to increases in AWT (Figure 2.6B and 2.6C). Rather, CC1 hearts had significantly reduced HW/BW relative to vehicle control (PBS) (Figure 2.6C). EF was increased in CC1 and CPC + MSC hearts starting at 3 WPI, and CC1 and CC2 had increased EF over PBS at 6 WPI (Figure 2.6D). CC and CPC + MSC-treated groups exhibited improved EF starting at 12 WPI, whereas the CPC-treated group was beneficial for cardiac function only at 18 WPI (Figure 2.6D). Heart rates and structural/functional data are detailed in Table 2.1. Correlating with improved EF, CC1 treatment significantly improved positive developed pressure over time (dP/dT) (Figure 2.6E) and negative dP/dT (Figure 2.6F). CC1, CC2, CPC + MSC and CPC had smaller infarct sizes relative to PBS (Figure 2.6G).

MSC groups exhibited increased infarct size when measuring scar between 4 and 12 WPI, CPC and CPC + MSC hearts remain unchanged, and CC1 and CC2 treatment reduced infarct size as represented by Masson's Trichrome staining (Figure 2.6G-2.6N).

Cellular engraftment of CardioChimeras 4 weeks after damage

Scar size measured at 4 WPI was not significantly different among infarcted heart groups (Figure 2.7A and 2.7B-2.7E). Next, we were interested in determining cell persistence at this time point and were able to detect CPCs labeled with mcherry in CPC alone and CPC + MSC treated hearts (Figure 2.7F and 2.7G). Interestingly, mcherry⁺ CPCs were detected near small c-kit⁺/cTNT⁺ cardiomyocytes in the infarct area (Figure 2.7H). CC1 was detected by both GFP and mcherry expression, but did not display evidence of commitment at this early time point (Figure 2.7I-2.7K).

CardioChimeras have increased engraftment, expression of cardiomyogenic markers and support the increased presence of c-kit⁺ cells in the myocardium 12 weeks after damage

C-kit⁺ cell recruitment in damaged regions supports endogenous differentiation and myocardial repair¹²¹. Although infarction sizes were similar at the 4-week time point, induction of endogenous c-kit cells in the infarcted area was increased in MSC, CPC + MSC, and CC1 treated hearts (Figure 2.8A-2.8C). At 12 WPI, a high number of c-kit⁺ cells were observed in PBS and MSC treated hearts, yet c-kit⁺ cells remained visually present in CPC + MSC, CC1 and CC2

treated hearts surrounding mcherry⁺ cells in the border zone regions (Figure 2.8D-2.8G). The percentage of cell engraftment was increased in CC1 and CC2 hearts at 1.9% and 1.1% respectively relative to 0.21% and 0.29% in CPC and CPC + MSC hearts (Figure 2.8H and 2.8K-2.8O). MSCs were detected at a much lower level or 0.04% of the total left ventricular free wall (Figure 2.8H, 2.8I, and 2.8J). CPCs discovered in the border zone areas co-expressed c-kit and mcherry in CPC hearts and expressed mcherry alone in CPC + MSC hearts (Figure 2.8K and 2.8L). However, both CC1 and CC2 showed increased levels of engraftment and co-localized with cTNT, surrounded by endogenous c-kit⁺ cells (Figure 2.8M-2.8O).

CardioChimeras increase capillary density in the infarct area

Capillary density was measured in the border zone and infarcted areas at 12 WPI. Shams, non-injured controls, are included as a standard for capillary density compared to injured hearts (Figure 2.9A, 2.9B, and 2.9C). Parent cells, individual or combined, or CC treatment did not significantly increase capillary density in the border zone regions relative to PBS (Figure 2.9A and 2.9C-2.9I). MSC, CPC or CPC + MSC treated hearts similarly did not affect the number of capillaries discovered in the infarct zone (Figure 2.9B and 2.9J-2.9M). Notably, CC1 and CC2 treated hearts had significant increases in isolectin⁺ structures in the infarct regions at 12 WPI (Figure 2.9B and 2.9N-2.9O).

CPC, MSC and CardioChimera treatment normalizes cardiomyocyte size in the remote and infarcted regions

Cellular treatment and long term engraftment of cells is reported to induce compensatory hypertrophy in areas of damage preventing progression of heart failure after MI¹²³. MSC and vehicle controls had increased cardiomyocyte size in the remote area relative to sham, displayed no significant changes in the border zone cardiomyocytes and revealed decreased average cardiomyocyte size in the infarct regions (Figure 2.10A-2.10F). CPC + MSC, CC1 and CC2 treated hearts maintained cardiomyocyte size in the remote region similar to non-injured controls (Figure 2.10A, 2.10D and 2.10H-2.10J). Although stem cell treatments did not modify border zone cardiomyocyte size (Figure 2.10B and 2.10K-2.10P), injection of CPC, CPC + MSC, and both CCs increased cardiomyocyte size in the infarcted regions relative to PBS and MSC treated hearts up to 12 WPI (Figure 2.10C and 2.10Q-2.10V). This data indicates that improved engraftment of stem cells correlates with the presence of microvascular structures and preservation of cardiomyocyte size in the remote and infarct regions relative to failing and severely damaged hearts.

DISCUSSION

The restorative impact of cell therapy to advance regenerative medicine remains to be fully realized and continues to be the focus of intense investigation. Increased knowledge of stem cell biology emerges from the use and application of a variety of adult stem cells. Unfortunately, ideal cellular properties are compromised by massive cellular death upon introduction into damaged myocardium⁴⁷. In this report, we demonstrate a novel approach by using cell fusion to enhance delivery of novel and unique stem cell properties created within a single cell. Cardiac-derived CPCs and bone marrow derived MSCs were chosen for this study as both of these cell types have established roles in the heart: CPCs contribute to direct cardiomyogenic differentiation whereas MSCs provide for protective immunomodulatory and growth factor paracrine secretion^{105, 106}. CCs were not significantly impaired in proliferation and did not exhibit signs of genomic instability due to increased DNA content (Figure 2.1 and 2.2). Furthermore, CCs had decreased expression c-kit⁺ and increased expression of cardiac specific factors at basal levels and after co-culture with cardiomyocytes, which is concurrent with the ability of stem cells to provide for increases in cardiomyocyte growth, survival and *sdf-1* mRNA in stressed cultured conditions (Figure 2.3, 2.4, and 2.5). CCs injected into the acutely damaged heart improved structural integrity and reduced infarct size (Figure 2.6). Furthermore, functional improvements were observed in CC treated hearts, and increased engraftment was apparent in the border zones after 12 WPI (Figure 2.8). In conclusion, CardioChimeras are a superior cellular therapy to single cell

injections of either CPCs or MSCs alone, comparable to CPC + MSC treatment but with the advantage of increased survival and persistence relative to either parental cell line.

BMCs, the most common stem cell for cardiac therapy, apparently undergo engraftment through a combination of cell fusion and to a lesser degree by direct transdifferentiation events¹²⁴. Membrane fusion is dependent upon signaling mechanisms involving paxillin induced focal adhesions and recycling of integrins as demonstrated between macrophages and myoblasts¹²⁵. In the heart, cell fusion is increased between exogenous stem cells and apoptotic cardiomyocytes similar to enhanced myoblast fusion in the presence of phosphatidylserine presenting cells^{110, 126}. Altered DNA content has been raised as an issue following fusion events as genomic instability leads to cellular aging¹²⁷. However, CCs display normal stem cell function and continue to expand without undergoing replicative senescence after long-term culture (Figure 2.1). Somatic cells exhibiting chromosomal mosaicism such as through the loss or deletions of chromosomes do not significantly affect stem cell properties or cell fate¹²⁸. As a result, CCs do not appear transformed but rather retain properties of CPCs and MSCs to support enhanced myocardial repair.

Increased basal expression of cardiomyogenic factors was observed in CCs (Figure 2.3). Pre-committed cells, but not fully mature stem cell derived cardiomyocytes improve exogenous cell coupling and formation of gap junction proteins¹²⁹. CCs display coordinated phenotypic properties of commitment and increased paracrine abilities to promote cardiomyocyte health much like the MSC

parent and CPC + MSC parents combined (Figure 2.4). Furthermore, CC2 in particular had enhanced IL-6 production (Figure 2.5) indicating potential to mediate anti-inflammatory functions after acute MI compared to MSC alone¹²². Factor(s) that promote growth of cardiomyocytes and stabilization or the creation of microvasculature (Figure 2.9 and 2.10) remain to be established in our model of mouse CCs, but is certainly a subject of future investigations. Gene dosage effects as well as modifying the ratio of cell numbers before cell fusion leads to unique phenotypic properties such as proliferation and inhibition of senescence^{60, 61, 130}. Embryonic stem cell (ESC) fusion with somatic cells facilitates reprogramming using equal cellular ratios indicating that ESCs are the more dominant cell type¹³¹. In this report, the CPC parent phenotype dominates in the fused progeny and most likely mediates early cardiomyogenic factors in CCs, whereas paracrine mediated effects from the MSC parent is secondary. For future studies, selecting the optimal cells and gene dosage for fusion will allow us to more effectively design hybrids for stronger traits towards commitment or paracrine effects.

Therapeutic delivery of MSCs improves cardiac function and structure mainly through paracrine mediated effects. Secretion of factors such as SDF-1 and IGF-1 support endogenous recruitment of c-kit⁺ progenitor cells and further facilitates cardiomyocyte cell cycle entry and survival¹³²⁻¹³⁴. Immunomodulatory functions of MSCs to inhibit excess scar formation is an attractive therapy for several disease states¹³⁵. In this study, we did not see any significant improvements in AWT or EF over vehicle treated controls using the MSC

parental cells alone (Figure 2.6). The MSC treatment was unable to prevent increases in scar size or decreases in cardiac function up to 18 weeks similar to the deteriorating PBS treated hearts. Although, MSC addition did maintain size and survival of the responding cardiomyocytes, these beneficial effects were not recapitulated *in vivo* after MSC transfer (Figure 2.4 and 2.6). Apoptosis and slow proliferation rate are likely contributing factors to the disappearance of MSCs at later time points (Figure 2.1 and 2.6). Instead, MSC and PBS treated hearts sustained increases in c-kit⁺ cells, which are most likely increased through chronic inflammation and recruitment of hematopoietic derived c-kit⁺ mast cells (Figure 2.8).

The optimal cell number chosen for therapy is a critical aspect to promote structural and functional recovery after MI. Delivery of human CPC + MSC in a pig model of ischemia resulted in positive remodeling and engraftment using 200-fold more MSCs relative to CPCs¹⁰⁸. For our study, we placed CPCs to MSCs at a one-to-one ratio as the appropriate control compared to our CCs. The engraftment efficiency of MSCs could have been greatly limited from the beginning of the experiment due to reduced MSC cell numbers (Figure 2.8). Benefits of co-culture of CPCs with MSCs are consistent with previous findings as MSC co-incubation with CPCs at equal ratios increased basal differentiation markers such as *sm22*, which was not observed in CCs (Figure 2.3). Furthermore, during co-culture with NRCMs, CPC + MSC groups exhibited increased cardiomyogenic markers *sm22*, *pecam* and *cTNT* (Figure 2.5). It remains unclear if differentiation resulted from CPCs alone in culture with MSCs,

although significant cell death of MSCs alone was observed when co-cultured with NRCMs for seven days. The comparatively modest therapeutic benefit of unmodified CPCs has been previously shown from our laboratory^{48, 49}. Clearly, pinpointing the mechanistic contribution of MSCs to support CPCs in our CPC + MSC treated hearts is an important unanswered question to be resolved in future investigations. Although engraftment efficiency of CPCs co-injected with MSCs was not significantly improved relative to CPC hearts alone, function was improved in CPC + MSC hearts at a much earlier time point. We can hypothesize that MSCs in the acute stages of damage (<4weeks) facilitated protective endogenous cell reprogramming without long-term persistence, which was not sufficient to impact on exogenous CPC proliferation and/or engraftment, consistent with reports from other groups^{107, 136}.

From the numerous cell types touted to be efficacious for cardiac clinical therapy, CPCs and MSCs are particularly promising because of established protocols for cell isolation and expansion in clinical settings^{10, 32}. Although MSCs show much lower rates of persistence in the damaged heart than CPCs, cell therapeutic practices could benefit from investigation of how to enhance immunomodulatory effects of MSCs¹⁰⁶. Currently, “Off-the-shelf” allogeneic cellular options include cardiosphere derived cells and MSCs that may exert beneficial effects after MI but suffer from poor persistence following delivery^{32, 137}. In comparison, ESCs and induced pluripotent stem cells exhibit extended proliferation and are less prone to immuno rejection and/or cell senescence after transplantation¹³⁸. However, ESCs have reduced capacity for integrative

cardiomyogenesis as demonstrated by arrhythmogenic events in large animal models¹³⁹. Our cell fusion approach aims to capitalize on adult stem cells that have validated cardiac therapeutic effects in order to create a superior composite hybrid with anti-inflammatory functions. Additionally, fusion of aged stem cells with more youthful cells could confer cell rejuvenation and reverse signs of cellular aging^{60, 140}. In the era of human cord blood banking, the isolation of immunoprivileged stromal cells from the same patient can be easily fused with stem cells harboring tissue specific regenerative capacity, resulting in a novel cell type that is resistant to rejection in addition to having desired cellular effects such as proliferation and direct tissue commitment¹⁴¹. From a translational perspective, cell fusion is an adaptable genetic engineering strategy that qualitatively enhances adult stem cell properties such as persistence, anti-inflammatory and growth factor secretion and direct cardiomyogenesis to sustain long-term cardiac repair.

SUMMARY POINTS

- Cell fusion of CPCs with MSCs creates unique hybrids that have similar proliferative rates and survival capabilities compared to the parental cell lines.
- Hybrids or CardioChimeras have increased DNA content after fusion but do not exhibit signs of genetic instability and/or senescence.
- CardioChimeras have increased expression of cardiomyogenic markers during normal growth conditions.
- CardioChimeras co-cultured with cardiomyocytes improve myocyte growth, survival and expression of SDF-1 a beneficial paracrine factor.
- Intramyocardial transplantation of CardioChimeras improves myocardial structure and reduces infarct size at 12 weeks.
- CardioChimeras and dual transplantation of CPCs and MSCs increase cardiac function as measured by ejection fraction.
- CPC injection improves ejection fraction 18 weeks after MI.
- CardioChimeras promoted an increase in capillary density and normalized cardiomyocyte size in the infarct area 12 weeks after damage.
- CardioChimeras have increased engraftment in the left ventricle relative to groups treated with parental cells individually or combined.
- CardioChimeras combine the beneficial and cardioprotective properties of distinct stem cells into a single cell type for effective cardiac repair.

FIGURES

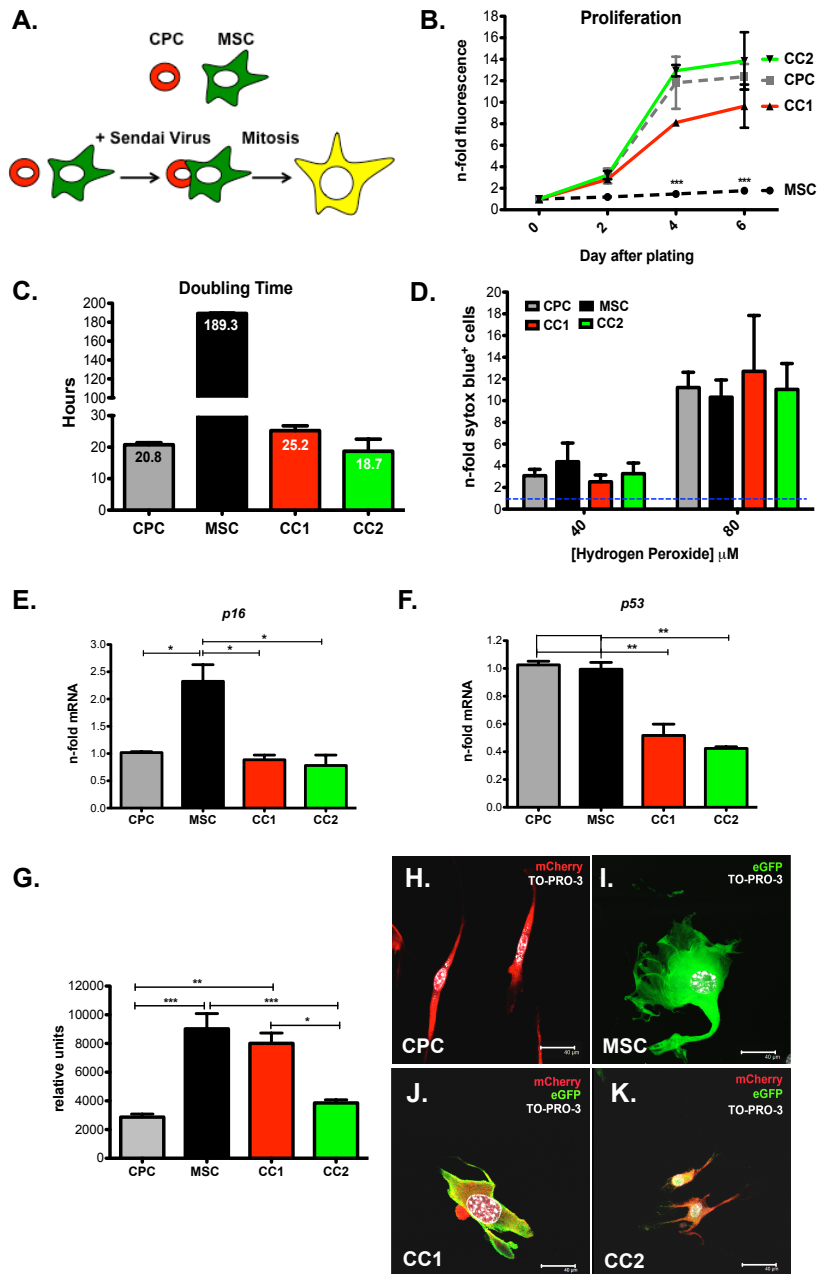


Figure 2.1: Phenotypic characterization of CardioChimeras.

(A) Schematic representation of the creation of CardioChimeras. (B) Proliferation of CCs, CPCs and MSCs represented as a fold change relative to day of plating. (C) Cell doubling time in hours. (D) Cell death assay of CCs and parents cells after treatment with 40 μ M or 80 μ M hydrogen peroxide represented, as a fold change relative to cells not treated with hydrogen peroxide. (E) p16 and (F) p53 gene expression normalized to ribosomal 18s and represented as a fold change relative to CPCs. (G) Surface area of (H) CPC, (I) MSC, (J) CC1 or (K) CC2. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Scale bar is 40 μ m.

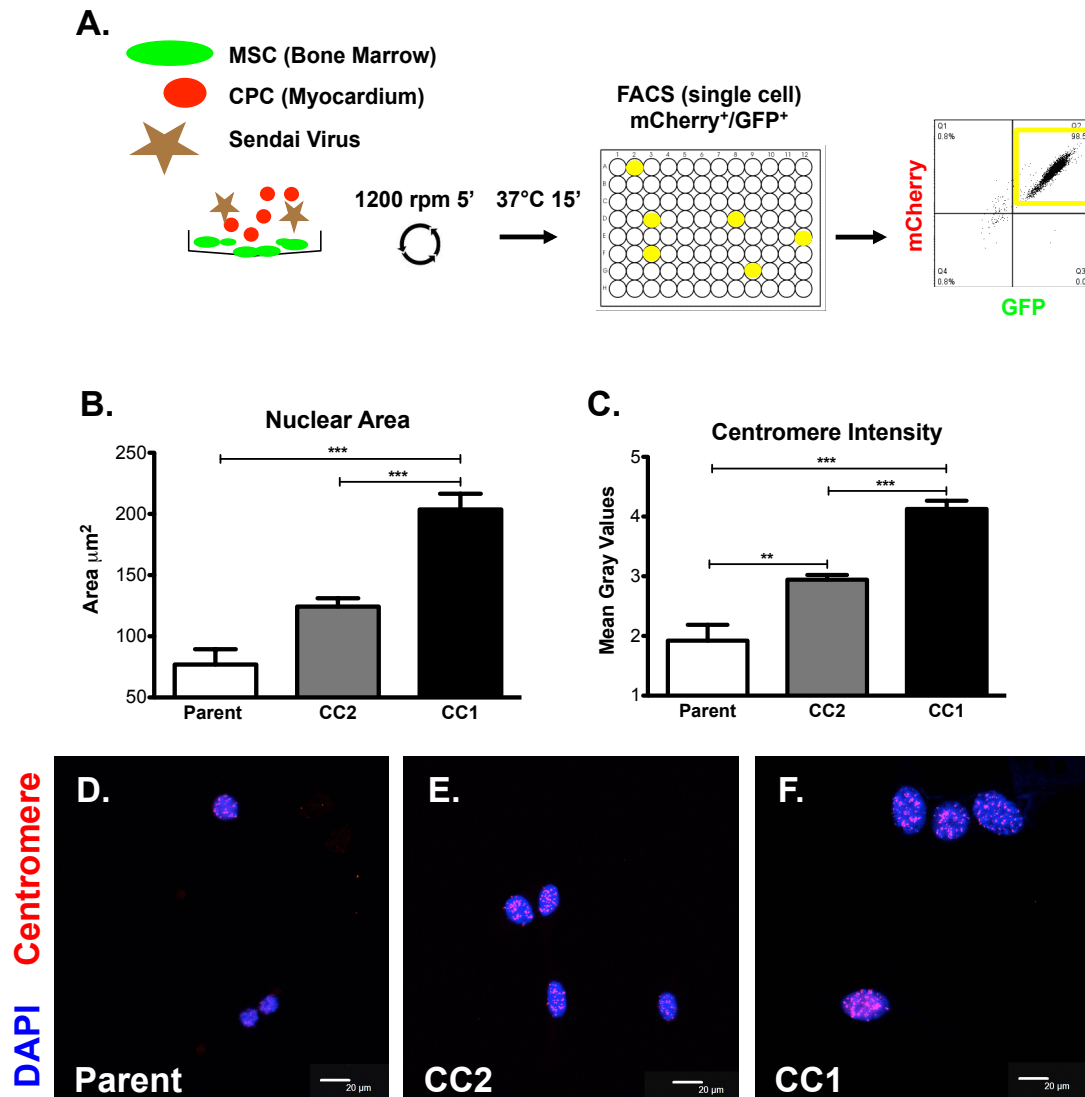


Figure 2.2: CardioChimeras have increased nuclear size and DNA content.

(A) Detailed protocol for the fusion and clonal expansion of CardioChimeras. Briefly, mouse CPCs were co-incubated with mouse MSCs at a 1:1 ratio with addition of Sendai virus. Cells were centrifuged to force cell contact and single cell sorted based on fluorescent expression of mCherry and GFP. Clones were confirmed by flow cytometric analysis. (B) Measurement of nuclear size and (C) Centromere intensity in parent MSCs, CC2 and CC1. (D) Representative images of nuclei in parent (E) CC2 and (F) CC1. Blue represents DAPI staining of DNA content and red represents centromere probe binding. Scale bar is 20 μm . * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

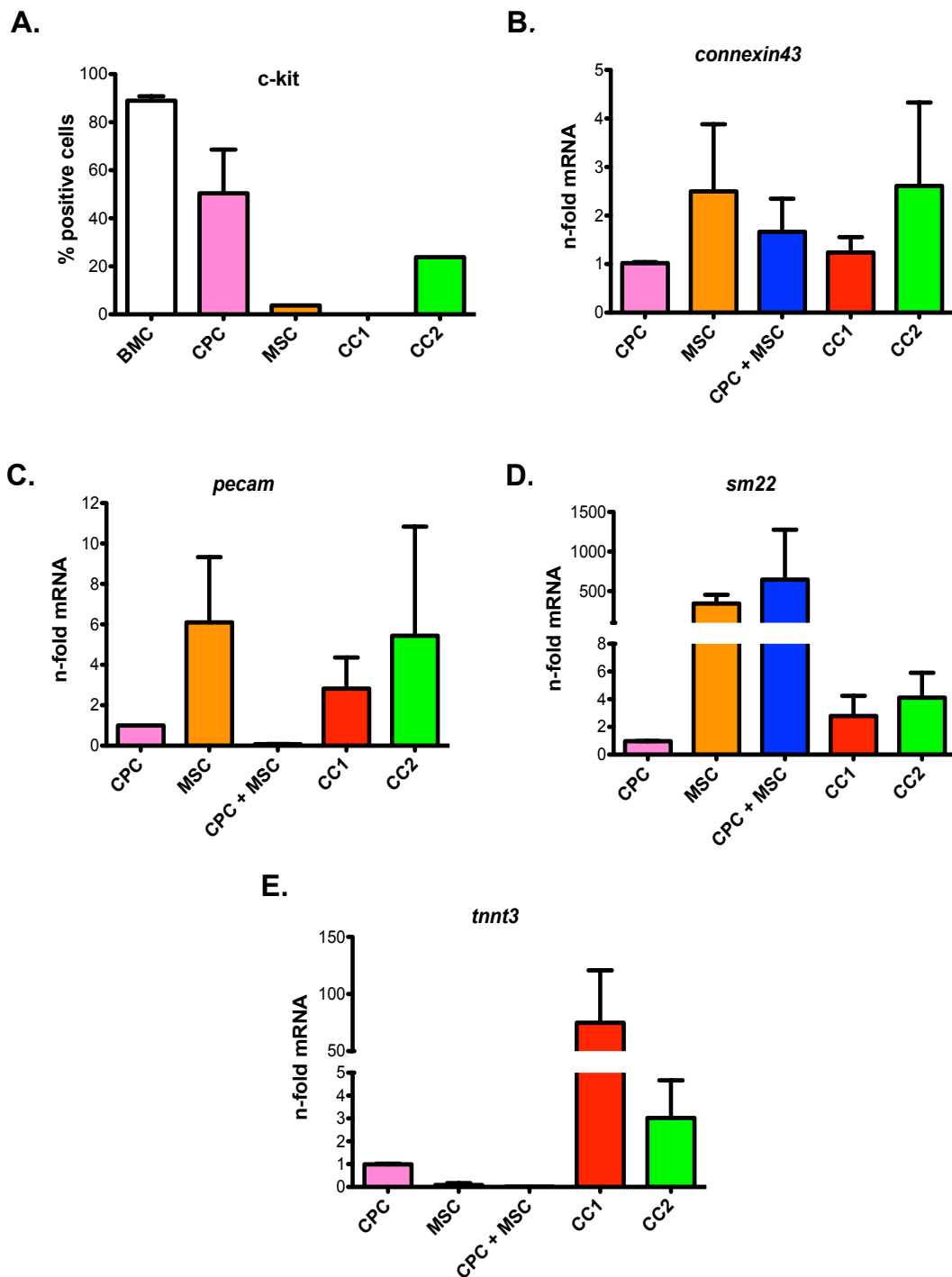


Figure 2.3: CardioChimeras have increased expression of cardiomyogenic commitment markers at basal levels.

(A) C-kit protein expression as analyzed by flow cytometry. C-kit purified bone marrow cells were utilized as a positive control. (B) *connexin 43*, (C) *pecam (cd31)*, (D) *sm22* and (E) *cTNT (tnnt3)* gene expression was analyzed by qRT-PCR in CPC, MSC, CPC + MSC, CC1 and CC2 after normalization to ribosomal 18s. Values are represented as a fold change relative to CPCs.

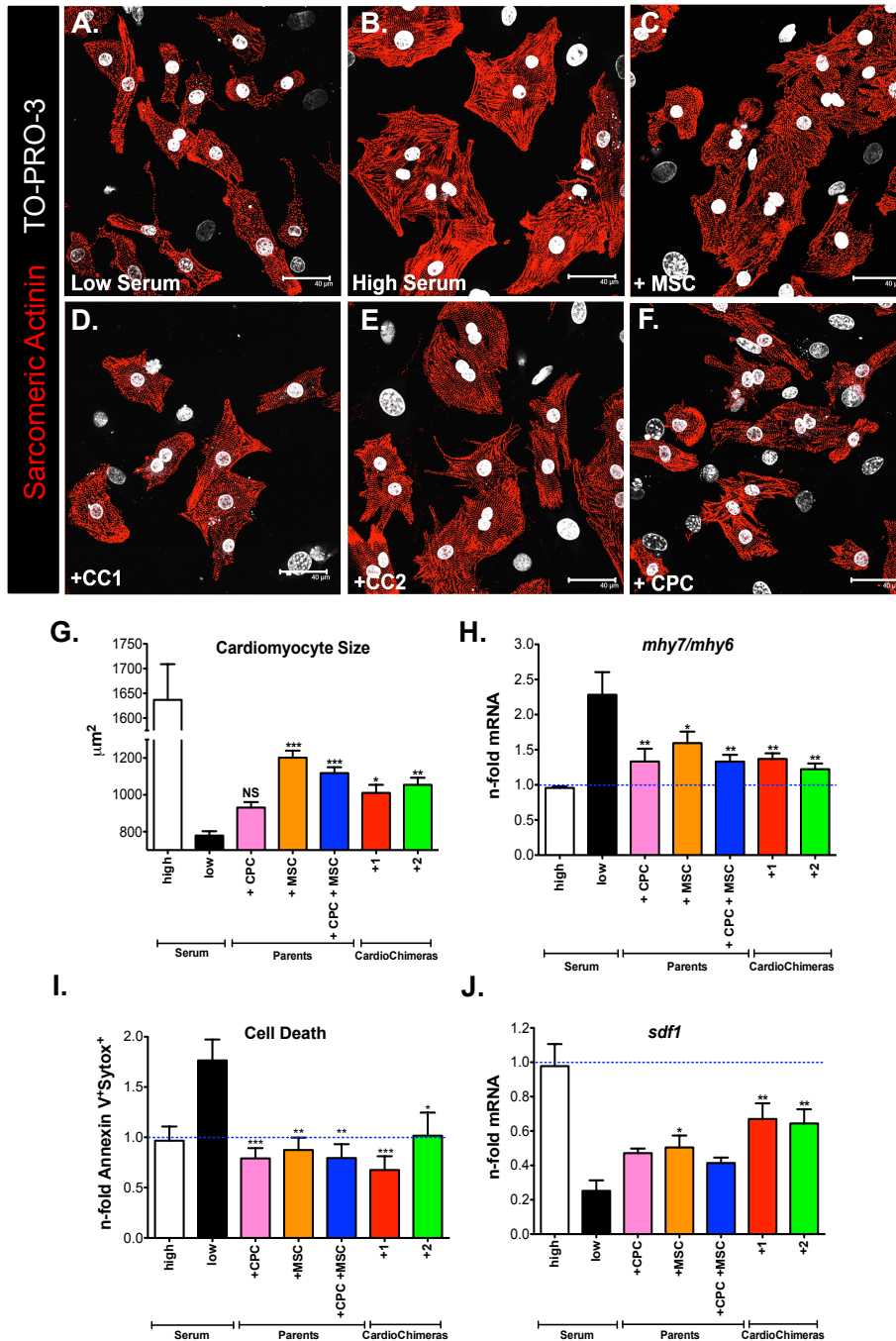


Figure 2.4: CardioChimeras promote cell growth after co-culture with cardiomyocytes. (A) NRCMs in low serum. (B) NRCMS in high serum. (C) NRCMs in low serum and the addition of MSCs, (D) CC1, (E) CC2 or (F) CPC for 24 hours. Cardiomyocytes were visualized by staining with sarcomeric actinin. TO-PRO-3 iodide was used to visualize nuclei. (G) Quantitation of cardiomyocyte size. (H) Gene expression of *mhy7* over *mhy6* represented as fold change relative to high serum. (I) Cardiomyocyte cell death. Values are represented as fold change of Annexin V⁺ and Sytox Blue⁺ cells relative to high serum. (J) *sdf-1* gene expression in cardiomyocytes alone after the addition of stem cells. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Scale bar is 40 μm .

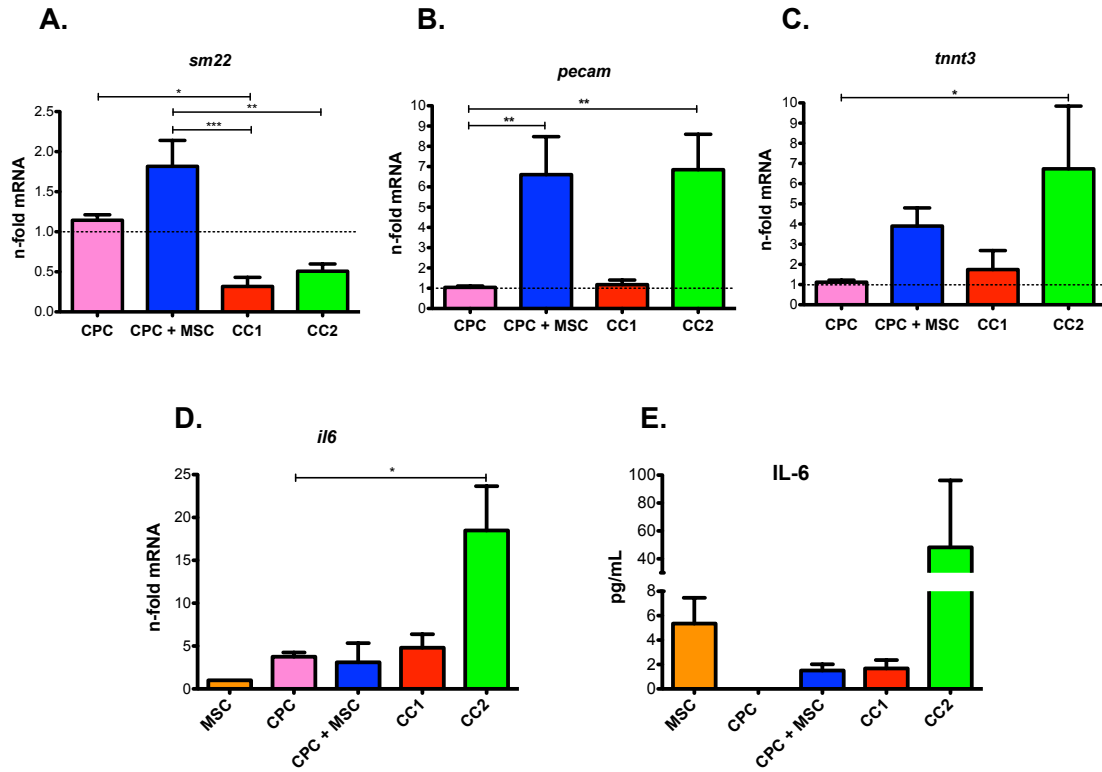


Figure 2.5: CardioChimeras have increased commitment and paracrine gene expression after co-culture with cardiomyocytes.

(A-C) Gene expression in stem cells after 7-day co-culture with NRCMs. (A) *sm22* (B) *pecam* and (C) *cTNT*. (D) *il6* gene expression was analyzed in stem cells after 24-hour co-culture with NRCMs. (E) IL-6 protein expression was confirmed by ELISA. (G-J) Statistical values were determined by one-way ANOVA compared to low serum controls. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

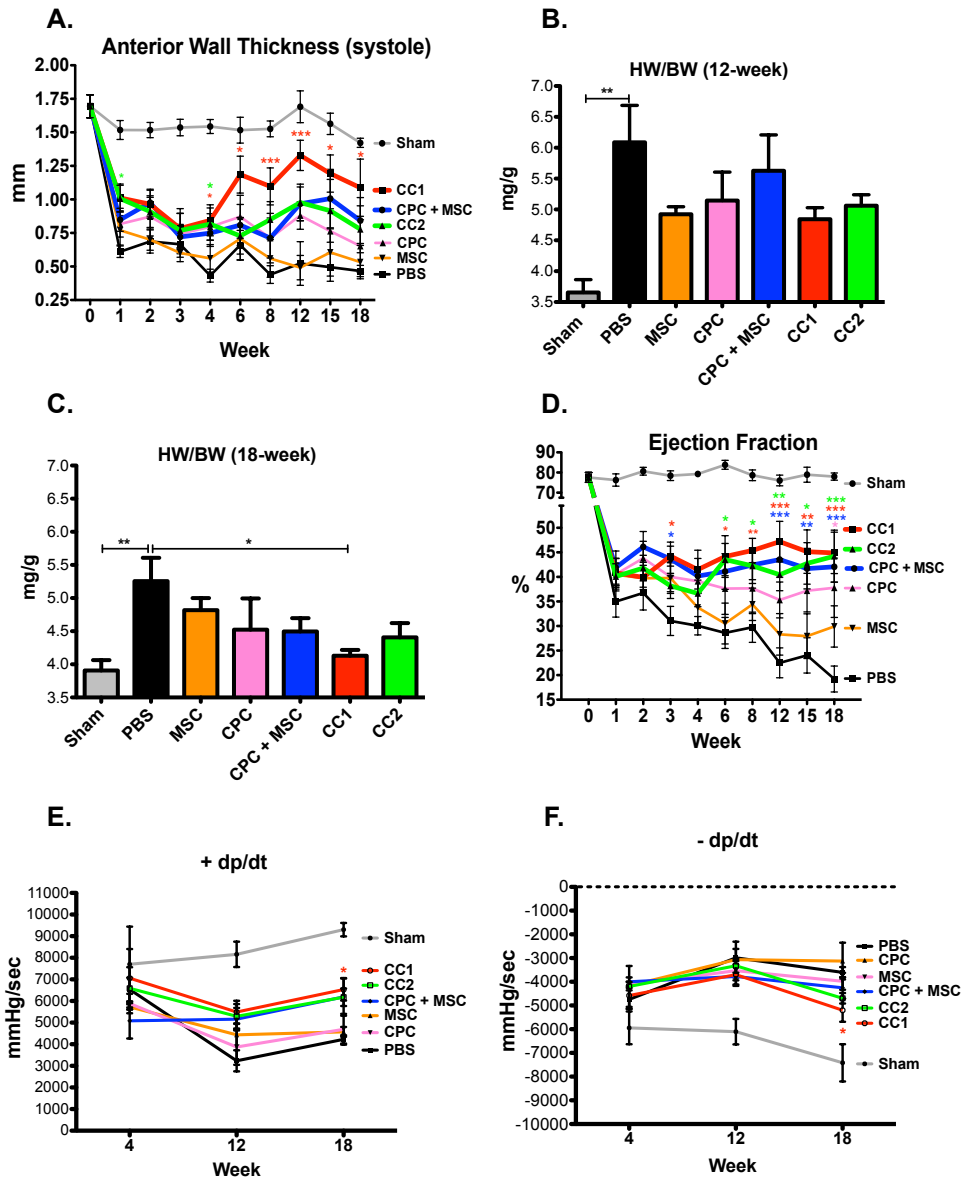


Figure 2.6: CardioChimeras improve left ventricular wall structure and cardiac function after myocardial injury.

(A) Longitudinal assessment of anterior wall thickness during systole (mm) over 18 weeks. (B) Heart weight to body weight ratio (mg/g) at 12 weeks and (C) 18 weeks post treatment and infarction. Sample sizes of at 3-5 mice per group. (D) Longitudinal assessment of ejection fraction (%). (E) Positive and (F) Negative developed pressure over time represented as mmHg/sec at 4, 12 and 18 weeks. (G) Change in infarct size between 4 and 12 weeks time points. P values were determined by one-way ANOVA compared to PBS treated controls. (H-N) Masson's Trichrome staining and representative images of infarct size and fibrosis in (H) Sham, (I) PBS, (J) MSC, (K) CPC, (L) CPC + MSC, (M) CC1 and (N) CC2. Sample sizes are specified in Table S1. All statistical values were determined by two-way ANOVA compared to PBS treated hearts. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Colors of asterisk(s) correspond to heart group. Scale bar is $250\mu\text{m}$.

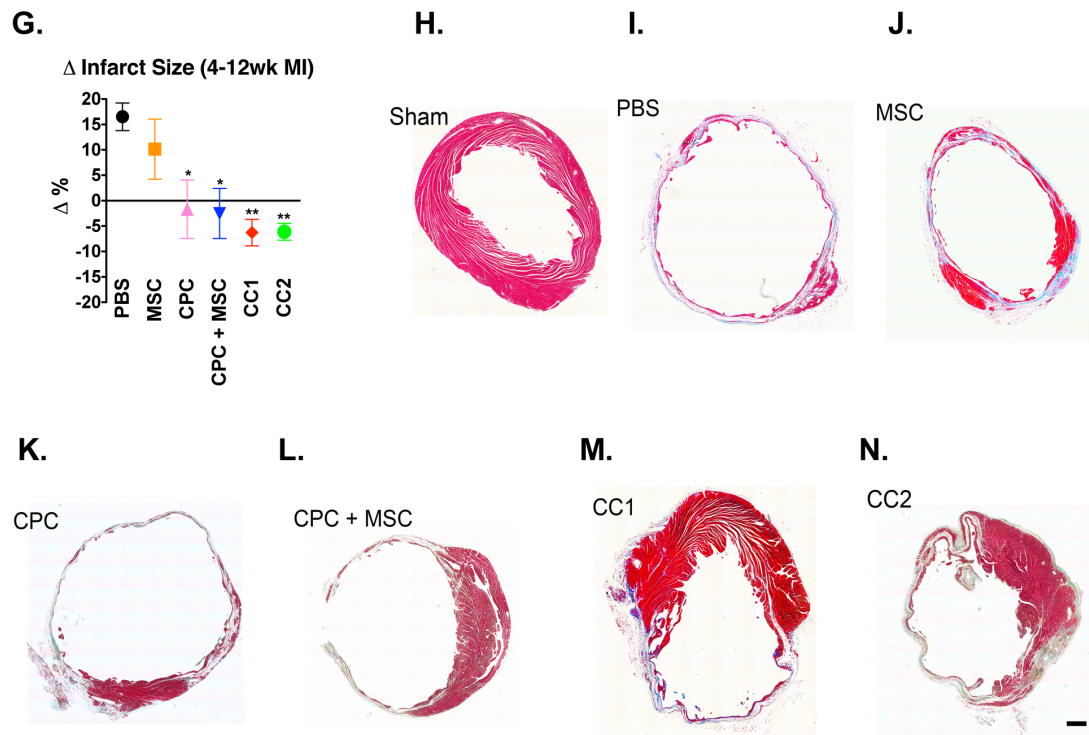


Figure 2.6: CardioChimeras improve left ventricular wall structure and cardiac function after myocardial injury, Continued.

(G) Change in infarct size between 4 and 12 weeks time points. P values were determined by one-way ANOVA compared to PBS treated controls. (H-N) Masson's Trichrome staining and representative images of infarct size and fibrosis in (H) Sham, (I) PBS, (J) MSC, (K) CPC, (L) CPC + MSC, (M) CC1 and (N) CC2. Sample sizes are specified in Table S1. All statistical values were determined by two-way ANOVA compared to PBS treated hearts. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Colors of asterisk(s) correspond to heart group. Scale bar is $250\mu\text{m}$.

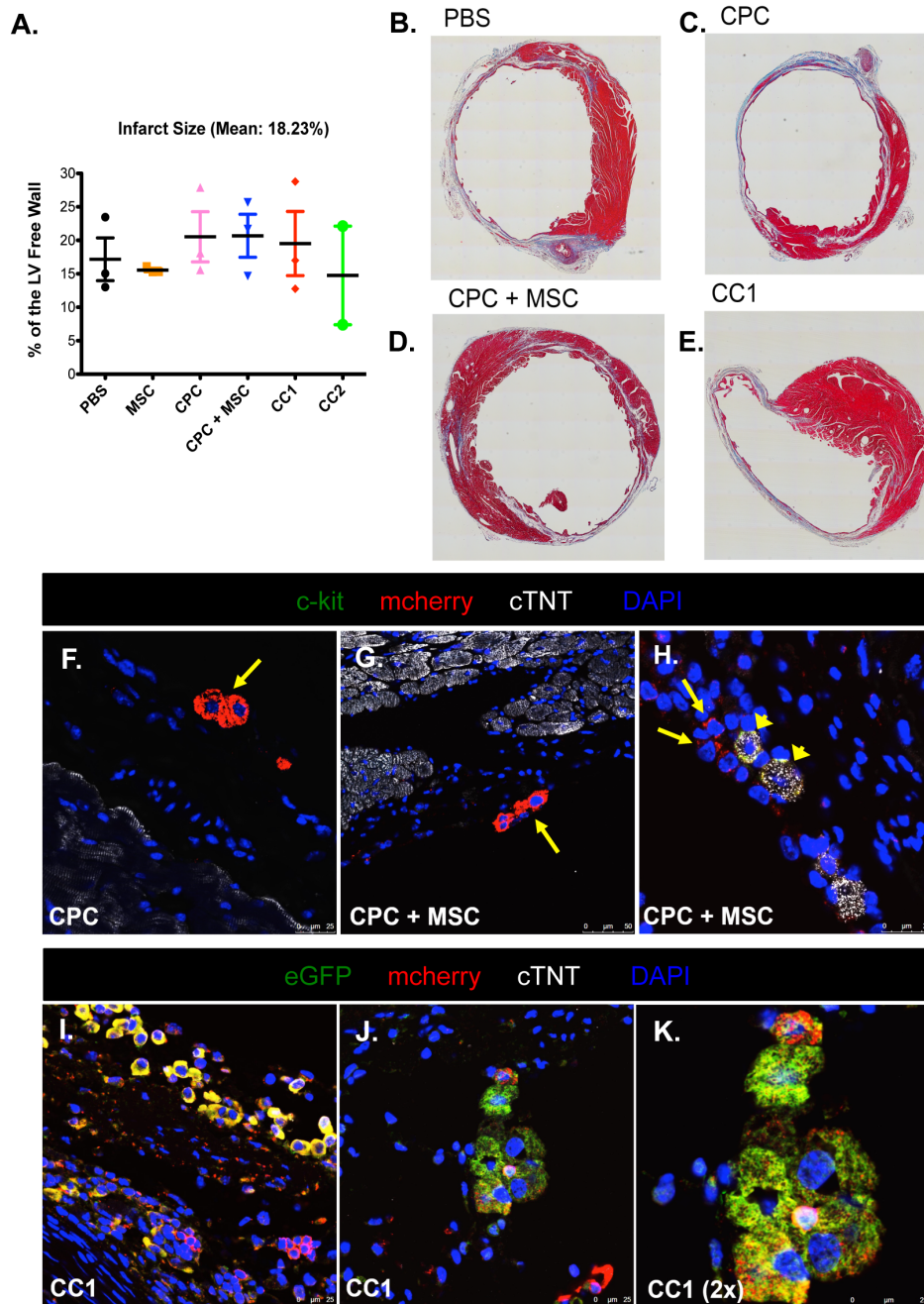


Figure 2.7: Cellular engraftment of CardioChimeras 4 weeks after damage.

(A) Infarct size was not significantly different between infarcted groups (mean=18.23%). N=2-4 per group. (B-E) Masson's Trichrome staining and representative images of (B) PBS, (C) CPC, (D) CPC + MSC and (E) CC1 hearts to visualize scar size and fibrosis. Scale bar is 250µm. (F) Mcherry⁺ CPCs detected in the infarct area in CPC treated hearts. (G) Mcherry⁺ CPCs detected in the infarct area in CPC + MSC treated hearts. (H) Mcherry⁺ CPCs adjacent to c-kit⁺ /cTNT⁺ cardiomyocytes in CPC + MSC treated hearts. (I) and (J) CC1 expressing eGFP and mcherry in the infarcted area. (K) 2x zoom of CC1. Scale bar is 25µm for confocal images. Scale bar is 50µm in (G).

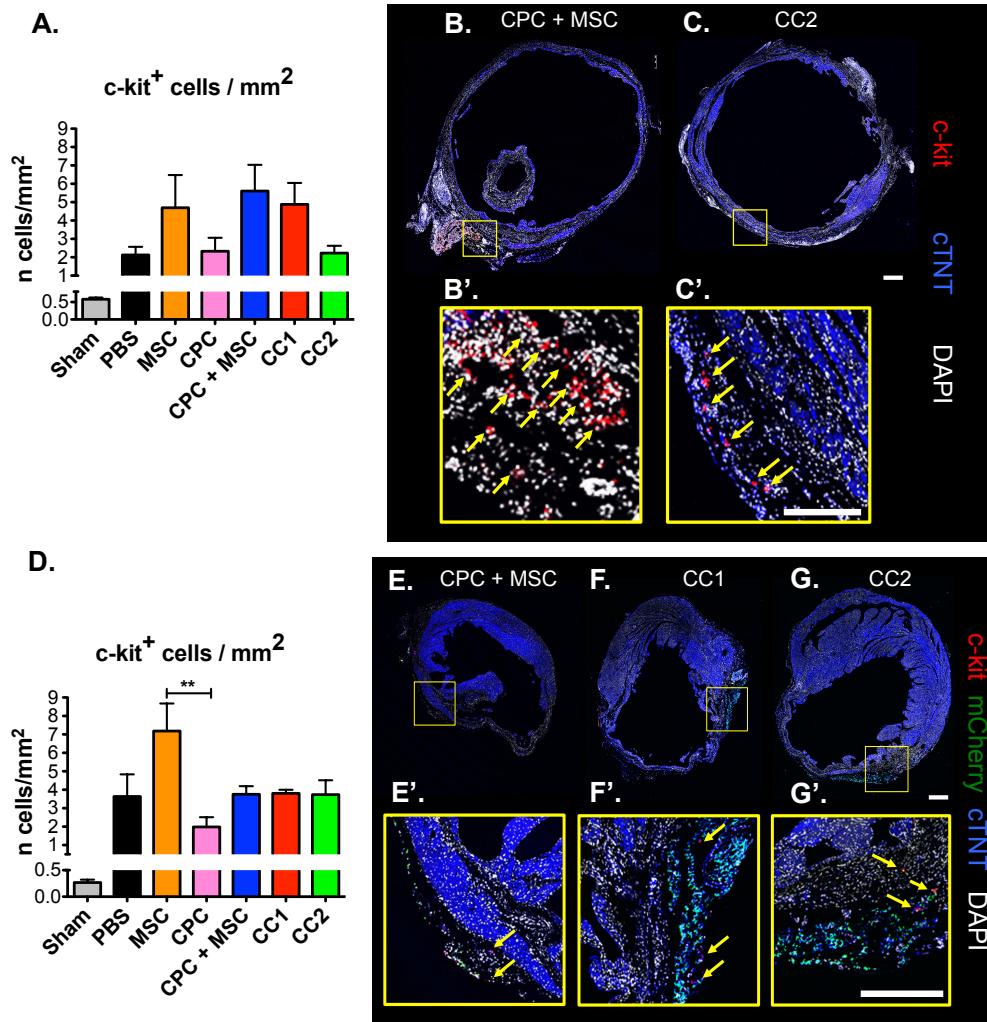


Figure 2.8: CardioChimeras have increased engraftment, expression of cardiomyogenic markers and support the increased presence of c-kit positive cells in the myocardium 12 weeks after damage.

(A) Number of c-kit⁺ cells represented as number of cells over the area of left ventricular free wall (mm²) in 4-week damaged hearts. Sample size of 3 mice per group. Representative whole heart scans of (B) CPC + MSC and (C) CC2 treated hearts to visualize c-kit⁺ cells (red). Scale bar is 100µm. (B') and (C') C-kit⁺ cells are identified by yellow arrows. Scale bar is 50µm. (D) Number of c-kit⁺ cells in 12-week damaged hearts. Sample size of 3 mice per group. Representative whole heart scans of (E) CPC + MSC, (F) CC1 and (G) CC2 treated hearts to visualize exogenous mcherry⁺ cells (green) and c-kit⁺ cells (red). Scale bar is 100µm. (E'), (F') and (G') C-kit⁺ cells are identified by yellow arrows. Scale bar is 100µm.

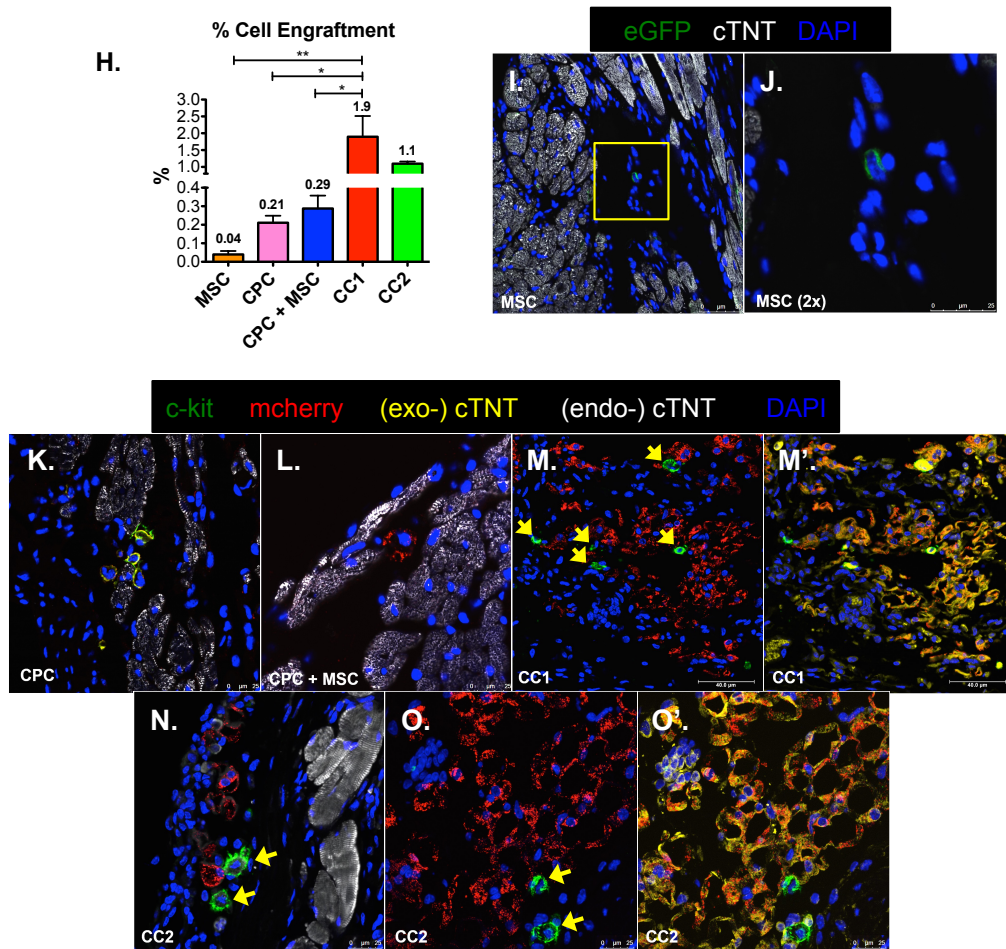


Figure 2.8: CardioChimeras have increased engraftment, expression of cardiomyogenic markers and support the increased presence of c-kit positive cells in the myocardium 12 weeks after damage, Continued.

(H) Cell engraftment efficiency (%). Sample size of 3 mice per group. (I) MSC detected by GFP protein staining at 12 weeks. (J) 2x zoom of MSC in the border zone area. (K) C-kit⁺/mcherry⁺ CPCs in the border zone area. (L) Mcherry⁺ CPC in CPC + MSC treated heart. (M) Mcherry⁺ CC1 visualized in the infarcted area surrounded by c-kit⁺ cells (green). (M') Overlay of cTNT (exogenous-cTNT, yellow) in CC1 mcherry labeled cells. (N) Mcherry⁺ CC2 visualized in the infarcted area surrounded by c-kit⁺ cells (green). (O) Mcherry⁺ CC2 (red) visualized in the infarcted area surrounded by c-kit⁺ cells (green). (O') Overlay of cTNT (exogenous-cTNT, yellow) in CC2 mcherry labeled cells. Endogenous-cTNT (white) labels existing cardiomyocytes. * p<0.05, ** p<0.01, *** p<0.001.

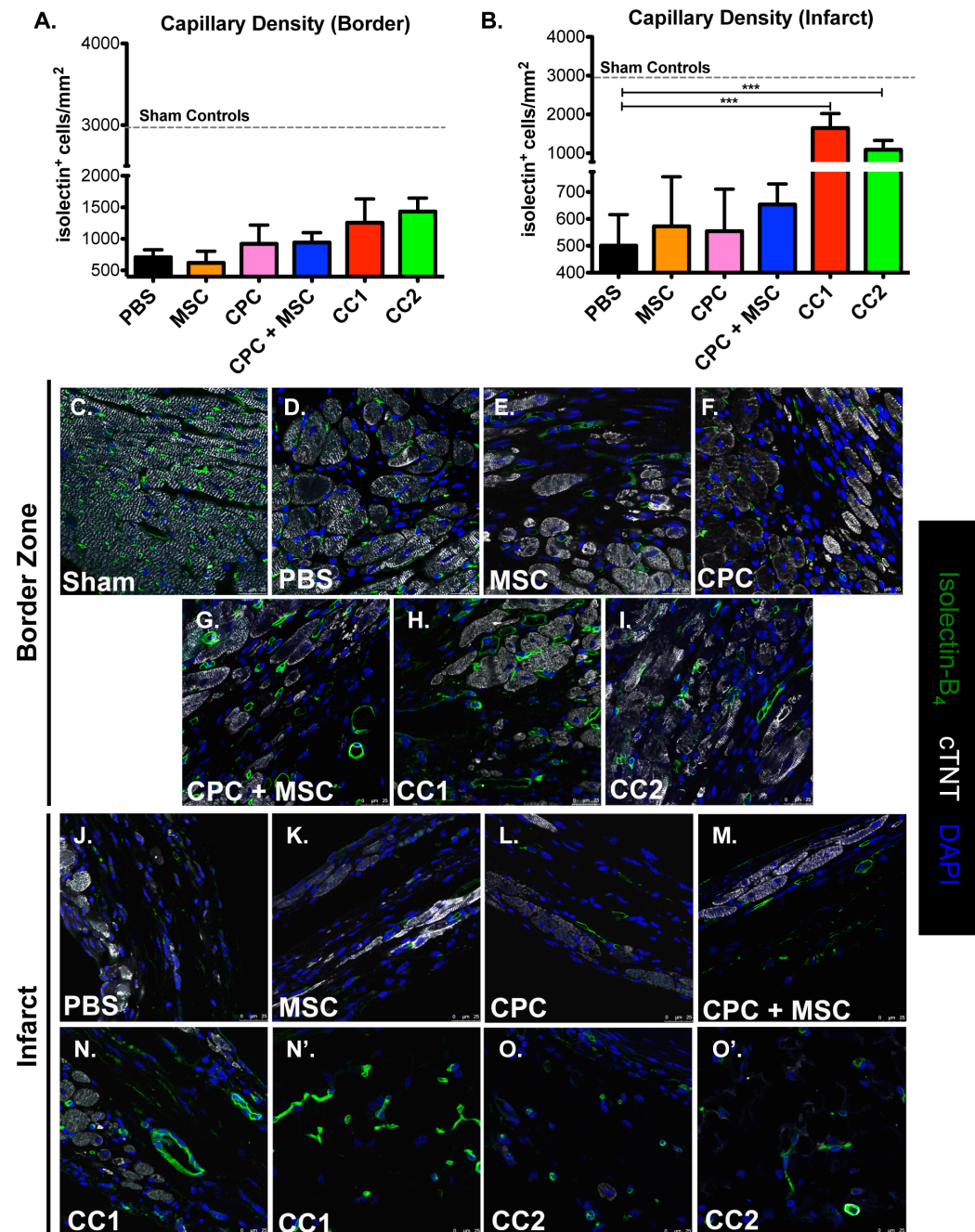


Figure 2.9: CardioChimeras increase capillary density in the infarct area.

(A) Capillary density in the border zone and (B) Infarcted heart regions. Sample sizes are 3-4 mice per group. Sham controls (dashed line) are represented as control for baseline density of isolectin⁺ structures per mm². (C-I) Representative border zone images to visualize isolectin⁺ structures. (J-O) Representative infarct zone images to visualize and quantitate isolectin⁺ structures. Green= Isolectin B₄, White=cardiac troponin T and Blue= DAPI to stain for nuclei. Scale bar is 25µm. * p<0.05, ** p<0.01, *** p<0.001.

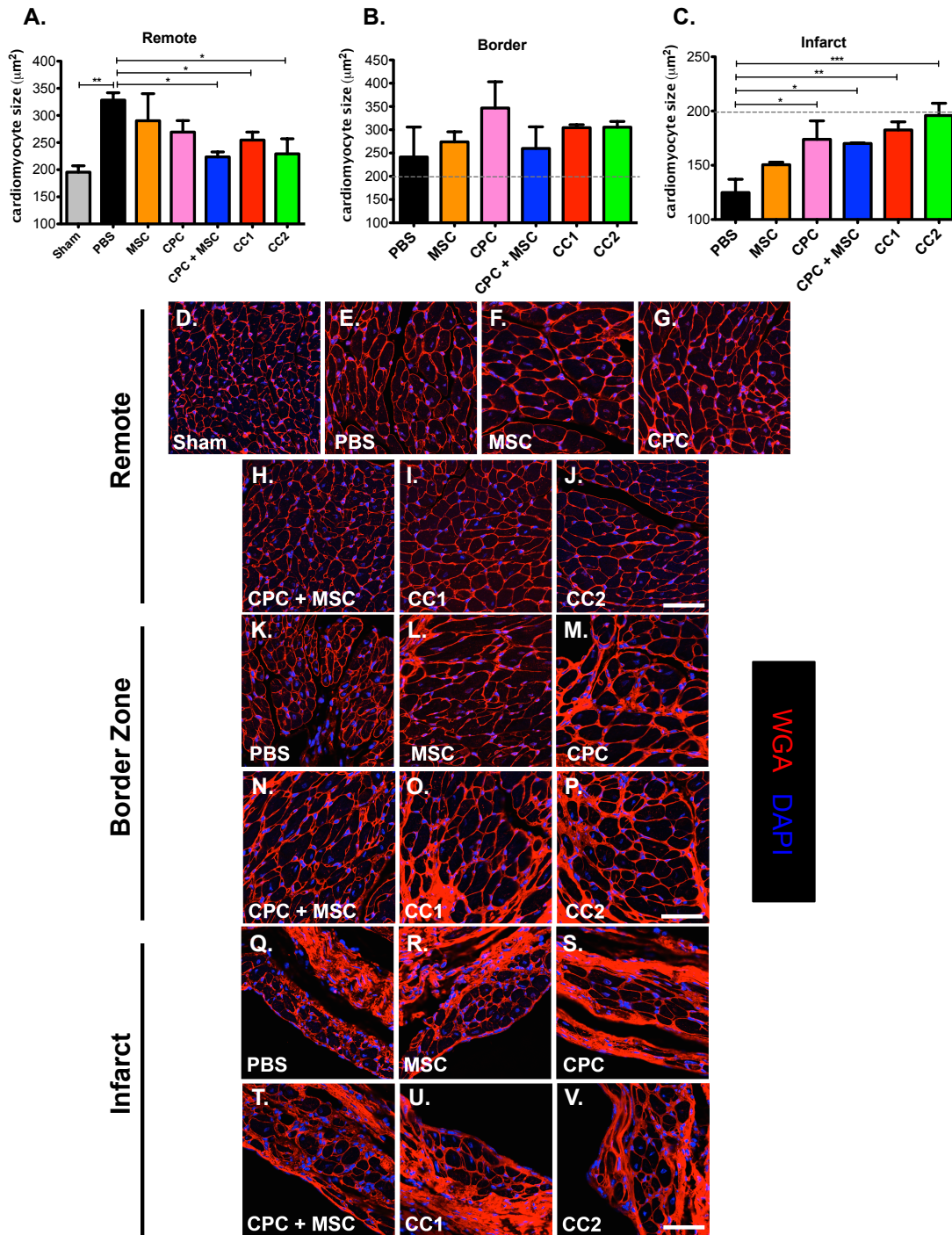


Figure 2.10: CPC, MSC and CardioChimera treatment normalizes cardiomyocyte size in the remote and infarcted regions.

(A) Mean cardiomyocyte size in the remote, (B) Border zone and (C) Infarct regions. Sample size is 3-4 mice per group. (D-J) Representative images of remote area cardiomyocyte size. (K-P) Representative images of border zone area cardiomyocytes. (Q-V) Representative images of infarct area cardiomyocytes. Red=Wheat germ agglutinin, White=cardiac troponin T and Blue=DAPI to stain for nuclei. Scale bar is 25μm. * p<0.05, ** p<0.01, *** p<0.001.

Table 2.1: Heart rate and echocardiographic data.

Echocardiographic data represented as mean ± SEM. Heart rate, anterior wall thickness, posterior wall thickness, left ventricular volume, ejection fraction and fractional shortening were measured at specified times after MI. (N) indicates the number of mice used in each group at the given time point.

WEEK	SHAM			PBS			CPC			MSC			CPC + MSC			CC1			CC2		
	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N
1	442.01	9.59	14.00	437.76	31.15	16.00	470.12	14.68	10.00	430.31	22.14	9.00	482.20	17.02	13.00	447.60	14.93	12.00	471.75	13.97	16.00
2	481.89	21.14	15.00	388.62	35.11	15.00	402.29	17.00	10.00	456.65	16.74	13.00	451.13	17.70	16.00	435.68	12.17	12.00	465.07	12.08	15.00
3	463.60	20.09	15.00	418.29	30.32	15.00	458.29	13.70	10.00	481.08	8.04	13.00	474.35	17.10	16.00	428.67	16.10	11.00	437.39	10.37	14.00
4	410.89	15.03	13.00	403.82	31.30	15.00	455.85	30.35	12.00	486.92	21.92	10.00	433.97	18.33	16.00	458.96	12.32	12.00	453.01	8.97	12.00
6	462.46	16.23	13.00	418.66	33.42	13.00	448.29	10.66	8.00	437.37	16.02	10.00	431.76	15.99	11.00	443.29	16.17	9.00	446.78	12.22	13.00
8	447.88	10.27	10.00	402.93	62.11	7.00	419.22	18.53	9.00	399.69	18.97	8.00	389.69	21.15	9.00	459.84	13.17	10.00	444.61	16.72	13.00
15	415.57	6.42	7.00	390.88	65.85	6.00	431.98	40.89	6.00	412.93	33.16	6.00	451.78	25.30	6.00	465.01	14.56	6.00	448.01	14.28	8.00
18	459.99	20.90	6.00	375.44	75.95	5.00	411.75	23.07	6.00	427.62	23.90	6.00	482.13	9.90	7.00	438.17	18.29	6.00	454.12	21.22	8.00

WEEK	SHAM			CPC			MSC			CPC + MSC			CC1			CC2			
	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	
1	1.52	0.07	0.61	0.94	0.62	0.10	0.77	0.11	0.65	0.59	1.01	0.10	1.01	0.10	1.01	0.10	1.01	0.10	
2	1.52	0.08	0.69	0.87	0.14	0.70	0.08	0.98	0.10	0.86	0.10	0.91	0.12	0.86	0.10	0.86	0.10	0.86	0.10
3	1.54	0.05	0.43	0.05	0.80	0.10	0.86	0.10	0.75	0.10	0.84	0.12	0.82	0.12	0.82	0.12	0.82	0.12	0.82
4	1.52	0.10	0.60	0.10	0.87	0.16	0.71	0.16	0.15	1.19	0.14	0.73	0.14	0.44	0.64	0.05	0.83	0.11	0.86
6	1.69	0.12	0.52	0.16	1.04	0.18	0.49	0.09	0.97	0.13	1.33	0.11	0.98	0.14	0.98	0.14	0.98	0.14	0.98
12	1.56	0.08	0.57	0.11	0.88	0.21	0.88	0.21	1.23	0.21	1.07	0.17	0.86	0.21	0.86	0.21	0.86	0.21	0.86
18	1.42	0.03	0.47	0.04	0.85	0.20	0.57	0.17	0.84	0.17	1.09	0.21	0.78	0.18	0.78	0.18	0.78	0.18	0.78

WEEK	SHAM			CPC			MSC			CPC + MSC			CC1			CC2		
	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N
1	1.40	0.08	0.70	0.68	0.64	0.07	0.73	0.07	0.71	0.07	0.65	0.04	0.75	0.07	0.65	0.04	0.75	0.07
2	1.55	0.07	0.83	0.06	0.64	0.10	0.61	0.05	0.72	0.06	0.87	0.07	0.82	0.09	0.82	0.09	0.82	0.09
3	1.54	0.05	0.61	0.09	0.52	0.08	0.72	0.10	0.53	0.08	0.64	0.05	0.74	0.10	0.74	0.10	0.74	0.10
4	1.24	0.05	0.61	0.09	0.52	0.08	0.72	0.10	0.53	0.08	0.64	0.05	0.74	0.10	0.74	0.10	0.74	0.10
6	1.43	0.05	0.50	0.06	0.81	0.07	0.82	0.07	0.85	0.12	0.88	0.09	0.70	0.11	0.88	0.09	0.70	0.11
12	1.52	0.07	0.49	0.06	0.45	0.06	0.40	0.04	0.54	0.08	0.61	0.08	0.75	0.11	0.75	0.11	0.75	0.11
18	1.38	0.12	0.40	0.08	0.81	0.07	0.80	0.13	0.82	0.08	0.89	0.10	0.87	0.13	0.87	0.13	0.87	0.13

WEEK	SHAM			CPC			MSC			CPC + MSC			CC1			CC2		
	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N
1	8.23	1.31	32.47	2.71	2.10	1.80	24.51	2.00	25.37	2.80	30.37	3.60	26.51	1.92	26.51	1.92	26.51	1.92
2	6.65	0.74	45.65	4.12	35.43	4.58	39.66	4.70	37.90	4.67	33.21	3.26	37.42	2.90	37.42	2.90	37.42	2.90
3	6.65	0.64	48.14	6.23	34.82	4.42	37.87	4.64	30.97	3.27	34.27	3.91	38.98	3.51	38.98	3.51	38.98	3.51
4	6.90	1.08	59.25	6.65	33.71	6.31	39.67	4.93	31.64	4.58	35.42	4.08	38.15	4.12	38.15	4.12	38.15	4.12
6	6.23	0.63	72.89	6.54	37.02	7.69	45.63	6.28	33.84	4.09	35.66	6.08	43.39	5.92	43.39	5.92	43.39	5.92
12	6.41	0.85	85.10	6.17	42.06	8.13	61.12	13.11	38.13	9.37	36.42	6.82	34.07	5.75	34.07	5.75	34.07	5.75
18	6.41	0.85	85.10	6.17	42.06	8.13	61.12	13.11	38.13	9.37	36.42	6.82	34.07	5.75	34.07	5.75	34.07	5.75

WEEK	SHAM			CPC			MSC			CPC + MSC			CC1			CC2		
	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N	MEAN	SEM	N
1	76.28	3.05	35.00	3.18	40.56	2.31	40.45	3.20	41.91	3.37	40.84	2.98	40.70	2.59	40.70	2.59	40.70	2.59
2	80.65	1.92	36.74	3.47	43.81	3.45	39.75	1.84	46.12	3.14	39.90	2.46	41.80	2.61	41.80	2.61	41.80	2.61
3	79.27	1.39	32.57	2.39	39.12	2.46	33.76	3.12	40.19	3.62	41.50	3.95	38.64	2.71	38.64	2.71	38.64	2.71
4	83.83	2.20	30.89	3.27	40.23	5.32	32.86	4.39	41.10	3.62	42.82	4.03	43.54	3.28	43.54	3.28	43.54	3.28
6	78.06	2.86	22.51	3.04	39.22	5.06	31.09	4.69	43.53	3.97	47.20	4.13	39.45	3.16	39.45	3.16	39.45	3.16
12	78.59	3.73	24.03	3.60	37.19	4.32	27.93	4.55	41.69	4.12	45.15	4.43	40.31	4.39	40.31	4.39	40.31	4.39
18	77.59	1.77	19.22	6.94	37.79	6.94	29.91	4.21	49.53	3.46	44.69	4.21	44.23	5.29	44.23	5.29	44.23	5.29

Chapter 2, in full, is prepared for submission. Cardiac Stem Cell Hybrids Enhance Myocardial Repair. Pearl Quijada, Hazel T. Salunga, Nirmala Hariharan, Jonathan Cubillo, Farid El-Sayed, Maryam Moshref, Kristin M. Bala, Jaqueline M. Emathingier, Andrea De La Torre, Lucia Ormachea, Roberto Alvarez Jr., Natalie A. Gude, and Mark A. Sussman. The dissertation author was the primary author and investigator on this manuscript.

CHAPTER 3

Characterization of Adult Stem cells with Altered DNA Content

INTRODUCTION

Physiological deterioration due to aging is coupled with the progression of cardiovascular disease. Myocardial aging is associated with reduced cardiac contractile and relaxation hemodynamics, metabolic dysfunction and cellular senescence¹⁴². Of the hallmarks of aging, stem cell exhaustion or a decline in stem cell regenerative capacity is particularly detrimental as resident c-kit⁺ cardiac progenitor cells (CPCs) give rise to cardiomyogenic structures during development and after damage^{73, 142}. In the era of cardiac cellular therapy, the ability to streamline the derivation of the most regenerative human adult stem is crucial. Isolation of youthful stem cells characterized by long telomeres and high telomerase activity is important for long-term maintenance of stem cell clonogenicity, self-renewal and differentiation¹⁴³⁻¹⁴⁶.

Growth properties of adult stem cells *ex vivo* are an important metric to predict endogenous cardiac repair. Patient recovery after infarction has been positively correlated with robust CPC proliferation¹⁴⁴. In addition, the cell surface receptor tyrosine kinase c-kit influences downstream signaling related to survival and proliferation in stem cells^{55, 115, 147, 148}. The heart contains a heterogeneous population of adult stem cells including resident mesenchymal stem cells (MSCs). MSCs from the heart are of pro-epicardial origin, express platelet derived growth factor- α (PDGF- α) and exhibit multipotency towards smooth muscle and endothelial lineages^{149, 150}. Although basic characteristics of

myocardial MSCs have been reported, the application of MSCs for cardiac therapy has not been investigated.

Diploid adult stem cells acquire tetraploidy after extended *in vitro* passaging leading to signs of cellular senescence and cell death¹⁵¹. Adipose derived MSCs frequently exhibit polyploidy in culture concurrent with increased p53 expression¹⁵². Chromosomal mosaicism or aneuploidy is reported in stem cells *in vivo*, yet chromosomal deletions or losses do not negatively effect stem cell properties such as self-renewal and/or differentiation¹⁵³. Aneuploidy is associated with extreme proliferative properties and decreased sensitivity to growth inhibitors¹⁵⁴. Recently, the stem cell field has highlighted the potential use of hybrids created through cell fusion as a potential therapeutic strategy to oppose cellular senescence and aging despite increased DNA content.

Cell fusion based nuclear reprogramming of somatic cells is a validated approach for production of pluripotent stem cells¹⁵⁵. Cross-species hybrids are utilized for ease in the identification of species-specific factors that aid in reprogramming¹⁴⁸. Identification of reprogramming factors after fusion between somatic fibroblasts and embryonic stem cells (ESCs) is accomplished with RNA sequencing (RNA-seq) of heterokaryons. Nuclear hybridization after fusion between human fibroblasts and immortalized mouse ESCs results in viable hybrids with enhanced survival and proliferation conferred by the ESC partner⁶¹. Related to our transplantation studies, electrofusion of MSCs with pancreatic islet cells improve β cell insulin release and cell survival compared to the co-injection non-fused β cells with MSCs in a diabetes mellitus mouse model¹⁵⁶.

Therefore, cell fusion may serve a novel therapeutic strategy to support the rejuvenation of somatic cells.

In this study we created a protocol to derive cross-species hybrids between mouse CPCs and human myocardial MSCs. CPCs were chosen due to enhanced proliferative properties and overall youthful cellular phenotype. Myocardial MSCs were utilized to further investigate paracrine-mediated secretion of stromal cells from the heart. Overall, we have identified an *ex vivo* strategy that allows for the successful propagation of mouse-human CardioChimeras. Furthermore, we have gained further understanding of the role ploidy plays in the regulation of stem cell characteristics and senescence.

METHODS

Stem cell isolation (mouse and human)

C-kit⁺ CPCs isolated from 3 month old male FVB mice hearts and CD90⁺/CD150⁺ MSCs were isolated from spontaneously aborted human fetuses and were cultured as previously described^{48, 54, 55}. Briefly, MSCs were isolated from whole fetal myocardial tissue, which was minced in small pieces and digested in collagenase (Worthington Bio Corporation) for 2 hours at 37°C. The cells were then passed through 100µm and 50µm filters (BD Biosciences), centrifuged at 1200rpm for 5 min and the pellet is incubated with c-kit labeled beads (Miltenyi Biotec,). The c-kit negative population was collected, washed once by centrifugation and cells were labeled with magnetic beads against CD90⁺/CD150⁺ (Miltenyi Biotec) and sorted according to manufacturer's protocol. MSCs were cultured in α-minimum essential media supplemented with 15% fetal bovine serum. Experiments with mCPCs and hMSCs were conducted between passages 10-20 and 4-10 respectively.

Lentivirus production

A third generation enhanced green fluorescent protein (eGFP) lentivirus with a phosphoglycerate kinase (PGK) and puromycin (puro) selection marker was purchased from Addgene (pLenti PGK GFP Puro (w509-5) was a gift from Eric Campeau, plasmid # 19070). pLenti PGK GFP Puro was used as a backbone to sub clone mcherry in the place of eGFP and bleomycin (bleo) to replace the puro gene in order to create pLenti PGK mcherry Bleo.

Stem cell transduction with lentivirus

Human MSCs at passage 6 were lentivirally transduced with pLenti PGK GFP Puro at a multiplicity of infection (MOI) of 10 and maintained in puromycin supplemented MSC media for one week starting at 48 hours post-infection. CPCs at passage 10 were lentivirally transduced with pLenti PGK mcherry Bleo at a MOI of 10 and subjected to fluorescent activated cell sorting (FACS) to purify mcherry positive CPCs. Fluorescent protein expression in MSCs and CPCs (CPC-mcherry) was confirmed by fluorescent microscopy and flow cytometric analysis.

Cell fusion and creation of cross-species CardioChimeras

Cell fusion was conducted using the GenomONE™ CF EX Sendai virus (Hemagglutinating Virus of Japan or HVJ) Envelope Cell Fusion Kit (Cosmo Bio. USA). According to the manufacturer's protocol, we subjected MSCs and CPCs to the suspension method. Here, human MSC labeled with GFP were mixed with mouse CPC labeled with mcherry at ratio of 3:1 and suspended in 20µL of cell fusion buffer and 10µL of Sendai virus and placed on ice for 5 minutes for absorption of the virus on the cell membrane. To induce cell fusion, cells were placed at 37°C for a total of 15 minutes. Cells were suspended in cell fusion media consisting of Hams F12 (Fisher Scientific), 15% FBS, 1% PSG, 5mU/mL human erythropoietin (Sigma Aldrich), 10ng/mL basic fibroblast growth factor (Peprotech) 0.2mM L-Glutathione (Sigma Aldrich), 10ng/mL leukocyte inhibitory factor (LIF) and 10ng/mL interleukin-6 (IL-6). The next day, media was changed,

and within 48 hours cells were trypsinized and subjected to fluorescence activated cell sorting (FACS) to purify GFP and mcherry double positive cells as a population. Once the population expanded, the cells were subjected to puromycin and bleocin selection for one week to remove single positive stem cells. The population was then subjected to a second round of FACS to purify GFP and mcherry double positive cells and placed as a single cell per well of a 96 well microplate and allowed to undergo clonal expansion. 12 double positive clones expanded from single cell sorted were confirmed by secondary flow cytometric analysis.

Cell proliferation assay

Cell proliferation was determined using the CyQuant Direct Cell Proliferation Assay (Life Technologies) according the manufacturer's instruction and as previously described¹¹⁵.

Cell death assay

Stem cells were plated in a 6-well dish (80,000 cells per well) and incubated in starvation media (growth factor and FBS depleted media) with 1% PSG for 18 hours. The cells were then treated with either 40 μ M or 80 μ M hydrogen peroxide for 4 hours. Cells were resuspended with TO-PRO-3 iodide to label for dead cells. Data was acquired on a FACS Canto (BD Biosciences) and analyzed with FACS Diva software (BD Biosciences). Cell death was quantitated by measurement of TO-PRO-3 positive cells and represented as a percentage of the entire population.

G-band karyotype analysis

Karyotype analysis was carried in cultured cells during the growth phase of cells. G-banding reports were performed by Cell Line Genetics, Inc. Chromosome analysis was measured in at least 20 cells per cell line.

Immunoblotting

Protein lysates from cultured cells were prepared as previously described¹¹⁵. All protein samples for western blot analysis were separated on a 4%–12% Bis-Tris mini-gel (Life Technologies) and transferred to a polyvinylidene difluoride membrane. Membranes were blocked for 1 hour with 10% milk in TBST (1% Tris-buffered saline/0.1% Tween) and then probed with primary antibody overnight in milk. Next day blots were washed with TBST buffer and incubated in secondary antibodies in milk for 1.5 hours. Primary antibodies for western blot are as follows: mouse anti GAPDH (1:1000, Millipore); goat anti HP1 γ (1:200, Santa Cruz Bio.).

Immunocytochemistry

Stem cells were placed at a density of 7,000 cells per well of a two-chamber permanox slide and stained according to previous studies⁵³. Before scanning, cells were washed in PBS containing DAPI (Sigma Aldrich) to stain for nuclei. Slides were visualized using a Leica TCS SP8 confocal microscope. Primary antibodies are as follows: rat anti-mcherry (1:100, Life Technologies); rabbit anti-GFP (1:100, Life Technologies); goat anti-GFP (1:100, Rockland); rabbit anti-tubulin (1:40, Sigma Aldrich); goat-anti-c-kit (1:40, mouse specific,

R&D Systems); goat anti-c-kit (1:40, human specific, R&D); mouse anti-cardiac troponin T (1:40, Abcam); mouse anti-smooth muscle actin (1:40, Sigma Aldrich); mouse anti p16 (clone F9) (1:10, Santa Cruz Bio.); rabbit anti p53 (1:40, Abcam).

RESULTS

Analysis of ploidy in adult stem cells from mouse and human origin

Mouse c-kit⁺ CPCs are abnormal tetraploid (4N), whereas myocardial human stem cells are diploid (2N) as confirmed by G-band karyotyping (Figure 3.1A and 3.1B). Bone marrow derived c-kit⁺ cells (BMCs) are euploid based on karyotype reports (Figure 3.1C). Non-transformed tetraploid cells which fail to undergo cell division exhibit signs of phenotypic and molecular senescence¹⁵⁷. Therefore, we were interested in evaluating the proliferation and expression of senescent makers in 2N and 4N cells. C-kit⁺ BMCs have slower proliferative capabilities relative to mono-nucleated 4N CPCs (Figure 3.1D). Low passage BMCs are p16 and p53 negative (Figure 3.1E), proteins that are involved in cell cycle inhibition and senescence associated cell death¹¹⁵. Mouse CPCs express p16 during normal growth conditions (Figure 3.1F). Additionally, 4N and 6N cells express high levels of p53 based on immunoblot analysis, while 2N BMCs express low levels of p53 (Figure 3.1G). Heterochromatin protein 1 (HP1 γ) is involved in chromatin regulation and transcriptional silencing by association with heterochromatin complexes¹⁵⁸. HP1 γ is highly expressed in 4N and 6N cell lines indicating that increased ploidy is correlated with suppression of transcription (Figure 3.1G).

Phenotypic properties of cross-species CardioChimeras

Mouse CPCs labeled with mcherry fluorescence and human MSCs labeled with GFP fluorescence were incubated at a ratio of 1:3 before fusion with

an inactivated RNA sendai virus. Cross-species hybrids were purified by these successive steps: 1) population sort by FACS 2) puromycin (puro) and bleocin (bleo) antibiotic treatments in culture and 3) clonal expansion after FACS single cell sorting (Figure 3.2A). 12 clones were confirmed to co-express mcherry and GFP based on flow cytometric analysis (Figure 3.2A). Of the 12 clones, two mouse and human CardioChimeras (MH-CCs) were characterized for properties of proliferation, cell survival and expression of stem and differentiation markers relative to the parental cell lines. MH-CCs were confirmed to express mcherry and GFP from mouse CPC and human CPC parents (Figure 3.2B and 3.2C). Clones are mono-nucleated indicating that cells underwent nuclear hybridization after fusion (Figure 3.2C). MH CCs exhibit a modest increase in proliferation relative to human MSCs (Figure 3.2D). Furthermore, cell survival between MH-CCs was comparable (blue) or slightly elevated (purple) relative to the parent cells during serum free and hydrogen peroxide conditions (Figure 3.2E).

Mouse/Human CardioChimeras have increased expression of mature cardiomyogenic markers and reduced c-kit expression

CPCs express c-kit *in vitro* and *in vivo*⁷⁴ and do not express mature markers such as cardiac troponin T (cTNT) during basal growth conditions (Figure 3.3A and 3.2B). Human derived MSCs are c-kit and cTNT negative (Figure 3.3D). However, both mouse CPCs and human MSCs express high levels of α -smooth muscle actin (α -SMA) (Figure 3.3C and 3.3D). MH-CC expresses low levels of c-kit using a mouse specific c-kit antibody (Figure 3.2E)

and express cTNT (Figure 3.2F). MH-CCs are uniformly α -SMA positive similar to parental cell lines (Figure 3.3G).

DISCUSSION

Myocardial CPCs and MSCs contribute to the heart during development and human cardiac disease^{73, 150}. In order to make advanced use of the distinct mechanistic properties of CPCs to directly contribute to regeneration and MSCs to provide for paracrine secretion we turned to the technique of cell fusion to create stem cells hybrids or CardioChimeras. We utilized two distinct stem cell types derived from different species allowing for use of species-specific reagents to better understand the basic phenotypic and molecular characterization of resulting CardioChimeras. Mouse CPCs in combination with human myocardial MSCs were used to create cross-species CCs, which undergo nuclear hybridization and exhibit distinct proliferative and survival properties (Figure 3.2 and 3.3).

Initial analysis of chromosome number in our stem cells revealed c-kit⁺ BMCs are 2N and c-kit⁺ CPCs are 4N confirmed by karyotyping although cells were derived from the same mouse strain (FVB/NJ) (Figure 3.1A and 3.1C). Long-term passaging of HSCs show decreased telomerase activity leading to genomic instability and cellular senescence¹⁵⁹. Furthermore, up regulation of p53 and p16 in polyploid cells is a reported mechanism to induce cell cycle arrest^{115, 152}. Tetraploid complementation, or the combination of a tetraploid embryo with a diploid embryo, results in a fetus that comes to term as tetraploid cells are confined to the extraembryonic tissue and removed by p53-mediated apoptosis¹⁶⁰. It is possible that the clearance of tetraploid cells from the embryo is incomplete leaving behind aneuploid cells with tissue specific residency in the

adult mouse. Currently, the source of 4N c-kit⁺ CPCs is not known and/or if this is an artifact of extended culture, but future investigations are currently underway to determine if 4N cells exist in the intact heart.

Mono-nucleated tetraploidy is a hallmark of cancer stem cells, which bypass G1 and G2/M cell cycle check points leading to a transformed cellular phenotype¹⁵⁴. Adult human CPCs from the myocardium have been shown to undergo replicative senescence as early as passage 15 out of the heart⁵⁵. In contrast, mouse CPCs display an indefinite replicative potential while expressing high levels of p53 (Figure 3.D, 3.F, 3.G), yet CPCs still possess the ability to undergo cardiomyogenic commitment⁴⁸. In our laboratory, mouse CPC senescence is induced after down regulation of stem cell maintenance protein nucleostemin as evidenced by senescence associated β -galactosidase staining and bi-nucleated cell cycle arrest¹¹⁵. Recent reports suggest that replicative and oxidative stresses are strong agents for increasing genomic instability and aneuploidy in proliferative cell types^{161, 162}. Future studies will investigate the relation of ploidy and senescence in c-kit⁺ CPCs, which may facilitate our understanding of stem cell exhaustion associated with cardiac aging.

Fusion between two human derived stem cells has been attempted, but nuclear hybridization was not observed. We posit that creation of heterokaryons between two human cells may up regulate p53 and inhibit nuclear fusion. Although observed at a low frequency, fusion of mouse CPCs to human MSCs yielded hybrids with optimal proliferative properties (Figure 3.2D). Interestingly, MH CCs express c-kit and retain expression of smooth muscle markers while up

regulating cTNT (Figure 3.3E and 3.3G). Aneuploidy is observed in MSCs undergoing osteogenic differentiation¹⁶³. Furthermore, aneuploidy is observed in induced pluripotent stem cells, which retain properties of ESCs such as alkaline phosphatase expression and pluripotency¹⁶⁴.

Our initial cell fusion approach focused on the functions of mouse derived stem cell hybrids in Chapter 2, yet this technology can be applied for the creation of cross-species and human-to-human hybrids. Fusions between two different species facilitates our understanding of novel expression patterns, enabling production of critical factors that define stem cells for commitment, paracrine secretion or both. The inability of human adult stem cells to accomplish high impact restoration of myocardial structure and function continues to frustrate and impede progress in the regenerative medicine field because of limited inherent properties of the stem cell types employed. Hybrids are an attractive and provocative novel method for developing innovative paracrine-based and genetically linked cellular properties that will enhance efficacious actions of a single cell population preceding adoptive transfer to the injured myocardium. The ultimate goal of cardiac stem cell hybrids therapy is to empower the adult stem cell with multiple properties in order to blunt myocardial scar formation, stimulate endogenous regeneration and survival and repopulate the damaged myocardium with new cardiomyogenic cells and structures. Genetic modification of stem cells through cell fusion creates hybrids that have never existed in nature but can be formulated as a superior regenerative tool.

SUMMARY POINTS

- Stem cells for cardiac therapy display differences in DNA content, which may affect cellular properties such as cell division and cellular senescence.
- Cell fusion followed by nuclear hybridization is feasible between stem cells derived from different species.
- Mouse and human CardioChimeras exhibit proliferative capabilities comparable to human MSCs.
- Mouse and human CardioChimera clones exhibit variability in survival, which may be dependent on genomic stability after nuclear hybridization.
- Mouse and human CardioChimeras down regulate expression of c-kit and up regulate expression of cardiomyogenic markers.

FIGURES

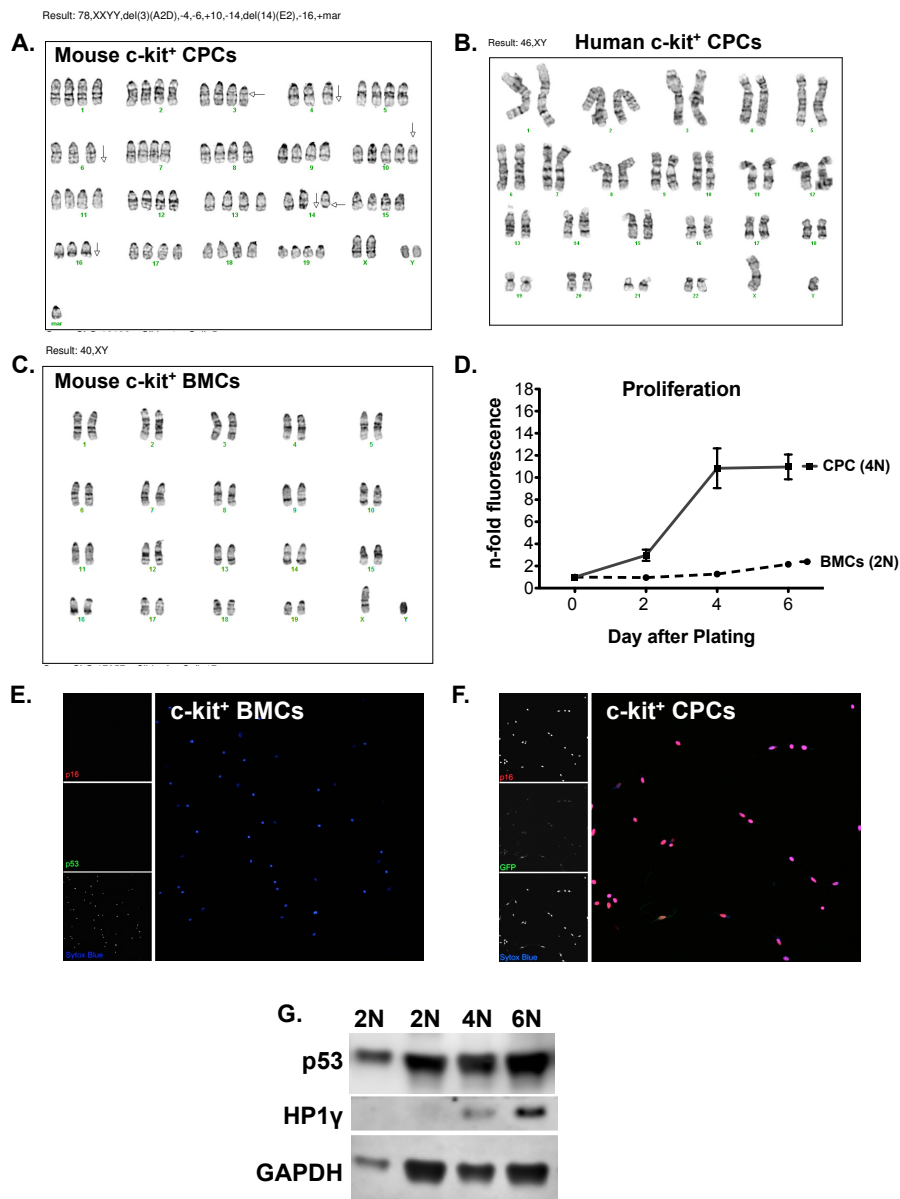


Figure 3.1: Analysis of ploidy in stem cells from mouse and human origin.

(A) Karyotype report of c-kit⁺ CPCs from mouse cardiac origin. Cells were characterized as abnormal tetraploidy with loss and deletion of chromosomes across all chromosomes. Cell line is derived from male FVB/NJ. (B) Karyotype report of human c-kit⁺ CPCs derived from a male fetal heart. (C) Karyotype report of c-kit⁺ bone marrow cells derived from mouse bone marrow. Cell line is derived from male FVB/NJ. (D) Proliferation of mouse diploid (2N) BMCs and tetraploid (4N) CPCs based on fluorescent based assay to stain for nucleic acid. (E) Expression of p16 and p53 in mouse BMCs. (F) Expression of p16 and GFP in mouse CPCs. Prior to immunocytochemical analysis of cells, CPCs were transduced with a p16-GFP reporter plasmid. (G) Expression of senescent protein p53 and heterochromatin marker HP1 γ in 2N and 4N mouse cell lines.

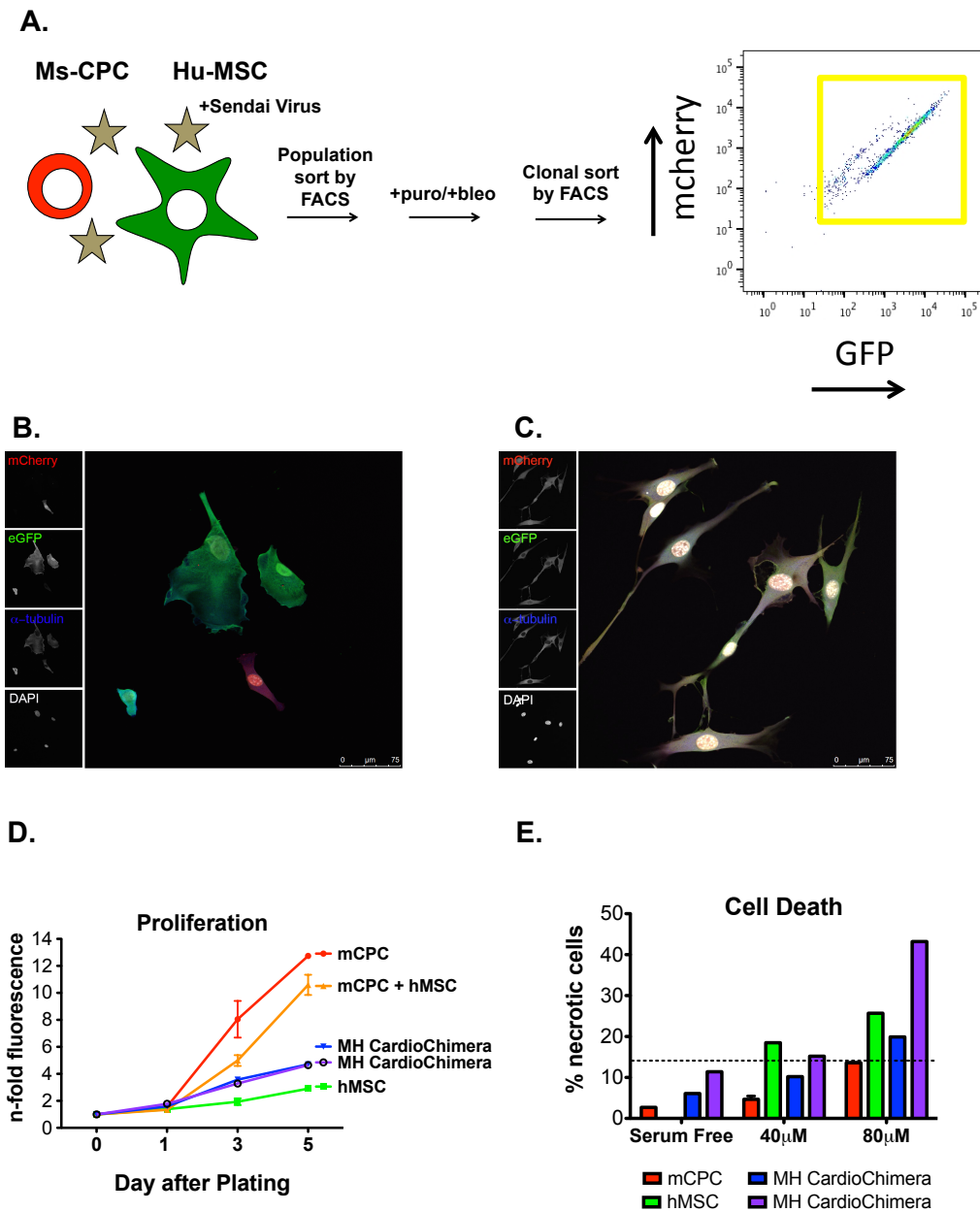


Figure 3.2: Phenotypic properties of cross-species CardioChimeras.

(A) Schematic representation of the fusion protocol to derive hybrids between mouse CPCs (Ms-CPC) and human (Hu-MSC). An initial population sort followed by a clonal sort selected for stable Mouse-Human CardioChimeras, which expressed mcherry and GFP from parental cell lines. (B) Non-fused mixed parental cell lines. Human MSCs express GFP and mouse CPCs express mcherry. (C) Representative Mouse-Human CardioChimera expresses both GFP and mcherry. (D) Proliferation of parental cells, individual or combined and two representative CardioChimeras based on fold change in fluorescence using a nucleic acid stain. (E) Cell death assay in parental cells compared to Mouse-Human CardioChimeras. Cell death was measured by percentage of TO-PRO-3 iodide positive cells. DAPI staining is used to visualize nuclei. Scale bar is 75µm.

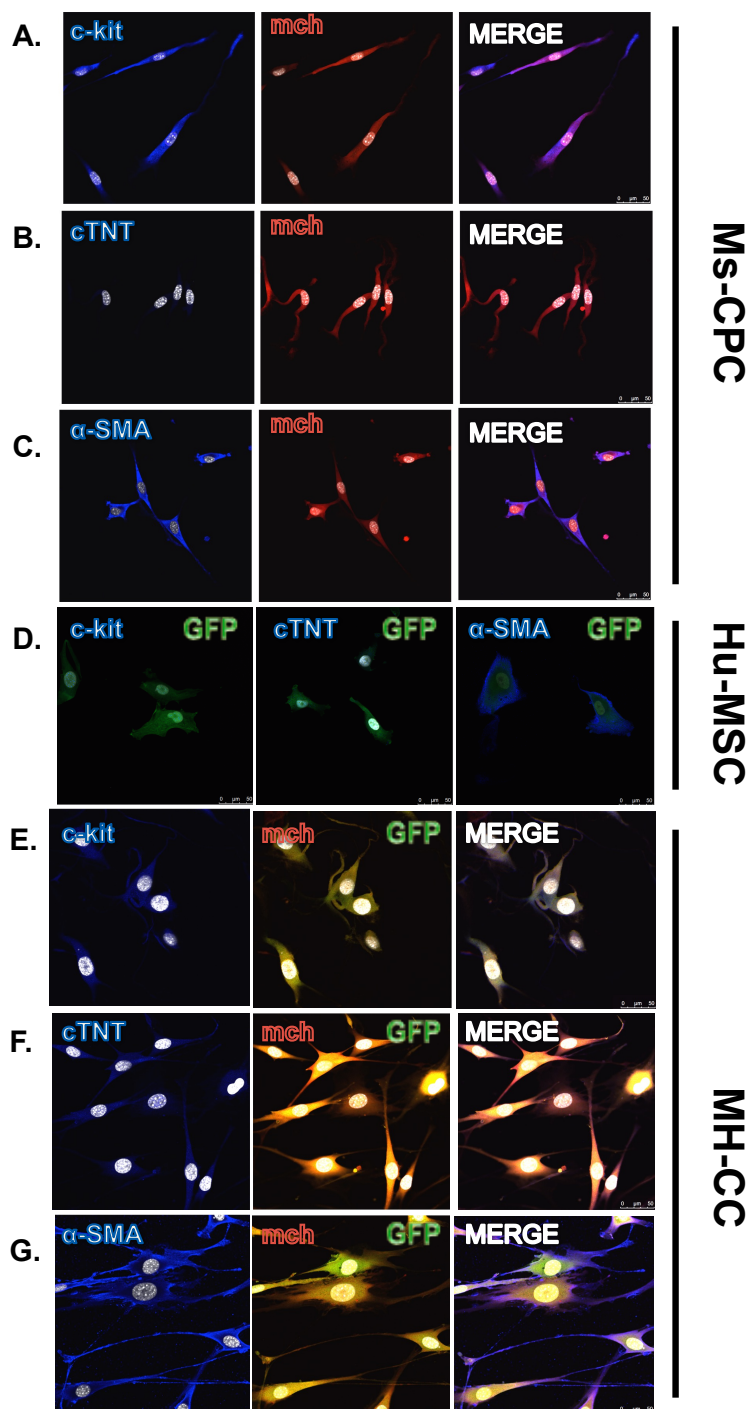


Figure 3.3: Mouse-Human CardioChimeras have increased expression of mature cardiomyogenic markers and reduced c-kit expression.

(A-C) Expression of (A) c-kit, (B) cTNT and (C) α -SMA in mouse CPCs, which co-express mcherry. (D) Expression of c-kit, cTNT and α -SMA in human MSCs, which co-express GFP. (E-G) Expression of (E) c-kit, (F) cTNT and (G) α -SMA in mouse-human CardioChimeras, which co-express mcherry and GFP. MERGED images are combination of left and center panels. Scale bar is 75 μ m.

Chapter 3 is presented in this dissertation as an extension of Chapter 2 to support the creation CardioChimeras between human derived stem cell lines. I would like to acknowledge Megan Monsanto for the isolation of fetal adult stem cells, Sarmistha Ganguly for her part in creating CardioChimeras between mouse and human adult stem cells and Michael McGregor for his studies identifying senescence markers in stem cells.

CONCLUSION OF THE DISSERTATION

The inability of cardiomyocytes to self-renew after myocardial damage has sparked extensive research into the underlying mechanisms that influence cardiomyocyte cell cycle entry and/or stimulation of endogenous stem cells to promote cardiac repair. Non-mammalian vertebrates such as the newt and the zebrafish display a remarkable ability to regenerate damaged hearts through cardiomyocyte de-differentiation and/or proliferation^{165, 166}. The early postnatal mouse heart displays a similar ability to regenerate damaged heart regions, although this capacity is diminished a few days after birth⁷. Recently, there has been a surge of studies utilizing the neonatal mouse to understand the molecular and physiological factors that limit cardiomyocyte replacement observed in the adult heart^{7, 167}. Coincident with decreased cardiomyocyte regeneration is an increase in the bi-nucleation of cardiomyocytes with age. Bi-nucleation occurs in 15% of cardiomyocytes identified in a toddler and is increased by 4-fold in young adults¹⁶⁸. Additionally, robust neonatal heart regeneration is facilitated by a surge in hormones during adolescent years, the lack of a mature immune system and/or increased exposure to hypoxia, which are all physiological responses that stabilize or diminish with age¹⁶⁹⁻¹⁷¹. Although cardiomyocytes show limited capacity for regeneration, adult resident cardiac stem cells show promise in the development of nascent cardiomyogenic structures⁷³. Therefore, the theme of this dissertation is to investigate novel techniques such as genetic modification and cell fusion of adult stem cells to enhance stem cell cardioprotective abilities.

In the past decade, defining the optimal stem cell types for cardiac-based cellular therapy is becoming increasingly difficult, as there has been a rush in the

discovery of distinct stem cells. One strategy to enhance stem cell function and phenotypic youthfulness is by analysis of proteins that confer survival and cardiomyogenic commitment. Chapter 1 of this dissertation focused on defining proteins that promote differentiation of cardiac progenitor cells (CPCs). Regulation of calcium is required for proper cardiomyocyte contractility, but the role of Calcium Calmodulin Kinases (CaMKs) in stem cells derived from the myocardium has not been addressed. CaMKs contributes to cardiomyocyte development and growth, while nuclear-targeted CaMKs have been implicated in the regulation of gene transcription through HDAC signaling⁸³. In adult myocytes, increases in cytosolic CaMKII δ lead to decreased cardiomyocyte function, pathological hypertrophy and heart failure¹⁷². Conversely, nuclear CaMKII δ (B isoform) increases cellular growth through activation of myocyte enhancing factor 2 (MEF2), contributes to cellular protection by regulation of transcription factor GATA4, and promotes cell lineage commitment^{83, 87, 93}. In conclusion, this study identified a significant role of CaMKII δ B to promote cell specific lineage commitment and survival of CPCs, increasing the potential impact of these cells for cardiac therapy.

In Chapter 2 of this dissertation, we believe this study is highly significant and is the first report utilizing a novel application of cell fusion to create adult stem cell hybrids between cardiac progenitor and bone marrow derived mesenchymal stem cells (MSCs) for mitigation of myocardial injury. Moreover, we believe that this study increases our understanding of the positive impact of combinatorial cell delivery of CPCs with MSCs into the infarcted heart. Although

CPCs are valued for cardiomyogenic potential, the low persistence rates of MSCs prevent paracrine mediated endogenous reparations after damage. In this study we created CardioChimeras in order to ensure the long-term persistence of MSCs coupled with CPCs. CardioChimeras conferred significant improvements in anterior wall thickness and ejection fraction 18 weeks after adoptive transfer. Improvements in myocardial structure and function can be attributed to increased CardioChimera engraftment, which provides for stabilization of microvasculature and preserves cardiomyocyte size in the infarcted area not observed in CPC and MSC dual cell injected hearts. We believe that this report would be of interest to researchers in the field of stem cells as identification of novel strategies to enhance stem cell therapy continues to be an intense area of focus. Additionally, this study supports the application of cell fusion to create hybrid stem cell populations that combine optimal characteristics for directing cardiomyogenesis and protective paracrine secretion in a single cell type.

Application of CardioChimeras, a fused combinatorial cell delivery approach, provides for unique cell variability that is not unlike the inherent cell heterogeneity observed in tissue^{173, 174}. In the bone marrow niche, hematopoietic stem cells undergo cellular fusion creating genetic variation without compromising mitotic ability or clonogenicity of stem cells¹⁷⁵. Mosaic aneuploidy, or abnormal chromosome number, is observed in the inner cell mass and neural progenitor cells, a well known characteristic of stem cells that leads to somatic variation in several tissue types^{128, 153}. Overall, these reports support the existence of chromosomal heterogeneity in stem cell populations, yet the

contribution of hybrids as a cell therapeutic geared towards cardiac tissue regeneration has only started to become of interest.

The heart and bone marrow are common sources of clinically relevant and heterogeneous adult stem cells. Therefore, it was no surprise that isolated cells from these tissues not only exhibit phenotypic variability but also chromosomal heterogeneity. Although, our studies could not identify the main mechanism of increased cellular ploidy in mouse CPCs relative to human CPCs, this topic is certainly a topic of several projects in the laboratory. The liver, which has a large number of tetraploid cells, much like what is observed in the heart, is further increased with telomere dysfunction leading to polyploidization¹⁶². Cardiomyocytes, which are primarily bi-nucleated tetraploid, have been reported to undergo a process of dedifferentiation a mechanism of cardiomyocyte remodeling¹⁷⁶. Dedifferentiation of cardiomyocytes yields progenitor cells that re-express c-kit and are morphologically similar to progenitor cells with cardiomyogenic potential¹⁷⁷. Although, cardiomyocyte dedifferentiation during homeostatic conditions is quite low, it is possible that this process promoted the residency of 4N CPCs derived from young adult mice. Furthermore, laboratory mice such as the FVB/NJ and C57/Bl6, which are subjected to long-term inbreeding exhibit unusually long telomeres (30-120kb), whereas the average human telomere length is 8-12kb¹⁷⁸. Indicating that there can be certain issues with the use universal mouse strains that exhibit dysfunctions in the telomere/telomerase axis, which is known to contribute to altered DNA content.

From this point, the stem cell field should have better understanding of the cell biology of stem cells beyond focusing on presumed actions to mediate cardiac repair. Herein, two novel approaches are described that may improve the use of existing single cell or combinatorial delivery approaches through the use of 1) CaMKII δ B over expression in CPCs to promote cardiomyogenic commitment and survival and 2) CardioChimeras to compel communication between two chosen stem cell types resulting in a hybrid with blended phenotypic traits and genetic material derived from the individual parental cell lines. The field of cellular therapy will benefit from more “outside the box” thinking and approaches to more effectively take advantage of the unique traits of adult stem cells for the advancement of cardiac regeneration.

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