

Myeloid IL4R α In Cardiovascular Remodeling

by

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To everyone who has helped me and everyone who loves me

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LIST OF ABBREVIATIONS

AAM/M2	alternative activated macrophage
ACE	angiotensin-converting enzyme
AHA	American heart association
ALK1	activin receptor-like kinase
AngII	angiotensin II
ANP	atrial natriuretic peptide
Arg1	arginase 1
BMDM	bone marrow derived macrophages
BME	Eagle's basal medium
BMP9	bone morphogenetic protein 9
BNP	brain natriuretic peptide
C/EBP β	ccaat-enhancer-binding protein β
CAM/M1	classical activated macrophage
CCL11	C-C motif chemokine ligand 11
CCL17	C-C motif chemokine ligand 17
CCR2	C-C motif chemokine receptor type 2
CD11b	cluster of differentiation molecule 11b
CD14	cluster of differentiation 14
CD16	cluster of differentiation 16
CD206	mannose receptor C type 1 (MRC1)
CD3	cluster of differentiation 3
CD301	macrophage galactose-type C-type lectin
CD31	platelet endothelial cell adhesion molecule
CD45	cluster of differentiation 45
Col1A1	collagen type 1 α 1
Col3A1	collagen 3A1
CSA	cross-sectional area
CVD	cardiovascular disease
DALY	disability-adjusted life year

DAMP	damage associated molecular pattern
DOCA	deoxycorticosterone acetate
DTI	Doppler tissue imaging
DTR	diphtheria toxin receptor
EC	endothelial cells
ECM	extracellular matrix
EDTA	ethylenediaminetetraacetic acid
F13A1	coagulation factor XIII A1
F4/80	EGF-like module-containing mucin-like hormone receptor-like 1
FBS	fetal bovine serum
FC	floxed controls
Gal3	galectin-3
Grb2	growth factor receptor-bound protein 2
H&E	hematoxylin and eosin
HF	heart failure
HFpEF	heart failure with preserved ejection fraction
HFrEF	heart failure with reduced ejection fraction
HIF1	hypoxia-inducible factor 1
HSC	hematopoietic stem cell
HSPC	hematopoietic stem and progenitor cell
HW/BW	heart weight to body weight ratio
HW/TL	heart weight to tibia length ratio
ID1	inhibitor of DNA binding 1
ID2	inhibitor of DNA binding 2
iDTR	Cre-inducible DTR
IFN γ	interferon γ
IgE	immunoglobulin E
IL-10	interleukin-10
IL-12	interleukin-12
IL-13	interleukin-13
IL-15	interleukin-15
IL-1Ra	interleukin 1 receptor antagonist
IL-1 β	interleukin-1 β
IL-2	interleukin-2
IL-4	interleukin-4

IL-6	interleukin-6
IL-7	interleukin-7
IL-9	interleukin-9
IL13R α 1	IL-13 receptor α 1
IL13R α 2	IL-13 receptor α 2
IL4R	interleukin-4 receptor
IL4R α	interleukin-4 receptor α
IRS	insulin receptor substrate
JAK	Janus kinase
JAK1	Janus kinase 1
JAK3	Janus kinase 3
LAD	left anterior descending coronary artery
LPS	lipopolysaccharide
LV	left ventricle
LVID	left ventricle internal diameter
Ly6C	lymphocyte antigen 6 complex
Ly6G	lymphocyte antigen 6 complex locus G6D
LysM	lysozyme M
MAPK	mitogen-activated protein kinase
MCP1/CCL2	monocyte chemoattractant protein1/C-C motif chemokine ligand 2
MDP	macrophage and dendritic cell progenitor
MI	myocardial infarction
MMP	matrix metalloproteinase
MRC1/CD206	mannose receptor C type 1
MRP8	myeloid-related protein 8
MyIL4R α KO	myeloid-specific IL4R α knockout
NADPH	nicotinamide adenine dinucleotide phosphate
NF κ B	nuclear factor κ B
NK cell	natural killer cell
Nox1	NADPH oxidase 1
Nox4	NADPH oxidase 4
p22phox	neutrophil cytochrome b light chain (CYBA)
p47phox	neutrophil cytosolic factor 1 (NCF1)
PAI-1	plasminogen activator inhibitor-1
PBS	phosphate-buffered saline

PDGFA	platelet derived growth factor subunit A
PI3K	phosphoinositide 3-kinase
Plod2	procollagen-lysine 2-oxoglutarate 5-dioxygenase 2
PSR	picrosirius red
qPCR	quantitative polymerase chain reaction
qRT-PCR	quantitative reverse transcription–polymerase chain
RAAS	renin-angiotensin-aldosterone system
RAG1	recombinase-activating gene 1
RBC	red blood cell
Relma/Fizz1	resistin-like molecule α /found in inflammatory zone
RNS	reactive nitrogen species
ROS	reactive oxygen species
S100a8/a9	S100 calcium-binding protein a8/a9
SHR	spontaneously hypertensive rat
SMC	smooth muscle cells
SOS	son of sevenless
STAT3	signal transducing and activation transcription 3
STAT6	signal transducing and activation transcription 6
t-PA	tissue-type plasminogen activator
TGF β	transforming growth factor β
TGF β 1	transforming growth factor beta 1
Th1	T helper cell type 1
Th17	T helper cell type 17
Th2	T helper cell type 2
TIMP	tissue inhibitors of metalloproteinase
TLR	toll-like receptors
TNF α	tumor necrosis factor α
Trib1	tribbles homolog 1
TTC	2,3,5-triphenyltetrazolium chloride
u-PA	urokinase-type plasminogen activator
UUO	unilateral ureteral obstruction
Ym1	chitinase 3-like 3
γ c	γ -signaling chain

ABSTRACT

Cardiovascular disease is the leading cause of death, and understanding the pathophysiological changes that occur in response to injury is important for identifying novel drug targets and developing improved therapeutics. The process of cardiovascular remodeling, which occurs after injury and includes structural and functional changes has been identified as a target for therapeutic intervention.

Reprogramming macrophages towards a reparative phenotype in cardiovascular remodeling is a potential therapeutic approach. Interleukin-4 receptor (IL4R) signaling is an inducer of alternatively activated macrophages (AAM or M2), and M2 macrophages are critically involved in inflammation resolution, tissue repair and pathological development of fibrosis. IL-4 administration can be beneficial, but the important IL-4 responsive cell types mediating the protection have not been identified. We hypothesized that macrophages are the critical target cell type of IL-4, and macrophage IL4R signaling plays an important role in cardiovascular remodeling by controlling macrophage polarization.

In order to test this hypothesis, we generated myeloid (macrophage/monocyte and neutrophil)-specific IL-4 receptor α knockout (MyIL4R α KO) mice. Bone marrow derived macrophages from MyIL4R α KO mice showed a significantly blunted response to the M2 macrophage stimulus IL-4 and a markedly augmented response to the M1 macrophage stimulus LPS, indicating the importance of IL4R α signaling in macrophage polarization *in vitro*. In addition, significant decreases of M2 macrophage markers at basal levels were shown in the heart suggesting that endogenous IL4R is required for appropriate macrophage polarization of resident cardiac macrophages.

In cardiac remodeling post myocardial infarction (MI), the infarct size of MyIL4R α KO mice at 1 week post-MI was significantly smaller than that of control

mice and infarct thickness at 3 weeks was significantly increased, indicating the involvement of myeloid IL4R α signaling in cardiac remodeling post-MI. No changes in collagen deposition were detected within the infarct, but there was evidence of an important role for endogenous cytokine action at the myeloid IL-4R since there was greater cardiac dysfunction in MyIL4R α KO mice. Surprisingly, IL4R α knockout in myeloid cells did not change the percentage or number of M2 macrophages in infarct tissues post-MI. This does not support the hypothesis that IL4R α signaling mediates cardiac remodeling via its control of macrophage polarization, but rather that the effect on myeloid phenotype is considerably subtler.

In angiotensin II and high salt-induced hypertensive cardiovascular injury, cardiac and vascular fibrosis was substantially decreased in MyIL4R α KO mice. This corresponded to significant changes in fibrosis-related signaling pathways including TGF β , Gal3 and BMP9 signaling. MyIL4R α KO mice also showed significantly increased mRNA expression of reactive oxygen species (ROS) generation related genes. This suggests that myeloid IL4R α signaling significantly alters cardiovascular remodeling post hypertensive injury by regulating collagen accumulation and ROS generation. Similar to what we found in the MI model, ablation of IL4R α in myeloid cells did not induce changes in the polarization of M2 macrophages in the heart and aorta during hypertensive injury. This suggests that the changes in cardiovascular remodeling may not be attributed to a simple alteration in global macrophage polarization.

In conclusion, results from both injury models suggest that myeloid cells are critical targets of endogenous IL4R α signaling, and myeloid IL4R α signaling is very important in modulating cardiovascular remodeling post injury. However, the mechanism by which myeloid IL4R α signaling regulates cardiovascular remodeling is not simply through a global change in M2 macrophage polarization in vivo, and the exact mechanism needs to be determined further.

CHAPTER I

INTRODUCTION

Overview

Cardiovascular disease (CVD) is the leading cause of death worldwide. Based on the statistics reported in 2016, globally more than 17.3 million people die from CVD per year¹, representing 31% of all deaths², and this number is projected to grow to 23.6 million by 2030³. CVD is also the No. 1 cause of death in the United States. CVD accounted for 30.8% of all deaths in 2013 in the U.S, which is more than all forms of cancer combined^{4, 5}. On average, about 2,200 Americans die each day from CVD, one death every 40 seconds. Moreover, the estimated annual direct cost of CVD in the U.S from 2011 to 2012 is \$193.1 billion, more than any major diagnostic disease, and this total direct cost is projected to grow to \$918 billion by 2030^{6, 7}. These numbers indicate that CVD not only claims the most lives, but is also a serious financial burden, and its prevalence and cost are growing substantially.

This raises the urgent need to improve our understanding of the pathophysiology or response to injury in cardiovascular remodeling in order to identify novel targets and develop therapies to advance CVD treatment. Cardiovascular remodeling is the response of heart and vessels to an injury such as myocardial infarction (MI) and hypertension. The remodeling involves changes in the structure of the organs, often proliferation or hypertrophy of cells, modulation of the extracellular matrix, and ultimately functional adaptation of the organ. In this dissertation, we focus on cardiovascular remodeling occurring following two of the most common CVDs: myocardial infarction and hypertension. We investigate the involvement of modifying macrophages in these remodeling processes.

Macrophage

Monocytes and macrophages are types of leukocytes that phagocytize any pathogens not recognized as healthy tissues, including necrotic cells, apoptotic cells, cell debris and microorganisms. They play a central role in inflammatory responses following injury/stress and are essential for wound healing and tissue repair.

Macrophage Heterogeneity

Macrophages are highly heterogeneous in function, with a lifespan varying from hours to months or even years for tissue resident macrophages⁸. There is a wide spectrum of macrophage activation states, but the two main types often discussed are based on different in vitro stimulation leading to different activation states (Figure 1.1). Macrophages stimulated by lipopolysaccharide (LPS) and/or T helper cell type 1 (Th1) cytokine interferon γ (IFN γ) and damage associated molecular patterns (DAMPs) undergo classical activation, resulting in the polarization state of the classical activated macrophage (CAM) also called M1 macrophages⁹. They are characterized by production of reactive oxygen species (ROS), reactive nitrogen species (RNS) and pro-inflammatory cytokines such as tumor necrosis factor α (TNF α), interleukin-1 β (IL-1 β) and interleukin-6 (IL-6). They play a crucial role in inflammation and tissue injury¹⁰.

In contrast, macrophages stimulated by T helper cell type 2 (Th2) cytokines interleukin-4 (IL-4) and/or interleukin-13 (IL-13) undergo alternative activation, resulting in the polarization state of the alternative activated macrophage (AAM), also named M2 macrophage (reflecting the Th1-Th2 polarization). M2 macrophages are characterized by expression of mannose receptor C type 1 (MRC1 or CD206), arginase 1 (Arg1), and resistin-like molecule α that is found in inflammatory zone (Relm α /Fizz1), producing cytokines like interleukin-10 (IL-10) and transforming growth factor β (TGF β)¹¹, and are significantly involved in immunomodulation, wound healing and fibrosis^{9, 12-16}. Although distinct, both subsets contribute to the initiation and progression of cardiovascular, chronic inflammatory and autoimmune diseases¹⁷⁻¹⁹. Macrophages also have substantial plasticity in function depending on their microenvironment²⁰. Macrophages evaluate the status of local tissue frequently

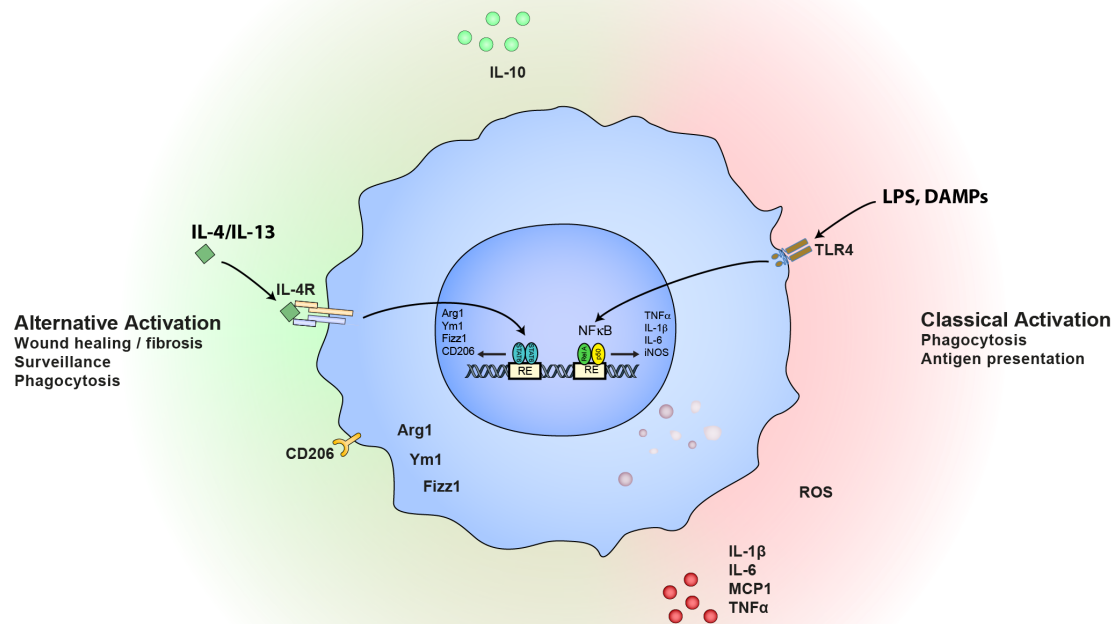


Figure 1.1 Graphical representation of classical and alternative activation of macrophages (M1 vs M2). M1 is induced by stimulus like lipopolysaccharide (LPS) and/or damage-associated molecular patterns (DAMPs) and stimulates production of pro-inflammatory cytokines (red) and also contributes to the expression of some anti-inflammatory cytokines like IL-10 (green). IL-4/IL-13 is the standard in vitro stimulus for activation of M2 macrophages and stimulates markers Arg1, Ym1, Fizz1 and the cell surface marker CD206 (mannose receptor C type 1) that is often used for histologic identification of M2-like macrophages. M1 macrophages are more involved in antigen presentation and tissue damage, while M2 macrophages are more involved in wound healing and fibrosis, but both M1 and M2 macrophages can phagocytize pathogens, dead cells and debris et al.

and change their phenotype accordingly²¹. They have a reversible transcriptional program that allows transformation of an activated pro-inflammatory macrophage phenotype into an anti-inflammatory and pro-resolution phenotype in response to local stimuli²².

Macrophage in Fibrosis

Macrophages are also very important in secretion of extracellular matrix (ECM) components and ECM remodeling. They are the major cell type producing matrix metalloproteinases (MMPs) and tissue inhibitors of metalloproteinases (TIMPs)²³, which are important in collagen degradation. Among phenotypically and functionally diverse macrophages, the M2 macrophage subtype is important in fibrosis²⁴. M2 macrophages also ingest collagen by endocytosis via a mannose receptor, representing their pleiotropic role in ECM homeostasis²⁵. In addition, immune cells like neutrophils, lymphocytes and eosinophils also contribute to fibrotic remodeling in multiple organs²⁶. The communication between stromal cells, immune cells and the ECM actively modulates fibrosis in cardiovascular remodeling²⁷⁻²⁹.

Origin of Macrophages

Resident Homeostatic Macrophages: Macrophages exist in essentially all tissues but can have different origins (Figure 1.2). Resident cells can be either derived from embryonic yolk sac or later through definitive hematopoiesis from hematopoietic stem cells (HSCs). The portion derived from each source is different in each tissue. Many types of these resident macrophages have a location specific name, for example macrophages in the brain are named microglia, macrophages in the liver are named Kupffer cells^{30,31}. In the absence of injury, the homeostasis of resident macrophages in many tissues is maintained by local proliferation without hematopoietic precursors³²⁻³⁵. In the steady state, macrophages have minimal inflammatory characteristics, for instance cardiac resident macrophages express high levels of 22 AAM-associated genes although they also express some inflammatory genes like IL-1 β ³⁶.

Macrophages after Injury: Macrophages present during inflammation can have a totally different origin. After injury, macrophages come from two

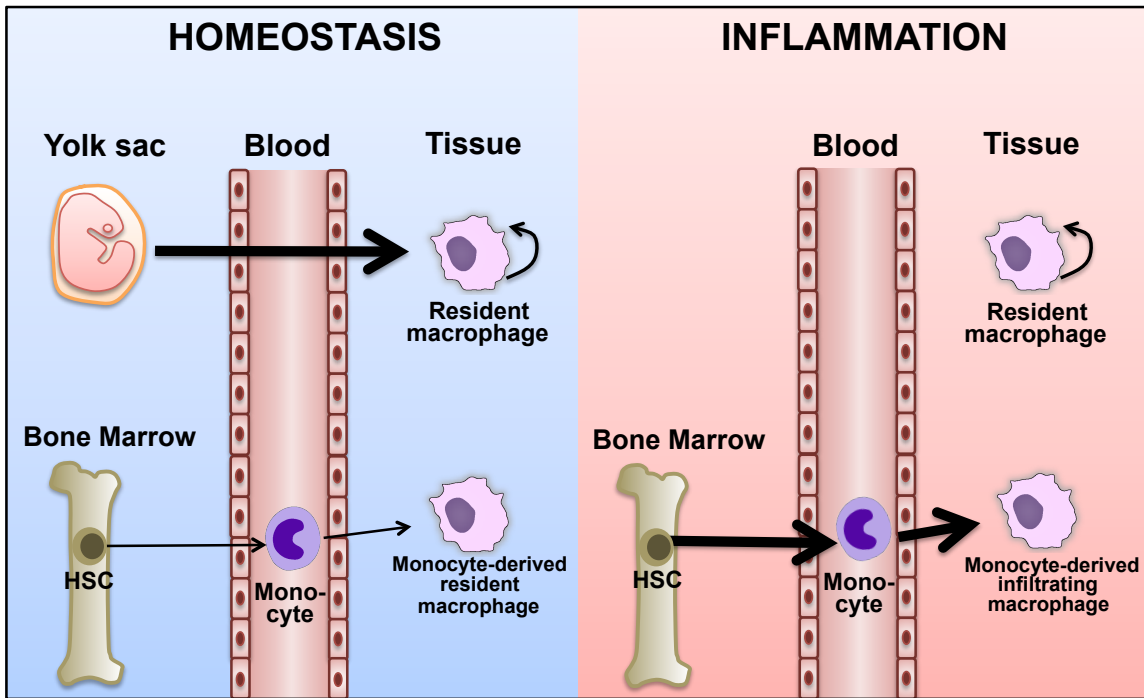


Figure 1.2 Macrophages can arise from two main sources: embryonic yolk sac and the hematopoietic stem cell (HSC) through definitive hematopoiesis. Initially, tissue-resident macrophages come from the yolk sac but with age they can be replaced with HSC derived macrophages to different degrees depending on the tissue. Macrophages developed from yolk sac can be maintained through adult by self-renewal. Upon stress or injury, macrophages can also originate from resident macrophage via proliferation and maturation from HSC derived monocytes.

distinct processes: recruitment of circulating monocytes that then differentiate into macrophages and proliferation of resident macrophages. Stimulated by injury, a small fraction of HSCs in bone marrow become active and produce progenitors that give rise to monocytes. These monocytes migrate from blood into the injured tissue where they differentiate into macrophages³⁷. The spleen also contributes to macrophages generation during inflammation. It is reported that the subcapsular red pulp in spleen is a monocyte reservoir, which expels monocytes that then accumulate in infarcted tissue post MI, and differentiate and mature into macrophages³⁸. In addition to the circulating monocytes, resident macrophages repopulate the inflamed tissue by proliferation. Tissue-resident macrophages are maintained locally by proliferative self-renewal during inflammatory responses^{33, 34, 39}. Jenkins et al. demonstrated that IL-4 signaling directly drives resident macrophage proliferation during Th2-biased tissue infection^{33, 40}. Meanwhile, resident macrophages also promote the recruitment of monocytes by communication with the surrounding parenchymal and non-parenchymal cells⁴¹. Recruitment of C-C chemokine receptor type 2 (CCR2) positive inflammatory macrophages has been shown to be crucial in both acute and chronic inflammatory diseases⁴²⁻⁴⁵.

Monocytes, as circulating precursors of macrophages, display heterogeneity based on the expression of lymphocyte antigen 6 complex (Ly6C)⁴⁶⁻⁴⁹. Monocytes are designated as inflammatory Ly6C^{high} monocytes and less-inflammatory Ly6C^{low} monocytes. During inflammation post MI, inflammatory Ly6C^{high} monocytes are abundantly recruited into the injured tissue as early as 30 min after the onset of ischemia, exceeding even neutrophils⁵⁰, although the number of neutrophils peaks earlier than monocytes. The recruitment of monocytes from blood relies on monocyte chemoattractant protein 1 (MCP1 or CCL2)/CCR2 signaling^{51, 52}. Ly6C^{high} monocytes then differentiate into inflammatory macrophages, and both monocytes and macrophages produce inflammatory cytokines that activate macrophages. Activated macrophages function to clear debris, necrotic myocytes, and apoptotic neutrophils. Recruitment of monocytes from the spleen is dependent on angiotensin II

(AngII)³⁸, so splenic monocytes mobilization after MI can be suppressed by angiotensin-converting enzyme (ACE) inhibitor that inhibits AngII signaling⁵³.

IL-4 Receptor Signaling

IL-4 and IL-13

IL-4 and IL-13 are both Th2 cytokines and are produced by activated T lymphocytes including Th2 cells, NK T cells, γ/δ T cells, as well as several other cell types including mast cells, basophils, eosinophils, and natural killer (NK) cells^{54, 55}, among which Th2 cells are particularly important sources, which also require IL-4 and IL-13 for their own differentiation. Although IL-4 and IL-13 only share 20-25% amino acid sequences, their tertiary structure are of high homology and they have a common subunit—IL-4 receptor α (IL4R α) in their respective receptor complexes that they have numerous overlapping biologic properties, eliciting a diverse array of biologic responses in immune system^{56, 57}.

IL-4 Receptor

IL-4 induces biological responses by binding to two receptor complexes: type I and type II IL-4 receptor (IL4R)^{57, 58} (Figure 1.3). The type I IL4R is composed of a 140kDa ligand-specific chain—IL4R α and a common γ -signaling chain (γ c) that is shared by some other cytokine receptors such as IL-2, IL-7, IL-9 and IL-15. The type II IL4R consists of an IL4R α subunit and an IL-13 receptor α 1 (IL13R α 1) subunit⁵⁹. Unlike the type I IL4R, which can only be bound by IL-4, the type II IL4R can bind both IL-4 and IL-13. IL-13 can also bind to a second receptor IL13R α 2 subunit although this does not initiate cell signaling⁶⁰, as IL13R α 2 serves as a decoy receptor. IL4R is expressed on a wide range of cell types including T cells, B cells, monocytes/macrophages, fibroblasts⁶¹, keratinocytes, epithelial cells, endothelial cells, and hepatocytes^{62, 63}.

Signaling Pathways Mediated by IL-4 Receptor

Both IL-4 and IL-13 signaling are mainly mediated via the IL4R α chain and both include the activation of transcription factor signal transducing and activation transcription 6 (STAT6)^{58, 64}. One of the pathways is initiated by Janus kinase (JAK) family members, JAK1 and JAK3⁶⁵. IL-4 binds to type I IL4R and induces the phosphorylation of JAK1 that is associated with the IL4R α subunit, and the

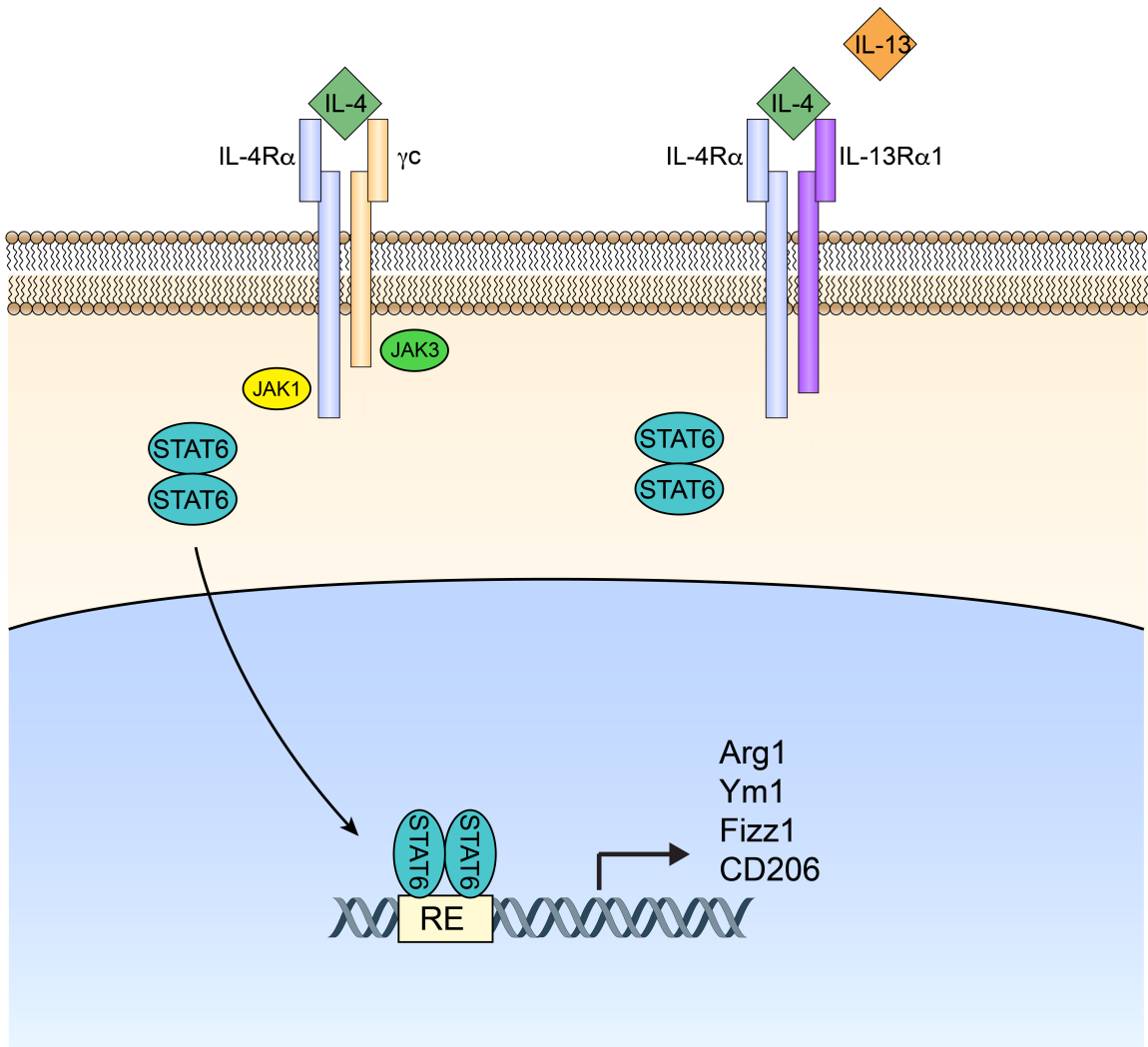


Figure 1.3 Type I and Type II IL-4 receptor. Type I IL-4 receptor is a heterodimer of subunits IL4Rα and γc. Type II IL-4 receptor is a heterodimer of IL4Rα and IL13Rα1 that can bind both IL-4 and IL-13. Activation of IL-4 receptor results in STAT6 signaling and induction of alternative M2 macrophage genes. IL4Rα knockout will block IL-4 signaling through both types of receptors as well as IL-13 through the Type II IL-4 receptor. RE: response element.

phosphorylation of JAK3 associated with γ_c subunit. The phosphorylated JAKs in turn phosphorylate and activate IL4R α chain itself and STAT6. Once activated by phosphorylation, cytoplasmic STAT6 dimerizes and translocates to the nucleus where it promotes the transcription of IL-4-responsive genes that contain STAT6 binding site in their promoter region⁶⁵.

IL-4 and IL-13 also signal through type II IL4R and subsequently activate the JAK1/STAT6 downstream signaling. STAT6 functions to mediate most responses of IL-4, such as Th2 cell differentiation^{66, 67}, B cell growth and immunoglobulin E (IgE) secretion^{68, 69}.

IL-4 and IL-13 activate a second signaling pathway when they interact with the membrane-bound form of IL4R⁶⁵ through the phosphorylation of an insulin receptor substrate (IRS), referred as IRS-2. Phosphorylated IL4R α stimulates the recruitment and phosphorylation of IRS-2, which in turn activates the phosphoinositide 3-kinase (PI3K) pathway. This pathway is critical in IL-4/IL-13-induced protection against apoptosis, cell survival and proliferation responses^{58, 65, 68}. Another signaling pathway triggered by binding of IL-4 to IL4R that contributes to cell growth and proliferation through phosphorylation of the adaptor protein Shc, resulting in recruitment of growth factor receptor-bound protein 2 (Grb2) and son of sevenless (SOS), which then activate Ras/MAPK pathway. This IL4R dependent Ras/MAPK signaling occurs only in human keratinocytic cells but not in T cells⁷⁰.

The soluble form of IL4R α does not mediate IL-4 signaling, but rather protects IL-4 from proteolytic degradation^{71, 72}. IL-4 binds to the soluble receptor with a lower affinity and IL-4 soluble receptor performs as a carrier for IL-4 promoting its presentation to the cell surface bound receptor⁷².

Biological Activities of IL-4/IL-13 Signaling

Although IL-4 and IL-13 have low amino acid sequence homology, they have similar tertiary structure and have a common IL4R α chain in their receptors, so IL-13 mediates virtually all of the IL-4 actions in nonhematopoietic cells and, to some extent, in hematopoietic cells⁷³. The functional differences between IL-4

and IL-13 are attributable to cell-dependent differential receptor expression and IL-13 shows similar but less effective biological activities than IL-4⁶¹.

The major function of IL-4 includes promoting Th2 cell differentiation^{57, 69}, stimulating B lymphocyte growth and differentiation⁷⁴, facilitating IgE secretion⁷⁵, regulating eosinophil recruitment⁷⁶, and an important role in myeloid cells such as monocytes/macrophages and neutrophils. IL-4 directly and predominantly promotes Th2 cell differentiation via type I IL4R, while IL-13 does not directly participate in Th2 cell development because Th0 cells do not express IL13R α 1 on their surface. However, IL-13 is to some extent involved in Th2 differentiation as IL4R α deficient mice display more severely diminished Th2 cell differentiation than IL-4 deficient mice, implying some indirect role of IL-13 in Th2 cell development^{77, 78}. Moreover, mature CD4⁺ T cells from IL-13^{-/-} mice produce significantly less Th2 cytokines⁷⁷. IL-4 also antagonizes the IL-12-mediated Th1 cell differentiation^{69, 79}. IL-4 stimulates B cell growth and differentiation and drives B cells to produce IgE. IL-13 has similar biological functions to those of IL-4 in B cells. IL-13 knockout mice showed significantly lower basal level of IgE in serum⁷⁷, suggesting the essential role of IL-13 in IgE secretion. IL-4 and IL-13 are also growth factors for mast cells, and regulate allergic responses via IgE-mediated mast cell degranulation.

IL-4 and IL-13 also exert critical biologic activities in macrophages and neutrophils. Both IL-4 and IL-13 are potent anti-inflammatory cytokines with the capability to inhibit monocytes/macrophages from producing pro-inflammatory cytokines and chemokines such as TNF α and IL-1 β , and interfere with their generation of ROS and nitrogen intermediates, and suppress IFN γ -induced expression of cellular adhesion molecules. IL-4 and IL-13 are also crucial inducers of alternative activation of macrophage (AAM or M2), which promotes tissue repair⁸⁰⁻⁸² and is pathologically associated with type 2 immune responses like allergy and fibrosis^{81, 83, 84}. Furthermore, the anti-inflammatory activity of IL-4 and IL-13 is also partially mediated through their induction of anti-inflammatory interleukin 1 receptor antagonist (IL-1Ra). IL-4 and IL-13 can augment the production of IL-1Ra, which binds IL-1 receptor type 1 with similar affinity to that

of IL-1 α and IL-1 β but transduces no signal^{85, 86}. Neutrophils were originally reported to express the type I (IL4R α / γ c) but not the type II (IL4R α /IL13R α 1) IL4R⁸⁷⁻⁸⁹, however it was reported recently that type II IL4R is also expressed in neutrophils⁹⁰. IL-4 and IL-13 display both pro- and anti-inflammatory activities in neutrophils although neutrophils are less effective in response to IL-13. Similar to macrophages, neutrophils up-regulate the production of IL-1Ra in response to IL-4 and IL-13⁹¹. Type II IL4R signaling antagonizes the expansion and migration of neutrophils during infection and inflammation⁹⁰, which indicates an anti-inflammatory role in IL4R signaling in neutrophils. Illustrating the pro-inflammatory role of IL-4 in neutrophils, IL-4 delays neutrophil apoptosis and enhances neutrophil-derived IL-8 production⁸⁹, which contributes to the recruitment of leukocytes to the inflammatory site. Moreover, neutrophil infiltration together with IL-4 elevation contributes to the severity of asthma^{92, 93}.

Although IL-13 can partially substitute for IL-4, it has its own independent properties, which was demonstrated by IL-4^{-/-} mice⁹⁴⁻⁹⁷. There is an additive effect when both IL-4 and IL-13 are deleted⁹⁷, indicating a unique role of IL-13 in type 2 immune responses. IL-13 plays a more important role than IL-4 in worm expulsion⁹⁴, effector activity in asthma⁹⁶, hepatic fibrosis and granuloma formation⁹⁵. Moreover, although IL-13 normally participates in type 2 immunity, IL-13 also has a significant role in regulating type 1 immune responses. In parasite-infected IL-13^{-/-} mice, IFN γ (Th1 cytokine) production was dramatically inhibited, while IL-4 and IL-10 (Th2 cytokines) production was significantly enhanced, supporting the involvement of IL-13 in type 1 responses^{98, 99}. This is consistent with the increased parasite burdens in IL13^{-/-} mice⁹⁸. IL-13 has also been shown to prime monocytes for IL-12 production¹⁰⁰ and exhibits a protective type 1 immune response during listeriosis¹⁰¹.

IL-13 signaling is mediated by type II IL4R, which consists of IL4R α and IL13R α 1, however, another IL-13 binding receptor IL13R α 2, which acts as a non-signaling decoy receptor, shows strong suppression of IL-13 activity¹⁰². For example, IL13R α 2 overexpression inhibits the expression of fibrotic markers induced by IL-13 in vitro and suppresses bleomycin-induced pulmonary fibrosis,

highlighting the antagonism of IL13R α 2 to the pro-fibrotic effector function of IL-13¹⁰³. Animals lacking IL13R α 2 fail to attenuate granuloma inflammation in the chronic phase after infection, and develop severe IL-13-dependent fibrosis and show increased mortality^{104, 105}, although IL13R α 2 has no effect on the inflammatory responses at the acute stage post infection¹⁰⁵. As IL-13 binds both type II IL4R and IL13R α 2 with high affinity, when IL13R α 2 is induced by IL-13, it acts as a inhibitor of IL-13 via negative feedback by competing for its interaction with type II IL4R¹⁰⁶. Conversely, there are also conflicting result showing that IL-13 plays an important role in mediating fibrosis partially via IL13R α 2 in chronic infectious and autoimmune diseases¹⁰⁷. Blocking both IL4R and IL13R α 2 signaling in double knockout mice IL4/IL13^{-/-} may be responsible for the augmented protection against chronic pancreatitis progression, compared with blocking IL4R signaling only in the IL4R α ^{-/-} mice¹⁰⁸. Therefore, IL13R α 2, originally regarded as a decoy receptor, probably also has the ability to mediate signaling. This is further supported by the ability of IL13R α 2 to signal on cell surface or in the cytoplasm with the soluble form in inducing TGF β 1 production in macrophages and mediating fibrosis¹⁰⁹.

IL4R α signaling also functions in cells outside of the immune system. IL4R α deficient mice exhibited significantly decreased bone marrow-derived fibroblasts (myeloid fibroblasts) and myofibroblasts in their kidneys¹¹⁰, indicating that IL4R α signaling is involved in renal fibrosis via bone marrow-derived fibroblasts.

IL-4 Receptor Signaling in Macrophage

IL-4 and IL-13 promote alternative macrophage activation^{12, 111}. Compared with their wild-type counterparts, macrophage/neutrophil-specific IL4R α knockout mice revealed significant suppression of parasite infection progression, indicating the significance of IL-4/IL-13-IL4R signaling induced M2-like macrophage polarization in inflammatory disease¹¹². IL4R α ^{flox/-}-LysM^{cre} mice, subjected to worm infection, showed impaired alternative macrophage activation with significantly decreased CD206 expression and enhanced Inducible nitric oxide synthase (iNOS) production¹¹³. In addition, M2 macrophages activated by IL-4

and/or IL-13 mediate fibrotic remodeling through IL4R. When activated by IL-4 and/or IL-13, macrophages secrete proteins that are directly involved in tissue repair, such as collagen type 1 α 1 (Col1A1) that is deposited in the ECM. These proteins also include α 1(I) procollagen, which eventually acts to cross-link collagen with fibrils, developing strength or stiffness to the tissue¹¹⁴. However, IL-4 and/or IL-13 are not sufficient to induce tissue repair in vivo. IL-4 or IL-13 stimulated macrophages are not able to initiate the tissue-repair program until they receive signals showing the presence of apoptotic (dying) neutrophils¹¹⁵. Loss of the ability to sense of apoptotic cells by genetic ablation impairs proliferation of tissue-resident macrophages and the expression of genes involved in inflammation resolution and tissue repair in infected lung or gut with colitis¹¹⁵. After clearing pathogens and debris in the wounded or infected tissue, macrophages switch to repair mode and activate tissue repair programs, by sensing local tissue-specific cues or signals from dying cells, and then result in the production of tissue-building factors¹¹⁶.

In addition to macrophage polarization, IL4R signaling may also be involved in macrophage proliferation. Compared with wild type mice, myeloid-specific IL4R α knockout (IL4R $\alpha^{\text{flox/-}}$ LysM^{Cre}) mice display a decrease in the absolute and relative number of macrophages (CD11b⁺F4/80⁺) during the early and middle phase of repair, which may be attributable to the decreased potential of macrophage proliferation caused by IL4R α deficiency¹¹⁴.

Models of Cardiovascular Remodeling

We are using two widely used models of cardiovascular damage, permanent myocardial infarction and pressure overload by treatment with angiotensin-II, in order to test the role of IL-4 stimulated macrophages in the pathophysiology.

Myocardial Infarction

Myocardial infarction (MI) is the irreversible death of heart muscle due to blood flow deprivation (ischemia). MI strikes Americans approximately once every 42 seconds¹¹⁷. About 550,000 Americans have a first-time attack annually, and about 200,000 have recurrent attacks¹¹⁷. Each year, about 116,000 people

die of MI in the U.S.¹¹⁷. Patients who survived the first MI are at high risk of having a secondary injury (second MI) because of complications, so prevention of secondary injury is very important in reducing mortality. Around 47% of the decrease in heart disease mortality in America is attributed to secondary injury prevention⁴. Inhibiting secondary injury can also substantially decrease the indirect cost of MI caused by loss of future productivity, which is estimated to reach \$308.2 billion by 2030¹¹⁷. Benefitting from medical advances, annual death from MI has declined over time, however the development of heart failure (HF) post MI is alarmingly high and continues to increase¹¹⁸. Based on pooled data, people who are 45 years old or older have a 20% chance of developing HF within five years after a first MI¹¹⁷.

Cardiac Remodeling post Myocardial Infarction

In response to MI, cardiomyocytes die by necrosis followed by a reparative process, which includes a series of complicated and finely orchestrated events. The whole process can be divided into three partially overlapping phases: inflammation, proliferation and maturation. These are summarized in Figure 4.

In the inflammatory phase, the sudden death of cardiomyocytes rapidly activates transient but intense inflammatory responses characterized by neutrophil and monocyte/macrophage infiltration¹¹⁹. The death of myocytes results in the loss of passive tension leading to infarct expansion in the first few days, which is characterized by acute ventricular dilation, infarct wall thinning, and cardiomyocyte elongation. When infiltrating neutrophils undergo apoptosis, inflammation resolution is induced by anti-inflammatory and pro-fibrotic signals.

In the proliferation phase, fibroblasts transdifferentiate into myofibroblasts, which proliferate, produce contractile and ECM proteins, and secrete collagens. Macrophages participate in remodeling by activating mesenchymal reparative cells^{51, 119}. Communication between macrophages and fibroblasts and myofibroblasts, together with Th2 responses, sustain the pro-fibrotic remodeling. Apoptosis of the majority of reparative cells marks the end of proliferative stage

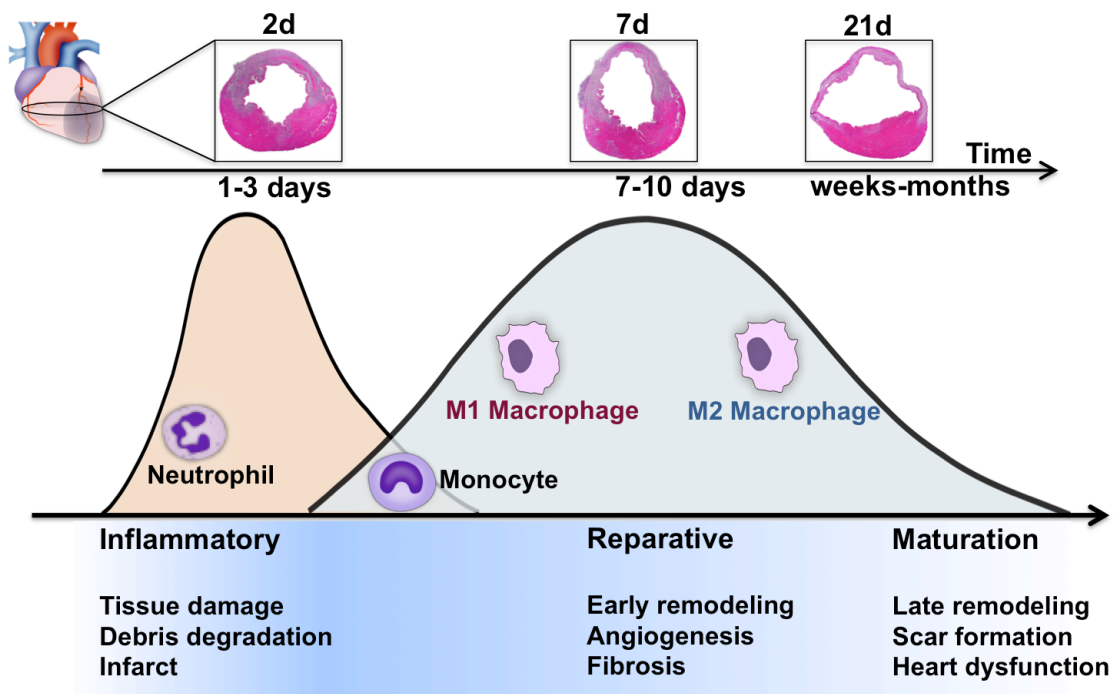


Figure 1.4 Cardiac remodeling post MI. Ischemia in part of the heart cause sudden death of myocytes, which activates transient but intense inflammatory responses characterized by neutrophil and monocyte/macrophage recruitment. Initially the infarct expands and the infarct wall gets thinner and thinner as a result of losing cardiomyocytes and extracellular matrix degradation. The apoptosis of neutrophils represents the start of inflammation resolution that is induced by anti-inflammatory signals. Infiltrating macrophages phagocytize apoptotic neutrophils and M1 and M2 macrophages sequentially dominate in the late inflammatory phase and the following reparative and maturation phase.

and pro-fibrotic remodeling. Conversely, failure to undergo apoptosis or extension of pro-fibrotic signaling results in pathological remodeling.

In the maturation phase, the infarct zone undergoes fibrotic replacement with the formation of cross-linked collagen, while the adjacent non-infarct zone exhibits perivascular and interstitial fibrosis. Scar forms to preserve the structural integrity and maintain cardiac pump function by preventing dilatation, aneurysm or myocardial rupture¹²⁰. Depending on the infarct size and the quality of repair, the extent of cardiac remodeling post-MI varies.

Cellular and Molecular Adaptation post MI

The innate immune system plays an important role in the remodeling post MI. In the inflammatory response after injury, immune cells including neutrophils and monocytes/macrophages recognize DAMPs by toll-like receptors (TLRs), and then activate downstream inflammatory pathways. Inflammation is further prolonged by secretion of pro-inflammatory cytokines such as MCP1, TNF α and IL-6. MCP1 contributes to the recruitment of monocytes, and TNF α promotes adhesion and extravasation of leukocytes through endothelium. The role of IL-6 in inflammation and cardiac remodeling is ambiguous. Augmented IL-6 expression aggravates the inflammatory responses and exacerbates deleterious effects of MI¹²¹. However, neither deficiency of IL-6 nor blocking the IL-6 receptor confers no protection^{122, 123}. The neutrophils and monocytes/macrophages phagocytize and clear the dead cells and debris. In addition to these infiltrating immune cells, resident cells such as fibroblasts, surviving cardiomyocytes and resident macrophages contribute to the development of inflammation. Macrophages in the proliferation phase are less inflammatory and express M2 macrophage-associated genes¹²⁴. They secrete cytokines and growth factors, and mediate tissue repair and neovasculogenesis^{51, 119}. Galectin 3 (Gal3), a pro-fibrotic protein predominantly produced by macrophages, is actively involved in post-MI remodeling^{125, 126}. TGF β , another major pro-fibrotic cytokine secreted by macrophages, suppresses inflammation, promotes hypertrophic cardiomyocyte growth, enhances ECM deposition by increasing collagen and fibronectin synthesis and down-regulates ECM degradation^{127, 128}.

The importance of monocytes/macrophages in cardiac remodeling post MI is increasingly appreciated. In response to injury, Ly6C^{high} monocytes efficiently migrate to the injured area and give rise to inflammatory macrophages¹²⁹⁻¹³¹, while Ly6C^{low} monocytes infiltrate less efficiently and are believed to differentiate into resident macrophages. Clodronate-loaded liposome mediated depletion of monocytes/macrophages showed that both Ly6C^{high} and Ly6C^{low} monocytes are essential for infarct healing^{132, 133}. Depletion of monocytes/macrophages resulted in impaired dead cardiomyocytes removal, delayed matrix regeneration and inefficient angiogenesis⁵¹. In mice with MI, Ly6C^{high} and Ly6C^{low} monocytes are sequentially recruited to the infarcted heart. Ly6C^{high} monocytes dominate early, display phagocytic and inflammatory functions, and participate in damaged tissue digestion. In contrast Ly6C^{low} monocytes dominate later, exhibit blunted inflammatory properties, and contribute to tissue repair via myofibroblasts accumulation, collagen deposition and angiogenesis⁵¹. A similar time course of pro-inflammatory monocytes/macrophages in the inflammatory phase and less inflammatory monocytes/macrophages in the proliferation phase was also described in human patients with MI. CD14⁺CD16⁻ (corresponding to Ly6C^{high}) monocytes dominated early in blood and infarcted tissues, whereas abundance of CD14⁺CD16⁺ (corresponding to Ly6C^{low}) monocytes was only detected in infarcted tissues of patients who died later^{134, 135}. Although macrophages are necessary for proper wound healing and scar formation to preserve left ventricle geometry, excessive macrophages during the inflammation phase are harmful. Patients with more CD14⁺CD16⁻ monocytes in blood in the acute inflammatory phase exhibited severely dilated left ventricles¹³⁵, and monocyte cell counts are positively correlated with HF progression^{136, 137}.

During post MI remodeling, fibroblasts contribute to fibrosis by proliferation and transdifferentiation into myofibroblasts, which along with myeloid cells, account for a significant portion of the ECM¹³⁸. Persistent activation by mechanical stress or pro-fibrotic molecules such as TGF β and Gal3 released by neighboring myofibroblasts or macrophages drives quiescent fibroblast transformation into active collagen-producing myofibroblasts^{126, 127}. Although

fibrosis initially benefits the injured myocardium, continued and uncontrolled fibrosis can be harmful and results in cell death and chronic inflammation, which consequently cause impaired cardiac function and organ failure¹³⁹⁻¹⁴¹. One factor that limits fibrosis is that myofibroblasts are programmed to undergo apoptosis after accomplishing their reparative “tissue-building” task. Conversely, sustained myofibroblasts result in extensive fibrosis¹⁴².

Limiting Inflammation and Fibrosis post MI

To optimally repair the infarcted tissue, inflammatory or pro-fibrotic reactions have to be contained and resolved^{143, 144}. Excessive inflammation, insufficient resolution, or excessive fibrosis leads to extended tissue damage, improper healing, defective scar formation, unnecessary cell loss and contractile dysfunction, all of which promote infarct expansion, adverse remodeling, chamber dilatation and the development of HF¹⁴⁵. Inflammatory and pro-fibrotic signaling pathways are critically involved in dilative and fibrotic remodeling, and drive major events in the pathogenesis of post-MI HF¹¹⁹. Therefore, in order to understand the progression of HF post MI, and to develop novel therapeutic strategies to suppress the development of HF, investigation of the inflammation and fibrosis post MI is critical. The switch from pro-inflammatory macrophage phenotype that phagocytize necrotic tissue to macrophages with anti-inflammatory and pro-fibrotic phenotype is thought to be critical to the proper healing of the damage. IL4R signaling and the AAM/M2 macrophage is thought to be critical to this transition.

Hypertension

Hypertension or high blood pressure is a major risk factor for CVD^{146, 147}. A systematic analysis using disability-adjusted life years (DALYs) showed that hypertension went from the number 4 leading risk factor in 1990 to the number 1 risk factor in 2010¹⁴⁸. Hypertension contributes to 40.6% and 34.7% of CVD and ischemic heart disease mortality, respectively, much higher than any other factor¹⁴⁹. In America, about 33% of adults have high blood pressure¹¹⁷, and this will increase to \approx 41.4% by 2030 (unpublished AHA computation, based on methodology described by Heidenreich et al⁷). Obviously, there is a considerable

financial burden in treating hypertension¹¹⁷, which is projected to be up to \$274 billion by 2030 (unpublished AHA computation, based on methodology described in Heidenreich et al⁷). Regardless, only 77 percent of people with hypertension are under current antihypertensive medication, and only 54% of those have their condition controlled¹¹⁷. Being a principal risk factor of CVD, hypertension can progressively lead to HF. Absence of hypertension in middle age is associated with lower risk of developing HF through the remaining life course, and prevention of hypertension during middle age substantially prolongs HF-free survival¹⁵⁰. Adjusting for age and HF risk factors in a Framingham Heart Study, the chance of developing HF in hypertensive subjects compared with the normotensive ones is about 2-fold higher in men and 3-fold higher in women¹⁵¹.

Hypertensive Cardiovascular Remodeling

Hypertension induces the development of CVDs through cardiovascular remodeling such as cardiovascular hypertrophy, inflammation and cardiovascular fibrosis via direct hemodynamic mechanisms and/or overactivation of the renin-angiotensin-aldosterone system (RAAS)¹⁵². For example, angiotensin II (AngII) increases significantly in Dahl salt-sensitive hypertensive rats in the phase of compensated left ventricle hypertrophy, but does not show further increase in subsequent congestive heart failure¹⁵³. In addition, both renin and aldosterone have been implicated in a causal relationship with cardiac remodeling caused by hypertension via fibrosis-dependent or –independent mechanisms^{154, 155}, and directly inhibiting renin decreases myocardial fibrosis and improves cardiac function¹⁵⁶. Persistent hypertension results in cardiovascular remodeling, which includes hypertrophy of cardiomyocytes and smooth muscle cells, cardiac and vascular inflammation, perivascular and interstitial fibrosis, and microvascular rarefaction.

Hypertensive Cardiac Remodeling

Hypertension can result from pressure or volume overload. Cardiac remodeling due to a predominantly pressure overload hypertension comprises concentric left ventricle hypertrophy characterized by thickening of the left ventricle wall and increase in heart mass at the expense of chamber volume¹⁵⁷⁻

¹⁵⁹. In contrast, cardiac remodeling due to a volume overload hypertension consists of eccentric cardiac hypertrophy characterized by increase in both heart mass and chamber volume^{157, 160}. Left ventricle hypertrophy is an intermediate phenotype in the progression of hypertension-induced HF. If pressure overload persists, diastolic dysfunction progresses, the concentric remodeled left ventricle decompensates, and hypertensive HF with preserved ejection fraction (HFpEF) ensues. Patients with HFpEF exhibit left ventricle hypertrophy, epicardial coronary artery lesions, coronary microvascular rarefaction, and myocardial fibrosis^{150, 161}. If volume overload persists, left ventricle dilatation progresses, the eccentric remodeled left ventricle decompensates, and HF with reduced ejection fraction (HFrEF) ensues^{150, 162, 163}. Longstanding pressure or volume overload ultimately leads to cardiovascular diseases that consist of dilated cardiomyopathy with diastolic dysfunction and reduced ejection fraction^{150, 151}. In animal models, changes are more dramatic in sudden pressure overload-induced hypertension, with earlier onset of cardiac fibrosis and accelerated cardiomyocyte loss¹⁶⁴.

Hypertensive Vascular Remodeling

In vascular remodeling (Figure 1.5), pathological changes occur in all three compartments of the vessel wall: the innermost layer intima, middle layer media, and the outermost layer adventitia, and their respective resident mesenchymal cells: endothelial cells (EC), smooth muscle cells (SMC) and fibroblasts. Local signals secreted by stressed or injured cells antagonize vascular homeostasis with cell-cell communications between mesenchymal cells like SMCs and/or fibroblasts and macrophages. As a result, these cells are persistently activated in a pro-inflammatory and pro-remodeling phenotype, which promotes the progression of non-resolving chronic inflammation and remodeling of vessel²². Coronary microvascular dysfunction may conceivably attribute to a systemic inflammatory state and oxidative stress accelerated by complications of HFpEF^{165, 166}. Animals with severe hypertension showed significant intimal fibrosis, dramatic medial thickening along with adventitia fibrosis, and eventually died from heart failure^{167, 168}.

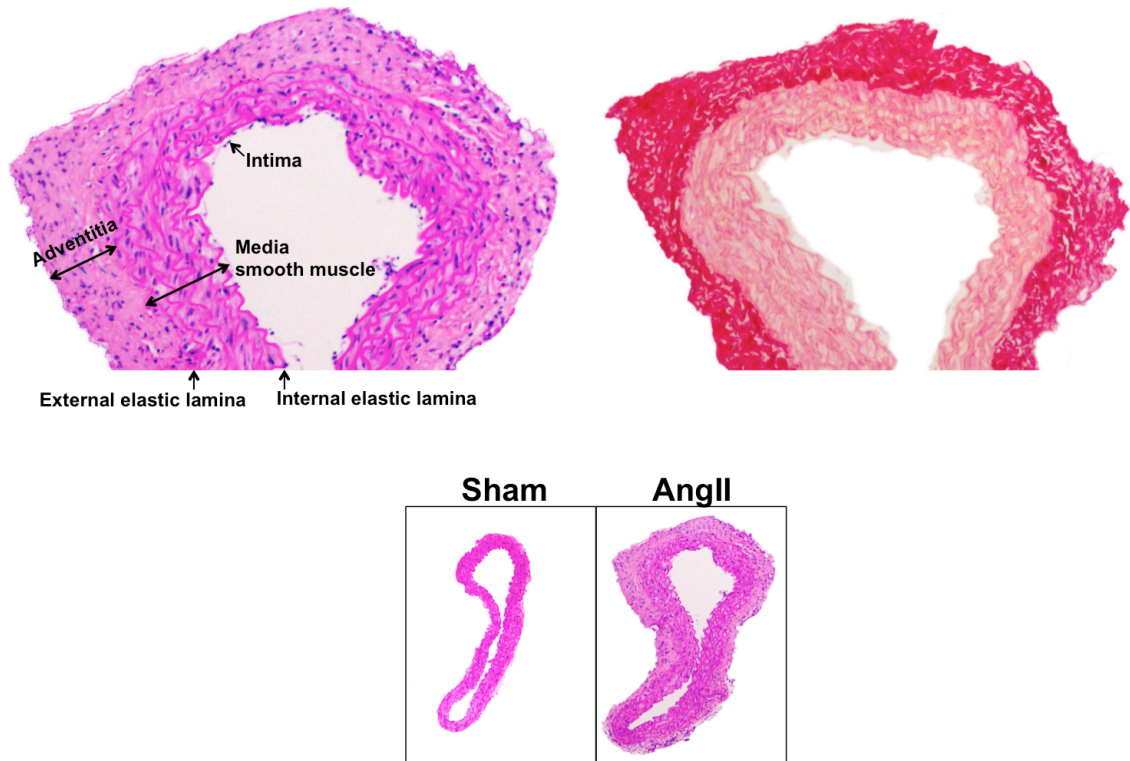


Figure 1.5 Vascular remodeling induced by Angiotensin II. The haematoxylin and eosin (H&E) stained aorta (up left) shows significant hypertrophic and hyperplasia remodeling in the middle layer media and the outermost layer adventitia. The picrosirius red staining (up right) of the same aorta section shows the substantial fibrosis (red) in adventitia, and the lower panel is the comparison of aorta cross section between sham and angiotensin II exposure.

Upon hypertension, changes in intima are characterized by endothelial hypertrophy, subendothelial edema and fibrosis due to collagen deposition¹⁶⁹, intimal thickening because of endothelial hypertrophy and hyperplasia and thickening of the subendothelial space¹⁷⁰⁻¹⁷². Endothelial injuries caused by shear stress induce ECs to produce vasoactive mediators, inflammatory molecules and growth factors¹⁷³⁻¹⁷⁵, and increase the permeability of endothelial cells, which consequently promotes the influx of plasma proteins, vasoactive substances and vascular wall protease¹⁷⁶. Increase of endothelial permeability also exposes SMCs to vasoactive mediators and leads to subendothelial edema. Stressed or injured endothelial cells also produce more laminin, fibronectin and elastin, contributing to pro-fibrotic remodeling that consequently impairs EC and SMC function. Direct changes of ECs as well as molecules and cytokines secreted by ECs lead to intimal thickening, recruitment of circulating cells, local cell proliferation, smooth muscle contraction, hypertrophy and hyperplasia, all of which contribute to intima-related vasculature remodeling and stiffness²².

The hypertrophic and hyperplasia responses of SMCs in media of large vessels and collagen deposition in the ECM contribute to medial thickening, which leads to compliance reduction of the vessels¹⁷⁷. Cumulative data suggest that, non-resident smooth muscle-like cells that are with the potential of differentiating into “mature SMCs”, cumulated in the distal media of large vessels and proliferate²². These smooth muscle-like cells are of high proliferation potential, resistant to apoptosis, and secrete factors to continually stimulate pro-proliferative and pro-signaling pathways¹⁷⁸. The recruitment of these cells contributes to extended, severe vascular remodeling.

The adventitia is the outermost layer of the vessel, and is also the most heterogeneous compartment of the vessel wall due to its cellular and structural complexity. The Adventitia contains lymphatic vessels, vasa vasorum, trophic nerves and resident cells including progenitor cells, fibroblasts and immune cells such as macrophages and dendritic cells. In response to hypertensive stress, the adventitia undergoes substantial remodeling: dramatic expansion of vasa vasorum, activation and proliferation of residential cells like progenitor cells,

fibroblasts and possibly macrophages, transdifferentiation of fibroblasts into myofibroblasts, recruitment of circulating progenitor cells and leukocytes such as macrophages and lymphocytes, as well as significant increase of collagen and ECM protein deposition¹⁷⁹. The expansion, activation, proliferation and infiltration of cells in the adventitia synergistically promote remodeling, and the sustained hypertension persists this process, and finally causes massive fibrosis.

Immune Cells in Hypertensive Cardiovascular Remodeling

Hypertensive stimuli promote oxidative stress and up-regulate pro-inflammatory molecules and cytokines, which leads to rolling, adhesion, and transcytosis of inflammatory immune cells^{180, 181}. As a result, a robust accumulation of immune cells in the cardiovascular system is induced in hypertension¹⁸²⁻¹⁸⁴, including monocytes, macrophages, neutrophils and lymphocytes.

Monocytes/Macrophages

Increases in monocytes and macrophages have been repeatedly demonstrated in experimental hypertension¹⁸⁵⁻¹⁸⁹. Circulating monocytes increase in AngII-induced hypertension^{188, 190}, and monocyte elimination results in decrease of hypertension severity, reduction of vascular reactive oxygen species (ROS) generation and improvement of vascular function¹⁸⁸. Monocytes are circulating precursors of macrophages that accumulate in perivascular adipose tissue and adventitia during hypertension^{153, 191}. Infiltrating macrophages release pro-inflammatory cytokines, produce ROS and disrupt vascular homeostasis¹⁹²⁻¹⁹⁴. Wenzel et al. used myeloid (monocytes/macrophages and neutrophils)-specific LysM-diphtheria toxin receptor mice and completely eliminated neutrophils and monocytes/macrophages by exposing the mice to diphtheria toxin, and they found that the hypertensive responses to AngII were abrogated, as well as hypertrophy, ROS production and vascular dysfunction caused by hypertension¹⁸⁸. Replacement of monocytes, but not neutrophils reversed hypertension¹⁸⁸, indicating the importance of monocyte/macrophage lineage cells in hypertension.

Infiltrating macrophages during hypertension differentiate from circulating monocytes that are initially produced by hematopoietic stem cells (HSCs) in bone marrow^{37, 195}. These macrophages are distinct from yolk sac macrophages that are developed in the embryo before the appearance of HSCs³⁰. In monocyte development, HSCs first give rise to cell progenitor intermediates such as macrophage and dendritic cell progenitors (MDPs), and then finally differentiate into monocytes¹⁹⁶. These hematopoietic stem and progenitor cells (HSPCs) can differentiate into monocytes, macrophages and dendritic cells et al. Besides proliferation and differentiation in bone marrow, HSPCs also constitutively exit bone marrow during inflammation and undergo myelopoiesis in tissues outside of the medulla of the bone¹⁹⁶⁻¹⁹⁸. Spleen tissue is identified experimentally and clinically in patients with CVDs¹⁹⁹⁻²⁰¹. Myelopoiesis from HSPCs in spleen supply a reservoir of monocytes³⁸, which is able to mobilize and contribute to macrophage infiltration in distant lesions^{202, 203}. AngII, independent of hemodynamics, plays a critical role in splenic release of monocytes²⁰⁴. AngII administration significantly induces the amplification of HSPCs in spleen instead of bone marrow²⁰⁴. By amplifying the HSPCs, AngII maintains splenic monocyte reservoir and allows tissue outside of medulla of bone to constantly supply new inflammatory macrophages, which highlights the central role of AngII as upstream of an effective macrophage amplification program. Instead of proliferation, AngII controls splenic monocyte/macrophage amplification by reprogramming HSPC trafficking, and increasing their retention in spleen^{197, 204}. It's worth mentioning that the monocytes generated from splenic HSPCs driven by AngII are mostly Ly6C^{high}²⁰⁴, indicating their pro-inflammatory characteristic. Although the production of monocytes in spleen is mediated by AngII, the recruitment of monocytes from circulation is not through AngII but through via the MCP1/CCR2 axis^{205, 206}, which suggests the production and recruitment of mononuclear phagocytes are two distinct processes that are managed separately.

Neutrophils

The involvement of neutrophils in hypertension is unclear. Selective depletion of circulating neutrophils protects against oxidative stress although has no effect on AngII-induced hypertension²⁰⁷, which suggests neutrophils may be not involved in blood pressure regulation, but are probably associated with hypertension-induced inflammation. Restoration of neutrophils into myeloid cells (monocytes/macrophages and neutrophils)-depleted mice did not restore pathophysiological action of AngII¹⁸⁸, which is inconsistent with the involvement of neutrophils in hypertension or hypertension-induced inflammation.

T Cells

In addition to the innate immune system, the adaptive immune system also contributes to hypertension and hypertension-induced cardiovascular remodeling. T cells, as major components of adaptive immune system, contribute to the development of hypertension by infiltrating into organs that control blood pressure such as vessels and kidney^{188, 189, 208}. Infiltrating T cells, contribute to hypertension and renal glomerular and tubular damages via production of ang-II. Hypertensive stimuli like AngII and deoxycorticosterone acetate (DOCA)-salt, induce T cell accumulation in kidney and vasculature. Higher T cell infiltration results in higher production of pro-inflammatory cytokines and ROS, which further enhances leukocyte recruitment, and leads to renal and vascular dysfunction and exacerbates hypertension²⁰⁸⁻²¹¹. A landmark study by Guzik et al. showed that recombina-activating gene 1 (RAG1) deficient mice, which fail to develop B and T cells, were protected from hypertension induced by AngII or DOCA-salt. Hypertensive responses were restored in these mice by adoptively transferring T but not B cells¹⁸⁹, which confirms the significance of T cells in hypertension. Furthermore, they demonstrated that the T cells are recruited into perivascular adipose tissue and adventitia of these mice¹⁸⁹.

Molecules in Hypertensive Cardiovascular Remodeling

Molecular pathways are essential for hypertension-induced cardiovascular remodeling. These pathways include reactive oxygen species (ROS) and inflammatory cytokines that promote inflammation and TGF β signaling that promotes pro-fibrotic remodeling.

Reactive Oxygen Species

ROS generation has been shown in multiple organs during hypertension, including brain, kidney, heart and the vasculature²¹², which contributes to the comorbidities of hypertension. ROS enhance inflammation, induce hypertrophy of cardiomyocytes and vascular smooth muscle, and mediate pathophysiological remodeling of stressed/injured tissues^{119, 184, 212-214}. ROS generation is attributed to the endothelium, SMC, neutrophils, macrophages, epithelium and fibroblasts, and the production of ROS promotes recruitment of monocytes/macrophages, which in turn generates more ROS, substantially exaggerating the impact of ROS^{179, 215, 216}. ROS also modulate the phenotype of resident cells and infiltrating cells by regulating their proliferation, migration, differentiation and matrix production, meanwhile, ROS function as molecular signals to activate downstream signaling pathways. A substantial clinical challenge targeting ROS production is that routine antioxidant administration is not effective in preventing cardiovascular diseases and hypertension and their treatment, which is likely due to the non-targeted fashion in which the drugs act, they clear away not only the harmful ROS but also those needed in normal cell signaling²¹².

Inflammatory Cytokines

The inflammatory cytokine TNF α is one of the principal cytokines regulating inflammation. TNF α activates nuclear factor κ B (NF κ B) and nicotinamide adenine dinucleotide phosphate (NADPH) oxidase²¹⁷, which importantly contribute to the induction of oxidative stress and up-regulation of chemokines and adhesion molecules²¹⁸. TNF α signaling is also involved in macrophage recruitment. In AngII-induced hypertensive cardiac injury, the pro-fibrotic response mediated by M2 macrophages is dependent on TNF α signaling, although the primary inflammatory stage characterized by M1 macrophages is TNF α signaling independent²¹⁹.

The pro-inflammatory cytokine IL-6 also promotes hypertension and hypertension-related remodeling. High levels of IL-6 correlate with blood pressure increase and may be an independent risk factor for hypertension²²⁰⁻²²⁴. Brands et al. demonstrated that IL-6 is essential for hypertension induced by

AngII²²², which is supported by a human study showing that acute AngII infusion caused dramatically exaggerated plasma IL-6²²⁵. Higher levels of circulating IL-6 were found in hypertensive patients and blocking AngII signaling by AngII receptor inhibition or AngII downstream product antagonist reduced circulating IL-6^{224, 226}. Moreover, IL-6 ablation attenuates AngII and high salt-induced hypertension²²⁷, and IL-6 deficiency prevents cardiac inflammation, fibrosis and dysfunction without affecting myocyte hypertrophy and angiogenesis²²⁸. IL-6 also controls vascular remodeling by mediating superoxide production, endothelial impairment²²⁹, vascular SMC proliferation and migration, which contributes to vascular medial hypertrophy^{230, 231}.

AngII also stimulates MCP1 secretion²³². By activating the receptor of MCP1–CCR2, chemokine MCP1 elicits the activation and migration of monocytes and leukocytes to inflammatory sites.

Fibrosis Associated Signaling Pathways

Instead of a single signaling pathway, multiple pathways contribute to the pro-fibrotic remodeling following cardiovascular injury. We summarized the ones that are associated with our study (Figure 1.6).

Transforming Growth Factor β

Inflammatory response is usually followed by pro-fibrotic remodeling in hypertensive cardiovascular diseases, in which transforming growth factor β (TGF β) signaling plays an important role. Patients with essential hypertension show significantly higher levels of both active and total TGF β 1 in plasma than normotensive subjects²³³. Compared with normotensive rats, spontaneously hypertensive rats (SHR) with HF displayed significant increase in TGF β 1 mRNA expression in left ventricle, although SHR without HF did not show any increase²³⁴. Higher TGF β 1 mRNA level was also shown in aorta and kidney of DOCA-salt-induced hypertensive rats²³⁵. TGF β 1 promotes the deposition of ECM proteins²³⁶, which reduces the cardiovascular compliance and aggravates the stiffness.

TGF β Pathway – PDGF-A and PAI-1

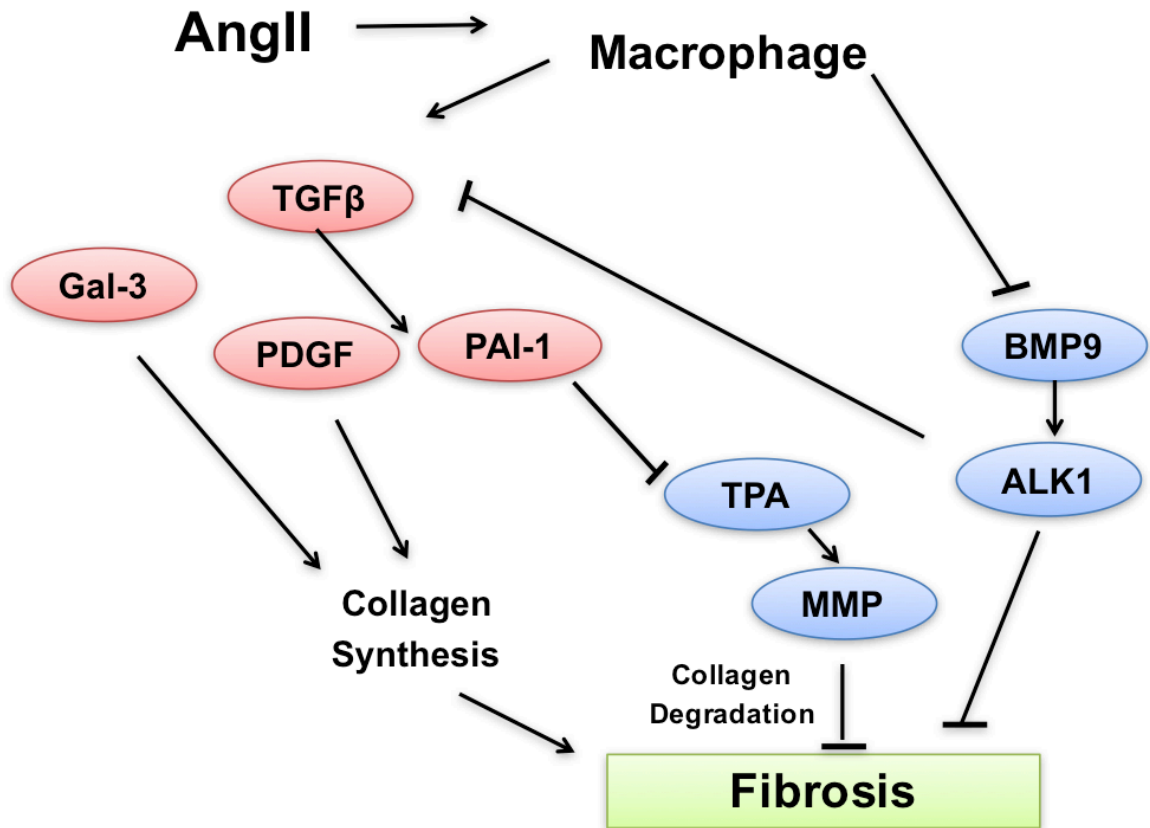


Figure 1.6 Signaling pathways involved in AngII-induced fibrotic remodeling. Pro-fibrotic signaling TGF β pathway (including TGF β itself, PDGF-A and PAI-1) and Gal3 pathway, and anti-fibrotic signaling BMP9 pathway are all involved in AngII-induced fibrotic remodeling. BMP9 binds with its receptor activin receptor-like kinase 1 (ALK1); PAI-1 regulates fibrosis through its inhibition of tPA that activates fibril degradation; TGF β functions via itself or its downstream signals like PDGF-A and PAI-1; and Gal3 can signal through Gal3-IL-6 axis. All of those signaling converge into their modulation of collagen synthesis and degradation by matrix metalloproteinases (MMPs) to regulate fibrotic remodeling.

The signaling pathways through which AngII/Salt induces fibrosis include both TGF β 1-dependent and –independent signaling²³⁷. Platelet derived growth factor subunit A (PDGF-A) is one of the downstream mediators in TGF β signaling pathway to promote fibrosis^{238, 239}.

TGF β and AngII can also induce plasminogen activator inhibitor-1 (PAI-1, or serpin E1)²⁴⁰. PAI-1 is a serine protease inhibitor (serpin) that serves as the principal inhibitor of tissue-type plasminogen activator (t-PA) and urokinase-type plasminogen activator (u-PA), the activators of plasminogen and hence fibrin degradation^{240, 241}. This is consistent with the substantial fibrotic upregulation in PAI-1 null mice²⁴², but converse to the pro-fibrotic role of PAI-1^{243, 244}, which suggests the plastic role of PAI-1 depending on context and specific tissue type. In macrophages, PAI-1 expression can inhibit uPA and abrogate proteolytic activity by the macrophage²⁴⁵

Galectin 3 Signaling

AngII also induces fibrosis through TGF β -independent signaling such as AngII-galectin 3 (Gal3)-IL-6 axis²³⁷. Gal3 is a matricellular glycan-binding protein and involved in cardiac pro-fibrotic remodeling^{125, 246}. Genetic ablation or pharmacologically blocking Gal3 ameliorated cardiac fibrosis induced by hypertension, highlighting the causative role of Gal3 in hypertension-related fibrosis^{247, 248}. Therefore, targeting the AngII-Gal3 axis utilizing Gal3 inhibitor or by neutralizing IL-6 could be a therapeutic method to decrease cardiac fibrosis^{228, 247}. Gal3 is also required in myofibroblasts for pro-fibrotic response to TGF β ²⁴⁹.

In addition to the well-known pro-fibrotic signaling pathways, S100 calcium-binding protein a8/a9 (S100a8/a9) produced by neutrophils was also found to activate fibroblasts in initiation of AngII-induced inflammation and fibrosis in the heart²⁵⁰. Moreover, osteopontin²⁵¹ and syndecan-1²⁵² have also been implicated in AngII-induced cardiac fibrosis.

Bone Morphogenetic Protein 9 Signaling

Bone morphogenetic protein 9 (BMP9) has been recently identified as a novel anti-fibrotic factor in a pressure overload hypertension model²⁵³. BMP9

can be synthesized in the liver but is also present in the heart. Its receptor is the activin receptor-like kinase 1 (ALK1) and can oppose actions of TGF β ²⁵⁴.

Matrix Metalloproteinase

Fibrosis is essential for tissue healing and repair. Fibrosis occurs when ECM protein synthesis exceeds degradation. The proteolysis enzymes that regulate ECM protein (e.g. collagen) degradation are mainly matrix metalloproteinases (MMPs), such as the collagenase MMP1 that cleaves mature collagen fibers²⁵⁵. MMP2 acts to remodel nascent collagens to enable correct fibril formation^{256, 257}. MMP9 is involved in inflammation-induced fibrosis via mediation of leukocyte migration. The activities of MMPs are antagonized by specific inhibitors: tissue inhibitors of metalloproteinases (TIMPs). The complex modulation between ECM protein synthesis, degradation by MMPs, and suppression of degradation by TIMPs coordinately determines the level of fibrosis. Other MMPs can also participate in ECM degradation.

Hypotheses Driving this Study

In this thesis, we will address the role of the myeloid IL-4 receptor in the response to two injury models: permanent occlusion of the left coronary artery as a model of MI (Chapter II) and chronic angiotensin-II and high salt diet as a model of hypertension (Chapter III). For each we will determine the importance of the myeloid IL4R α on a number of pathophysiological phenotypes of these two models. It will separate out functions of endogenous IL-4 on the myeloid line to determine the important cell types responding and the consequences of that response. This is a critical study since IL4R α is present on a variety of cell types including T cells, B cells, monocytes/macrophages, fibroblasts⁶¹, keratinocytes, epithelial cells, endothelial cells, and hepatocytes^{62, 63}, all of which could be contributing to the phenotype of IL-4 action. While IL4R α in macrophages is thought to play an important role, particularly in the polarization of macrophages, fibrosis and cardiovascular injury response, this assumption has not been tested in vivo. As a result, these studies will determine the importance of the macrophage response to endogenous IL-4 during the pathogenic processes.

1. We have tested the hypothesis that IL4R α is important in determining the AAM/M2 macrophage phenotype. While other cytokines and factors can influence macrophage polarization, IL-4 is thought to be a major determinant. Certainly, it is clear that AAM/M2 macrophages increase with administration of IL-4. We present analysis of both the number of macrophages and the level of expression of macrophage gene markers to detect changes in phenotype. Our original hypothesis was that this receptor would be critical for the determination of macrophage phenotype, with knockouts showing decreased AAM/M2 macrophages and marker gene expression.
2. Because of the AAM/M2 role in fibrosis and inflammation, we anticipated that cardiac remodeling would be aberrant with decreased fibrosis and the potential for increased tissue damage. To assess this, we analyzed collagen fibrosis by histology and gene expression. We also evaluated histology for evidence of increased tissue damage. To determine if fibrotic gene pathways were being activated, we determined the expression of pro- and anti-fibrotic genes and identified significant changes of these pathways in some circumstances.
3. We further hypothesized that with the loss of AAM/M2, we would have increased inflammation. We analyzed this aspect by evaluation of CAM/M1 markers and other inflammatory cytokine genes were increased.
4. Because IL-4 has been linked to improvements in cardiac function, we evaluated cardiac function and blood pressure. Cardiac function was evaluated by echocardiography and structural changes in the heart were evaluated including heart size and cardiomyocyte hypertrophy. We proposed that function in the myeloid (monocyte/macrophage and neutrophil)-specific IL4R α knockout (MyIL4R α KO) mice would be worse than control mice thus demonstrating that the phenotype had significant contributions from the IL-4 dependent induction of AAM/M2 phenotype. To assess vascular changes in the heart, we evaluated endothelial histology.

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CHAPTER II

MYELOID INTERLEUKIN-4 RECEPTOR SIGNALING IS NECESSARY FOR EFFICIENT CARDIAC REMODELING AND CARDIAC FUNCTION AFTER MYOCARDIAL INFARCTION

Abstract

Cardiac remodeling can be a critical determinant of outcome for patients after myocardial infarction (MI). Well-contained inflammation results in successful infarct healing while either inadequate or excessive inflammation can cause adverse remodeling and lead to heart failure. Reprogramming macrophages towards a resolving and reparative phenotype is a potential therapeutic approach. Interleukin-4 (IL-4) is a major inducer of alternative macrophage activation (M2) *in vitro*, and IL-4 treatment in MI has been shown to be beneficial although the target cell types have not been experimentally defined. We tested whether myeloid cells were important targets in a mouse model of MI using myeloid (monocyte/macrophage and neutrophil)-specific IL-4 receptor α knockout (MyIL4R α KO) mice.

MyIL4R α KO and floxed control (FC) mice were subjected to permanent ligation of the left coronary artery. Initial infarct size at 2 day post-MI was not affected by IL4R α knockout, but at 1 week post-MI, infarct size of MyIL4R α KO mice was significantly smaller than that of FC mice indicating changes in remodeling. At 3 week post-MI, infarct thickness of MyIL4R α KO mice was significantly increased compared with FC mice. These changes were accompanied by decreased expression of fibrosis markers: collagen 1A1 (Col1A1) and procollagen-lysine 2-oxoglutarate 5-dioxygenase 2 (Plod2). A significantly lower ejection fraction was observed in MyIL4R α KO mice compared with FC mice at 3 week. Importantly, MyIL4R α KO did not decrease the percentage of CD206⁺ M2-like macrophages post-MI and the expression of

macrophage markers was largely unchanged.

Myeloid-specific IL4R α knockout results in alterations in cardiac remodeling and decreased cardiac function post-MI, demonstrating that these cells are important targets of IL-4. Importantly, macrophage polarization markers were not significantly changed, suggesting that the functional changes observed and the protection from IL-4 is not through global changes in macrophage polarization; thus a simple macrophage polarization model is inadequate.

Introduction

Patients with acute myocardial infarction (MI), who survive the initial ischemia, are at higher risk of developing heart failure in a process named cardiac remodeling¹⁻⁴. Cardiac remodeling refers to structural changes in size and shape, such as dilation, sphericity, wall thinning, as well as epigenetic, molecular, cellular, compliant and functional changes that include both resident (cardiomyocytes, fibroblasts, macrophage) and non-resident (infiltrating leukocytes) cells of the heart, in the infarct area and in the peri-infarct and remote viable myocardium^{5, 6}. In the initial few days post MI, the infarct expands, which is characterized by acute ventricle dilation (without additional necrosis), infarct wall thinning and cardiomyocyte enlargement^{7, 8}. Extracellular matrix degradation augments cardiomyocyte slippage and infarct wall thinning. Cardiac fibroblasts and myofibroblasts produce a noncompliant collagen scar to maintain the ventricle geometry and prevent the development of aneurysm^{2, 3, 7, 9}. Cardiac remodeling is a powerful prognostic factor after MI and has been identified as a target for intervention^{4, 8, 10}.

Adverse cardiac remodeling post-MI can lead to impaired cardiac function and ultimately cause heart failure. Immune cells are a critical component of post-MI healing and have major regulatory effects on the healing and remodeling process. Following ischemic injury, there is an intense influx of leukocytes, mainly characterized by infiltration of neutrophils, followed by monocytes/macrophages and lymphocytes, which are involved in a complex inflammatory response to facilitate cardiac healing. Through interactions with cardiomyocytes and fibroblasts, these immune cells are directly involved in the

regulation of hypertrophic, fibrotic and wound healing responses during cardiac injury¹¹.

In addition to cardiomyocytes and fibroblasts, macrophages represent a major resident immune cell type in the heart that are maintained under normal, steady state conditions through local proliferation^{12, 13}. Macrophages exist within a spectrum of phenotypes and have been previously characterized as ranging from classically activated macrophages (CAM or M1) to alternatively activated macrophages (AAM or M2). Importantly, these characterizations are clearly inadequate^{14, 15}. At rest, the heart contains a heterogeneous population of resident macrophages with gene expression profiles that more closely resemble the AAM/M2 macrophage phenotype^{12, 16}. After MI, there are dynamic changes in macrophage phenotype. Kinetic analysis has shown that the early inflammatory phase is composed of a high percentage of macrophages expressing CAM/M1 markers, which most likely reflects the need for immune cell recruitment, phagocytosis and clearance of necrotic tissue^{17, 18}. During the later phase of injury, macrophages expressing AAM/M2 markers predominate and are thought to be involved in wound healing, angiogenic and profibrotic cardiac remodeling^{18, 19}.

Apoptosis of infiltrating neutrophils and a switch in macrophages from CAM/M1 to AAM/M2 phenotype are involved in the resolution of the inflammatory phase^{4, 18, 20}. Neutrophils undergo apoptosis, indicating the start of inflammation resolution, and leads to a gradual stop of the infiltration. Macrophages remove apoptotic neutrophils by phagocytosis and release cytokines and growth factors to potentiate the resolution^{21, 22}. Uncontrolled or delayed resolution of inflammation with an abundance of CAM/M1 is thought to be responsible for impaired wound healing and adverse cardiac remodeling post-MI. However, simply depleting or blocking macrophages does not appear to be a viable therapeutic strategy. Several studies have found that depleting macrophages results in decreased clearance of necrotic tissue, impaired collagen deposition, and decreased survival post-MI²³⁻²⁶. AAM/M2 macrophages are known to be involved in wound healing, and it is thought that enhanced AAM/M2 polarization

may be critical for efficient infarct remodeling; therefore, depletion of macrophages likely prevents this critical process.

There is increasing evidence to suggest that AAM/M2 macrophages are important for efficient cardiac remodeling and function after MI, and numerous studies have shown that enhanced AAM/M2 phenotypes correlate with cardiac protection^{27, 28}. Although there are many regulators of macrophage polarization, IL-4 and IL-13 are the major inducers of the AAM/M2 phenotype in vitro. These Th2 cytokines induce an AAM/M2 phenotype by activating the IL-4 and IL-13 receptors, both of which initiate signal transduction through the common IL-4 receptor α subunit (IL4R α). Global deletion of IL-13 has been shown to decrease survival and impair cardiac remodeling after MI in male mice²⁹. In addition, IL-4 administration has been shown to increase survival and improve cardiac function after MI²⁷. Importantly, tribbles homolog 1 (Trib1)^{-/-} mice that have an impaired capacity for AAM/M2 polarization are not protected by IL-4 administration. However, in addition to myeloid cells, IL4R α is expressed in a number of cell types including T cells³⁰, endothelial cell, smooth muscle cells³¹, and cardiomyocytes³². In fact, macrophage IL4R α inactivation did not affect allergic airway disease³³ even though IL-4 deficiency does³⁴.

To delineate the contribution of macrophage phenotypes mediated by IL-4 during cardiac injury and repair, we genetically ablated IL-4 receptor α in myeloid cells to prevent IL-4/IL-13-induced AAM/M2 polarization. We hypothesized that the myeloid cells are an important target of IL-4/IL-13 and that inhibition of IL4R α signaling in myeloid cells would block AAM/M2 responses post-MI and would lead to ineffective cardiac remodeling and decreased cardiac function.

Materials and Methods

Animals

IL4R $\alpha^{\text{flox/flox}}$ mice were previously produced on a BALB/c background³⁵. IL4R $\alpha^{\text{flox/flox}}$ mice were first backcrossed to C57BL/6 background for more than 10 generations, and then intercrossed with LysM-Cre mice (The Jackson Laboratory) to generate myeloid-specific IL4R α knockout (MyIL4R α KO) mice. Experiments used 10-12 weeks old male MyIL4R α KO mice (IL4R $\alpha^{\text{flox/flox}}$;LyzM^{Cre})

and littermate floxed controls (FC, IL4R α ^{flox/flox}). Numbers of mice for each experiment are shown in figure legends. Mice were randomly assigned to intervention (myocardial infarction, MI) or sham (no MI, NM) groups. Animal died from experimental MI within 24 hours (6.9%) or that displayed excessively small infarct size (2.7%) as a result of variations in vascular tree were excluded. All animal procedures were performed in accordance with the Guide for the Care and Use of Laboratory Animals (8th Edition) and were approved by the Institutional Animal Care and Use Committee of the University of Michigan.

Myocardial Infarction Model

Myocardial infarction (MI) was induced in mice by permanent ligation of the left anterior descending (LAD) coronary artery. Mice were anesthetized with 2% isoflurane, intubated, and maintained on mechanical ventilation while a thoracotomy was performed between the left 3rd and 4th intercostal space. The left ventricle was visualized and the LAD was ligated using 7-0 surgical silk suture. Occlusion of the LAD was confirmed by the presence of blanching of the myocardium in the LAD territory. The chest wall was closed with 6-0 silk suture, the intercostal and pectoral muscles were realigned, and the skin incision was closed with surgical staples. At the end of experiments, mice were euthanized by isoflurane. Simply, mice were first induced anesthesia by 3-4% isoflurane, once anesthesia was achieved, the isoflurane was increased to 5% to induce death. Mice were remained in the chamber for extra 3 minutes after no breath could be noticed. Afterwards euthanasia was further confirmed by exsanguination.

Infarct Size and Thickness

Infarct size at short-term (2 days and 1 week post-MI) was measured based on 2,3,5-triphenyltetrazolium chloride (TTC) stained heart sections with the area-based measurement. As the infarct wall thins over time, the area-based infarct size measurement is considerably compressed and becomes less appropriate, infarct size at late short-term to long-term (1 week and 3 week post-MI) was measured based on picosirius red (PSR) stained heart sections with length-based measurement.

Area-based infarct measurement: Hearts were arrested in diastole by

intraventricular injection of saturated KCl, and then excised, rinsed and briefly frozen at -20°C. The frozen hearts were cut into 1 mm thick transverse sections, and then incubated with 1% TTC solution at 37°C for 10 minutes with flipping. The stained sections were fixed in 4% paraformaldehyde. The infarct area and the area of left ventricle (LV) were traced by a blinded observer and quantified using ImageJ 1.45s software, and the area-based infarct size was calculated as: infarct size= (total infarct area/total area of left ventricle) x 100%.

Length-based infarct measurement: Hearts were arrested in diastole, fixed in 4% paraformaldehyde, and embedded in paraffin. Serial 5- μ m sections were cut through the heart from apex to base with an interval of 500- μ m distance. Heart sections were used for hematoxylin and eosin (H&E) and picosirius red (PSR) staining. Infarct length and left ventricle (LV) circumference were traced and measured using ImageJ 1.45s software based on PSR stained sections. Epicardial infarct ratio = epicardial infarct length/epicardial LV circumference. Endocardial infarct ratio = endocardial infarct length/ endocardial circumference. Infarct size was then calculated as a ratio of [epicardial infarct ratio + endocardial infarct ratio)/2] x 100%.^{36, 37}

To measure infarct thickness, a representative PSR-stained heart section from the middle of the heart and with the most significant LV cavity dilatation was chosen. Nine evenly spaced radians were marked through the infarct with the section center as a reference. The Infarct thickness of each segment was measured by ImageJ 1.45s software and the average was calculated.³⁶

Histopathological Analysis

Hearts were arrested in diastole, rinsed in PBS, fixed in 4% paraformaldehyde for 48 hours, and embedded in paraffin. Serial transverse sections (5 μ m) were cut through the heart with an interval of 500 μ m between sections, and then subjected to H&E and PSR staining. In order to determine myocyte cross-sectional area (CSA), pictures were taken of all regions in peri-infarct zone and remote zone of left ventricle in H&E stained sections using a Zeiss Axio Imager 2 microscope (Carl Zeiss, Jena, Germany). Myocytes with similar-sized nuclei and intact cellular membranes were outlined by a blinded

observer, and CSA was calculated using ImageJ 1.45s software. The average CSA was calculated from approximately 200 myocytes per sample. For fibrosis analysis, pictures were taken of all regions in infarct zone, peri-infarct zone and remote zone in PSR stained heart sections. Fibrotic (PSR positive) areas and areas of cardiomyocytes were traced and measured with ImageJ 1.45s software. The percentage of fibrotic area was calculated as: $\text{area of fibrosis}/(\text{area of cardiomyocytes} + \text{area of fibrosis}) \times 100\%$.³⁸ 5- μm thick heart sections were also used for immunohistochemical staining for endothelial cells forming vasculature (CD31, DIA310, Diavona), and images captured. CD31-positive vessels were quantified using ImageJ 1.45s and reported as 'percent per field'.

Bone Marrow-Derived Macrophage

Anesthesia was induced in mice by 3-4% isoflurane, once anesthesia was achieved, the isoflurane was increased to 5% to induce death. Mice were remained in the chamber for extra 3 minutes after no breath could be noticed. Afterwards euthanasia was further confirmed by exsanguination. When the death was confirmed, mice were dissected and bones were collected for producing bone marrow-derived macrophages, and peritoneal macrophages were collected by peritoneally flushing with ice cold PBS.

Bone marrow-derived macrophages (BMDMs) were produced by flushing bone marrow from femurs and tibias. Briefly, bone marrow cells were flushed out with ice-cold PBS in a laminar flow hood. After centrifugation, cells were resuspended in RPMI 1640 medium with 10% fetal bovine serum (FBS), 100 units/ml penicillin and streptomycin, 30% L929-conditioned medium, 1% Glutamax® and 0.1% Eagle's basal medium (BME). The cells were then cultured in a humidified incubator under 95% air and 5% CO₂ at 37°C for 4 days. On day 4, medium was replaced by fresh medium. After two more days culturing, BMDMs were differentiated and ready for experiments on day 6.

Alternative macrophage activation was achieved by treatment with IL-4 (50 ng/ml) for 24 h, while classical macrophage activation was achieved by treatment of 100 ng/ml lipopolysaccharide (LPS) for 3 h.

Immunofluorescence

After deparaffinization and rehydration, 5- μ m thick sections of heart tissue were subjected to microwave epitope retrieval in 10 mM Tris-HCl (pH 9) containing 1 mM EDTA. After rinsing several times in 10 mM Tris-HCl buffer (pH 8) containing 0.154 M NaCl (TBS), non-specific binding of the antibodies was extinguished by a 30 min incubation with ‘Background Sniper’ (BioCare Medical, Concord, CA). The slides were labeled simultaneously with CD206 (Alexa Fluor® 488, BioLegend, San Diego CA, #141710), and F4/80 (PE, BioLegend, San Diego CA, #123110) overnight at 4 °C. The slides were washed with 3 changes of TBS and stained with the nucleus staining dye 4',6-diaminodo-2-phenylindole (DAPI) in a non-fading mounting media (ProLong Gold, Molecular probes, Carpinteria, CA).

Gene Expression Analysis

Relative mRNA expression was determined using quantitative reverse transcription–polymerase chain reaction (qRT-PCR). Total RNA was extracted using TRIzol reagent and RNA (1 μ g) was reverse transcribed to cDNA with a High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems). Quantitative polymerase chain reaction (qPCR) was performed using a 7900HT fast real-time PCR system (Applied Biosystems) and relative mRNA expression was analyzed using the comparative method and normalized to the internal control L32. All qPCR primers are listed in Table 2.1.

Gene	Forward	Reverse
ANP	GCTTCCAGGCCATATTGGAG	GGGGGCATGACCTCATCTT
Arg1	ACCTGGCCTTTGTTGATGTCCCTA	AGAGATGCTTCCAACCTGCCAGACT
BNP	ATGGATCTCCTGAAGGTGCTG	GTGCTGCCTTGAGACCGAA
CCL11	GAATCACCAACAACAGATGCAC	ATCCTGGACCCACTTCTTCTT
CCL17	CATGAGGTCACTTCAGATGCTG	CCTGGAACACTCCACTGAGG
Col1A1	GCTCCTCTTAGGGGCCACT	CCACGTCTCACCATTGGGG
Col3A1	CCTGGCTCAAATGGCTCAC	CAGGACTGCCGTTATTCCCG
F13A1	GAGCAGTCCCGCCCAATAAC	CCCTCTGCGGACAATCAACTTA
Fizz1	ACTGCCTGTGCTTACTCGTTGACT	AAAGCTGGGTTCTCCACCTCTTCA
IL-6	GAGGATACTCACTCCCAACAGACC	AAGTGCATCATCGTTGTTTCATACA
IL-1 β	AAGAGCTTCAGGCAGGCAGTATCA	TGCAGCTGTCTAATGGGAACGTCA
IL4R α	TCTGCATCCCGTTGTTTTGC	GCACCTGTGCATCCTGAATG
L32	TTAAGCGAAACTGGCGGAAAC	TTGTTGCTCCATAACCAGATG
MCP1	TCACCTGCTGCTACTCATTACCA	TACAGCTTCTTTGGGACACCTGCT
Plod2	GAGAAGTGGCATGTTTCCTC	CCCAAAGTGTAAACGGAAGGAG
TNF α	CCCTCACACTCAGATCATCTTCT	GCTACGACGTGGGCTACAG
Ym1	CACCATGGCCAAGCTCATTCTTGT	TATTGGCCTGTCTTAGCCCAACT

Table 2.1. Sequences of all primers used in chapter II. They were synthesized by Integrated DNA Technologies. L32, 60S ribosomal protein L32, was used as internal control.

Flow Cytometric Analysis

Single cell suspensions were prepared from peripheral blood and by mincing heart tissue into small pieces followed by digestion in DMEM containing collagenase I (450 U/mL), collagenase II (600 U/mL), collagenase XI (125 U/mL), DNase I (60 U/mL), and hyaluronidase (60 U/mL) for 1 h at 37°C with agitation. Cells were incubated in Fc Block for 10 min and then stained on ice for 1 h with the following antibodies: anti-mouse CD45 Pacific Blue™ (clone 30-F11, Biolegend, cat # 103126), anti-mouse/human CD11b PE/Cy7 (clone M1/70, Biolegend, cat # 101216), anti-mouse F4/80 PE (clone BM8, Biolegend, cat # 123110), anti-mouse Ly6C PerCP/Cy5.5 (clone HK1.4, Biolegend, cat # 128011), anti-mouse CD206 Alexa Fluor® 488 (clone C068C2, Biolegend, cat # 141709), and anti-mouse CD301 APC (clone LOM-14, Biolegend, cat # 145707). Stained cells were washed twice in PBS and fixed in 0.1% paraformaldehyde before analysis. Flow cytometry was performed using a BD FACS Canto II flow cytometer and analyzed with FlowJo V10.1 software. Neutrophils were defined as CD45⁺CD11b⁺F4/80⁻Ly6C⁻SSC^{high}FSC^{low}, macrophages as CD45⁺CD11b⁺F4/80⁺Ly6C⁻SSC^{low}, and monocytes as CD45⁺CD11b⁺F4/80⁻Ly6C^{high-low}SSC^{low}, and monocytes were further divided into Ly6C^{high} and Ly6C^{low} monocyte populations. Within macrophages, AAM/M2 macrophages were further defined as CD206⁺CD301⁺. For calculation of total cell numbers in heart, normalization to weight of indicated tissues was performed. The total number of each cell population per 100 milliliter of blood was calculated by multiplying the total cell number by the percentage of each cell population within the gate.

Echocardiography

Mice were anesthetized with isoflurane, and echocardiography was performed using a Vevo 2100 Micro-Imaging System (VisualSonics Inc.) with a 18-38-MHz linear array ultrasound transducer. LV ejection fraction was determined from the two-dimensional long axis view. Ejection fraction and

fractional shortening were calculated based on the M-mode parasternal short axis view. Systolic and diastolic dimensions and wall thickness were determined by M-mode in the parasternal short axis view. Diastolic function was assessed by conventional pulsed-wave spectral Doppler analysis of mitral valve inflow patterns (early [E] and late [A] filling waves). Doppler tissue imaging (DTI) was used to measure the early (Ea) diastolic tissue velocities of the septal and lateral annuluses of the mitral valve in the apical 4-chamber view.

Statistical Analysis

Results are presented as mean \pm SEM. For statistical analysis, one-way ANOVA, two-way ANOVA with a Bonferroni post-test and unpaired, two-tailed Student's *t* test were used. All statistical analysis of data was performed in GraphPad Prism (version 6; GraphPad Software, Inc). *P* < 0.05 was considered significant.

Results

Myeloid IL4R α deficiency changes macrophage polarization in vitro and cardiac macrophage markers at steady state in vivo

To test the role that myeloid IL4R α signaling and AAM/M2 polarization have during MI and post-MI cardiac remodeling, we used myeloid-specific IL-4 receptor α knockout mice (MyIL4R α KO). As expected, bone marrow-derived macrophages (BMDMs) from MyIL4R α KO mice had a significant reduction in IL4R α gene expression (Figure 2.1A), and importantly, this resulted in significant ablation of IL-4-induced AAM/M2 polarization. IL-4 treatment resulted in a significant increase in gene expression of AAM/M2 markers: Arg1, Ym1, and Fizz1 in macrophages from FC mice; however, this response was significantly abolished in MyIL4R α KO mice (Figure 2.1A). Like IL-4 stimulated AAM/M2 markers activation, LPS significantly activated the gene expression of CAM/M1 markers including TNF α , IL-1 β , IL-6 and MCP1 (Figure 2.1A). Moreover, BMDMs from MyIL4R α KO mice showed significant increase in the mRNA level of TNF α , IL-1 β and IL-6 (Figure 2.1A) although not in MCP1 (Figure 2.1A), which suggests the increase of CAM/M1 polarization as a result of IL4R α deficiency. Taken together, myeloid-specific IL4R α knockout significantly inactivates IL4R α

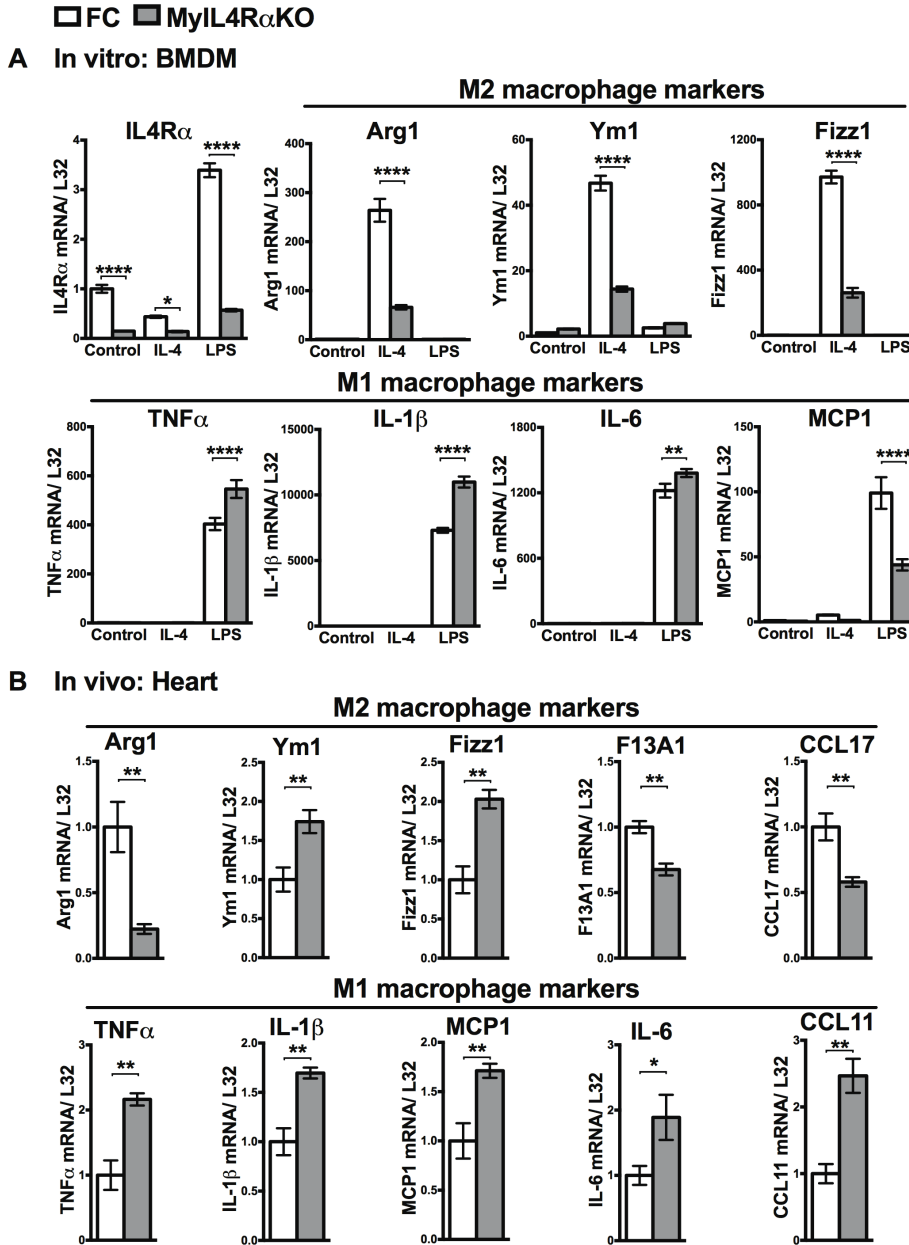


Figure 2.1. IL4R α deficiency in myeloid cells efficiently inactivates IL4R α signaling in macrophages and changes the macrophage markers expression in heart at steady state. (A) Bone marrow-derived macrophages (BMDMs) were produced from bone marrow of floxed control (FC) and myeloid-specific IL4R α knockout (MyIL4R α KO) mice, and treated by M2 macrophage stimulus IL-4 or M1 macrophage stimulus LPS. mRNA levels of IL4R α , AAM/M2 markers: Arg1, Ym1 and Fizz1 and CAM/M1 markers: TNF α , IL-1 β , IL-6 and MCP1 were determined using qRT-PCR. **(B)** Baseline mRNA gene expression of AAM/M2 markers: Arg1, Ym1, Fizz1, F13A1 and CCL17 and CAM/M1 markers TNF α , IL-1 β , MCP1, IL-6 and CCL11 was analyzed in intact hearts by qRT-PCR. Results are presented as means \pm SEM. $n = 5-6$. Two-way ANOVA and Student's t test were used for statistical analysis. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; **** $P < 0.0001$.

signaling in macrophages, and induces less AAM/M2 macrophage polarization and more CAM/M1 macrophage polarization in vitro.

In order to test whether the IL4R α signaling in myeloid cells also changes macrophage polarization in vivo especially in resident macrophages in heart, we analyzed the basal expression of selected AAM/M2 markers (Arg1, Ym1, Fizz1, F13A1 and CCL17) in the hearts of MyIL4R α KO mice, then we measured the basal expression of CAM/M1 markers (TNF α , IL-1 β , MCP1, IL-6 and CCL11) by qRT-PCR. The mRNA level of AAM/M2 markers Arg1, F13A1 and CCL17 was significantly decreased in MyIL4R α KO mice, although Ym1 and Fizz1 oppositely showed increase (Figure 2.1B). The mRNA level of CAM/M1 markers was consistently increased in MyIL4R α KO mice (Figure 2.1B). This basal level increase in CAM/M1 markers and the decrease in several AAM/M2 markers indicate the disturbance of macrophage polarization in vivo by IL4R α deficiency in myeloid cells, with more CAM/M1 polarization and relatively less AAM/M2 polarization, although the Ym1 and Fizz1 mRNA were increased in MyIL4R α KO mice, which may indicate not only macrophages, but also the other cell types contribute to the mRNA expression of Ym1 and Fizz1.

Myeloid IL4R α knockout has differential effects on infarct size and hypertrophy post-MI

We subjected mice to experimental MI by left anterior descending coronary artery ligation and first determined the effect that MyIL4R α KO had on early infarct development at 2 days and 1 week after MI. For early infarct size estimation, area measurement based on 2,3,5-triphenyltetrazolium chloride staining was used, whereas for later time points, as a result of wall thinning, the area measurement approach becomes less appropriate that length measurement based on picosirius red staining was used.³⁷ Results showed that there was no difference in infarct size between MyIL4R α KO and FC mice at 2 days post-MI (Figure 2.2A and B). However, both area- and length-based measurement of infarct size displayed a significant decrease in MyIL4R α KO mice 1 week post-MI (Figure 2.2A and B), although there was no significant change detected at 3 weeks post-MI (Figure 2.2B and C). Consistent with the decreased infarct size of

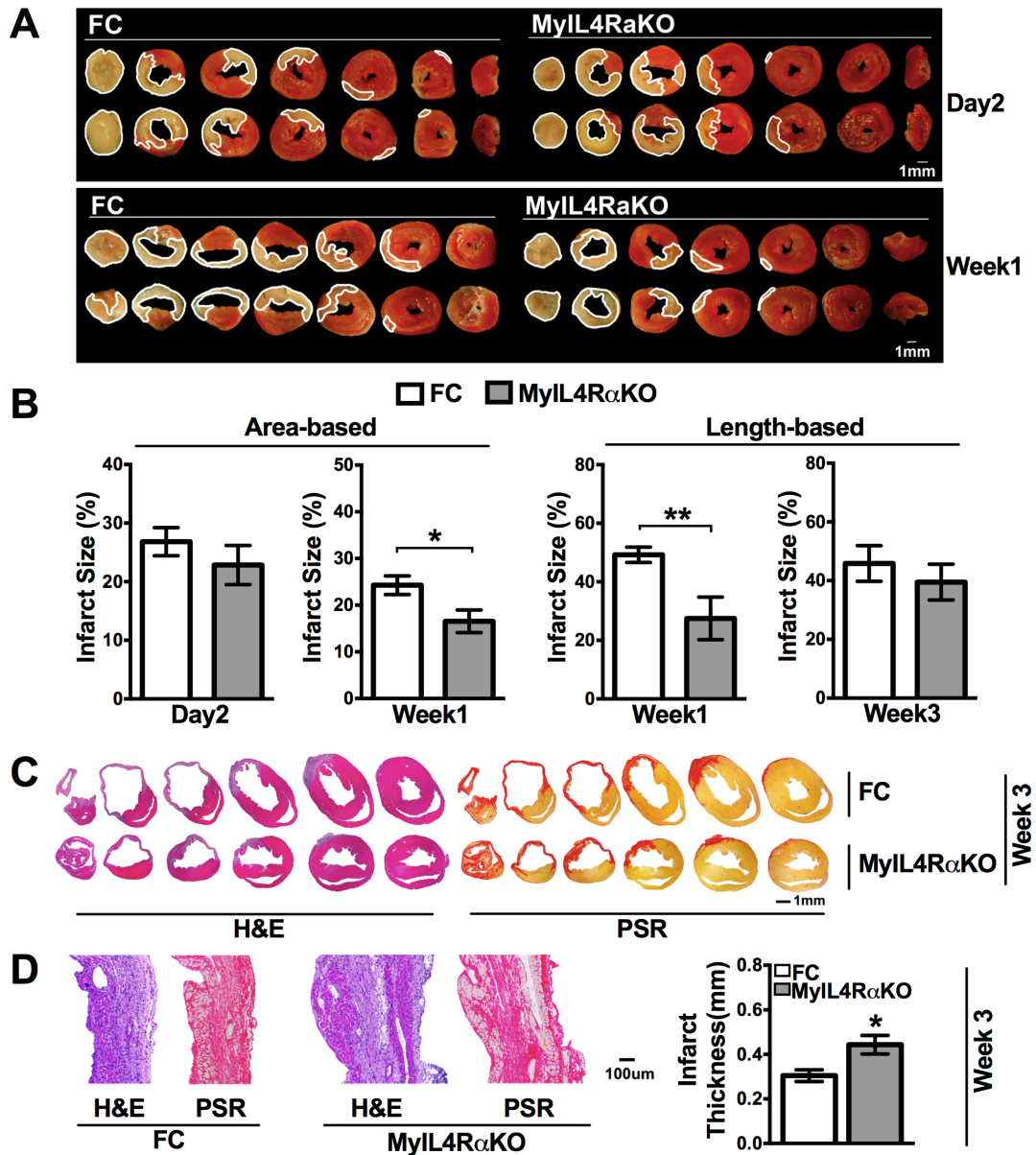


Figure 2.2. Myeloid IL4R α knockout changes infarct size and thickness. (A) Representative images of serial 2,3,5-triphenyltetrazolium chloride (TTC) stained heart sections at 2 day and 1week post-MI. Infarct areas were outlined in white. **(B)** Measurement of infarct size. Area-based infarct size measurement of hearts at 2 day ($n = 5-6$) and 1 week ($n = 11-16$) post-MI based on TTC staining and length-based infarct measurement of hearts at 1 week ($n = 5-8$) and 3 week ($n = 7-9$) post-MI based on picosirius red (PSR) staining. **(C)** Representative images of serial PSR stained heart sections at 3 week post-MI, and their hematoxylin and eosin (H&E) counterstaining. **(D)** Representative photomicrographs of PSR stained heart sections showing infarct thickness at 3 week post-MI, and their counterstaining of H&E and infarct thickness determination based on PSR stained heart sections ($n = 9-11$). Results are shown as means \pm SEM. Unpaired Student's t test was used for statistical analysis. * $P < 0.05$; ** $P < 0.01$.

MyIL4R α KO mice at 1 week post-MI, infarct thickness was shown significant increase in MyIL4R α KO mice at 3 weeks post-MI compared to FC mice (Figure 2.2D), suggesting that IL4R α signaling in myeloid cells may have an important role in post-MI cardiac remodeling.

Since immune cells can influence the hypertrophic response to cardiac injury, we next investigated whether myeloid IL4R α inactivation altered cardiac hypertrophy post-MI. We detected significant increases in heart weight to body weight ratio (HW/BW) in FC mice at 2 days, 1 week and 3 weeks post-MI and a significant increase in heart weight to tibia length ratio (HW/TL) at 1 week post-MI when compared to mice with no MI (Figure 2.3A). A small decrease in HW/BW was shown in MyIL4R α KO mice at 1 week post-MI when compared to FC mice, however this difference was undetectable by 3 week (Figure 2.3A). Similarly, cardiomyocyte size was significantly increased due to MI, but no difference was detected between FC and MyIL4R α KO mice (Figure 2.3B). We also analyzed the expression of hypertrophy-induced fetal genes atrial natriuretic peptide (ANP) and brain natriuretic peptide (BNP) in heart tissues by qRT-PCR. Although there was significant induction of ANP and BNP by MI, there was no difference detected between FC and MyIL4R α KO mice post-MI (Figure 2.3C). To be noticed, among mice with no MI, MyIL4R α KO showed significant increase in BNP expression compared with FC mice (Figure 2.3C), suggesting the difference between FC and MyIL4R α KO mice at basal level. Collectively, these data indicate that myeloid IL4R α inactivation does not significantly alter the hypertrophic response post-MI.

Myeloid IL4R α signaling is involved in fibrosis post-MI

IL-4 is thought to play an important role in fibrosis although whether effects are mediated through an AAM/M2-like macrophage phenotype in vivo has not been determined³⁹⁻⁴¹. We, therefore, determined the effect of IL4R α inactivation on fibrosis during the remodeling response post-MI. Cardiac interstitial fibrosis and perivascular fibrosis were examined using picosirius red staining. The interstitial fibrosis did not show any change due to the lack of IL4R α in myeloid cells whether in infarct zone, peri-infarct zone or remote zone (Figure

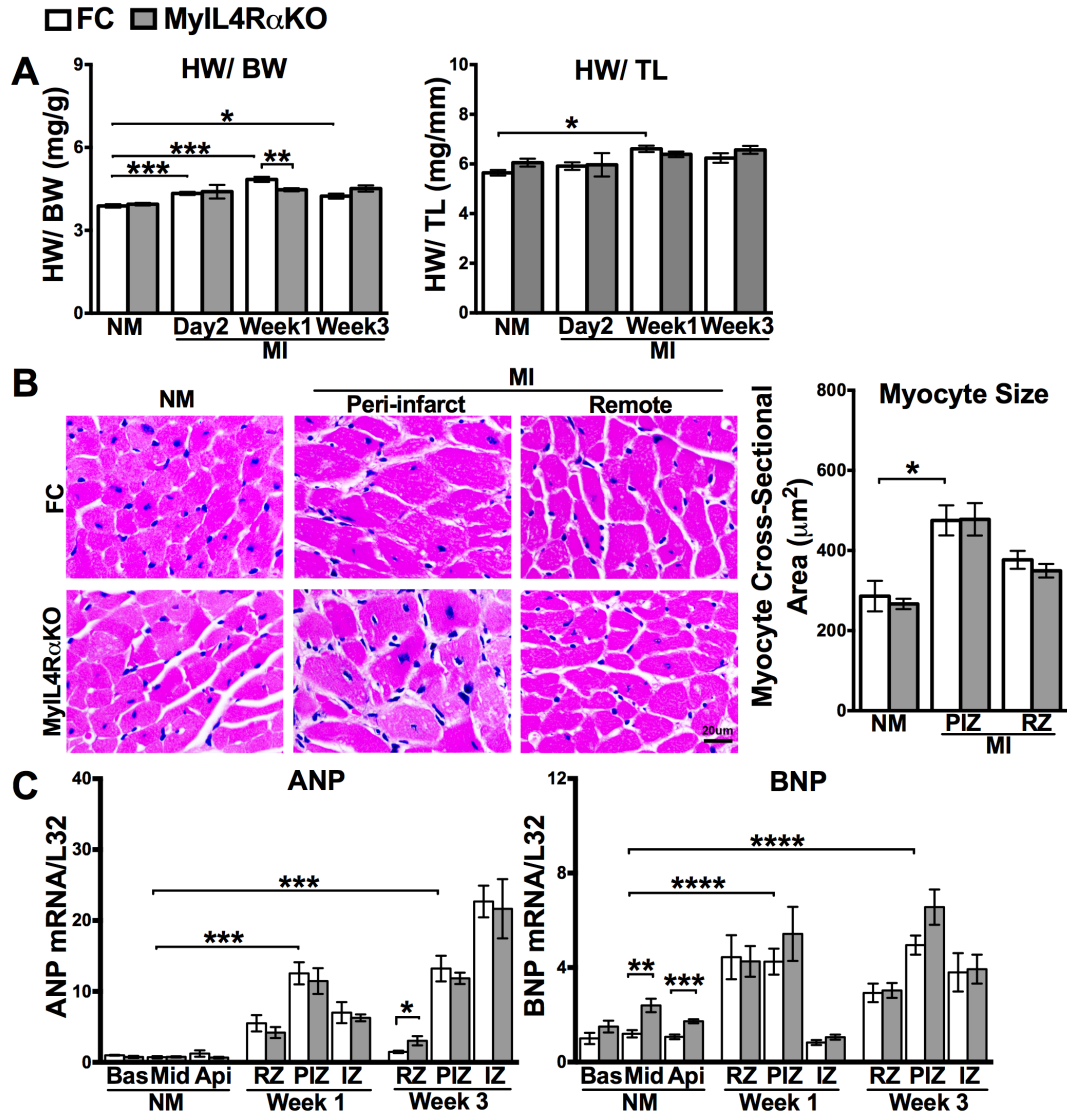


Figure 2.3. Myeloid-specific IL4Rα is not involved in hypertrophic cardiac remodeling. (A) Heart weight to body weight ratio (HW/BW) and heart weight to tibia length ratio (HW/TL) were measured at 2 day, 1 week and 3 week post-MI. Mice with no MI (NM) were served as controls. (FC, $n = 8$ and MyIL4RαKO, $n = 13$ in no MI controls; FC, $n = 6$ and MyIL4RαKO, $n = 4$ at 2 day; FC, $n = 49$ and MyIL4RαKO, $n = 42$ at 1 week; FC, $n = 18$ and MyIL4RαKO, $n = 22$ at 3 week). (B) Representative images of H&E stained heart sections 3 week post-MI and the cardiomyocyte cross-sectional area in peri-infarct (PIZ) and remote zone (RZ) was determined. $n = 9-12$. (C) The mRNA expression of fetal genes ANP and BNP of heart tissues at 1 week and 3 week post-MI was analyzed by qRT-PCR at infarct zone (IZ), peri-infarct zone (PIZ) and remote zone (RZ) respectively. Hearts from mice with no MI (NM) were dissected similarly into apical (Api), middle (Mid) and basal (Bas) regions and served as controls. $n = 4-8$. All results are shown as means \pm SEM. Unpaired Student's t test was used for statistical analysis. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; **** $P < 0.0001$.

2.4A). However, perivascular fibrosis in peri-infarct zone was significantly increased in MyIL4R α KO mice compared to FC (Figure 2.4B). In order to find out whether the change in perivascular fibrosis results in any change in angiogenesis after infarction, we investigated the expression of CD31 by immunohistochemistry in heart sections post-MI. CD31 showed significantly higher expression in remote zone than in infarct or peri-infarct zone (Figure 2.4D), indicating the deteriorated vasculogenesis system in infarct and peri-infarct zone. However, the expression of CD31 did not show any difference between FC and MyIL4R α KO mice (Figure 2.4D), which is consistent with the CD31 expression between IL4R α ^{flox/flox} and IL4R α ^{flox/-}LysM^{Cre} mice during wound healing after injury in skin⁴¹. These results suggest that the change in perivascular fibrosis does not affect angiogenesis post-MI.

We next quantified the mRNA expression of fibrotic markers like collagen 1A1 (Col1A1), collagen 3A1 (Col3A1) and procollagen-lysine 2-oxoglutarate 5-dioxygenase 2 (Plod2) in heart tissues post-MI. These genes were all significantly increased as a result of MI (Figure 2.4C), and MyIL4R α KO mice displayed a significant decrease in Col1A1 and Plod2 mRNA level in infarcted tissues at 3 weeks post-MI when compared with FC (Figure 2.4C), which is consistent with the pro-fibrotic role of IL-4 signaling in myeloid cells³⁹, although the increase of perivascular fibrosis in MyIL4R α KO mice is surprisingly the opposite. These suggest the possibility that without anti-inflammatory activity of IL-4 action in myeloid cells, there is increased perivascular pro-fibrotic effect from persistent inflammatory stimulation, and this may be unrelated to angiogenesis.

Myeloid IL4R α deficiency deteriorates cardiac function post-MI

To determine if the changes in cardiac remodeling caused by IL4R α knockout in myeloid cells result in functional deficits, we performed echocardiography on mice at 3 weeks post-MI to assess cardiac function (Figure 2.5A). No differences were detected in baseline cardiac function in FC and MyIL4R α KO mice without MI (Figure 2.5B). When compared with mice with no MI, mice at 3 weeks post-MI had significantly reduced ejection fraction and fractional shortening (Figure 2.5B). More importantly, a significant decrease in

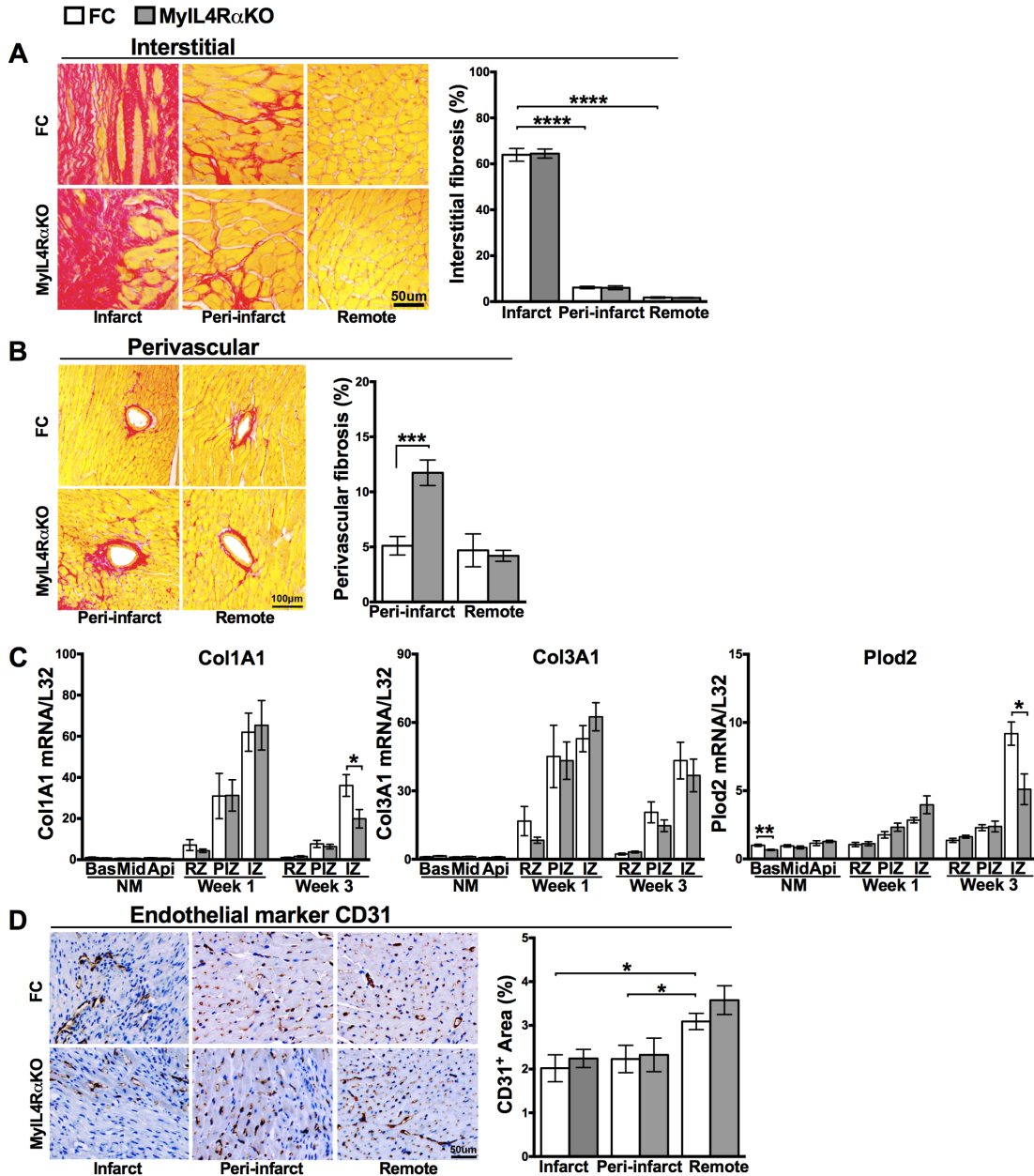


Figure 2.4. IL4R α signaling in myeloid cells is involved in fibrotic cardiac remodeling post-MI. Representative images of picrosirius red stained heart sections at 3 week post-MI to show interstitial (A) and perivascular (B) fibrosis in hearts at 3 week post-MI, and their respective quantification. $n = 7-9$. (C) mRNA gene expression of fibrosis markers Col1A1, Col3A1, and Plod2 by qRT-PCR at 1 week and 3 week post-MI. Heart tissues were dissected into remote zone (RZ), peri-infarct zone (PIZ) and infarct zone (IZ), and hearts of mice with no MI (NM) were dissected similarly into basal (Bas), middle (Mid) and apical (Api) region. $n = 6-8$. (D) Representative images of heart sections 3 week post-MI by CD31 staining and the quantification of the percentage of CD31 positive areas. $n = 6-7$. All results are shown as means \pm SEM. Unpaired Student's t test was used for statistical analysis. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; **** $P < 0.0001$.

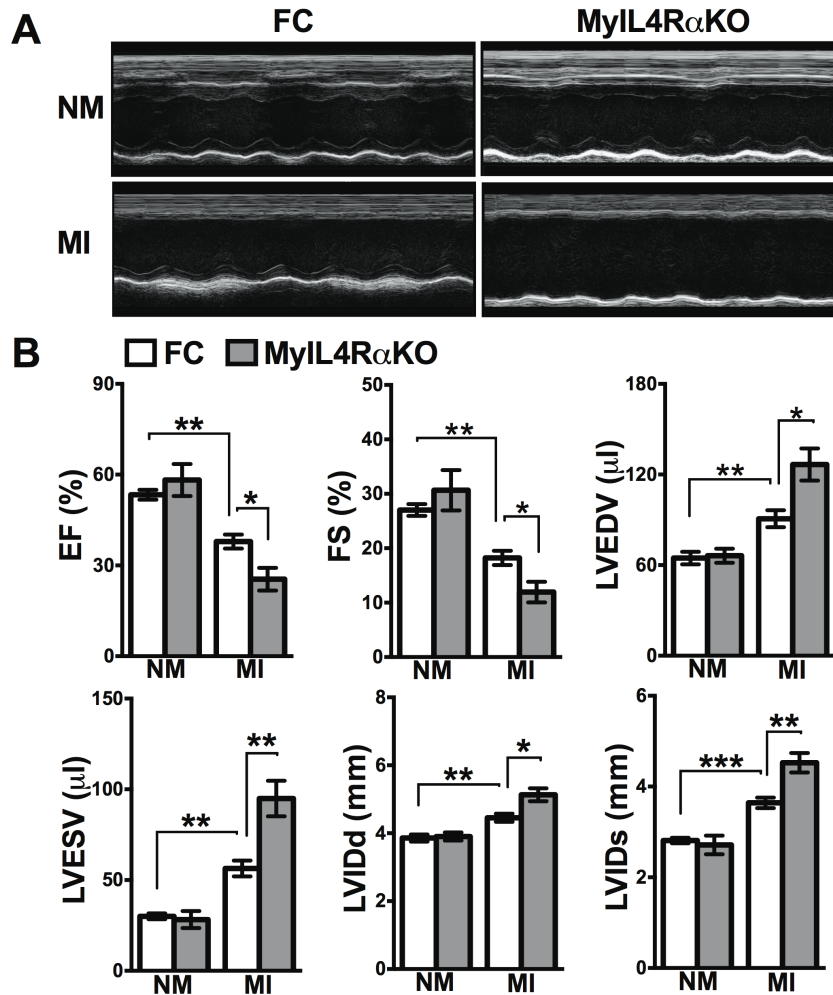


Figure 2.5. Myeloid IL4R α knockout impairs cardiac function after MI. Cardiac function was analyzed at 3 week post-MI by echocardiography. **(A)** Representative echocardiographic images of FC and MyIL4R α KO mice 3 week post-MI. **(B)** Quantitative evaluation of echocardiography data collected 3 week post-MI including ejection fraction (EF), fractional shortening (FS), left ventricle end diastolic volume (LVEDV), left ventricle end systolic volume (LVESV), left ventricular internal diameter diastole (LVIDd), and left ventricle internal diameter systole (LVIDs). Mice that did not receive MI are labeled as NM (no MI) and served as controls. $n = 4-5$. Results are presented as means \pm SEM. Unpaired Student's t test was used for statistical analysis. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

ejection fraction and fractional shortening was detected in MyIL4R α KO mice 3 weeks post-MI when compared to FC mice (Figure 2.5B). Similarly, MyIL4R α KO mice had significantly increased left ventricle end diastolic volume, left ventricle end systolic volume, left ventricular internal diameter diastole, and left ventricle internal diameter systole (Figure 2.5B), indicating that MyIL4R α KO mice have impaired cardiac function. In conclusion, these results suggest that IL4R α signaling in myeloid cells is critical in cardiac remodeling that loss of this signaling impairs cardiac function.

Myeloid IL4R α inactivation does not change macrophage polarization post-MI

Although we found impaired cardiac function in MyIL4R α KO mice, the mechanism by which myeloid IL4R α deficiency decreases cardiac function is still unknown. In order to test our hypothesis that IL4R α signaling in myeloid cells changes macrophage polarization, we measured the mRNA expression of CAM/M1 and AAM/M2 markers in heart tissues post-MI. There was increased expression of both CAM/M1 markers and AAM/M2 markers at 1 week and 3 weeks post-MI with highest levels found predominantly in the infarct zone (Figure 2.6). However, no differences in CAM/M1 marker expression were detected between FC and MyIL4R α KO mice post-MI (Figure 2.6). Similarly, no difference was found in the expression of the AAM/M2 marker: Arg1, but increased expression of Ym1 was found in infarct tissues of MyIL4R α KO mice at 1 week, and increased expression of Fizz1 in both infarct and peri-infarct tissues at 1 week and in infarct tissues at 3 weeks post-MI (Figure 2.6). Expectedly, the expression of CAM/M1 markers and AAM/M2 markers in heart tissues with no MI was consistent with the basal level expression (Figure 2.1B), which showed increase in CAM/M1 markers and decrease (Arg1) or increase (Ym1 and Fizz1) in AAM/M2 markers, indicating the disturbance of macrophage polarization in vivo by IL4R α deficiency in myeloid cells with more CAM/M1 polarization at steady state. Collectively, these data suggest that IL4R α deficiency in myeloid cells significantly changes macrophage polarization at steady state with increase of inflammation in heart; however, most of the changes disappear in

□ FC ■ MyIL4R α KO

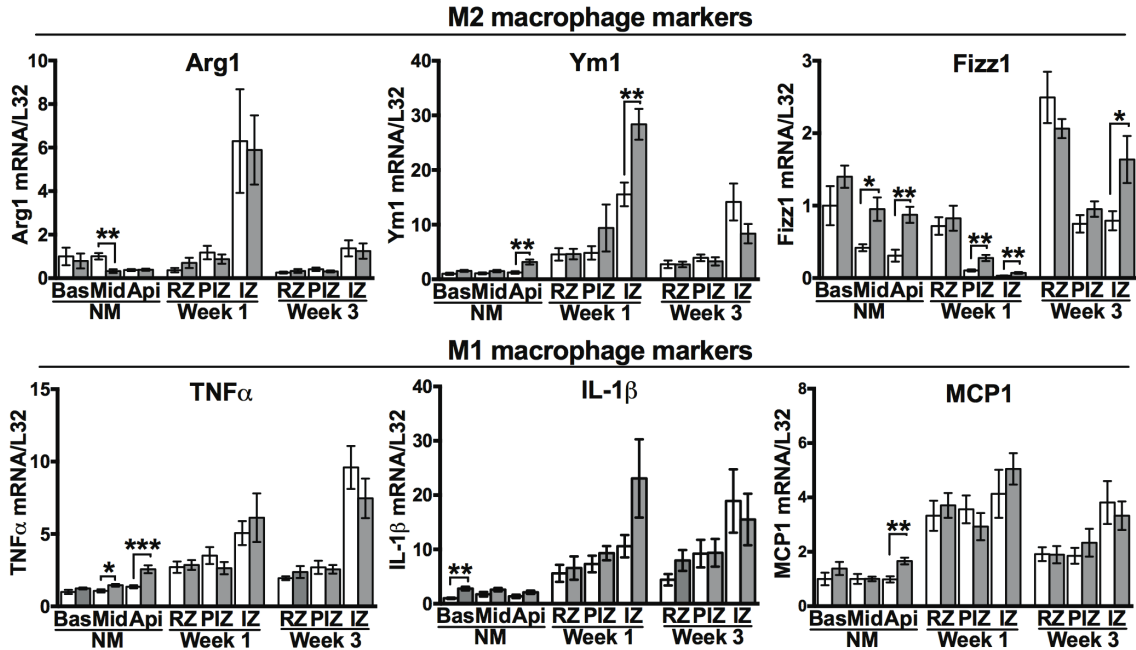


Figure 2.6. Gene expression analysis of pro-inflammatory CAM/M1 and anti-inflammatory AAM/M2 markers in heart tissues post-MI. The mRNA level of anti-inflammatory AAM/M2 markers: Arg1, Ym1 and Fizz1 and pro-inflammatory CAM/M1 markers: TNF α , IL-1 β and MCP1 was measured at 1 week and 3 week post-MI in tissues from heart. Hearts post-MI were dissected into remote zone (RZ), peri-infarct zone (PIZ) and infarct zone (IZ) while mice with no MI (NM) were dissected similarly into basal (Bas), middle (Mid) and apical (Api) regions. $n = 5-8$. Results are presented as means \pm SEM. Unpaired Student's t test was used for statistical analysis. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

inflammatory state (post-MI).

In order to further determine if myeloid-specific IL4R α knockout changes macrophage polarization during MI, we used flow cytometry to characterize the macrophage subtypes defined by cell surface markers expression. At 1 week post-MI, there was a marked decrease in the percentage of CD301⁺CD206⁺ AAM/M2 macrophages in infarct tissues compared with non-infarct tissue or heart tissues with no MI, but no differences were detected as a result of myeloid IL4R α inactivation (Figure 2.7A). This is supported by the results that neither the percentage of Ly6C^{high} nor Ly6C^{low} monocytes showed any difference between FC and MyIL4R α KO mice (Figure 2.7B and C). The number of CD206⁺CD301⁺ AAM/M2 macrophages was significantly increased in infarct tissues (Figure 2.7A), indicating the recruitment of AAM/M2 macrophages into the infarcts, however similarly, no difference was shown between MyIL4R α KO and FC mice, as well as the number of macrophages, neutrophils and Ly6C^{high} and Ly6C^{low} monocytes (Figure 2.7B), which suggests that the inactivation of IL4R α signaling in myeloid cells does not change the recruitment and trafficking of myeloid cells to infarct tissue, neither their polarization. This was further confirmed by the quantification of neutrophils and monocytes in blood of mice post-MI. The number of neutrophils and monocytes was significantly increased in blood because of MI (Figure 2.7D), indicating the circulation and trafficking of myeloid cells after MI, however the percentage or the number of neutrophils and monocytes in blood did not change as a result of IL4R α knockout in myeloid cells (Figure 2.7D). We also performed immunofluorescent staining of heart sections to independently investigate the effect of IL4R α knockout on macrophage polarization. F4/80 and CD206 were used to identify macrophage and AAM/M2 macrophages respectively, and showed no changes due to IL4R α deficiency in myeloid cells (Figure 2.8). These results again indicate that myeloid-specific IL4R α inactivation does not change the polarization of AAM/M2 macrophages post-MI, although it did cause significant changes in cardiac remodeling and function.

□ FC ■ MyIL4RαKO

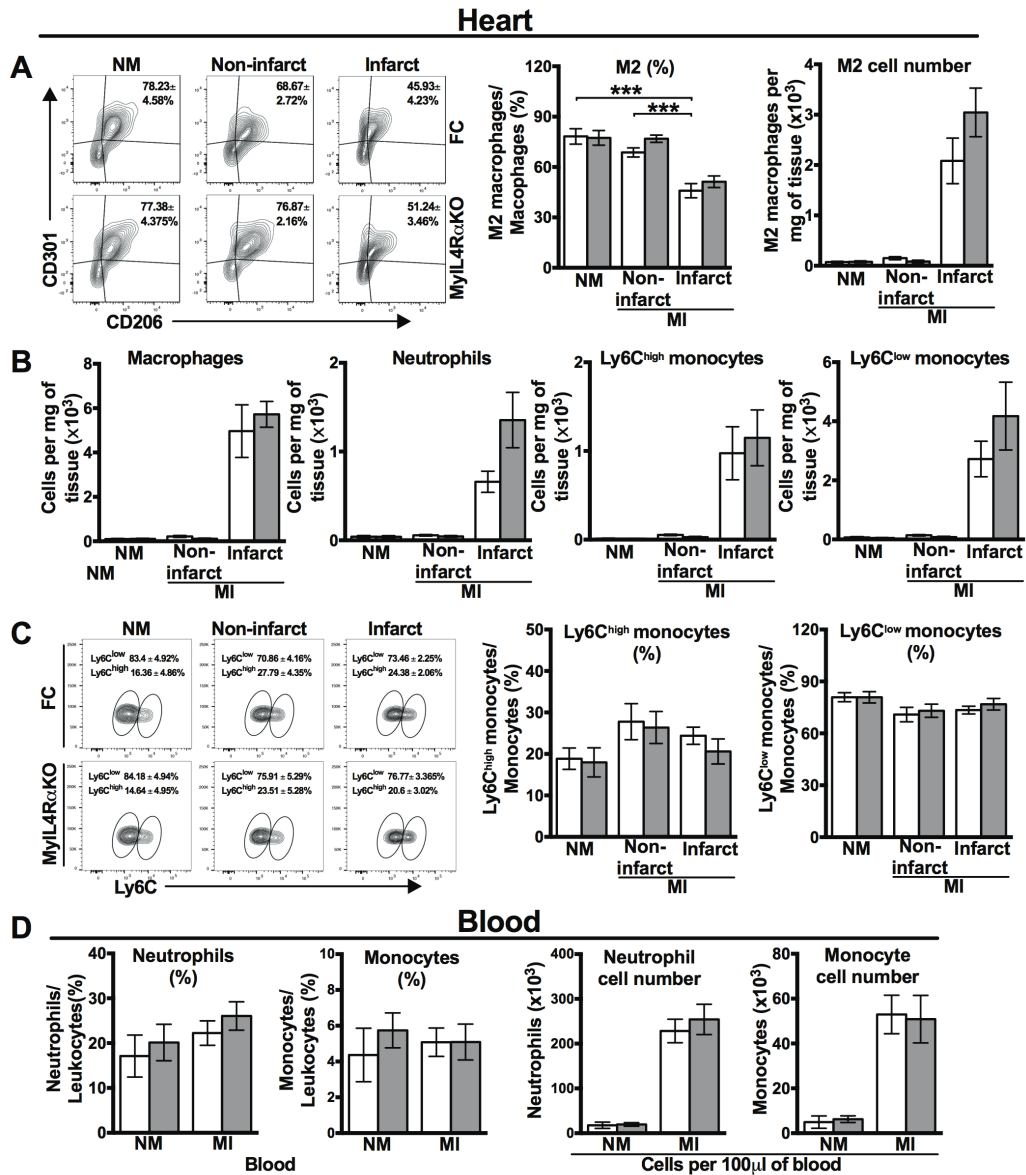


Figure 2.7. Myeloid IL4Rα knockout does not alter myeloid cells recruitment or macrophage polarization. Flow cytometric analysis of macrophages, neutrophils and monocytes in intact hearts of control mice (NM, no MI), infarcted and non-infarcted (including remote and peri-infarct) heart tissues of FC and MyIL4RαKO mice 1 week post-MI. Representative FACS contour plots of CD206⁺CD301⁺ M2-like macrophages gated from macrophages (**A**) and Ly6C^{high} and Ly6C^{low} monocytes gated from total monocytes (**C**) and the quantification of their percentage and number per milligram of indicated tissues. (**B**) Total number of macrophages, neutrophils and Ly6C^{high} and Ly6C^{low} monocytes per milligram of indicated tissues. n=5-7. (**D**) The percentage of neutrophils and monocytes in total CD45⁺ leukocytes in blood from mice 1 week post-MI, and the number of neutrophils and monocytes per 100 microliter of blood. n=5-7. Results are shown as means ± SEM. Unpaired Student's *t* test and one-way ANOVA were used for statistical analysis. ****P* < 0.001.

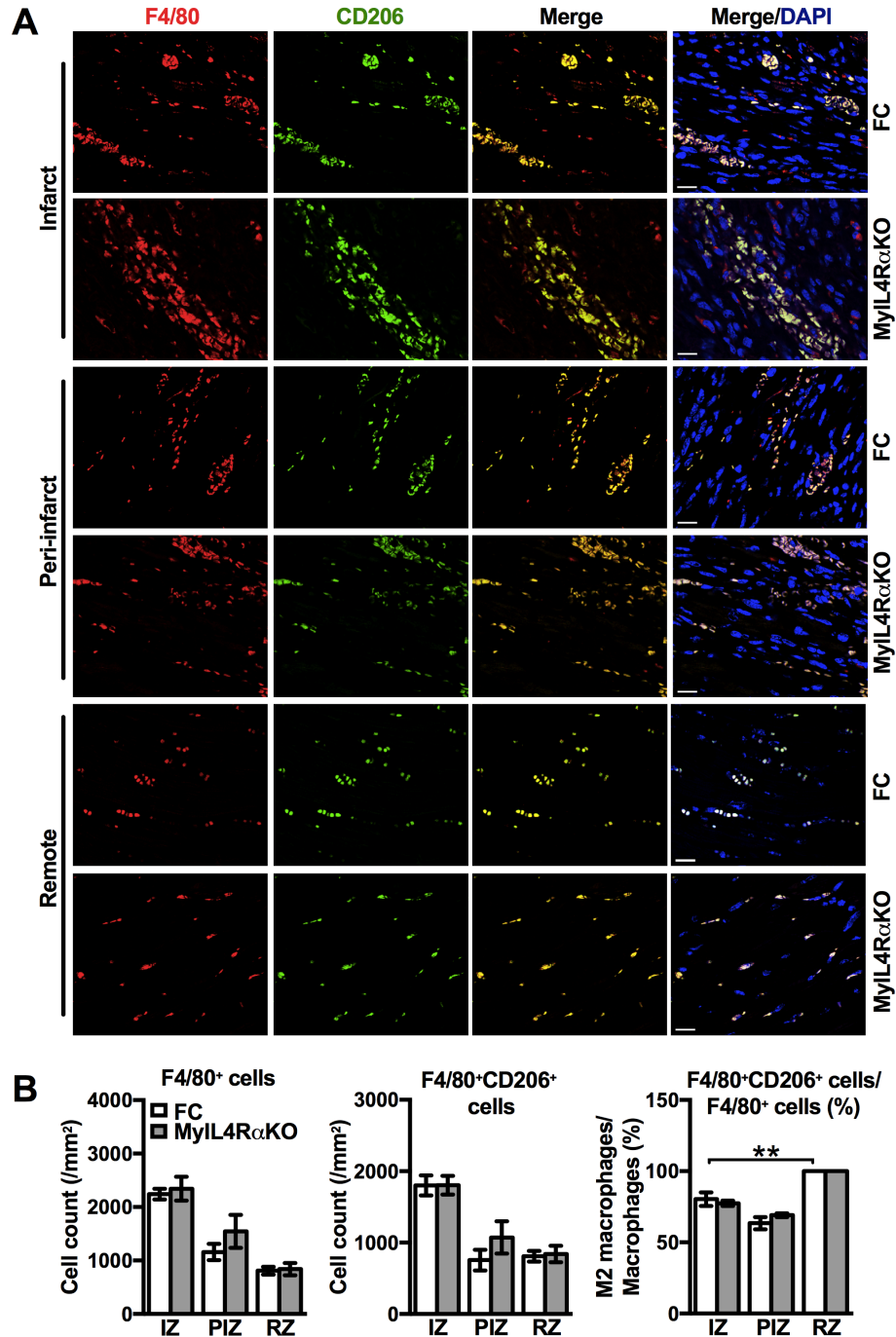


Figure 2.8. Immunofluorescent analysis of F4/80⁺CD206⁺ M2-like macrophages in heart sections post-MI. (A) Representative immunofluorescent photos of remote zone (RZ), peri-infarct zone (PIZ) and infarct zone (IZ) of heart sections 3 wk post-MI. F4/80⁺CD206⁺ macrophages were detected by co-localization of immunofluorescent signals from F4/80 and CD206 antibodies. **(B)** Quantification of F4/80⁺ macrophages and F4/80⁺CD206⁺ M2-like macrophage subpopulation. $n = 5$. Results are shown as means \pm SEM. Unpaired Student's t test was used for statistical analysis. ****** $P < 0.01$.

Taken together, IL4R α knockout in myeloid cells significantly changes macrophage polarization in vitro and changes macrophage polarization at steady state in heart with increase in inflammation. It impairs cardiac function post-MI by increasing the adverse cardiac remodeling, however, this is not caused by altering the M1/M2 macrophage polarization balance or myeloid cells recruitment post-MI, which suggests IL4R α signaling in myeloid cells is very important in cardiac remodeling in inflammatory state, but through a more subtle mechanism rather than changing the number of polarized macrophages or myeloid cells trafficking.

Discussion

Adverse cardiac remodeling after MI is a major contributor to heart failure and is a significant cause of cardiovascular morbidity and mortality. Inflammation occurs rapidly after MI, and immune cells have important roles in post-MI cardiac remodeling. IL-4 is a major inducer of AAM/M2 macrophage polarization, and while IL-4 administration has been recently shown to be protective in post-MI cardiac remodeling, the target cell types have not been identified.

In the present study, we investigated how myeloid IL4R α changes cardiac remodeling and function post-MI by cell-type specific knockout of this receptor subunit. We found that myeloid-specific knockout of IL4R α does not change cardiac hypertrophy or initial infarct size. It does alter remodeling leading to a smaller infarct at 1 week and by 3 weeks there is increased scar thickness. These results show that IL4R α in myeloid cells is an important target for IL-4/IL-13 and that its activity is required for normal infarct healing. In addition, IL4R α knockout in myeloid cells increases perivascular fibrosis although it does not change interstitial fibrosis in the heart indicating a direct or indirect role in the peri-infarct area. All of these changes in cardiac remodeling result in decreased cardiac function, which suggests myeloid IL4R α itself is protective in MI. Importantly, this is not a simple global change in AAM/M2 macrophages since the number or percentage of cells with AAM/M2 markers remains mostly unchanged. Despite the lack of global AAM/M2 changes, without IL4R α signaling in myeloid cells there is impaired healing resulting in decreased cardiac function.

Cardiac hypertrophy occurs after MI,^{36, 42} showing as an increase in ventricle wall mass and cardiomyocyte size. Increases of HW/BW and HW/TL were detected in our data as a result of MI, but there was no difference between FC and MyIL4RαKO mice, indicating that IL4Rα knockout in myeloid cells does not affect cardiomyocyte growth. The only difference in HW/BW between FC and MyIL4RαKO mice was at 1 week post-MI, which showed decreased HW/BW in MyIL4RαKO mice, but the difference was not confirmed in HW/TL. Further, the expression of cardiac fetal genes associated with cardiac hypertrophy, did not show significant difference between FC and MyIL4RαKO mice. Fetal gene BNP mRNA level was higher in hearts from MyIL4RαKO mice, but the increase only was present in hearts without surgery and there were no differences in heart tissues post-MI. The expression of ANP mRNA did show increase at 3 weeks post-MI, but it was only in the area remote from the infarct. Overall these data do not support the involvement of myeloid IL4Rα in cardiomyocyte growth post-MI.

Infarct size and infarct thickness correlate with the prognosis of MI.³⁷ IL-4 administration before MI was recently shown to reduce infarct size and increase infarct wall thickness.²⁷ It was also found that the mice injected with IL-4 showed improved cardiac function post-MI. However, in our study, knockout of IL4Rα from myeloid cells caused abnormal remodeling and decreased infarct size 1 week post-MI. By 3 week, the infarct size was comparable in knockout and wild type animals. The infarct thickness increased in MyIL4RαKO mice at 3 week, but was associated with decreased cardiac function in MyIL4RαKO mice. The change in infarct thickness may be similar to the impaired collagen fibril assembly seen in a wound-healing model.⁴¹ Since IL-4 administration also resulted in increased scar thickness and improved function, infarct thickness may not be a universal measure of improved healing. Potential explanations include that the increased thickness is due to altered remodeling that is not complete. Alternatively, the protective effect that resulted from IL-4 administration may not be through or only through myeloid cells, but also the involvement of the other cell types. It is possible that the changes in infarct size and infarct wall thickness are time point-dependent. Importantly, the improved cardiac function after IL-4

administration in the literature²⁷ is consistent with the decreased cardiac function in our MyIL4R α KO mice, which suggests that the protective effect of IL-4 administration is significantly through IL4R α signaling in myeloid cells.

At the later stages of cardiac remodeling post-MI, inflammatory reactions are typically suppressed and reparative processes dominate. Fibroblasts proliferate and transdifferentiate into myofibroblasts, extracellular matrix deposition occurs in the injured area, and fibrosis is enhanced to form supportive tissue and scarring to maintain the structure and function of ventricles. Although the mRNA levels of Col1A1 and Plod2 were significantly decreased in the infarct tissues of MyIL4R α KO mice, the interstitial fibrosis based on picrosirius red staining did not show any difference whether in infarct area, peri-infarct area, or remote area. It was reported that administration of IL-4 increased both the number and the activation of fibroblasts after MI, which resulted in increased fibrosis²⁷. The differences between IL-4 treatment and our study using myeloid-specific IL4R α knockout may reflect other target cell types for IL-4 or that other effects may be due to IL-13, which is also a ligand for IL4R α and has been shown to be involved in cardiac remodeling after MI.²⁹

It was previously found that IL-4 administration during MI increased the number of CD206⁺ macrophages (sometimes used to identify AAM/M2-like macrophages) post-MI²⁷. We found no change in either the number or the percentage of CD206⁺ cells due to myeloid IL4R α knockout. While this is not a full characterization of the macrophage phenotype, this staining is the almost universally used measure of M2 macrophages. This indicates two important points: first, that the presence of the CD206⁺ cells is not dependent on IL-4 signaling effects in myeloid cells, and second, that global changes in macrophage polarization are not necessary for important effects of IL-4 and that IL-4 is not a required determinant of “M2” macrophage polarization. This points to inadequacy in this system of the M1-M2 paradigm as has recently been shown.¹⁵ Although neither the number or the percentage of classically defined CD206⁺ AAM/M2 macrophages showed any significant differences in MyIL4R α KO mice, we did see significantly impaired responses in BMDMs and PEMs treated with IL-

4, confirming that IL4R α signaling in myeloid cells contributes to cardiac remodeling post-MI.

We did not detect any large, consistent differences in pro- and anti-inflammatory macrophage markers after MI, although we did find significant differences at baseline. In uninjured hearts, there was a clear pattern of increased pro-inflammatory markers and decreased anti-inflammatory markers in MyIL4R α KO mice. There were no differences in the pro-inflammatory markers in heart tissues post-MI, and the differences in anti-inflammatory markers varied depending on marker. The decrease in Arg1 mRNA disappeared in tissues post-MI, while both Ym1 and Fizz1 mRNA increased in heart tissues both in steady state and post-MI although the increase of Ym1 only showed up at 1 week post-MI. Part of the differences may be due to differential dependence of resident and recruited macrophages. This raises a very important question of different role of myeloid IL4R α signaling in resident macrophages and circulating macrophages, but to clarify this question will require further investigation with experiments of lineage tracing, which will be a promising direction of study in the future.

Previous reports using MyIL4R α KO mice in other injury models did not specifically show a reduction in the number or percentage of AAM/M2 macrophages, but they did find that the expression of the AAM/M2 marker CD206 was decreased in macrophages induced by pancreatitis or skin injury in MyIL4R α KO mice.^{39, 41} MyIL4R α KO mice in models of pancreatitis and skin injury showed decreased or perturbed collagen fibril formation that is different from ours, suggesting a model-dependent function of myeloid IL4R α .^{39, 41} IL4R α was also shown significantly decreased in neutrophils in MyIL4R α KO mice³⁵, and IL-4 signaling restricts neutrophil expansion in bone marrow and their migration from bone marrow to tissues⁴³, which suggests the IL4R α signaling-induced changes in neutrophils might contribute to the altered cardiac remodeling of MyIL4R α KO mice. Although we did not find any change in neutrophil recruitment and circulation, it worth further clarification of the contribution of IL4R α signaling in neutrophils, either by isolating primary neutrophils in vitro or neutrophil-specific IL4R α knockout in vivo by MRP8^{Cre}.

In conclusion, myeloid IL4R α is important for efficient cardiac remodeling and cardiac dysfunction after MI, indicating that it is likely an important target for IL-4-mediated protection during MI. However, despite being necessary for IL-4 induced AAM/M2 macrophage polarization in vitro, myeloid IL4R α is not required for the polarization of CD206⁺ macrophages in vivo during MI.

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CHAPTER III
MYELOID INTERLEUKIN-4 RECEPTOR SIGNALING IS IMPORTANT FOR
CARDIOVASCULAR REMODELING INDUCED BY ANGIOTENSIN II AND
HIGH SALT

Abstract

Hypertension is the first leading risk factor for death from cardiovascular diseases. Hypertension-induced cardiovascular remodeling results in chronic low-grade inflammation, fibrosis and tissue stiffness, which lead to development and progression of cardiovascular diseases. Macrophages are the central participants in remodeling, and modulating the remodeling process by reprogramming macrophages is a potential strategy to prevent cardiovascular diseases.

We investigated the role of myeloid IL4R α in cardiac and vascular remodeling in angiotensin II (AngII) and high salt-induced hypertension. Myeloid-specific knockout of IL4R α (MyIL4R α KO) did not show any effect on hypertrophic remodeling in the cardiovascular system, but it increased the expression of reactive oxygen species (ROS) generation related genes. MyIL4R α KO also resulted in substantial decreases in cardiovascular fibrosis through systemic suppression of pro-fibrotic pathways including TGF β and Gal3 signaling and enhancement of anti-fibrotic BMP9 signaling, which indicates an important role for myeloid IL4R α signaling in cardiovascular remodeling. The pathophysiologic alterations in inflammation and fibrosis resulted in a relatively mild preservation of cardiac function in MyIL4R α KO mice while that of floxed control mice was significantly impaired by AngII and high salt. However, no change in macrophage polarization was shown in injured heart and aorta tissues. Neither the percentage or cell number of M2 macrophages was decreased by IL4R α deficiency although IL-4 receptor signaling is very important in M2 macrophage activation. These

results suggest that the decreased fibrosis and functional preservation in MyIL4R α KO mice is not simply due to a change in macrophage polarization.

In conclusion, myeloid IL4R α signaling is significantly involved in cardiovascular remodeling induced by AngII and high salt, but it is not simply through blocking the M2 macrophage activation in vivo, suggesting a more complicated change in macrophages, which needs to be determined in the future.

Introduction

Hypertension is a major risk factor for cardiovascular disease¹. Being the first-leading risk factor, hypertension contributes to 40.6% of total cardiovascular mortality². Antihypertensive therapy has been shown to reduce the risk of death from cardiovascular disease, but only half of hypertensive patients using antihypertensive medication have controlled hypertension, and 25% of hypertensive patients do not take any type of antihypertensive medication³. Based on recent reports from preclinical research and clinical trials, none of the newly developed drugs or interventions have been successful in preventing cardiovascular disease outcomes or death in hypertensive patients⁴. Novel therapeutic targets need to be identified and target-based therapeutic strategies need to be developed to improve cardiovascular outcomes.

Uncontrolled hypertension can exert deleterious effects on the cardiovascular system by adverse cardiovascular remodeling, which includes a complex spectrum of pathophysiological events including cardiovascular hypertrophy, inflammation and fibrosis. These remodeling events result in myocardial stiffening, vascular stiffness, oxidative stress, and long-term low-grade systemic inflammation, which promote the pathological transition from hypertension to hypertensive cardiovascular diseases⁵.

In response to hypertension, left ventricle and vasculature geometry undergoes structural remodeling, which is a pro-inflammatory and pro-fibrotic process that leads to adverse accumulation of collagen. Collagen deposition in extracellular matrix gives rise to interstitial fibrosis, which initially reduces myocardial compliance without cardiomyocyte loss, and clinically displays as heart failure with preserved ejection fraction⁶. As advanced hypertension

progresses, cardiomyocytes undergo pathological hypertrophy and cardiomyocyte loss occurs. This results in irreversible replacement by fibrosis and collectively leads to impairment of cardiac systolic function and clinically manifests as heart failure with reduced ejection fraction⁷⁻⁹. Shear stress and low-grade systemic inflammation during hypertension also cause endothelial damage and results in perivascular fibrosis with substantial collagen accumulation in the adventitia of intramural arteries. This leads to a reduction in vascular compliance and changes in permeability¹⁰. Low-grade systemic inflammation also elicits structural and functional alterations in the microvasculature, which cause microvasculature remodeling and rarefaction¹⁰.

In addition to structural remodeling, hypertension also induces cardiovascular consequences via neurohumoral activation – renin-angiotensin-aldosterone system (RAAS). RAAS functions to maintain blood pressure homeostasis, however stimulating RAAS exerts detrimental consequences such as high blood pressure, adverse cardiovascular remodeling and increase of cardiovascular morbidity and mortality^{11, 12}. Angiotensin II (AngII) is a crucial component in the system and is commonly used in experimental models of hypertension or hypertensive cardiovascular diseases^{13, 14}.

Macrophages are one of the central cell types that mediate cardiovascular remodeling induced by hypertension. Macrophages accumulate and infiltrate into injured tissues through two distinct mechanisms: recruitment of monocyte precursors from circulation and proliferation of resident macrophages. Selective ablation of monocyte/macrophage and neutrophil using inducible diphtheria toxin receptor driven by lysozyme M (LysM) resulted in blunted oxidative stress, reduced arterial hypertension and attenuated vascular dysfunction induced by AngII, in contrast, adoptive transfer of monocytes but not neutrophils restored the adverse effects suggesting an essential role of monocytes/macrophages in AngII-induced hypertension¹⁵.

There is a wide spectrum of macrophage phenotypes with two main extremes: classically activated macrophage (CAM/M1) and alternatively activated macrophage (AAM/M2). M1 macrophages are characterized by the production of

reactive oxygen species (ROS), reactive nitrogen species (RNS) and pro-inflammatory cytokines including tumor necrosis factor α (TNF α), interleukin-1 β (IL-1 β) and interleukin-6 (IL-6), and are considered to play a crucial role in inflammation and tissue damage¹⁶. M2 macrophages are defined as macrophages stimulated by Th2 cytokines such as interleukin-4 (IL-4) and interleukin-13 (IL-13) in vitro. They are characterized by expression of mannose receptor C type 1 (MRC1/CD206), arginase 1 (Arg1), and resistin-like molecule α that also named found in inflammatory zone (Relm α /Fizz1), and are significantly involved in wound healing and fibrosis¹⁷⁻²². Although distinct, both populations contribute to the initiation and progression of cardiovascular diseases²³⁻²⁵.

IL-4 and IL-13 function by binding to IL-4 receptor (IL4R), so IL4R signaling plays a very important role in cardiovascular remodeling potentially through its control of macrophage polarization. IL4R includes type I and type II IL4R: type I IL4R consists of IL-4 receptor α (IL4R α) chain and common γ chain (γ c), while type II IL4R consists of IL4R α and IL-13 receptor α 1 (IL13R α 1) subunits, highlighting the importance of IL4R α subunit that is required by both type I and type II IL4R. IL-4 can signal through both receptors, while IL-13 can only signal through type II IL4R. IL4R α ^{-/-} mice and IL-4/IL-13 double knockout mice showed significantly decreased fibrosis in chronic pancreatitis, indicating the critical role of IL4R signaling in fibrosis²⁶. In AngII-induced hypertension, IL-4^{-/-} mice exhibited significantly reduced interstitial myocardial fibrosis and protected left ventricle chamber dilatation²⁷. A pro-fibrotic role for IL-4 signaling in cardiac remodeling is further supported by data showing that inhibition of IL-4 with neutralizing antibodies significantly reduces cardiac fibrosis during transverse aortic constriction²⁸.

Alternative macrophage activation through IL4R α signaling has been proposed as a mechanism by which IL-4 and/or IL-13 mediate tissue fibrosis^{17, 22, 29, 30}, and M2-like macrophages have been hypothesized as regulators of fibrosis^{29, 31}. Mice lacking myeloid (monocyte/macrophage and neutrophil)-specific IL4R α (LysM^{cre}IL4R α ^{flox/flox}) were less susceptible to pancreatic fibrosis, and compared with wild type mice, IL4R α ^{-/-} and LysM^{cre}IL4R α ^{flox/flox} mice

displayed similar decrease in fibrosis, which suggests the principal role of myeloid or probably macrophage IL4R α in pro-fibrotic remodeling²⁶. Moreover, pancreatic macrophages from both IL4R α ^{-/-} and LysM^{Cre}IL4R α ^{flox/flox} mice showed comparable and significantly decreased expression of the M2 macrophage marker CD206, implicating that IL4R α deletion in myeloid cells reduces fibrosis likely by limiting M2 macrophage activation and polarization²⁶. Work by the Sabine laboratory also showed attenuated alternative macrophage activation in LysM^{Cre}IL4R α ^{flox/-} BALB/c mice in skin wound healing, and they demonstrated that the M2 macrophage marker Relm α (Fizz1) is critical for collagen fibril assembly, which further suggests an important role of myeloid-specific IL4R α signaling and M2-like macrophages in adverse pro-fibrotic remodeling³².

In addition to pro-fibrotic remodeling, IL4R signaling and IL4R signaling-mediated M2 macrophage activation are also importantly involved in inflammation, although their role in inflammation in vivo is ambiguous. Both IL-4 and IL-13 were up-regulated in hypoxic pulmonary hypertension, as well as early recruitment of alveolar macrophages characterized by M2 macrophage markers Arg1, Fizz1, chitinase-3-like protein 3 (Ym1) and CD206, all of which contributed to the development of pulmonary hypertension³³. *Schistosoma mansoni* infected LysM^{Cre}IL4R α ^{flox/-} mice showed massive inflammatory cell infiltration in intestine, associated with enhanced production of the type 1 cytokine interferon γ (IFN γ) in gut, supporting the anti-inflammatory role of myeloid IL4R α signaling³⁴. Furthermore, it was demonstrated that macrophages but not neutrophils stimulated by IL-4/IL-13 are essential for the survival in acute schistosomiasis, and LysM^{Cre}IL4R α ^{flox/-} mice showed impaired M2 macrophage activation with reduced CD206 levels. This indicates that IL4R signaling-mediated M2 macrophage activation protects against schistosomiasis by down-regulation of inflammation³⁴.

In this study, we generated myeloid (macrophage/monocyte and neutrophil)-specific IL4R α knockout (MyIL4R α KO) mice, and then subjected them to AngII and high salt-induced hypertension to investigate the role of myeloid-specific IL4R α signaling in hypertensive injury-induced cardiovascular remodeling.

We hypothesized that IL4R α signaling in myeloid cells promotes fibrosis but inhibits inflammation in cardiovascular remodeling by regulating M2 macrophage activation and polarization; therefore blocking IL4R α signaling in myeloid cells may reduce cardiovascular fibrosis but enhance systemic inflammation and eventually result in cardiac function alterations. In order to test this hypothesis, we determined the hypertrophy, fibrosis, expression of inflammatory cytokines and ROS generation-related genes in heart and vessel (aorta), as well as cardiac function in hypertensive MyIL4R α KO mice to detect the effect of myeloid IL4R α deficiency on cardiovascular remodeling. In addition, we performed flow cytometry analysis to examine macrophage polarization in injured tissues and the migration and recruitment of myeloid cells in order to determine if myeloid IL4R α knockout induces phenotypic and functional changes in myeloid cells during cardiovascular remodeling.

Materials and Methods

Animals

IL4R $\alpha^{\text{flox/flox}}$ mice were previously generated on a BALB/c background³⁴. IL4R $\alpha^{\text{flox/flox}}$ mice were then backcrossed to a C57BL/6 background for at least 10 generations, and further mated with LysM-Cre C57BL/6 mice (The Jackson Laboratory) to generate myeloid (macrophage and neutrophil)-specific IL4R α knockout (MyIL4R α KO) mice. Male MyIL4R α KO (IL4R $\alpha^{\text{flox/flox}}$; LysM^{Cre}) mice at the age of 10-12 weeks were used for experiments, and their littermate floxed control mice (IL4R $\alpha^{\text{flox/flox}}$, referred to as FC) were used as wild type equivalents. Animals of each genotype were randomly assigned to treatment (hypertension) and sham groups. Hypertension was induced by subcutaneously implanting micro-osmotic pump (Alzet, Cupertino, CA, Model 1002) into each mouse to infuse angiotensin II (AngII, Sigma-Aldrich, St. Louis, MO, at. A9525) at a dose of 1.5mg/kg/day, and by feeding 4% NaCl high salt diet (Envigo, Cat. TD.03095) for 4 weeks. The pumps were implanted twice as they only last for 2 weeks. The mice in sham group were also subcutaneously implanted the pumps twice but with saline (0.9% NaCl) and were fed with regular chow. At the end of experiments, mice were euthanized by isoflurane. In brief, mice were first

induced anesthesia by 3-4% isoflurane, once anesthesia was achieved, the isoflurane was increased to 5% to induce death. Mice were remained in the chamber for extra 3 minutes after no breath could be noticed. Afterwards euthanasia was further confirmed by exsanguination. All animal procedures were performed in accordance with the Guide for the Care and Use of Laboratory Animals (8th Edition) and were approved by the Institutional Animal Care and Use Committee of the University of Michigan.

Histological Analysis

After euthanization, hearts and aortas were collected from mice following perfusion with PBS. The collected tissues were fixed in 4% paraformaldehyde for 48 hours, and then processed and embedded in paraffin for histological analysis. Tissue blocks were cut transversely and sections (5 μ m thick) were subjected to hematoxylin and eosin (H&E) staining. In order to measure myocyte cross-sectional area (CSA), pictures were taken of all regions through the H&E stained sections using a Zeiss Axio Imager 2 microscope (Carl Zeiss, Jena, Germany). Myocytes with similar-sized nuclei and intact cellular membranes were outlined by a blinded observer, and myocyte CSA was calculated using ImageJ 1.45s software. The average myocyte CSA was calculated from approximately 200 myocytes per heart. To determine wall thickness and medial area of aorta, digital images of H&E stained aorta cross sections were also obtained from the Zeiss Axio Imager 2 microscope. Similar to what was shown before³⁵, perpendicular lines were drawn from internal elastic lamina to the external lamina at a minimum of ten locations of the aorta section to measure the distance, and average distance was calculated as wall thickness of aorta. For medial area of aorta, the internal and external perimeters of elastic laminae were traced and the area between those two perimeters was quantified and reported as the aortic medial wall area. All measurements were performed using ImageJ 1.45s software.

Fibrosis Evaluation

Hearts, aortas and kidneys were harvested from euthanized mice after perfusion, and fixed in 4% paraformaldehyde for 48 hours, and then processed and embedded in paraffin to make tissue blocks. Tissue sections (5 μ m thick)

were then transversely cut from the blocks and subjected to picosirius red (PSR) staining for further fibrosis determination. To quantify fibrosis, pictures were taken of all regions through each section using a Zeiss Axio Imager 2 microscope (Carl Zeiss, Jena, Germany). For fibrosis in heart sections, cardiac interstitial fibrosis and cardiac perivascular fibrosis were measured separately. To measure interstitial fibrosis, the red-stained interstitial area (fibrotic area) and the area of cardiomyocytes were traced respectively and quantified using ImageJ 1.45s, and the percentage of fibrotic area was calculated as: $\text{area of fibrosis} / (\text{area of cardiomyocytes} + \text{area of fibrosis}) \times 100\%$ ³⁶. To measure cardiac perivascular fibrosis, all vessels across the section were traced and the area that was positively stained and immediately surrounding the intramyocardial vessel was considered perivascular fibrotic area, and perivascular fibrosis was calculated as the ratio between perivascular fibrotic area and luminal media area³⁷. Fibrosis in aorta was expressed as the ratio between the red-stained collagen area in aorta and the total area of aorta including tunica intima, tunica media and tunica adventitia. For kidneys, glomerular, tubulointerstitial and perivascular fibrosis were analyzed respectively. All glomeruli (matrix, cells, capillary loops and space surrounding glomerular segments) across the kidney section were included, and glomerular fibrosis was calculated as: $\text{PSR positively stained area} / \text{glomerular area} \times 100\%$ ³⁸, while the tubulointerstitial fibrosis was expressed as the ratio between PSR positively stained area and total area. In order to determine the perivascular fibrosis in kidney, all intraparenchymal vessels with a diameter of $\leq 100\mu\text{m}$ across the section were taken into account, and the fibrosis was calculated as: $\text{collagen area surrounding the vessel} / \text{luminal media area} \times 100\%$.

Gene Expression Analysis

Relative mRNA expression was determined using quantitative reverse transcription–polymerase chain reaction (qRT-PCR). Total RNA was extracted using TRIzol reagent and RNA (1 μg) was reverse transcribed to cDNA with a High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems). Quantitative polymerase chain reaction (qPCR) was performed using a 7900HT fast real-time PCR system (Applied Biosystems) and relative mRNA expression

was analyzed using the comparative method and normalized to the internal control L32. All qPCR primers are listed in Table 3.1.

Gene	Forward	Reverse
ANP	GCTTCCAGGCCATATTGGAG	GGGGGCATGACCTCATCTT
Arg1	ACCTGGCCTTTGTTGATGTCCCTA	AGAGATGCTTCCAACCTGCCAGACT
BMP9	CAGAACTGGGAACAAGCATCC	GCCGCTGAGGTTTAGGCTG
BNP	ATGGATCTCCTGAAGGTGCTG	GTGCTGCCTTGAGACCGAA
Col1A1	GCTCCTCTTAGGGGCCACT	CCACGTCTCACCATTGGGG
Col3A1	CCTGGCTCAAATGGCTCAC	CAGGACTGCCGTTATTCCCG
Fizz1	ACTGCCTGTGCTTACTCGTTGACT	AAAGCTGGGTTCTCCACCTCTTCA
Gal3	GGAGAGGGAATGATGTTGCCT	TCCTGCTTCGTGTTACACACA
IL-6	GAGGATACCACTCCCAACAGACC	AAGTGCATCATCGTTGTTTCATACA
IL-1 β	AAGAGCTTCAGGCAGGCAGTATCA	TGCAGCTGTCTAATGGGAACGTCA
L32	TTAAGCGAAACTGGCGGAAAC	TTGTTGCTCCCATAAACCGATG
MMP2	CAAGTTCCTCCGCGATGTC	TTCTGGTCAAGGTCACCTGTC
MMP8	TCTTCTCCACACACAGCTTG	CTGCAACCATCGTGGCATTG
MMP9	GGACCCGAAGCGGACATTG	CGTCGTGAAATGGGCATCT
MMP12	AATGCTGCAGCCCCAAGGAAT	CTGGGCAACTGGACAACCTCAACTC
MMP13	CTTCTTCTTGTGAGCTGGACTC	CTGTGGAGGTCAGTGTAGACT
Nox1	GGTGGTCACGGAGTTAAAAACA	TCGGCATCCATTGGGGTCT
Nox4	ACTTTTCATTGGGCGTCCTC	AGAAGTGGGTCCACAGCAGA
p22phox	TGCCAGTGTGATCTATCTGCT	TCGGCTTCTTTCGGACCTCT
p47phox	ACACCTTCATTGCCATATTGC	TCGGTGAATTTTCTGTAGACCAC
PAI-1	GCTTGGCAACCCACGTTAAAGGAA	ACAGCAGCCGGAAATGACACATTG
PDGF α	GAGGAAGCCGAGATACCCC	TGCTGTGGATCTGACTTCGAG
TGF β 1	CTCCCGTGGCTTCTAGTGC	GCCTTAGTTTGGACAGGATCTG
TIMP1	CCTAGAGACACACCAGAGCA	TACCGGATATCTGCGGCATT
TIMP2	GGCAACCCCATCAAGAGGA	CCTTCTGCCTTCTGCAATTAG
Timp3	CTTCTGCAACTCCGACATCGT	GGGGCATCTTACTGAAGCCTC
TNF α	CCCTCACACTCAGATCATCTTCT	GCTACGACGTGGGCTACAG
Ym1	CACCATGGCCAAGCTCATTCTTGT	TATTGGCCTGTCCTTAGCCCAACT

Table 3.1. Sequences of primers used in chapter III. The primers were synthesized by Integrated DNA Technologies. L32, 60S ribosomal protein L32, was used as internal control.

Echocardiography

Mice were anesthetized with isoflurane, and echocardiography was performed using a Vevo 2100 Micro-Imaging System (VisualSonics Inc.) with a 18-38-MHz linear array ultrasound transducer. LV ejection fraction was determined by the two-dimensional long axis view. Ejection fraction and fractional shortening were calculated based on the M-mode parasternal short axis view. Systolic and diastolic dimensions and the LV wall thickness were determined by M-mode in the parasternal short axis view at the level of the papillary muscles. Diastolic function was measured by conventional pulsed-wave

spectral Doppler analysis of mitral valve inflow patterns. The early diastolic tissue velocities of the septal and lateral annuluses of the mitral valve were measured by Doppler tissue imaging with the apical 4-chamber view.

Flow Cytometric Analysis

Preparation of single cell suspensions: after euthanization, whole blood was collected in a heparinized blood collection tube (BD Vacutainer, Ref 367871), and then 100ul blood was subjected to red blood cell (RBC) lysis with the diluted 1X RBC lysis buffer (Biolegend, Cat 420301). After the RBC lysis, peripheral blood single cell suspension was ready for further procedures. Organs including spleen, heart and aorta³⁹ were harvested from the euthanized mice after perfusion via left ventricle by 5ml of 2mM EDTA buffer and 2x10ml PBS. Single cell suspension from spleen was obtained by trituration followed by RBC lysis. Single cell suspensions from heart and aorta were achieved by mincing hearts and aortas into small pieces followed by digestion with a cocktail of 450 U/ml collagenase I (Worthington, Lakewood, NJ), 125 U/ml collagenase XI (Worthington, Lakewood, NJ), 60 U/ml DNase I and 60 U/ml hyaluronidase (Worthington, Lakewood, NJ) for 1 h at 37°C while agitating. The number of total viable cells was counted using Trypan Blue (Gibco, Ref 15250-061).

Cells were then blocked by incubating with anti-CD16/32 (Biolegend, San Diego, CA, Cat. 101302) for 5 min on ice. Antibodies including: anti-CD45-PerCP/Cy5.5 (Biolegend, San Diego, CA, Cat 103131), anti-CD45-PE/Cy7 (Biolegend, San Diego, CA, Cat 103113), anti-CD45-Pacific Blue™ (Biolegend, San Diego, CA, Cat 103126), anti-CD3-APC (Biolegend, San Diego, CA, Cat 100236), anti-CD11b-Brilliant Violet 605™ (Biolegend, San Diego, CA, Cat 101257), anti-Ly6G-FITC (Biolegend, San Diego, CA, Cat 127606), anti-Ly6C-PerCP/Cy5.5 (Biolegend, San Diego, CA, Cat 128011), anti-F4/80-PE (Biolegend, San Diego, CA, Cat 123110), anti-CD206-Alexa Fluor® 488 (Biolegend, San Diego, CA, Cat 141710), anti-TNFα-PE/Dazzle™ 594 (Biolegend, San Diego, CA, Cat 506345) were used for flow cytometric analysis in this study. T cells were identified as CD45⁺CD3⁺CD11b⁻Ly6G⁻ Ly6C⁻ in blood and spleen, and were identified as CD45⁺CD3⁺CD11b⁻Ly6G⁻ F4/80⁻ in heart and

aorta. Neutrophils were identified as CD45⁺CD3⁻CD11b⁺Ly6G⁺Ly6C⁻ in blood and spleen, and CD45⁺CD3⁻CD11b⁺Ly6G⁺F4/80⁻ in heart and aorta. Monocytes were identified as CD45⁺CD3⁻CD11b⁺Ly6G⁻Ly6C⁺, and within the monocyte population, monocytes were further divided into Ly6C^{high} and Ly6C^{low} monocytes based on the expression of Ly6C. Macrophages were identified as CD45⁺CD3⁻CD11b⁺Ly6G⁻F4/80⁺, and within the macrophage population, macrophages were further divided into M1-like macrophages (CD206⁻TNF α ⁺) and M2-like macrophages (CD206⁺TNF α ⁻). Cells were incubated with indicated antibodies on ice (light protected) for 30 min without permeabilization except anti-TNF α -PE/DazzleTM 594. Until after fixation and permeabilization (eBioscience, Cat 88-8824), cells were incubation with anti-TNF α -PE/DazzleTM 594 for 30 min on ice. Flow cytometry was performed using a BD LSRFortessaTM flow cytometer (BD Biosciences) and data were analyzed using FlowJo V10.1 software. For calculation of total cell numbers in heart and aorta, normalization to weight of indicated tissues was performed. The total cell number of each population was calculated by multiplying the total cell number by the percentage of each cell population within the gate.

Statistical analysis

Results are presented as mean \pm SEM. For statistical analysis, one-way ANOVA, and unpaired, two-tailed Student's *t* test were used. All statistical analysis of data was performed in GraphPad Prism (version 6; GraphPad Software, Inc). *P* < 0.05 was considered significant.

Results

Myeloid IL4R α signaling has no impact on cardiovascular hypertrophy

AngII infusion and high salt diet has been used as an experimental model for hypertension^{40, 41}, so we exposed myeloid-specific IL4R α knockout (MyIL4R α KO, LysM^{Cre}IL4R α ^{flox/flox}) mice and the floxed control mice (FC, IL4R α ^{flox/flox}) to AngII and high salt to induce hypertensive cardiovascular injury. As shown in Figure. 3.1A, the systolic blood pressure of both FC and MyIL4R α KO mice were significantly increased in response to AngII and high salt, although there was no significant difference between FC and MyIL4R α KO mice,

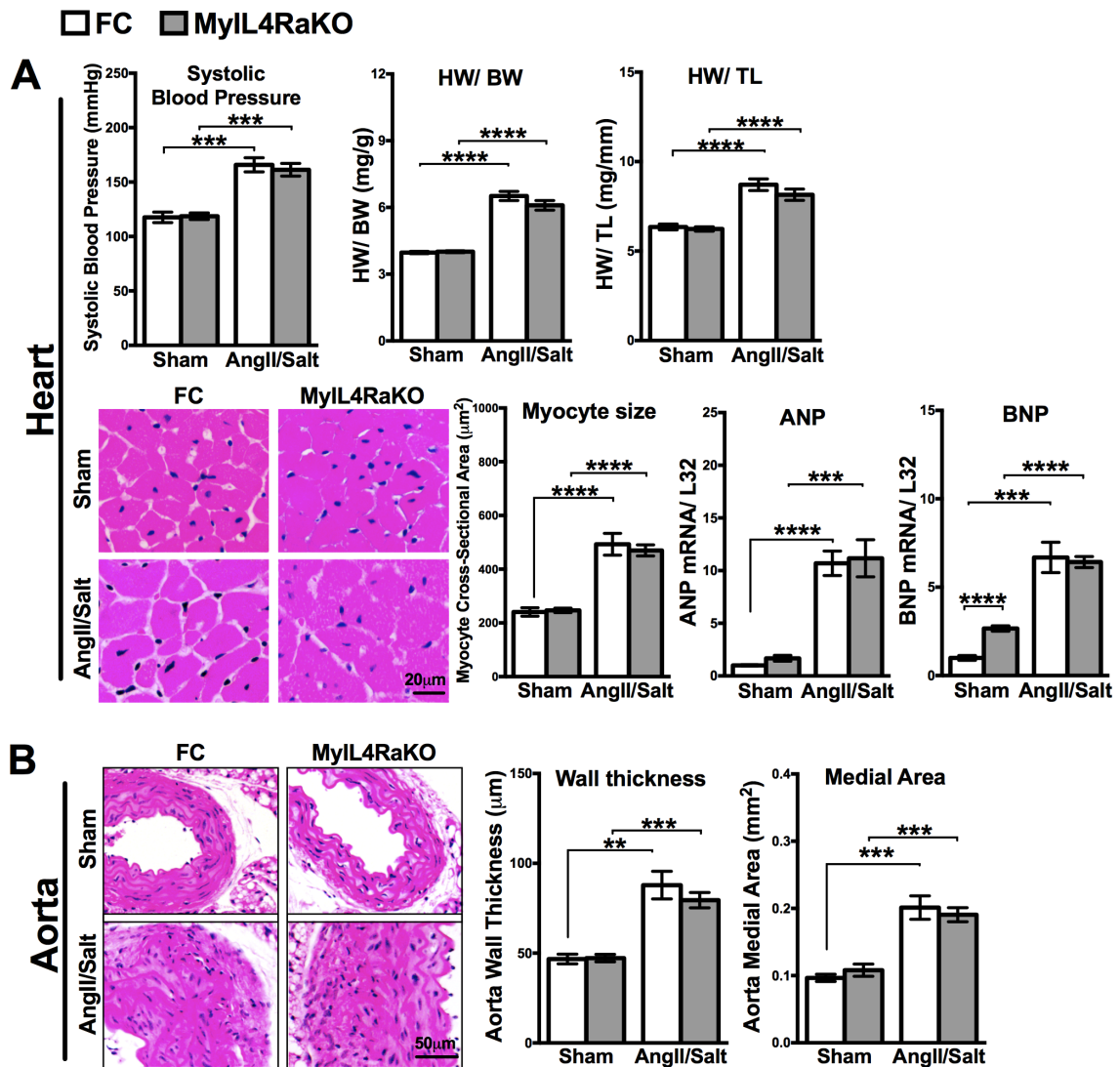


Figure 3.1. Myeloid-specific IL4R α knockout does not affect cardiovascular hypertrophy. (A) The systolic blood pressure of sham mice and mice subjected to AngII and high salt (n=5-6) was determined. The heart weight to body weight ratio (HW/BW, n=20-24) and heart weight to tibia length ratio (HW/TL, n=17-25), and the cardiomyocyte cross-sectional area were measured to determine the cardiac hypertrophy of sham mice and mice after AngII and high salt treatment. Representative images of hematoxylin and eosin (H&E) stained heart sections to show the size of cardiomyocytes (n=7-9). The mRNA level of fetal genes ANP and BNP in hearts of sham and AngII and high salt-treated mice was determined by qRT-PCR (n=5-9). (B) Representative pictures of H&E stained aorta sections, and the wall thickness and medial area of aorta were measured to determine the aortic hypertrophy (n=5-9). Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. ***P* < 0.01; ****P* < 0.001; *****P* < 0.0001.

which suggests that myeloid IL4R α does not control blood pressure.

As hypertrophy is one of the most important events in cardiovascular remodeling induced by hypertension, we determined both cardiac and vascular hypertrophy. Heart weight to body weight ratio (HW/BW) and heart weight to tibia length ratio (HW/TL), and the size of cardiomyocytes were measured. HW/BW, HW/TL (Figure. 3.1A), and cardiomyocyte size shown as myocyte cross-sectional area (Figure. 3.1A) were significantly increased in mice exposed to AngII and high salt, however no difference was shown between FC and MyIL4RaKO mice, which suggests that myeloid IL4R α signaling is not involved in hypertrophic cardiac remodeling. This is further supported by the expression of hypertrophy-induced fetal genes atrial natriuretic peptide (ANP) and brain natriuretic peptide (BNP) expression at mRNA level, which exhibited significant increase after AngII and high salt, but no difference between hypertensive FC and MyIL4RaKO mice (Figure. 3.1B). Of note, the expression of BNP mRNA was significantly increased in heart of sham MyIL4RaKO mice (Figure. 3.1B), and this is consistent with what was found in the acute myocardial infarction model showing higher basal level BNP mRNA in sham MyIL4RaKO mice (Figure. 2.3C).

Vascular hypertrophy was analyzed by measuring the wall thickness and medial area of aorta. Compared with the sham mice, mice treated by AngII and high salt displayed significant increase in aortic wall thickness and aortic medial area (Figure. 3.1B), but similar to the cardiac hypertrophy, there was no obvious difference between FC and MyIL4RaKO mice, indicating the comparable hypertrophic remodeling in aorta. Taken together, all results above indicate that AngII and high salt can successfully induce hypertension, cardiac hypertrophy and vascular hypertrophy, however IL4R α signaling in myeloid cells does not contribute to either blood pressure or hypertrophic cardiovascular remodeling.

Myeloid IL4R α signaling contributes to pro-fibrotic remodeling

IL-4 signaling has been shown to promote fibrosis^{26, 32}, so we hypothesized that knockout of IL4R α in myeloid cells suppresses cardiovascular fibrotic remodeling induced by AngII and high salt. To test this hypothesis, we analyzed the fibrosis in heart and aorta by picrosirius red staining, and quantified

the percentage of fibrotic areas. As shown in Figure. 3.2A, fibrosis was distinctively induced in aorta of hypertensive mice, and more importantly, hypertensive MyIL4R α KO mice showed significantly less fibrosis than hypertensive FC mice. As well as aorta, both cardiac interstitial and perivascular fibrosis were substantially induced by AngII and high salt, and compared with FC mice, the interstitial and perivascular fibrosis in heart of MyIL4R α KO mice were considerably decreased (Figure. 3.2B). The interstitial fibrosis in heart of MyIL4R α KO mice was only half of that in FC mice (Figure. 3.2B). These results strongly indicate that IL4R α signaling in myeloid cells contributes to pro-fibrotic cardiovascular remodeling induced by hypertension.

Prolonged hypertension also causes end organ damage in kidney⁴²⁻⁴⁶, which is associated with progressive fibrosis, so we also determined the fibrosis in kidney based on picrosirius red staining. The glomerular, tubulointerstitial and perivascular fibrotic areas were traced separately and the percentage of fibrotic areas in each region was calculated. AngII and high salt induced considerably increase in glomerular, tubulointerstitial and perivascular fibrosis, and the fibrosis in all three regions was significantly decreased when IL4R α was ablated in myeloid cells (Figure. 3.3). The tubulointerstitial fibrosis in kidney of MyIL4R α KO mice was even comparable to the basal level (Figure. 3.3).

In conclusion, these results suggest that myeloid IL4R α signaling critically contributes to a systemic pro-fibrotic remodeling in a variety of organs after hypertensive injury, and blocking IL4R α signaling in myeloid cells can protect heart and vasculature from adverse fibrotic remodeling and ameliorate kidney damage.

Signaling pathways mediating the decreased fibrosis in MyIL4R α KO mice

Accumulation of collagen in extracellular matrix (ECM), and ECM degradation by matrix metalloproteinases (MMPs) regulate the fibrotic cardiovascular remodeling^{47, 48}. Increase of collagen synthesis, decrease in the activity of MMPs but increase of tissue inhibitors of metalloproteinases (TIMPs) result in the accumulation of collagen. In order to investigate whether the fibrosis

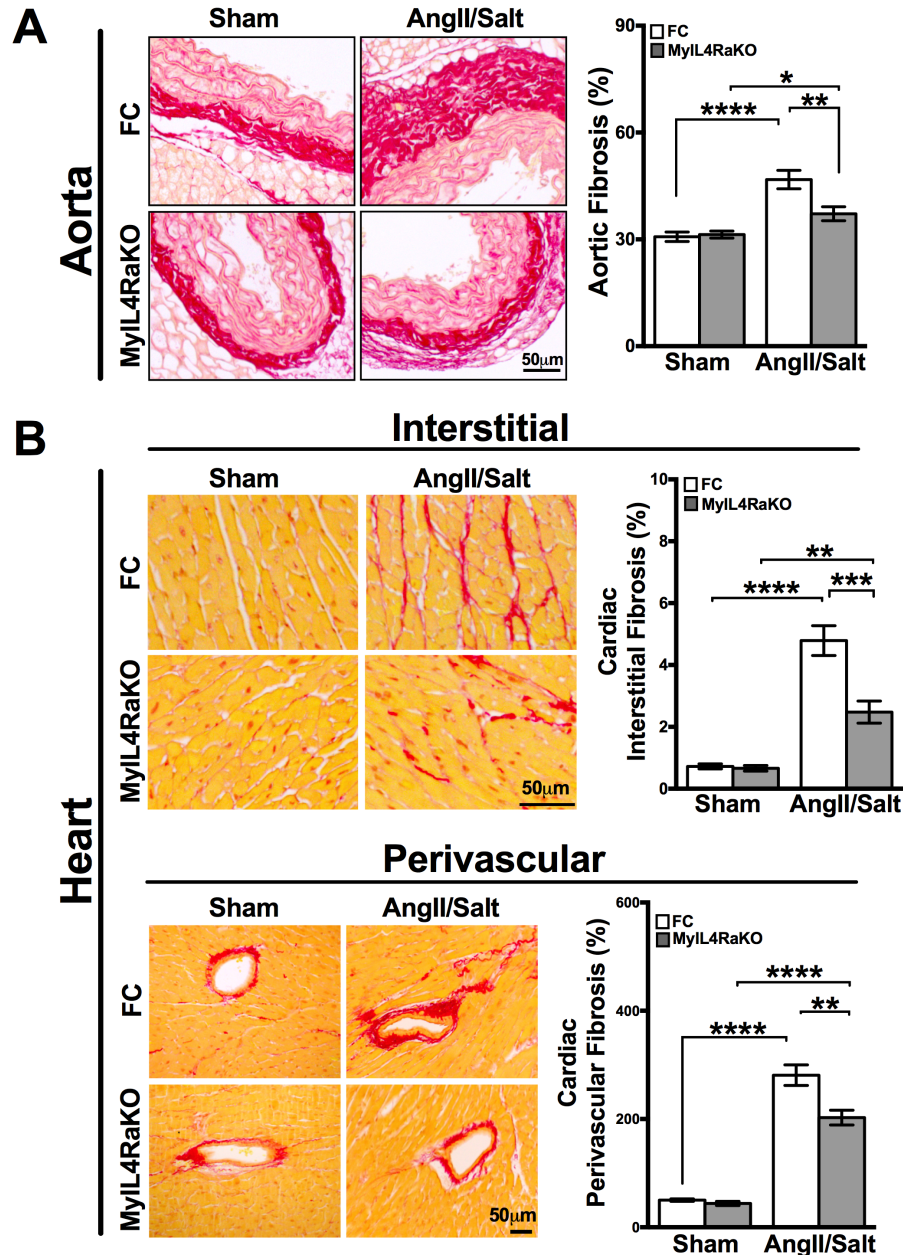


Figure 3.2. IL4R α deficiency in myeloid cells decreases fibrosis in aorta and heart. (A) Representative images of picosirius red stained aorta sections to show the fibrosis (red) in aorta, and the percentage of fibrotic areas in the whole section was quantified in sham and AngII and high salt-induced hypertensive mice (n=9-14). (B) Representative pictures of picosirius red stained interstitial and perivascular region of heart to display the cardiac interstitial and perivascular fibrosis (red) induced by AngII and high salt, and the quantification of interstitial and perivascular fibrosis in heart. Sham mice: n=6; AngII and high salt-treated mice: n=17. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. **P* < 0.05; ***P* < 0.01; ****P* < 0.001; *****P* < 0.0001.

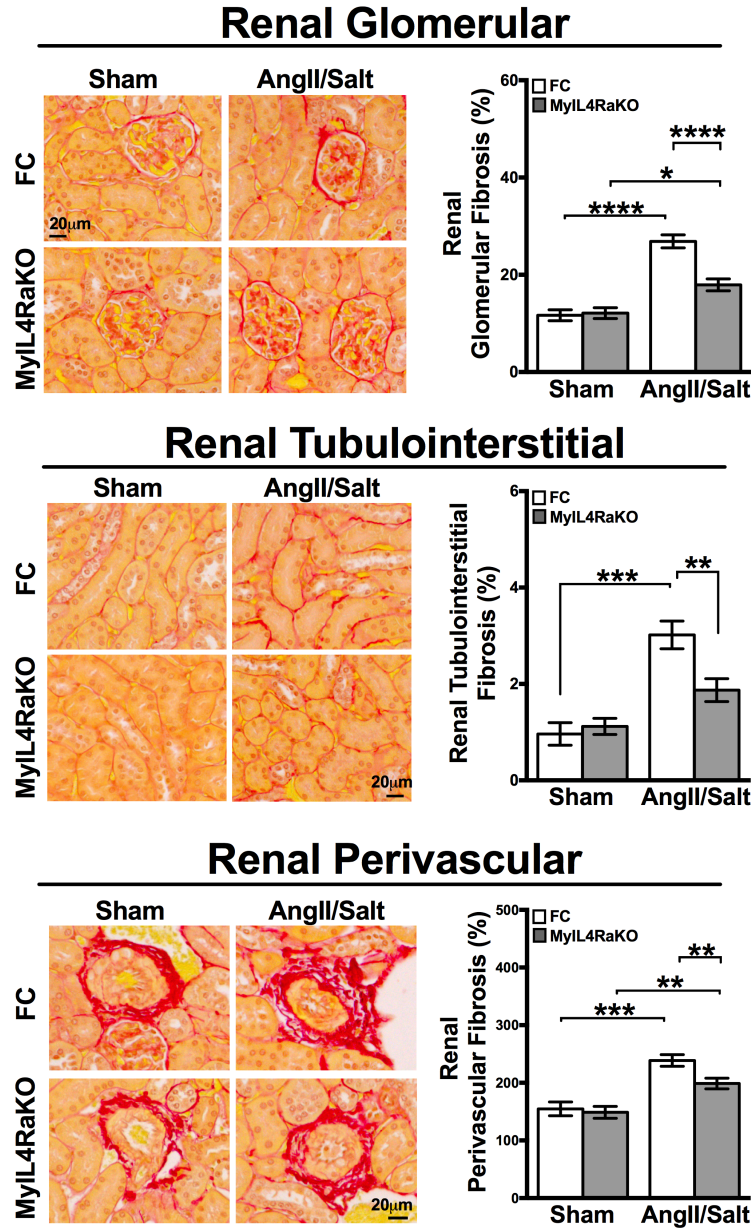


Figure 3.3. IL4R α deficiency in myeloid cells decreases fibrosis in kidney. Representative images of glomerular, tubulointerstitial and perivascular region of picosirius red stained kidney after exposure to AngII and high salt and the quantification of glomerular, tubulointerstitial and perivascular fibrosis in kidney based on the picosirius red staining in kidney. Sham mice: n=5-6; AngII and high salt-treated mice: n=13-14. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. **P* < 0.05; ***P* < 0.01; ****P* < 0.001; *****P* < 0.0001.

reduction in MyIL4R α KO mice attribute to the expression changes of collagens, MMPs and TIMPs, we determined the mRNA level of collagen 1A1 (Col1A1), collagen 3A1 (Col3A1), MMP2, MMP8, MMP9, MMP12, MMP13, TIMP1, TIMP2 and TIMP3 by qRT-PCR.

In heart tissues, both Col1A1 and Col3A1 were significantly up-regulated by AngII and high salt, but only Col3A1 mRNA showed significant decrease as a result of IL4R α deficiency in myeloid cells (Figure. 3.4). The expression of MMPs varies, MMP2 showed significant increase after exposing to AngII and high salt, while MMP9 and MMP13 exhibited significant decrease, and no change was noticed in MMP8 and MMP12 (Figure. 3.4). No significant differences were shown between FC and MyIL4R α KO mice in the expression of MMPs except MMP13 with dramatic increase in MyIL4R α KO mice (Figure. 3.4). The mRNA level of TIMP1 was up-regulated by AngII and high salt, but not TIMP2 and TIMP3, and there was no change induced by the knockout of myeloid IL4R α (Figure. 3.4). Taken together, the decreased fibrosis in heart of MyIL4R α KO mice attributes at least partially to the decreased expression of Col3A1 and increase in MMP13.

Regarding the signaling pathways through which AngII and high salt induces fibrosis, both TGF β -dependent and -independent signaling are involved⁴⁹. PDGF α is one of the downstream mediators in TGF β signaling pathway to promote fibrosis^{50, 51}, as well as plasminogen activator inhibitor-1 (PAI-1, or serpin E1)⁵², which is a serine protease inhibitor (serpin) that functions as the principal inhibitor of tissue-type plasminogen activator (t-PA) and urokinase-type plasminogen activator (u-PA), the activators of plasminogen and hence fibrin degradation^{52, 53}. AngII/galectin3 (Gal3)/IL-6 axis is one of the TGF β -independent signaling pathways that facilitate fibrosis in cardiovascular remodeling^{54, 55}. Genetically ablate IL-6 or Gal3, or pharmacologically neutralize IL-6 or block Gal3 reduces hypertension-related fibrosis^{13, 14, 56}. Another TGF β -independent signaling bone morphogenetic protein 9 (BMP9) pathway has been recently identified as a novel anti-fibrotic pathway in a pressure overload hypertension model⁵⁷.

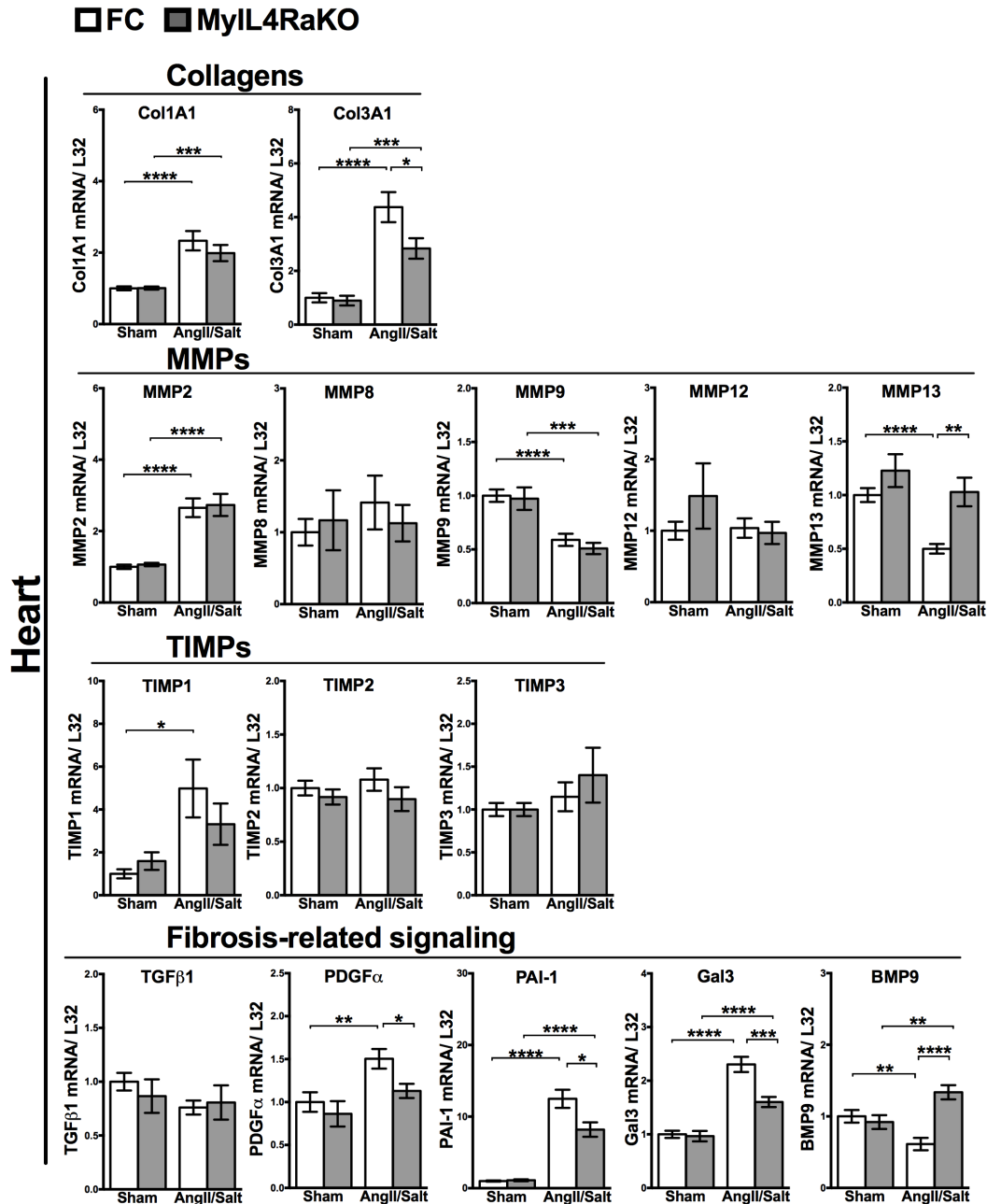


Figure 3.4. The fibrosis-related genes contributing to cardiac fibrosis decrease in MyIL4RaKO mice. The expression of collagens including Col1A1 and Col3A1 (n=11-18), matrix metalloproteinases (MMPs) including MMP2 (n=12-14), MMP8 (n=6-7), MMP9 (n=12-14), MMP12 (n=6-7) and MMP13 (n=13-14), tissue inhibitor of metalloproteinases (TIMPs) including TIMP1, TIMP2 and TIMP3 (n=6-7) and genes included in the fibrosis signaling pathways TGFβ1 (n=12-13), PDGFα (n=5-7), PAI-1 (n=12-14), Gal3 (n=12-14), and BMP9 (n=12-14) at mRNA level was determined in heart tissues of sham and AngII and high salt-induced hypertensive mice. Results are shown as means ± SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. **P* < 0.05; ***P* < 0.01; ****P* < 0.001; *****P* < 0.0001.

Based on the known pathways contributing to AngII and high salt-induced fibrotic remodeling, we determined the mRNA level of TGF β 1, PDGF α , PAI-1, Gal3 and BMP9 in order to identify the signaling pathways that are responsible for the fibrosis decrease resulted from myeloid-specific IL4R α deficiency. In heart tissues, TGF β 1 did not show any difference upon AngII and high salt, neither between FC and MyIL4R α KO mice (Figure. 3.4). PDGF α , PAI-1 and Gal3 all displayed significant increase after AngII and high salt, and more importantly, all of them showed significant decrease as a result of IL4R α ablation in myeloid cells (Figure. 3.4). As BMP9 limits cardiac fibrosis, BMP9 mRNA in heart was significantly reduced in response to AngII and high salt, furthermore, compared with hypertensive FC mice, hypertensive MyIL4R α KO mice exhibited significantly increased BMP9 mRNA (Figure. 3.4). In conclusion, instead of a single signaling pathway, TGF β signaling via the decrease of PDGF α and PAI-1, Gal3 signaling with reduced Gal3, and BMP9 signaling with increased BMP9 mRNA cooperatively mediate the cardiac fibrosis decrease induced by myeloid IL4R α deletion. This suggests that the reduced cardiac fibrosis because of IL4R α deficiency in myeloid cells is rather a systemic change caused by multiple signaling pathways.

In contrast to the gene expression in heart, both collagens (Col1A1 and Col3A1), all MMPs (MMP2, MMP8, MMP12 and MMP13) except MMP9, and all TIMPs (TIMP1, TIMP2 and TIMP3) in aorta were dramatically increased by AngII and high salt at mRNA level, however none of them showed any difference between FC and MyIL4R α KO mice (Figure. 3.5), suggesting the different mechanism contributing to cardiac or vascular fibrosis decrease. In terms of the signaling pathways involved in fibrosis induced by hypertension, the mRNA level of TGF β 1, PDGF α , PAI-1, Gal3 and BMP9 all showed significant increase in aorta in response to AngII and high salt, however none of these genes showed any difference between hypertensive FC and MyIL4R α KO mice except PAI-1 (Figure. 3.5). PAI-1 mRNA, instead of the expected decrease in hypertensive MyIL4R α KO mice based on fibrosis quantification in aorta, it surprisingly showed significant increase compared with hypertensive FC mice (Figure. 3.5). This is

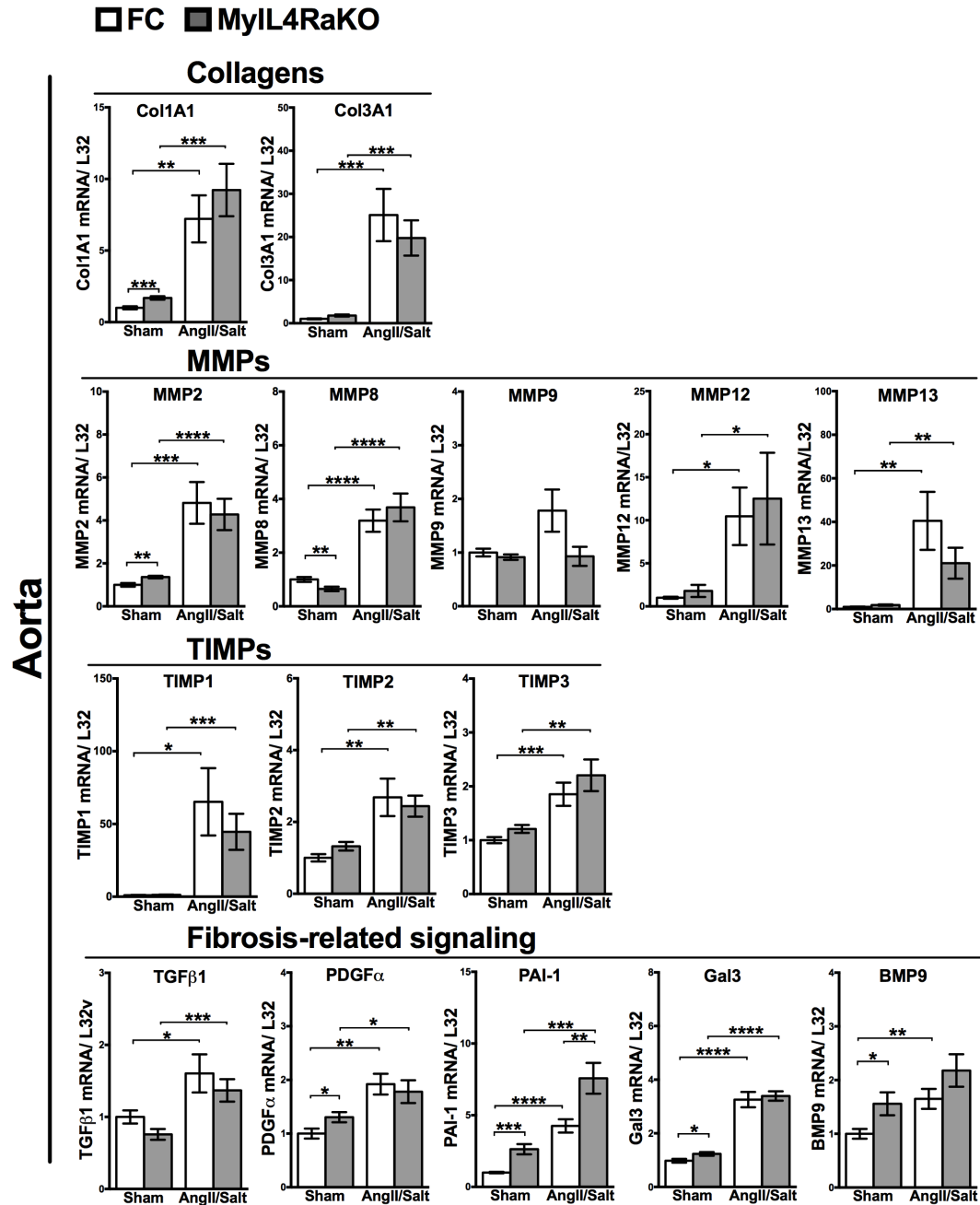


Figure 3.5. The fibrosis-related genes contributing to aortic fibrosis decrease in Myl4RaKO mice. The expression of collagens including Col1A1 and Col3A1 (n=12-15), matrix metalloproteinases (MMPs) including MMP2 (n=12-20), MMP8 (n=12-14), MMP9 (n=13-20), MMP12 (n=5-8) and MMP13 (n=12-19), tissue inhibitor of metalloproteinases (TIMPs) including TIMP1 (n=5-8), TIMP2 (n=5-8) and TIMP3 (n=13-14) and genes included in the fibrosis signaling pathways TGFβ1 (n=12-16), PDGFα (n=6-8), PAI-1 (n=14), Gal3 (n=12-13), and BMP9 (n=14) at mRNA level was determined in aorta tissues of sham and AngII and high salt-induced hypertensive mice. Results are shown as means ± SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. **P* < 0.05; ***P* < 0.01; ****P* < 0.001; *****P* < 0.0001.

consistent with the substantial fibrotic up-regulation in PAI-1 null mice⁵⁸, but contrary to the pro-fibrotic role of PAI-1^{59, 60}, which suggests the plastic role of PAI-1 depending on specific context. The increased PAI-1 mRNA in aorta of MyIL4R α KO mice is also opposite to what was shown in heart tissues (Figure. 3.4), which again suggests the different mechanism of fibrotic remodeling in heart and aorta, although the exact mechanism in aorta is not clear yet.

It's also noteworthy that a lot fibrosis-related genes including Col1A1, MMP2, MMP8, PDGF α , PAI-1, Gal3 and BMP9 in aorta revealed a significant change at basal level between FC and MyIL4R α KO mice although not after hypertension induction (Figure. 3.5), which strongly suggests a different role of myeloid IL4R α signaling at steady state and in the AngII and high salt-induced inflammatory state in fibrotic remodeling. Moreover, as most pro-fibrotic genes showed higher mRNA level in MyIL4R α KO mice at basal level, which probably suggests higher baseline inflammation as a result of the inactivation of anti-inflammatory IL4R α signaling in myeloid cells.

IL4R α deficiency in myeloid cells increases ROS-related genes expression

In addition to fibrosis, hypertension also elicits up-regulation of low-grade systemic inflammation and oxidative stress, the pathophysiological events that promote the transition of hypertension to cardiovascular diseases.

In order to investigate whether the ablation of IL4R α in myeloid cells enhances inflammation induced by AngII and high salt, we measured the mRNA level of inflammatory cytokines including TNF α , IL-1 β , and IL-6 in heart and aorta. As shown in Figure. 3.6, TNF α , IL-1 β and IL-6 mRNA were all significantly increased by AngII and high salt, indicating the increased inflammation in hypertensive mice, however, no difference was caused by the knockout of IL4R α in myeloid cells except IL-6 mRNA in aorta, suggesting that myeloid IL4R α signaling might have no effect on the expression of hypertension-induced inflammatory cytokines. The reduction of IL-6 mRNA in aorta of MyIL4R α KO mice (Figure. 3.6) may contribute to the decreased fibrosis as IL-6 is involved in the AngII/Gal3/IL-6 axis that regulates fibrosis^{13, 14, 54-56}. Although no difference was shown between hypertensive FC and MyIL4R α KO mice in heart, sham

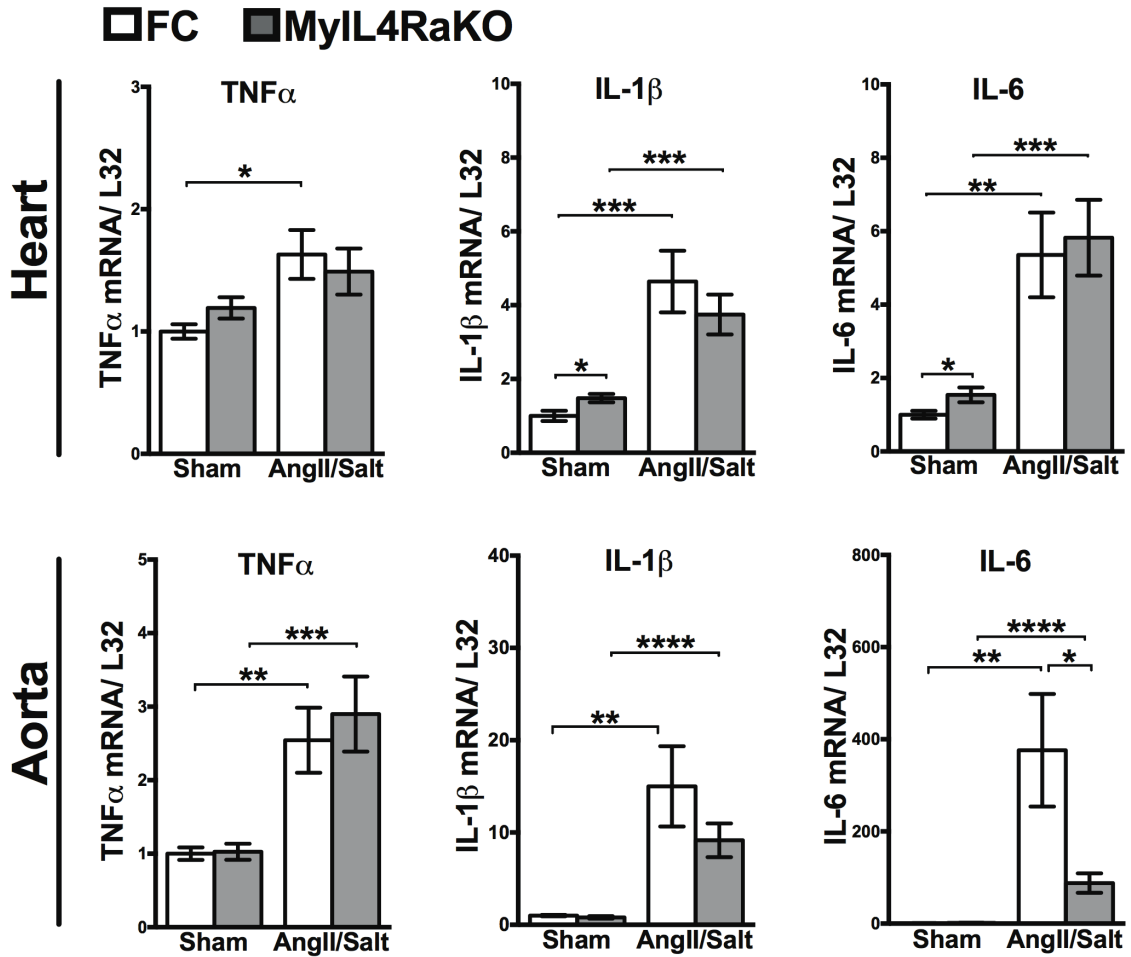


Figure 3.6. The mRNA expression of inflammatory cytokines in heart and aorta. The mRNA level of inflammatory cytokines TNF α , IL-1 β and IL-6 was measured in heart (n=11-17) and aorta (n=11-20) of sham mice and mice subjected to AngII and high salt. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. **P* < 0.05; ***P* < 0.01; ****P* < 0.001; *****P* < 0.0001.

MyIL4R α KO mice displayed significant increase of IL-1 β and IL-6 mRNA in heart compared with sham FC mice (Figure. 3.6). This is consistent with what was shown in the acute myocardial infarction model (Figure 2.1B), which probably suggests the aggravated inflammation at baseline caused by deficiency of IL4R α in myeloid cells.

Oxidative stress plays an important role in inflammation. In order to detect whether deletion of IL4R α in myeloid cells enhances inflammation by up-regulating oxidative stress, we measured the mRNA level of ROS generation-related genes including p22phox, p47phox, Nox1 and Nox4 by qRT-PCR. In heart tissues, the expression of p47phox, Nox1 and Nox4 were all significantly increased in hypertensive mice except p22phox, however no difference was detected between hypertensive FC and MyIL4R α KO mice (Figure. 3.7). However, both Nox1 and Nox4 exhibited significant increase at basal level of MyIL4R α KO compared with sham FC mice, what's more, the Nox1 mRNA at basal level was even comparable to that induced by hypertension in MyIL4R α KO mice (Figure. 3.7), indicating the relatively exacerbated oxidative stress caused by IL4R α deletion in myeloid cells. In aorta tissues, p22phox, p47phox and Nox4 mRNA were significantly up-regulated by AngII and high salt, and more importantly they displayed significant increase in hypertensive MyIL4R α KO mice compared with hypertensive FC mice (Figure. 3.7), which suggests probably higher oxidative stress caused by IL4R α ablation in myeloid cells. Moreover, Nox1 and Nox4 also showed significantly higher mRNA level in MyIL4R α KO mice at basal level than sham FC mice (Figure. 3.7), which also suggests probably higher basal level ROS in MyIL4R α KO mice.

Taken together, ROS generation related genes revealed significant increase as a result of IL4R α ablation in myeloid cells, suggesting the possible more ROS generation and higher oxidative stress, which in turn may result in aggravated inflammation. In conclusion, myeloid-specific IL4R α signaling is also involved in inflammatory regulation by modulating the expression of ROS generation related genes and hence oxidative stress.

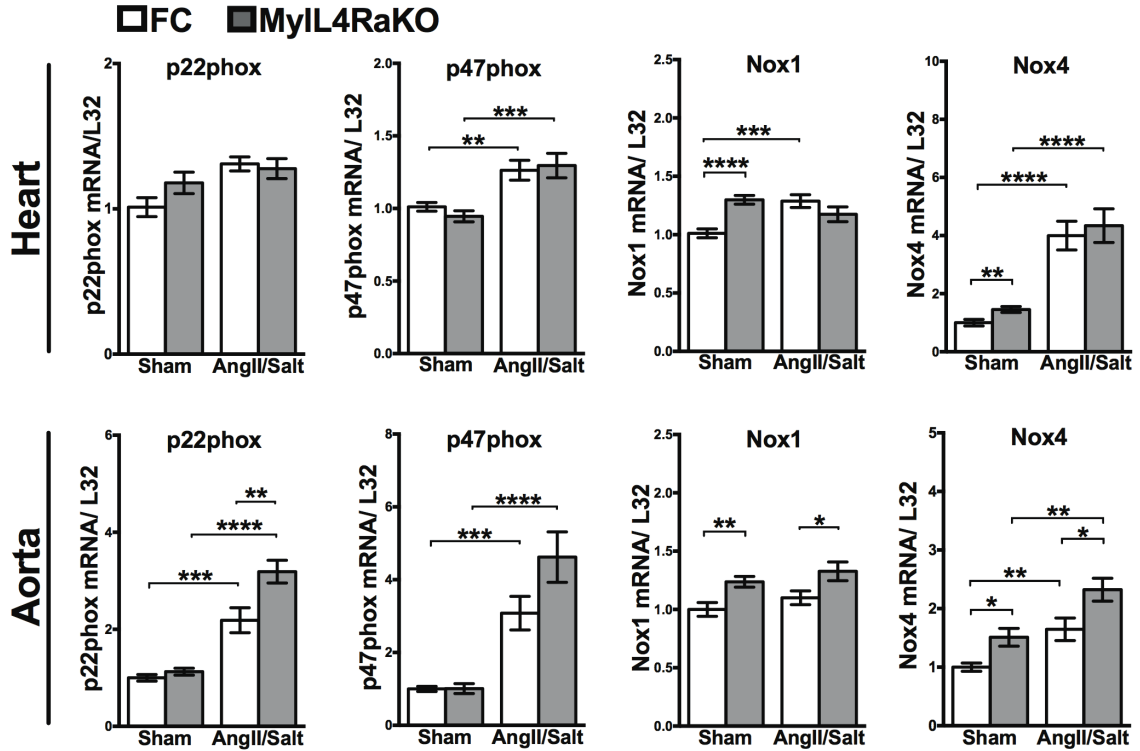


Figure 3.7. Myeloid-specific IL4R α deletion induces increase of ROS generation-related genes mRNA expression. The mRNA expression of ROS generation-related genes: p22phox, p47phox, Nox1 and Nox4 was determined by qRT-PCR in hearts (n=15-20) and aortas (n=11-20) of sham mice and AngII and high salt-treated mice. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. **P* < 0.05; ***P* < 0.01; ****P* < 0.001; *****P* < 0.0001.

Myeloid-specific IL4R α knockout preserves cardiac function in response to AngII and high salt

In order to clarify the overall impact of the myeloid-specific IL4R α knockout, after charactering its effect on fibrosis and inflammation, cardiac function was determined by echocardiography.

The ejection fraction of FC mice was significantly impaired by AngII and high salt, but MyIL4R α KO mice did not show any significant change with comparable ejection fraction of the sham mice (Figure. 3.8), indicating the preserved ejection fraction by IL4R α deficiency in myeloid cells. Similarly, systole and diastole left ventricle internal diameter (LVID) were also preserved in hypertensive MyIL4R α KO mice, while significantly increased in hypertensive FC mice (Figure. 3.8), which supports the suggestive protection of cardiac function by IL4R α deficiency in myeloid cells. In addition, compared with hypertensive FC mice, hypertensive MyIL4R α KO mice showed significant decrease in systole left ventricle area and left ventricle volume (Figure. 3.8), which indicates a stronger potential of cardiac contraction of MyIL4R α KO mice. In addition to left ventricle, MyIL4R α KO mice also displayed a protective role in the function of aorta. Compared with hypertensive FC mice, aorta velocity peak gradient was significantly increased in hypertensive MyIL4R α KO mice, which was even comparable to that of sham mice (Figure. 3.8). Ascending aorta diameter was also preserved in hypertensive MyIL4R α KO mice while that of hypertensive FC mice was significantly increased (Figure. 3.8).

In conclusion, hypertensive MyIL4R α KO mice showed relatively improved cardiovascular function compared with the hypertensive FC mice, which basically indicates a overall protective role of myeloid-specific IL4R α knockout by balancing the effect on fibrosis and inflammation.

Myeloid-specific IL4R α deletion does not change M2 macrophage polarization

IL-4 or IL4R signaling regulates fibrosis through controlling the M2 macrophages polarization²⁶. In our study, knockout of IL4R α in myeloid cells caused decreased fibrosis, so we hypothesized that this may through its down-

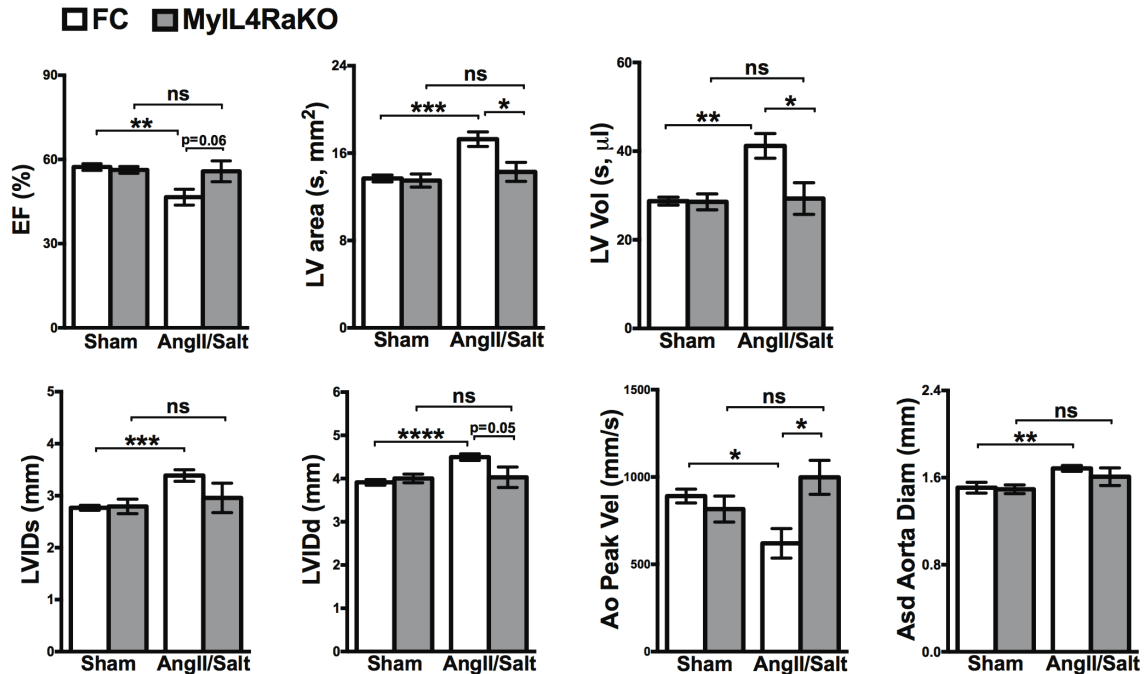


Figure 3.8. Myeloid IL4R α deficiency helps to preserve cardiac function after AngII and high salt treatment. Cardiac function was analyzed in sham and AngII and high salt-induced hypertensive mice by echocardiography. Quantitative evaluation of echocardiography data including ejection fraction (EF), systole left ventricle area (LV area, s) and systole left volume (LV Vol, s), systole and diastole left ventricular internal diameter (LVIDs and LVIDd), aorta velocity peak gradient (Ao Peak Vel) and ascending aorta diameter (Asd Aorta Diam) were shown. $n=6-8$. Results are shown as means \pm SEM. Unpaired student's t test and one-way ANOVA were used for statistical analysis. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; **** $P < 0.0001$.

regulation of M2 macrophage activation. In order to test this hypothesis, we first measured the mRNA level of M2 macrophage markers in heart and aorta. Unexpectedly, no significant difference was shown between hypertensive FC and MyIL4R α KO mice in the mRNA level of M2 macrophage markers including Arg1, Fizz1 and Ym1 (Figure. 3.9), which suggests that myeloid IL4R α deletion might not change M2 macrophages polarization at least in our model. It should be pointed out that, compared with sham FC mice, Arg1 showed significant decrease while Fizz1 showed significant increase in hearts of sham MyIL4R α KO mice (Figure. 3.9), which is consistent with the results in acute myocardial infarction model (Figure. 2.1B), strongly suggesting the control of macrophages at steady state by IL4R α .

As the gene expression of M2 macrophage markers were examined in heart and aorta tissues that consist of a wide range of cell types rather than macrophages only, the gene expression in non-macrophages may interfere with their expression profile in macrophages, which cannot truly manifest the M2 macrophage polarization change caused by IL4R α knockout. In order to specifically investigate the M2 macrophage polarization, flow cytometry analysis was performed to determine the M2-like macrophage population in heart. M1-like and M2-like macrophages were gated from CD11b⁺F4/80⁺ macrophages and characterized as TNF α ⁺CD206⁻ and TNF α ⁻CD206⁺ respectively. As shown in Figure. 3.10, the percentage of M1-like (TNF α ⁺CD206⁻) or M2-like (TNF α ⁻CD206⁺) macrophages was similar between FC and MyIL4R α KO mice as well as their cell numbers, although AngII and high salt induced a significant infiltration of both M1- and M2-like macrophages, which indicates that IL4R α signaling inactivation in macrophages does not change the M2 macrophage polarization in vivo. In order to test whether IL4R α signaling is involved in the regulation of macrophage recruitment, we examined macrophages in heart of sham and hypertensive mice. Both the percentage of macrophages in total leukocytes and the macrophage cell number were significantly increased upon AngII and high salt (Figure. 3.11), indicating the migration and infiltration of macrophages into hearts after hypertension, however, no significant change was shown between

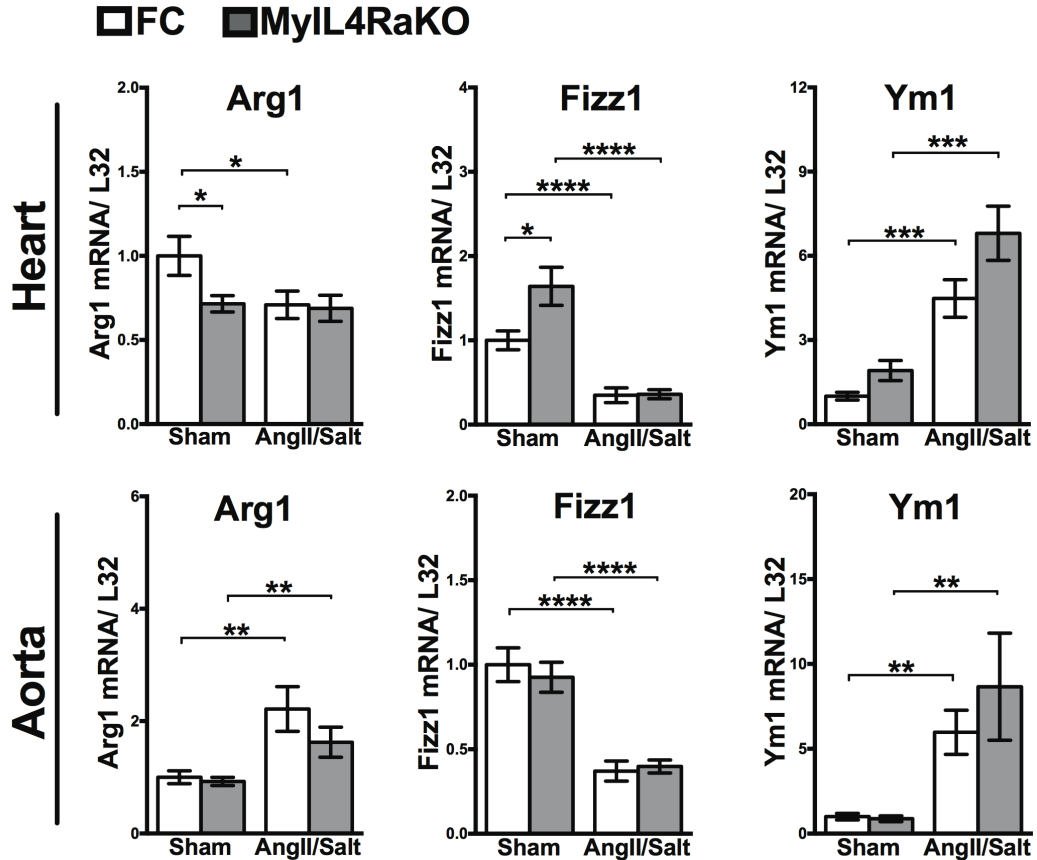


Figure 3.9. The mRNA level of M2 macrophage markers in heart and aorta. The expression of M2 macrophage markers including Arg1, Fizz1 and Ym1 at mRNA level was determined in heart (n=9-17) and aorta (n=5-20) tissues of sham mice and mice exposed to AngII and high salt. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. **P* < 0.05; ***P* < 0.01; ****P* < 0.001; *****P* < 0.0001.

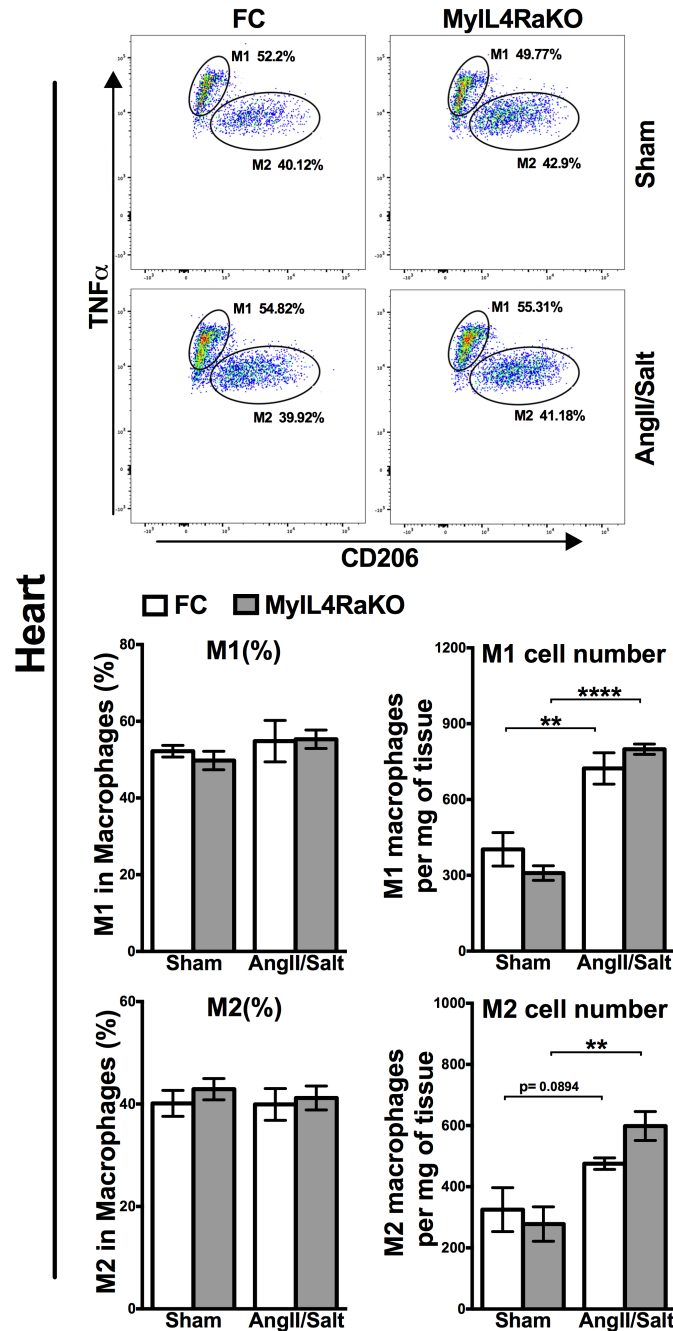


Figure 3.10. IL4R α knockout does not change macrophage polarization in vivo. Representative FACS dot plots of M1-like (CD206⁻TNF α ⁺) and M2-like macrophages (CD206⁺TNF α ⁻) gated from macrophages and the quantification of the percentage of M1-like and M2-like macrophages in total macrophages and their cell number. All cell numbers are expressed per milligram tissue. n=5. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. ***P* < 0.01; *****P* < 0.0001.

FC and MyIL4R α KO mice (Figure. 3.11), suggesting that IL4R α signaling inactivation in myeloid cells in vivo has no effect on macrophage recruitment either.

As, in addition to macrophages, myeloid cells also include neutrophils that have IL4R α deleted in MyIL4R α KO mice, it's worth determining whether IL4R α controls neutrophil infiltration into the heart. Like macrophages, neither the percentage of neutrophils in total leukocytes nor their number showed any change caused by IL4R α deficiency (Figure. 3.12), suggesting that IL4R α signaling in neutrophils does not affect their migration into the heart upon inflammation. This is consistent with the results from Eming lab, who reported no difference between IL4R α ^{flox/flox} and LysM^{Cre}IL4R α ^{flox/-} mice in the number of Ly6G⁺ cells in skin wound tissues³². No change was even shown in neutrophils as a result of AngII and high salt (Figure. 3.12), which may suggest that AngII and high salt does not significantly induce cardiac neutrophil infiltration or at least not at the time of examination.

T cells are known importantly involved in AngII-induced hypertension and inflammation, so we were curious whether deletion of IL4R α in myeloid cells changes T cells infiltration via the regulation of inflammation by IL4R α signaling. We then quantified T cell population in heart tissues by flow cytometry. No change in the cell number of T cells was shown in response to AngII and high salt or as a result of IL4R α deficiency in myeloid cells (Figure. 3.12), however, the percentage of T cells in total leukocytes in heart was decreased after AngII and high salt (Figure. 3.12), which probably attributes to the massive infiltration of macrophages that in turn decreases the fraction of T cells.

Taken together, suppressing IL4R α signaling in myeloid cells did not change M2-like macrophage polarization, neither macrophage or neutrophil recruitment, which suggests a more complicated microenvironment in vivo than in vitro, and the IL4R α signaling may change the characteristics of macrophage rather than simply change the M2 macrophage polarization, and IL4R α signaling may not be involved in the recruitment of myeloid cells into the heart in response to hypertension.

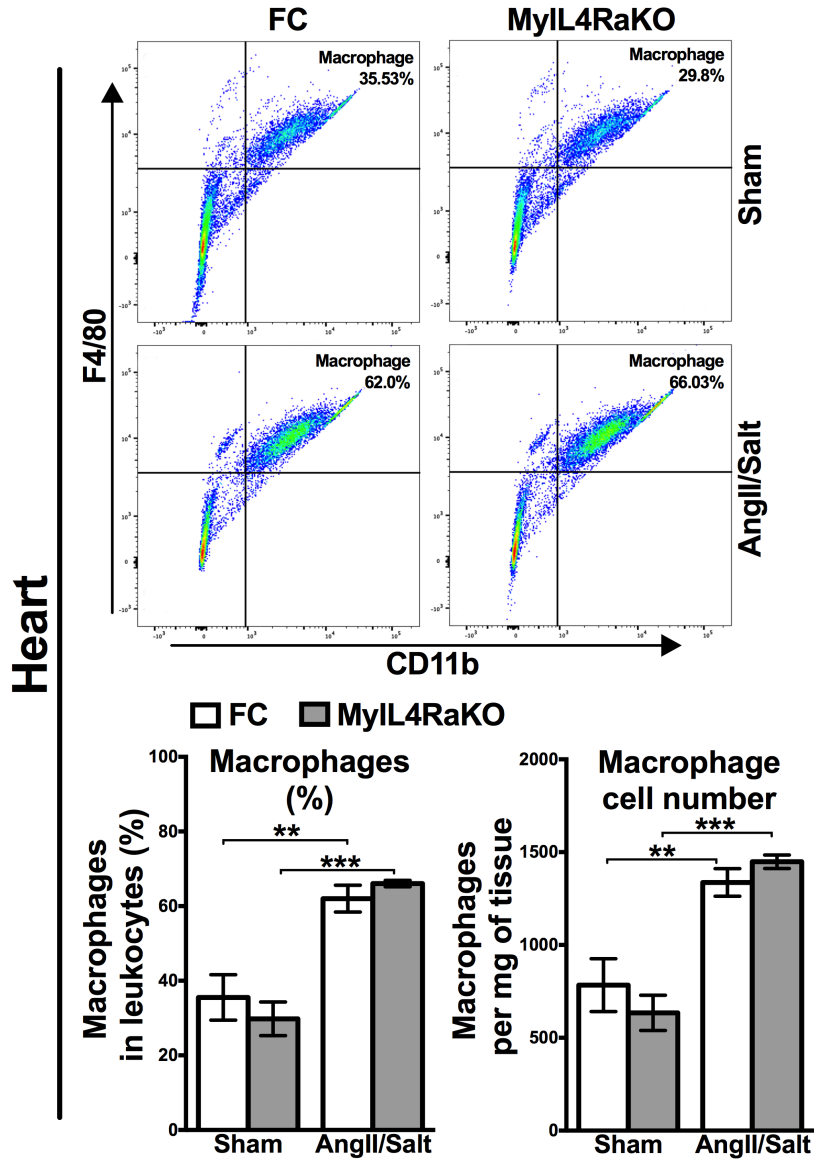


Figure 3.11. IL4R α knockout does not change macrophage recruitment induced by AngII and high salt. Representative FACS dot plots of macrophages (CD11b⁺F4/80⁺) gated from leukocytes in heart tissues of sham and AngII and high salt-treated mice, with quantification of the percentage of macrophages in total leukocytes and their cell number. All cell numbers are expressed per milligram tissue. n=5. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. ***P* < 0.01; ****P* < 0.001; *****P* < 0.0001.

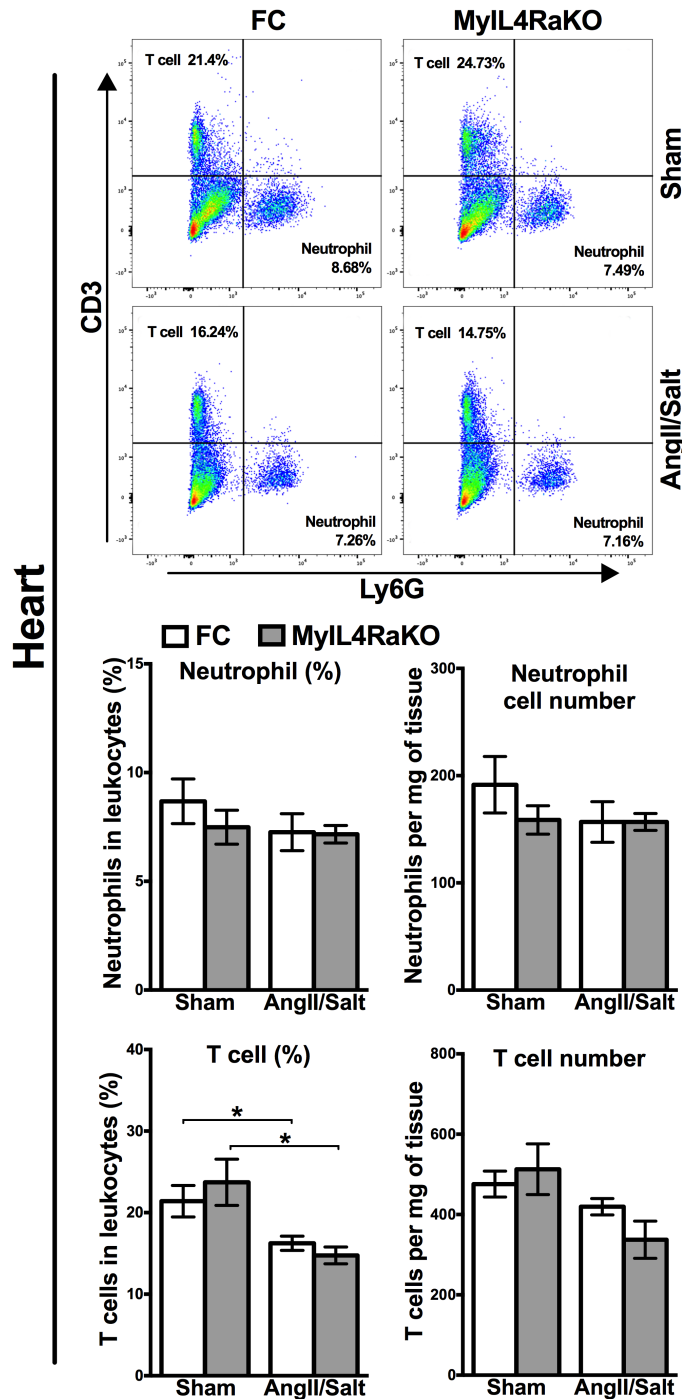


Figure 3.12. IL4R α knockout does not change neutrophils and T cells recruitment induced by AngII and high salt. Representative FACS dot plots of neutrophils (Ly6G⁺) and T cells (CD3⁺) gated from leukocytes in heart tissues of sham and AngII and high salt-treated mice and the quantification of the percentage of neutrophils and T cells in leukocytes and their cell number. All cell numbers are expressed per milligram tissue. n=5. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. **P* < 0.05; ***P* < 0.01; ****P* < 0.001; *****P* < 0.0001.

In addition to heart tissues, we also determined the M2-like macrophage population in aorta, another important organ in cardiovascular remodeling induced by hypertension. Similar to the results in heart, no change in M2-like macrophages was caused by IL4R α deletion (Figure. 3.13), which supports that IL4R α signaling alone may not be able to change macrophage polarization in vivo. However, AngII and high salt significantly exerted an increase in both the percentage of M2-like macrophages in total macrophage and their cell number (Figure. 3.13), indicating the involvement of M2-like macrophages in hypertensive inflammatory and pro-fibrotic vascular remodeling.

Macrophage and neutrophil population in aorta were also determined by flow cytometry. Both the percentage and number of macrophages were significantly up-regulated by AngII and high salt (Figure. 3.14), which indicates the migration and infiltration of macrophages into the hypertensive vasculature with enhanced inflammation. In contrast to the un-changed neutrophil in heart, both the percentage and the total number of neutrophils in aorta showed significant increase after exposure to AngII and high salt (Figure. 3.15), which indicates the recruitment of neutrophils into the vasculature and confirms the increased inflammation induced by AngII and high salt. Consistent with the results of heart tissues, no change in macrophage or neutrophil was induced by IL4R α deletion (Figure. 3.14 and Figure. 3.15), which supports the conclusion that IL4R α signaling may not contribute the recruitment of myeloid cells into injured tissues. Neither the percentage or number of T cells in aorta was changed by AngII and high salt or IL4R α deficiency in myeloid cells (Figure. 3.15).

Based on the above data from flow cytometry, knockout of IL4R α in myeloid cells does not change M2 macrophage polarization in vivo, neither macrophage and neutrophil infiltration into injured tissues and the T cell recruitment, which suggests that the phenotypic and functional changes in heart and vasculature induced by myeloid-specific IL4R α ablation does not simply attribute to a global change of M2-like macrophages as hypothesized.

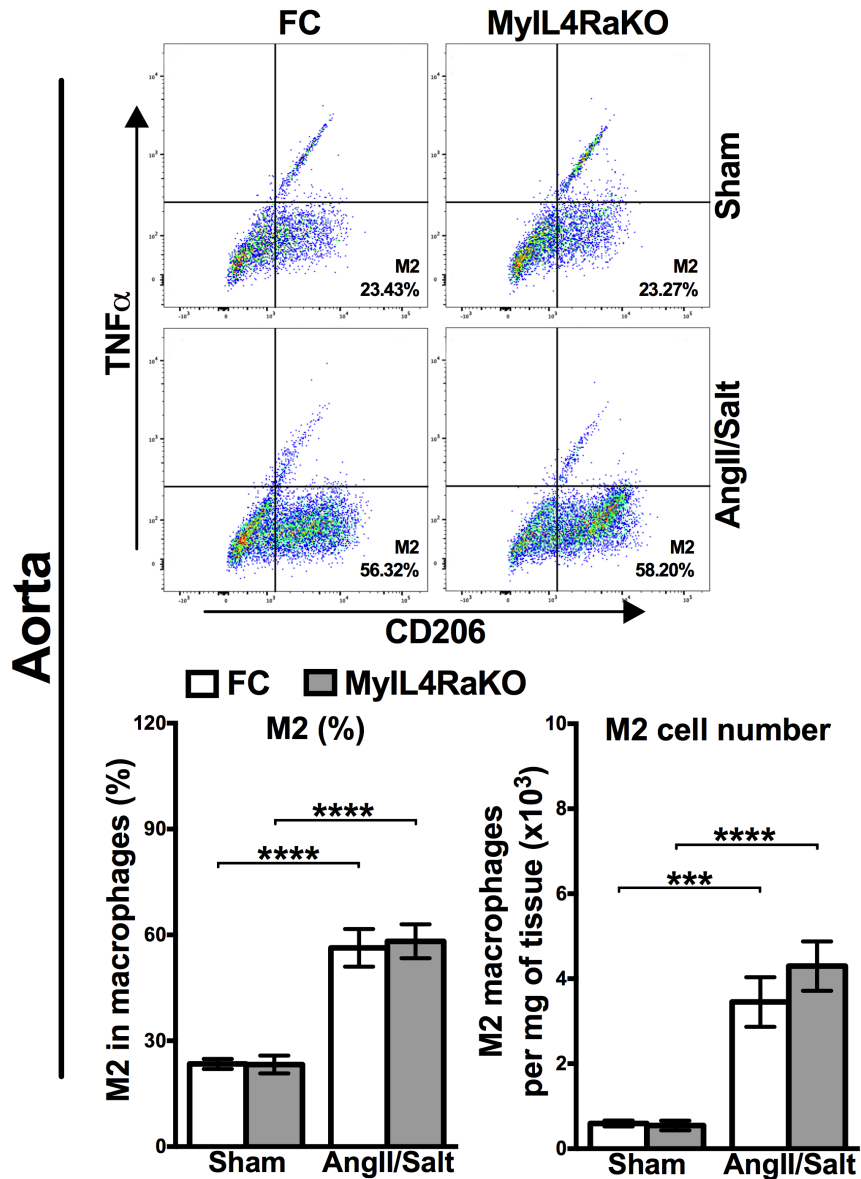


Figure 3.13. IL4R α deficiency does not change the polarization of macrophages in aorta. Representative FACS dot plots of M2-like macrophages (CD206⁺TNF α ⁺) gated from macrophages and the quantification of the percentage of M2-like macrophages in total macrophages and their cell number. All cell numbers are expressed per milligram tissue. n=9-10. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. ****P* < 0.001; *****P* < 0.0001.

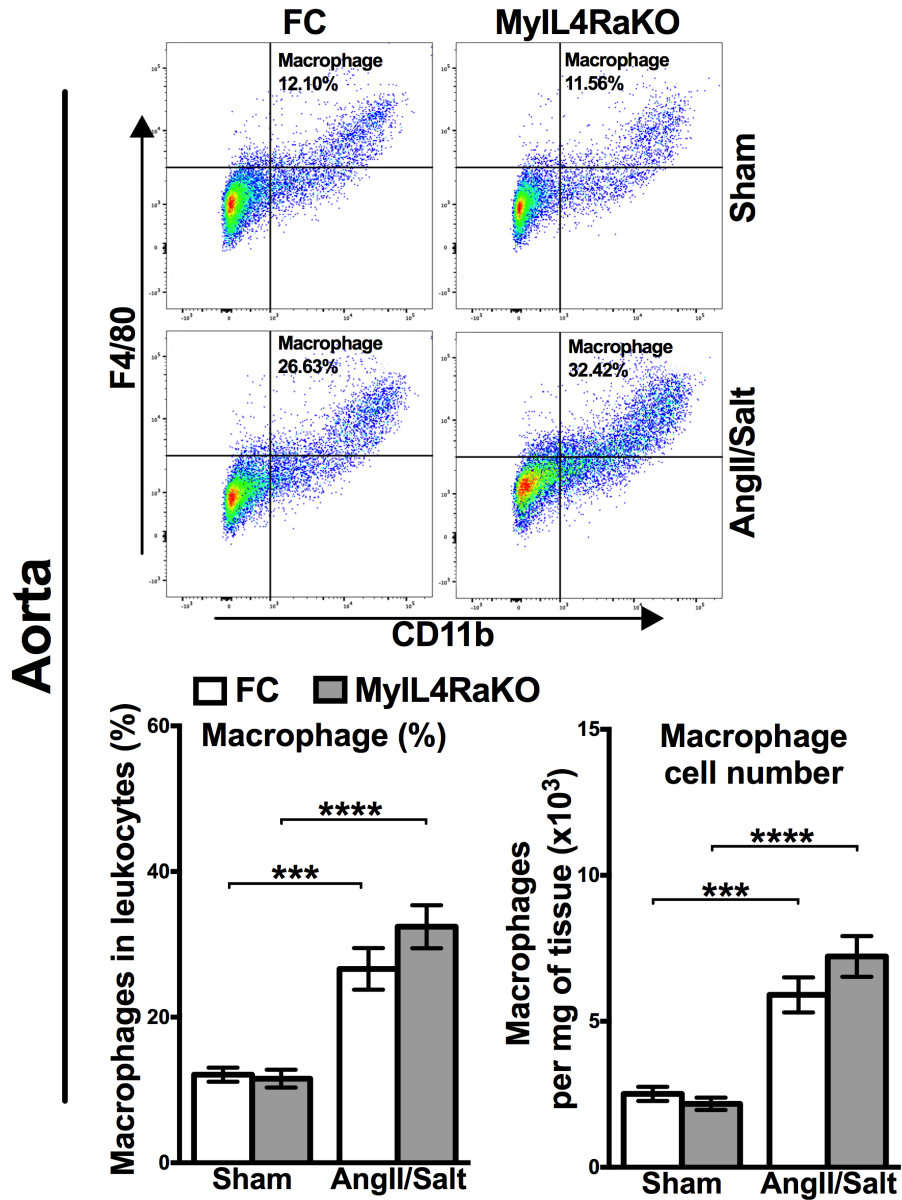


Figure 3.14. IL4R α deficiency does not change the recruitment of macrophages induced by AngII and high salt into aorta. Representative FACS dot plots of macrophages (CD11b⁺F4/80⁺) gated from leukocytes in aorta tissues of sham and AngII and high salt-treated mice, and the quantification of the percentage of macrophages in leukocytes and their cell number. All cell numbers are expressed per milligram tissue. n=9-10. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. ****P* < 0.001; *****P* < 0.0001.

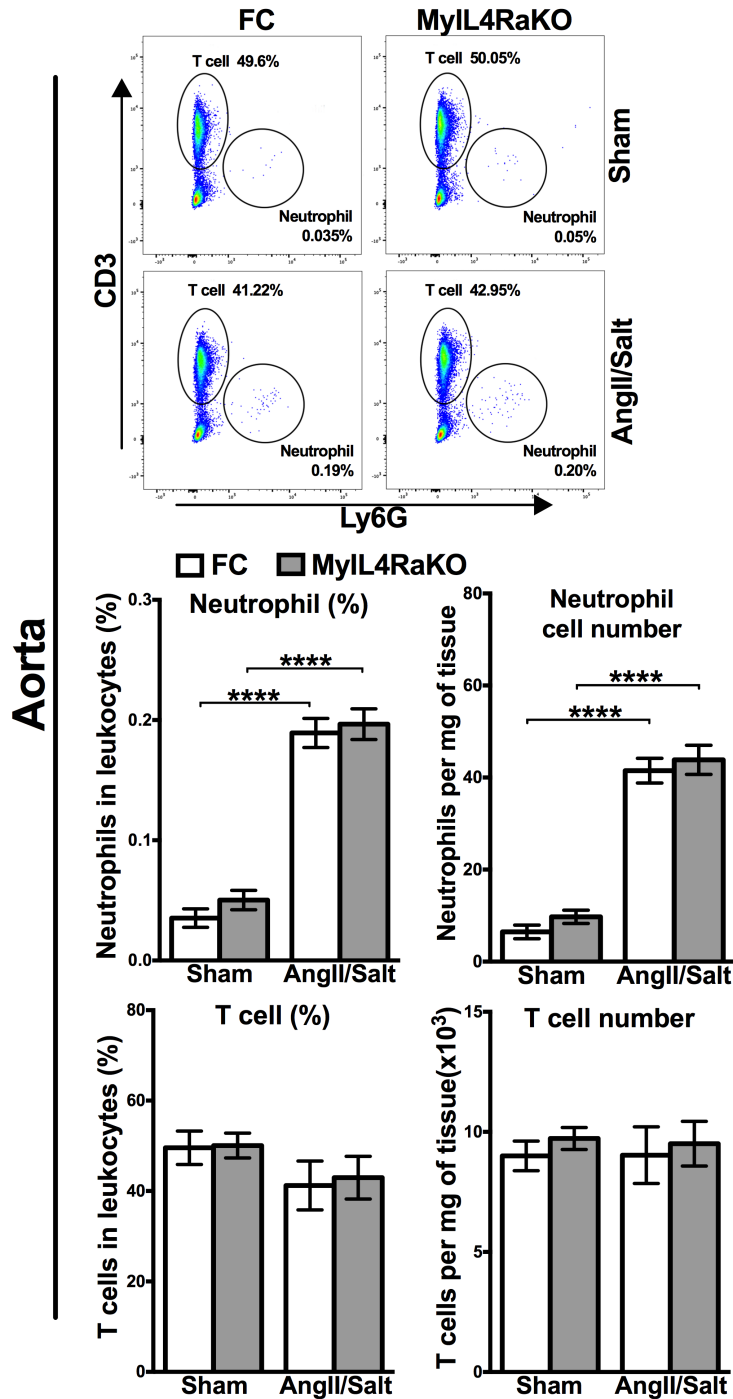


Figure 3.15. IL4R α deficiency does not change the recruitment of neutrophils and T cells induced by AngII and high salt into aorta. Representative FACS dot plots of neutrophils (Ly6G⁺) and T cells (CD3⁺) gated from leukocytes in aorta tissues of sham and AngII and high salt-treated mice, and the quantification of the percentage of neutrophils and T cells in leukocytes respectively and their cell number. All cell numbers are expressed per milligram tissue. n=5. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. *****P* < 0.0001.

Mildly enhanced circulating myeloid cells in MyIL4RαKO mice

As the infiltrating macrophages in heart and aorta are mostly derived from circulating monocytes, we were wondering whether the ablation of IL4Rα would cause any change in circulation monocytes. In order to answer this question, we determined the monocytes in blood by flow cytometry. Not only the percentage but also the number of monocytes increased significantly after exposure to AngII and high salt (Figure. 3.16A), which indicates the increase of circulating monocytes and inflammation in response to hypertensive injury, and more intriguingly, increased monocytes were shown in hypertensive MyIL4RαKO mice compared with hypertensive FC mice (Figure. 3.16A), which suggests the exaggerated inflammation induced by lack of IL4Rα in myeloid cells.

Because of the diversity and heterogeneity of monocytes⁶¹⁻⁶⁴, it was shown in infarcted hearts that Ly6C^{high} monocytes dominate early and undergo inflammatory functions to digest damaged tissue, while Ly6C^{low} monocytes dominate later and are less inflammatory to promote tissue healing and repair⁶⁵, which is parallel with the property and function of M1 and M2 macrophages^{66, 67}. In order to elucidate whether the knockout of IL4Rα disturbs the Ly6C^{low} and Ly6C^{high} monocytes interplay, we determined the circulating Ly6C^{low} and Ly6C^{high} monocytes in blood. The percentage of Ly6C^{low} or Ly6C^{high} monocytes in total monocytes was not changed (Figure. 3.16B), although the numbers of Ly6C^{low} and Ly6C^{high} monocytes were both increased and the number of Ly6C^{low} monocytes in MyIL4RαKO mice was higher than that in FC mice (Figure. 3.16B), which is likely attributable to the increase of total monocytes. Meanwhile, neutrophils in blood were also quantified by flow. Neutrophils were increased in hypertensive mice (Figure. 3.16C), indicating the increase of inflammation induced by AngII and high salt, but no difference was shown between hypertensive MyIL4RαKO and FC mice (Figure. 3.16C), however neutrophils at basal level were significantly increased in MyIL4RαKO mice (Figure. 3.16C), suggesting the enhanced inflammation at least at baseline by IL4Rα deficiency. No change was shown in T cells in blood (Figure. 3.16C), together with the

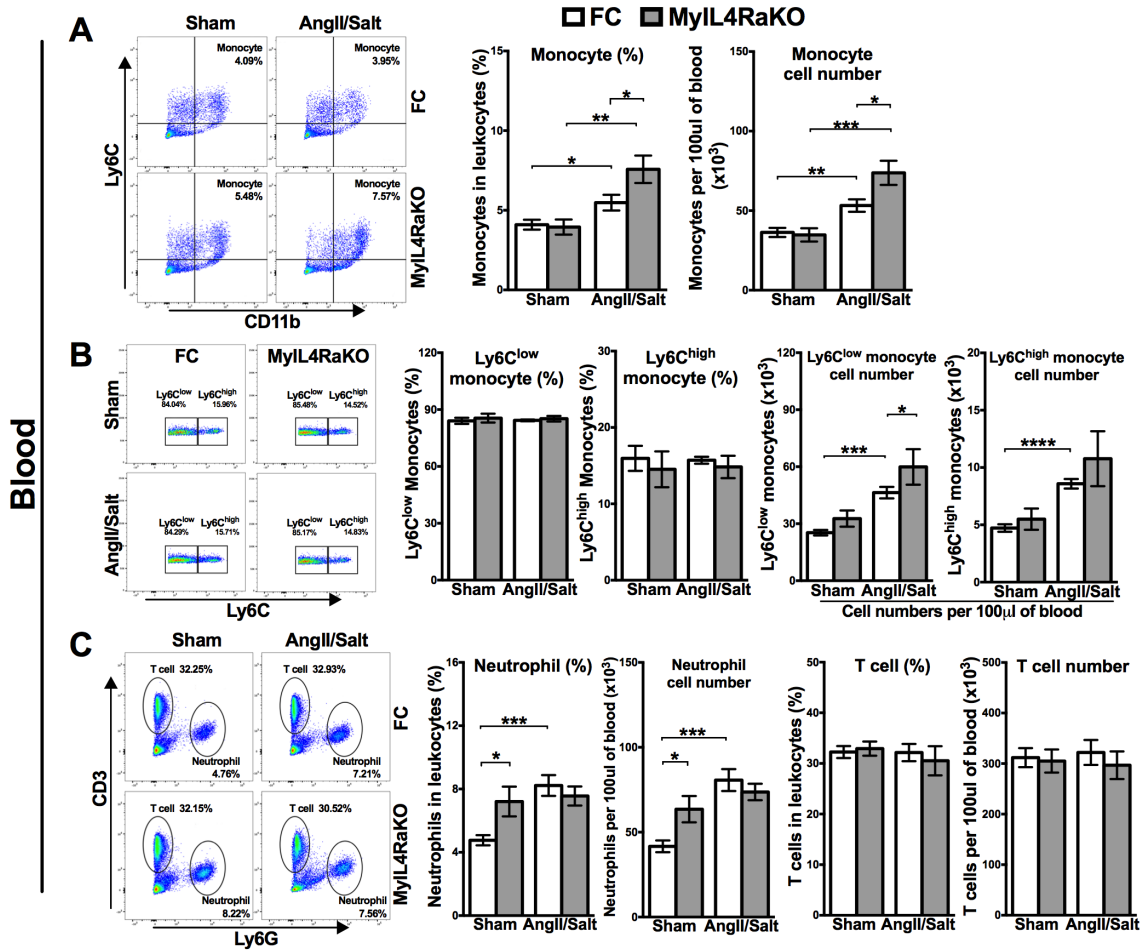


Figure 3.16. Myeloid-specific IL4R α ablation mildly increases circulating myeloid cells in blood. (A) Representative FACS dot plots of monocytes (CD11b⁺Ly6C⁺) gated from leukocytes in blood of sham and AngII and high salt-treated mice, and the quantification of the percentage of monocytes in leukocytes of blood and their cell number. n=9-10. (B) Representative FACS dot plots of Ly6C^{low} and Ly6C^{high} monocytes gated from total monocytes and the quantification of the respective percentage of Ly6C^{low} and Ly6C^{high} monocytes in total monocytes and their cell number per 100 μ l of blood. n=5. (C) Representative FACS dot plots of neutrophils (Ly6G⁺, n=8-10) and T cells (CD3⁺, n=5) gated from leukocytes in blood of sham and AngII and high salt-treated mice, and the quantification of the percentage of neutrophils and T cells in total leukocytes of blood and their cell number. All cell numbers are expressed per 100 μ l of blood. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. **P* < 0.05; ***P* < 0.01; ****P* < 0.001; *****P* < 0.0001.

quantification of T cells in heart and aorta, suggests that IL4R α signaling in myeloid cells is not involved in T cell infiltration from blood.

As spleen is also an important monocyte reservoir⁶⁸, and AngII can induce the release of monocytes from splenic reservoir^{68, 69}, and drive splenic macrophage progenitor amplification⁷⁰, we also characterized the cell populations in spleen after AngII and high salt-induced hypertension. Monocytes in spleen were significantly increased upon AngII and high salt (Figure. 3.17A), which is the opposite of reported decreased total monocytes in spleen after AngII⁶⁸, however, the increase of splenic monocytes is consistent with the enlargement of spleen in hypertensive mice (Figure. 3.17A). No difference was shown between FC and MyIL4R α KO mice in the number of monocytes in spleen or the size of spleen (Figure. 3.17A), suggesting that the IL4R α signaling may not participate in the splenic monocyte circulation (at least in our model).

As well as the Ly6C^{low} or Ly6C^{high} monocytes in blood, no change was shown in their percentage in total monocytes in spleen (Figure. 3.17B), and the increase of both Ly6C^{low} and Ly6C^{high} monocytes in response to AngII and high salt (Figure. 3.17B) is likely resulted from the increase of total monocytes (Figure. 3.12B). Neutrophils were also increased in spleen in response to AngII and high salt, with significant increase in MyIL4R α KO mice at basal level compared with FC mice (Figure. 3.17C), which probably suggests the enhanced inflammation in MyIL4R α KO mice at least at basal level. T cells were also significantly induced in hypertensive mice, but compared with FC mice, the number of T cells in spleen was reduced in MyIL4R α KO mice (Figure. 3.17C), which may suggest the involvement of myeloid IL4R α signaling in modulation of T cells in spleen.

Taken all the results in circulation together, knockout of IL4R α in myeloid cells showed increase in the number of neutrophils and monocytes in circulation, which suggests that myeloid-specific IL4R α knockout causes a mild systemic inflammation increase.

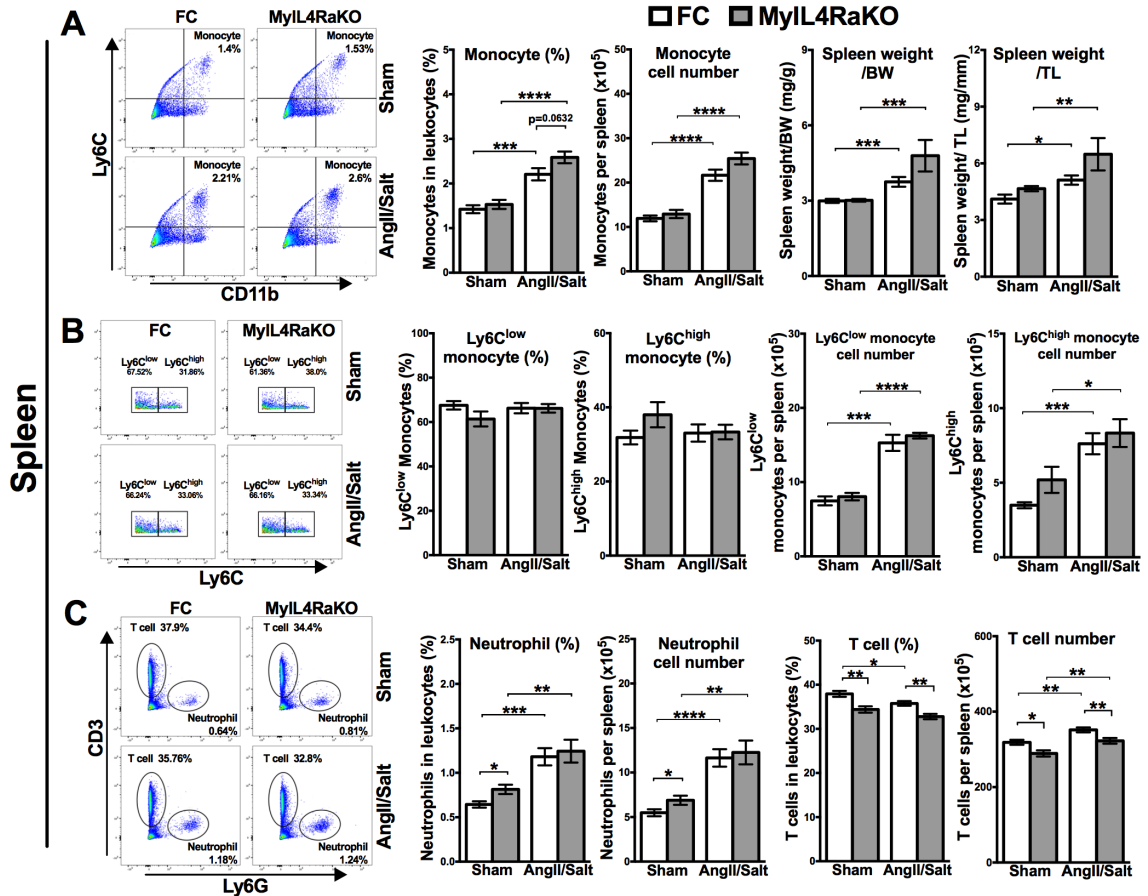


Figure 3.17. Myeloid-specific IL4R α knockout does not change the migration of myeloid cells from spleen after AngII and high salt. (A) Representative FACS dot plots of monocytes (CD11b⁺Ly6C⁺, n=9-10) gated from leukocytes in spleen of sham and AngII and high salt-treated mice, and the quantification of the percentage of monocytes and their cell number in spleen. The measurement of the spleen weight to body weight (BW) ratio and spleen weight to tibia length (TL) ratio. n=7-16. (B) Representative FACS dot plots of Ly6C^{low} and Ly6C^{high} monocytes gated from total monocytes, and the quantification of respective percentage of Ly6C^{low} and Ly6C^{high} monocytes in total monocytes of spleen and their cell number. n=5. (C) Representative FACS dot plots of neutrophils (Ly6G⁺) and T cells (CD3⁺) gated from leukocytes in spleen of sham and AngII and high salt-treated mice and the quantification of the percentage of neutrophils and T cells in leukocytes of spleen respectively and their cell number. n=8-10. Cell numbers indicated are per spleen. Results are shown as means \pm SEM. Unpaired student's *t* test and one-way ANOVA were used for statistical analysis. **P* < 0.05; ***P* < 0.01; ****P* < 0.001; *****P* < 0.0001.

Discussion

In the present study, we investigated the role of myeloid IL4R α signaling in cardiovascular remodeling during AngII and high salt-induced hypertension and cardiovascular remodeling. Knockout of IL4R α in myeloid cells had no effect on cardiovascular hypertrophic remodeling, but increased the expression of ROS generation related genes, and substantially decreased cardiovascular fibrotic remodeling via a systemic change of signaling pathways that mediate the development of fibrosis, such as TGF β , Gal3 and BMP9 signaling. These pathophysiologic changes lead to a relative mild preservation of cardiovascular function in MyIL4R α KO mice while that of FC mice was significantly impaired by AngII and high salt. However, the decreased fibrosis and the functional preservation in MyIL4R α KO mice are not simply due to the hypothesized M2 macrophage polarization reduction, because no decrease in M2-like macrophage population was shown. In conclusion, myeloid IL4R α signaling is significantly involved in cardiovascular remodeling induced by AngII and high salt, but it is not simply through blocking M2 macrophage activation in vivo, suggesting a more complicated change in macrophage phenotype that needs to be determined in the future.

Hypertrophic Remodeling

Hypertension is causally related to adverse cardiovascular remodeling, which includes hypertrophic structural changes. Clinical trials demonstrate that antihypertensive therapy prevents left ventricle hypertrophy. The prevention or reversal of left ventricle hypertrophy are correlated with cardiac function improvement and decline in risk of adverse cardiovascular outcomes. Cardiac hypertrophy, either from dilatation of left ventricle chamber or thickening of walls⁸, is an intermediate phenotype in the progression of hypertension to heart failure. Vascular smooth muscle hypertrophy is a critical component of vascular hypertrophic remodeling in hypertension⁷¹. In our study, hypertrophy was observed in both heart and aorta in AngII and high salt-induced hypertensive injury. Mice displayed increased heart weight, enlarged cardiomyocyte size, and increased aortic wall thickness (Figure. 3.1), which is consistent with previously

reports^{72, 73}. However, no change in hypertrophic remodeling was caused by myeloid IL4R α deficiency, which is also consistent with a previous report showing that global IL-4 deficiency does not affect hypertrophy during AngII-induced cardiac remodeling²⁷. These results together suggest that myeloid IL4R α signaling is not involved in cardiovascular hypertrophic remodeling.

Fibrotic Remodeling

In addition to hypertrophy, AngII and high salt also induces pro-fibrotic cardiovascular remodeling. Both hypertrophy⁷⁴ and fibrosis⁷⁵⁻⁷⁷ contribute to myocardial and vascular stiffness, which plays a critical role in deleterious functional disorders. In our study, MyIL4R α deficiency resulted in significant suppression of interstitial and perivascular fibrosis (Figure. 3.2) with modest changes in collagen gene expression (Figure. 3.4 and Figure. 3.5) during AngII and high salt treatment compared to floxed controls. In addition to collagens, MMPs and TIMPs also contribute to the pathogenesis of fibrosis. Decreased MMPs and increased TIMPs would lead to collagen accumulation. In heart tissues of AngII treated MyIL4R α KO mice, we detected decreased Col3A1 and increased MMP13 which could cooperatively contribute to the decreased fibrosis. No change in TIMP1 was found in hypertensive MyIL4R α KO mice compared with the sham, where as a significant increase in TIMP1 mRNA expression was shown in hypertensive floxed control mice (Figure. 3.4).

Fibrosis Associated Signaling Pathways

TGF β signaling: TGF β signaling is one of the classical pathways in fibrotic remodeling. TGF β 1 facilitates the deposition of extracellular matrix proteins on vascular walls in response to mechanical stress caused by hypertension⁷⁸, which attenuates vasculature compliance and increases stiffness. In our study, TGF β 1 mRNA in heart did not show any change upon AngII and high salt treatment (Figure. 3.4). Consistent with our results, spontaneously hypertensive rats (SHR) without heart failure also do not show any difference in TGF β 1 mRNA in left ventricle compared with normotensive rats, although a significant increase was shown in SHR with heart failure⁷⁹. Another study by Kim et al. showed that there is no significant difference in cardiac TGF β 1 mRNA

expression between deoxycorticosterone acetate (DOCA)-salt hypertensive rats and shams. However, TGF β 1 mRNA was significantly increased in aorta of DOCA-salt hypertensive rats⁸⁰, which is consistent with our results showing a significant increase of TGF β 1 mRNA in aorta tissues but no change in hearts after AngII and high salt treatment (Figure. 3.4 and Figure. 3.5). These studies suggest that the expression of TGF β 1 varies depending on the severity of disease and the tissue. Fibrosis development may not absolutely require an increase in TGF β 1 since TGF β 1 mRNA did not change, but its downstream target gene PDGF α mRNA increased upon AngII and high salt (Figure 3.4).

PAI-1 signaling: PAI-1 has been linked to both pro-fibrotic and anti-fibrotic actions. The pro-fibrotic role was shown in renal fibrosis either induced by unilateral ureteral obstruction (UUO) or protein overload, which displayed significantly diminished fibrosis in kidney of PAI-1^{-/-} mice⁵⁹. Its anti-fibrotic role was shown in PAI-1^{-/-} aging mice which revealed increased fibrosis in heart but not other major organs such as lung and kidney⁵⁸. As PAI-1 is an inhibitor of t-PA and u-PA, spontaneous cardiac fibrosis in PAI-1 deficient mice is consistent with cardiac fibrosis in u-PA overexpressing mice⁵⁸ and impaired collagenous scar formation in infarcted hearts of u-PA null mice⁸¹, which supports an anti-fibrotic role of PAI-1. This may explain the increased expression of PAI-1 mRNA in aorta in hypertensive Myl4R α KO mice compared with hypertensive FC mice, but with decreased aortic fibrosis in our study (Figure. 3.2A and Figure. 3.5). PAI-1 deficient mice with reduce perivascular fibrosis in infarcted hearts⁸² is consistent with PAI-1 overexpression resulting in augmented fibrosis, and PAI-1 deficiency or u-PA overexpression leads to decreased fibrosis in lung and kidney^{60, 83}, which supports a pro-fibrotic role of PAI-1. This may partially explains the reduced PAI-1 mRNA in heart of Myl4R α KO mice with decreased cardiac fibrosis (Figure. 3.2B and Figure. 3.4). However, it is not clear whether PAI-1 is pro- or anti-fibrotic in our model except using the PAI-1^{-/-} mice to demonstrate.

One of the possibilities is that the function of PAI-1 may vary depending on the severity of the damage or the progression of disease. PAI-1 inhibits fibrosis when fibrosis is harmful, but promotes fibrosis when fibrosis is required to

maintain the integrity of the injured tissue. A molecule may have opposite effects depending on the context. Another alternative explanation is that the role of PAI-1 is possibly tissue-dependent. In a specific context, it is likely that both damage severity and tissue type contribute to the function of PAI-1 in fibrosis.

BMP9 Signaling

As a TGF β 1-independent signaling pathway, BMP9 signaling has been recently identified as a novel pro-fibrotic⁸⁴⁻⁸⁶ or fibrosis-limiting factor⁵⁷, another molecule that may have opposite and context-specific effects. In our study, decreased cardiac fibrosis was shown in hypertensive MyIL4R α KO mice with increased BMP9 mRNA expression (Figure. 3.2B and Figure. 3.4), which probably supports the anti-fibrotic role of BMP9 in heart, however, this needs to be confirmed via a BMP9 knockout mouse model or pharmacologically blocking BMP9 signaling. BMP9 acts through the downstream target genes inhibitor of DNA binding 1 (ID1) and inhibitor of DNA binding 2 (ID2) via the Smad molecules to regulate the production of ECM proteins^{87,57,88}. However, in our study, compared with hypertensive FC mice, MyIL4R α KO mice did not show any difference in ID1 mRNA expression in heart, while showed significant decrease in ID2 mRNA (data not shown), which is not consistent with the increase in BMP9 mRNA. This may suggest that there are more than one signaling in addition to BMP9 contributing to the transcription of ID1 and ID2.

In contrast to the no change in ID1 and decrease in ID2 mRNA in heart of hypertensive MyIL4R α KO mice, ID1 significantly decreased while ID2 did not show any change in aorta (data not shown), which is not consistent with the expression of BMP9 in aorta either as BMP9 mRNA did not show any difference in hypertensive MyIL4R α KO mice compared with FC (Figure. 3.5). This may confirm that there may be other pathways contributing to the expression of ID1 and ID2, in addition to BMP9. The difference in BMP signaling between heart and aorta tissues also supports the tissue-dependent mechanisms that control fibrotic remodeling.

Inflammatory Responses

Hypertensive stimuli including AngII and high salt induce ROS production in a variety of tissues such as brain, heart, kidney and vasculature⁷¹, which promotes the pathological development of hypertensive remodeling like hypertrophy, inflammation and fibrosis. ROS generation related genes were increased in MyIL4R α KO mice (Figure. 3.7), suggesting there is increased inflammation as a result of IL4R α deficiency in myeloid cells.

Hypertensive stimuli also induce pro-inflammatory molecules, which then promote the rolling, adhesion and accumulation of inflammatory cells in injured tissues⁸⁹⁻⁹³. The pro-inflammatory molecules and oxidative stress mutually amplify each other. For instance, TNF α activates NADPH oxidase that further enhances oxidative stress⁹⁴. Meanwhile, TNF α facilitates the overexpression of chemokines and adhesion molecules⁹⁵. The migration of M2 macrophages at late stages of cardiac injury was shown to be TNF α signaling dependent⁹⁶.

IL-6, another major pro-inflammatory cytokine, also mediates superoxide production, which causes endothelial impairment⁹⁷. IL-6 is fundamental for the development of hypertension⁹⁸⁻¹⁰³ and contributes to hypertension-induced cardiovascular remodeling. AngII and high salt-induced hypertension and cardiac injury was significantly abrogated in IL-6 deficient mice¹⁰⁴, and high levels of circulating IL-6 can be considerably diminished by blocking AngII signaling^{103, 105}. Deletion of IL-6 prevents macrophage infiltration, ameliorates fibrosis and improves cardiac function in AngII and high salt-induced hypertension¹³. IL-6 also involves in vascular remodeling by promoting vascular smooth muscle cells migration and proliferation, which results in vascular medial hypertrophy^{106, 107}. In our study, TNF α was significantly induced by AngII and high salt, and a strikingly significant increase in IL-6 mRNA was also shown (Figure. 3.6).

The chemokine MCP1 (also known as CCL2) activates monocytes and mediates their migration towards the inflammatory site. AngII can stimulate the production of MCP1 by activating CCR2 receptor¹⁰⁸. A significant increase in MCP1 mRNA was observed in hypertensive aorta tissues in our study, however, no increase in heart has detected (data not shown), which indicates a differential remodeling mechanism in heart and aorta. No significant change in MCP1

expression was revealed in MyIL4RαKO mice compared with FC, suggesting that myeloid IL4Rα signaling effects on cardiovascular remodeling may not be through the MCP1/CCR2 axis.

Immune Cells in Cardiovascular Remodeling

The hypertrophic, inflammatory and fibrotic cardiovascular remodeling following hypertension is attributable to the interaction between cardiac- and vascular- parenchymal cells and inflammatory immune cells.

Monocytes and Macrophages

Circulating monocytes amplify in response to AngII^{15, 109}, which is also supported by our results (Figure. 3.16), showing significant increase of monocytes in blood. Elimination of monocytes results in attenuated hypertension, decreased ROS generation and improvement of cardiovascular function¹⁵. Monocytes are circulating precursors of macrophages that accumulate in perivascular adipose tissue, adventitia, heart and kidneys during hypertension^{110, 111}. Stimulated by hypertension, infiltrating macrophages release pro-inflammatory cytokines, produce ROS and promotes oxidative stress, disturb tissue homeostasis and initiate remodeling, all of which contributes to disease development and progression¹¹²⁻¹¹⁷. Massive infiltration of macrophages in the cardiovascular system was observed in our study (Figure. 3.11 and Figure. 3.14), characterized by a significant increase of macrophages in heart and aorta in hypertensive mice. In monocyte and neutrophil depleted LysM^{iDTR} mice by diphtheria toxin administration, hypertensive responses such as hypertrophy, ROS production and cardiovascular dysfunction were blocked. Restoration of monocytes rather than granulocytes reversed the hypertension¹⁵, which supports the essential role of monocytes/macrophage in hypertension and hypertension-induced cardiovascular remodeling.

Macrophages are present during injury with distinctive phenotypes depending on the stage. Initially they migrate into the injured tissue and adopt a pro-inflammatory phenotype (M1 macrophages) that serves to clear dead cells and debris, later on they polarize to anti-inflammatory phenotype (M2 macrophages) and produce cytokines against inflammation and other factors to

resolve inflammation and initiate tissue repair. Macrophages are more and more appreciated as master regulator of fibrosis^{29, 109}. The type 2 immune response maintains tissue homeostasis, but if not appropriately regulated, it can result in fibrosis by amplification of macrophages¹¹⁸. It has recently been shown that IL-4 or IL-13 alone is not sufficient to induced type 2 immune responses, but IL-4 or IL-13 together with signals from apoptotic cells activate macrophages to repair the damaged tissue¹¹⁹, i.e. IL-4 or IL-13 activated macrophages cannot initiate tissue repair program unless they receive signals from apoptotic neutrophils. Losing the ability to sense apoptotic cells interrupts the proliferation of tissue-resident macrophages and inhibits the activation of anti-inflammatory genes involved in tissue repair¹¹⁹. The sensing process occurs between macrophages and local tissue-specific signals, by which macrophages integrating various signals and then switch to repair mode to produce tissue-building factors¹²⁰. Macrophages generate proteins that are directly involved in tissue repair such as Col1A1 which deposits in ECM and Relm α which eventually acts to cross-link collagen with fibrils, enhancing the strength or stiffness of injured tissue³². Those macrophages participating in tissue repair are mostly M2-like macrophages.

M2 Macrophage Polarization In Vivo

M2 macrophages are importantly involved in the pro-fibrotic remodeling. Fibrosis in multiple tissues was found significantly decreased in MyIL4R α KO mice in our study (Figure. 3.2 and Figure. 3.3), and as IL4R α signaling is very important for M2 macrophage activation and polarization, we hypothesized that the decreased fibrosis attributes to M2 macrophage polarization suppression as a result of IL4R α deficiency. However, we were unable to demonstrate this hypothesis. Knockout of IL4R α in myeloid cells dramatically attenuated M2 macrophage polarization in vitro (Figure. 2.1A), but unfortunately not in vivo. First, no significant decrease was observed in the expression of M2 macrophage markers in heart or aorta tissues of hypertensive MyIL4R α KO mice (Figure. 3.9). On the contrary, one of the M2 macrophage markers Fizz1 displayed significant increase in heart of sham MyIL4R α KO mice compared with sham FC. This may contribute to the expression of Fizz1 in other cell types other than myeloid cells in

heart because Fizz1 also expresses in endothelial cells, vascular smooth muscle cells, T cells and myofibroblast-like cells¹²¹. Our result is supported by the comparable expression of Fizz1 in IL-4 knockout mice and WT mice in hypoxia-induced hypertensive lung¹²², which together suggests that there are more than one signaling pathway in addition to IL-4 signaling that contribute to Fizz1 expression. Second, no difference was shown in the percentage or number of M2 macrophages in MyIL4R α KO mice based on the results from flow (Figure. 3.10 and Figure. 3.13). These results conflict with data from other studies. Macrophages from LysM^{cre}IL4R α ^{flox/-} mice revealed significant reduction in genes characterizing M2 macrophages including CD206 and Fizz1 by qRT-PCR after specifically sorting CD11b⁺F4/80⁺ macrophages from wound tissues³². This inconsistency may attribute to the samples for gene expression: instead of macrophages only in vivo, we determined gene expression in tissues that include a lot other cell types. Macrophages from pancreas of LysM^{cre}IL4R α ^{flox/flox} mice also displayed significant decrease in CD206 expression in a chronic pancreatitis model²⁶, which was determined by flow. In order to further pursue that whether IL4R α deficiency changes the macrophages or not, sorting macrophages from heart and aorta and then characterize these macrophages by determining the mRNA expression profile of M2 and M1 macrophage markers with qRT-PCR will be very helpful.

To reconcile the results we have so far, we propose a 4-part hypothesis. First: timing; macrophages from wounded skin showed decreased expression of M2 macrophage markers at 7-day post injury, but none of the markers was maintained at very late stage (after 14 days) of repair³², which suggests the time dependence of gene expression. Second: genetic background; both mouse models that showed decrease in M2 macrophage polarization are on a background of BALB/c (LysM^{cre}IL4R α ^{flox/-} mice in the skin wound model and LysM^{cre}IL4R α ^{flox/flox} mice in the chronic pancreatitis model), in contrast, what we used in our study are on a C57BL/6 background. Totally different phenotypes were shown in mice of different background but with the same knockout¹²³, which highlights the importance of genetic background. Third: signaling pathways other

than IL4R signaling also contribute to M2 macrophage polarization *in vivo*. Instead of canonical IL-4/IL-13-STAT6 signaling, activated adventitia fibroblasts polarized naïve macrophages to a distinctive phenotype that promotes inflammation and fibrosis via IL-6-STAT3-HIF1-C/EBP β axis, which challenges the present paradigm of IL-4/IL-13-STAT6-mediated macrophage alternative activation as the sole driver of reparative remodeling¹²⁴. This is supported by other studies. Tumor-derived lactic acid from aerobic glycolysis enhanced Fizz1 expression in tumor-associated macrophages, which is dependent on HIF1 but not IL-4/IL-13¹²⁵. Feilding et al. demonstrated that IL-6 is required for the development of peritoneal fibrosis by switching acute inflammation to a chronic pro-fibrotic state¹²⁶. Therefore, signaling like IL-6-STAT3-HIF1 axis may compensate the lack of IL4R signaling and contribute to the polarization of M2 macrophages *in vivo*. Fourth: incomplete deletion of IL4R α by LysM^{cre}. Because of the heterogeneity, macrophages express LysM differently. Macrophages elicited by inflammatory stimuli have a lower level of LysM than the tissue resident macrophages, which was demonstrated by the results that naïve tissue resident macrophages from LysM^{Cre}IL4R α ^{flox/-} mice almost completely lost IL4R α function while a large fraction of inflammation-stimulated macrophages failed to repeal IL4R α ¹²⁷. Taken together, the four mechanisms mentioned above probably synergize or work independently and result in the unchanged M2 macrophage populations *in vivo* in our model.

Neutrophils

As LysM^{cre}IL4R α ^{flox/flox} also ablates IL4R α in neutrophils, our results also reflect the effect of IL4R α deletion in neutrophils. Based on our data from flow cytometry, no change was shown in neutrophils of heart and aorta as a result of IL4R α ablation (Figure. 3.12 and Figure. 3.15), which suggests that IL4R α deficiency in neutrophils does not at least change their migration into the injured tissues. This is consistent with the study by Wenzel et. Al. who showed that restoration of neutrophils in LysM^{iDTR} driven myeloid cells ablated mice did not restore pathophysiological action of AngII¹⁵. However, more neutrophils were shown in blood and spleen of sham MyIL4R α KO mice, which indicates the higher

level of inflammation and this is supported by the result that selective depletion of circulating neutrophils protects against oxidative stress in AngII-induced hypertension¹²⁸.

T cells

T cells have also been shown to be involved in hypertension via infiltrating into organs that control blood pressure^{129, 130}. A landmark study by Guzik et al. demonstrated that recombina-activating gene 1 (Rag1) deficient mice, which fail to develop B and T lymphocytes, were protected from hypertension induced by AngII or DOCA-salt. Importantly, the hypertensive responses were restored by adoptive transfer of T cells, but not B cells¹²⁹. These results were confirmed by Mattson et al. who observed a similar phenotype in Rag1^{-/-} mice¹³¹. T cells accumulate in the kidney and vasculature of hypertensive mice, release inflammatory cytokines, produce ROS, and promote renal and vasculature dysfunction^{132, 133}. Blocking T cell infiltration by immunosuppressive drug mycophenolate acid reduces intrarenal AngII and prevents hypertension and kidney damage^{112, 134, 135}. Furthermore, circulating T cells induced by AngII were described with effector phenotype *in vivo* and *in vitro*^{129, 136}. In addition to T effector cells, T regulatory cells are also involved in hypertension and play a role that is opposite of T effector cells. Adoptive transfer regulatory T cells (Tregs) diminished AngII-induced hypertension, vascular stiffening and inflammation, as Tregs are innate and adaptive immune responses suppressing cells¹³⁷. Innate immune system release signals to activate T effector cells and their differentiation towards pro-inflammatory Th1 and Th17 phenotypes. These T effector cells promote low-grade inflammation by producing pro-inflammatory cytokines, which eventually lead to increase in blood pressure and end-organ damage. In contrast, Tregs counteract effects associated with hypertension by suppressing immune responses. Imbalance of T effector cells and Tregs aggravates inflammation, elicits increase in blood pressure and leads to end-organ damage in hypertensive patients¹¹⁷. However, no significant increase of infiltrating T cells was shown in response to AngII and high salt in our study (Figure. 3.12, and Figure. 3.15), which partially can be explained technically. T

cells are known accumulating in perivascular fat^{111, 129} to impair endothelial function and cause vascular fibrosis^{136, 138-140}, but when we collect the aorta tissues, in order to more specifically analyze aorta, we tried to exclude the surrounding adipose tissues, where a lot T cells accumulate. Distinct from injured tissues and blood, more T cells were detected in spleen from hypertensive mice (Figure. 3.17C), which probably resulted from the enlargement of spleen (Figure. 3.17A). This is consistent with the significant spleen hypertrophy and more proliferative immature lymphocytes in AngII-infused apolipoprotein E (ApoE)^{-/-} mice¹⁴¹.

Prospect in Future

Overall, as IL4R α signaling in myeloid cells is significantly involved in cardiovascular remodeling induced by hypertension, specifically targeting myeloid IL4R α signaling pathway could suppress excess pro-fibrotic remodeling and protect cardiovascular function. However, the timing and the extent are very important. For example, attenuating inflammation in the early phase of myocardial infarction could be beneficial, however, inhibiting fibrosis initially could lead to cardiac rupture or aneurysm^{11, 142-144}. Myeloid IL4R α signaling involves both anti-inflammatory and pro-fibrotic pathways in cardiovascular remodeling. Targeting myeloid IL4R α to limit the pro-fibrotic role but not suppress the anti-inflammatory effect is not easy to control. Therefore, comprehensive and accurate spatio-temporal description of the components in the anti-inflammatory and pro-fibrotic pathways is necessary, and specific drugs that target these pathways need to be evaluated.

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CHAPTER IV

SUMMARY AND CONCLUSIONS

Overview

Previous work from our lab has demonstrated that macrophage activation and polarization are important for inflammation in response to cardiac damage and ischemic stroke^{1, 2}. The mineralocorticoid receptor controls macrophage polarization, and ablation of the mineralocorticoid receptor in macrophages results in an alternatively activated (M2) profile and suppresses classical activation (M1). This change in macrophage polarization contributes to the protective effect of mineralocorticoid receptor deficiency on L-N^G-nitroarginine methyl ester (L-NAME)/AngII-induced cardiac and vascular remodeling¹ and neuroprotection in experimental stroke². Most importantly, these results indicate that macrophages are critical target cell types for mineralocorticoid receptor antagonists that have been widely used in the treatment of cardiovascular diseases.

Based on these previous findings, the original goal of the present study was to regulate macrophage polarization by modifying macrophage-specific molecules that control macrophage phenotype and test the importance of macrophages as a target cell type in the cardiac injury models myocardial infarction and AngII/Salt-induced hypertensive cardiac injury. IL4R α signaling is a well established and potent inducer of alternative activation (M2) in macrophages, and M2 macrophages are significantly involved in resolution of inflammation, wound healing and tissue repair^{3, 4}, and pathological fibrosis^{5, 6}. We hypothesized that macrophage IL4R α signaling inhibits inflammatory responses, but promotes fibrosis in cardiovascular remodeling post injury through M2 macrophage activation and polarization; therefore blocking IL4R α signaling in macrophages could exaggerate systemic inflammation, but ameliorate fibrosis,

leading to alterations in cardiovascular remodeling and subsequent changes in cardiac function.

In order to test this hypothesis, we generated myeloid-specific IL4R α knockout mice (MyIL4R α KO), which have genetic ablation of IL4R α in myeloid lineage cells including monocytes, macrophages and neutrophils. We subjected these mice to cardiac injury/stress using experimental myocardial infarction and AngII/Salt-induced hypertensive cardiac injury models and investigated whether macrophages are the main target cell type of endogenous IL4/IL-13 signaling during cardiac remodeling and whether myeloid-specific IL4R α signaling affects inflammation, pro-fibrotic remodeling and cardiac function.

Based on the expression of M1/M2 macrophage markers, in vitro macrophages isolated from MyIL4R α KO mice showed significantly blunted responses to the M2 macrophage stimulus IL-4 and in contrast had markedly increased responses to the M1 macrophage stimulus LPS. This demonstrates the importance of IL4R α signaling in macrophage polarization, particularly with respect to the activation and polarization of M2 macrophages.

During myocardial infarction (MI), the infarct size of MyIL4R α KO mice was significantly decreased at 1-week post MI and the infarct thickness was significantly increased at 3-week. This suggests that IL4R α in macrophages is an important target for endogenous IL-4/IL-13 and that myeloid IL4R α signaling is importantly involved in cardiac remodeling post MI. In addition, IL4R α deletion in myeloid cells enhanced perivascular fibrosis and caused more severe cardiac dysfunction, suggesting a protective role for myeloid IL4R α signaling in cardiac remodeling post MI. Surprisingly, there was no obvious change in alternatively activated M2-like macrophage populations in infarct tissues post-MI, which indicates that the increased adverse cardiac remodeling caused by lacking of IL4R α in myeloid cells is not through a simple global change of M2-like macrophages. Taken together, myeloid IL4R α signaling is necessary for appropriate cardiac remodeling post MI, and macrophages are important target cell types for IL-4/IL-13 signaling, therefore myeloid IL4R α signaling may be a potential therapeutic strategy for patients post MI.

In AngII/Salt-induced hypertensive cardiac injury, myeloid-specific IL4R α ablation caused significant upregulation of ROS generation-related genes, indicating there is enhanced inflammation in MyIL4R α KO mice. This is accompanied by a substantial decrease in cardiovascular fibrosis, which may attribute to the significant down-regulation of TGF β signaling and Gal3 signaling. The results above suggest that myeloid IL4R α signaling is importantly involved the suppression of oxidative stress development and pro-fibrotic cardiovascular remodeling, two opposite effects regarding cardiac function. By performing echocardiography, we found that cardiac and aortic function of MyIL4R α KO mice was largely preserved in chronic hypertension, while that of control mice was significantly impaired. Surprisingly, but consistent with the infarction model, the changes in cardiovascular remodeling were not simply due to the disturbed macrophage polarization because no in vivo changes in M1/M2 macrophages were detected by flow cytometry. In conclusion, myeloid IL4R α signaling is significantly involved in cardiovascular remodeling induced by chronic hypertensive injury, and myeloid lineage cells are critical targets of endogenous IL-4/IL-13. Importantly, instead of M1/M2 macrophage polarization alteration, increased systemic inflammation and decreased pro-fibrotic remodeling in MyIL4R α KO mice is mediated by a more complicated mechanism of myeloid cells, which needs to be determined in the future.

Overall in this dissertation, we demonstrated the following important findings: 1) myeloid cells are critical targets of endogenous IL-4/IL-13 signaling; 2) myeloid IL4R α signaling involves more than simply regulating M1/M2 macrophage polarization, and the present M1/M2 paradigm is inadequate; 3) IL4R α signaling differentially affects resident and monocyte-derived infiltrating macrophages; 4) the effect of myeloid IL4R α signaling on cardiac and vascular remodeling varies depending on the type and severity of the injury/stress. The last two conclusions were not specifically emphasized, but will be discussed later in this chapter.

Myeloid cells are critical targets of IL-4/IL-13

IL-4 and IL-13 are anti-inflammatory cytokines, and the signaling pathways driven by these two cytokines have been shown to be very important in cardiac and vascular remodeling after injury. IL-4 administration improved post-MI prognosis and cardiac function⁷. Cardiac fibrosis induced by pressure overload was considerably attenuated by anti-IL-4 neutralizing antibody⁸, and IL-4 deficient mice displayed reduced interstitial myocardial fibrosis in response to AngII⁹. However, the target cell type(s) of IL-4/IL-13 in cardiovascular remodeling have been unclear.

IL4R α is the common chain of IL-4/IL-13 receptors by which IL-4 and IL-13 activate their signaling pathways, therefore we employed the use of myeloid specific IL4R α deficient mice to identify the contribution of macrophages in endogenous IL-4/IL-13 mediated cardiovascular remodeling. By blocking IL4R α signaling specifically in myeloid cells, infarct size post-MI was decreased temporarily, perivascular fibrosis was increased and cardiac function was more significantly impaired post-MI. Both interstitial and peri-vascular fibrosis were significantly decreased during AngII/Salt-induced hypertensive injury. These results indicate that myeloid cells are important mediators of endogenous IL-4/IL-13-induced changes in cardiovascular remodeling during acute and chronic cardiac injury. Macrophages represent the largest population of myeloid lineage cells in the heart and vasculature in the models we tested, and these results highlight a significant role of macrophages in IL4R α signaling-mediated remodeling. This is further supported by the similar degree of fibrosis detected in global IL4R α deficient and myeloid-specific IL4R α deficient mice during a chronic pancreatitis model. They found that myeloid-specific IL4R α knockout phenocopied the global IL4R α deficient mice indicating that myeloid cells were the critical cell types mediating the fibrotic effects of IL4R α signaling¹⁰.

The significant role of myeloid cells or macrophages in IL4R α signaling-mediated cardiac and vascular remodeling in our studies could be confirmed by generating the whole body IL4R α knockout (IL4R α ^{-/-}) mice, and then comparing the remodeling phenotypes between IL4R α ^{-/-} and MyIL4R α KO mice. If IL4R α ^{-/-} mice phenocopy the myeloid-specific IL4R α deficient mice, that would indicate

myeloid cells/macrophages are critical cell specific targets in endogenous IL-4/IL-13 mediated cardiovascular remodeling. An alternative scenario would be to administer IL-4 in MyIL4R α KO and control mice that are subjected to myocardial infarction. If administration of IL-4 decreases cardiac damage and improves cardiac function in control mice but not in MyIL4R α KO mice, that would also demonstrate a predominant role for myeloid cells or macrophages in IL-4-mediated protection.

Myeloid cells include monocytes/macrophages and neutrophils, and both monocytes/macrophages and neutrophils express IL4R α , so we cannot exclude the possible contribution of neutrophils in our studies. Although we did measure the neutrophil population in our studies by flow cytometry, further experiments testing the response of neutrophils to IL-4 or other inflammatory stimuli during IL4R α deficiency would provide additional insight. Furthermore, to particularly delineate the contribution of neutrophils in IL4R α signaling-mediated cardiovascular remodeling after injury/stress, neutrophil-specific IL4R α knockout using the Mrp8 (S100A8)-Cre would be a possible approach.

Inadequacy of M1/M2 macrophage paradigm

IL4R α signaling is a well-established mechanism of IL-4-induced M2 macrophage activation and polarization. Consistent with this role, IL-4 stimulation of IL4R α KO macrophages showed a dampened response in polarization compared with macrophages from control mice. Although we saw some similar changes at baseline in cardiac tissue, we did not see this phenotype in vivo in cardiac injury models. No change was detected in M2-like macrophages characterized by CD11b⁺F4/80⁺CD206⁺ in injured tissues between MyIL4R α KO and control mice either after MI or hypertensive cardiac injury. This raises the question that after injury macrophage polarization is not changed by deleting IL4R α , or the properties of macrophages are changed but the present M1/M2 paradigm is not adequate to describe it?

This would indicate a diminished role for endogenous IL-4/IL-13 since the in vitro data clearly showed that deficiency of IL4R α in macrophages significantly decreased the expression of M2 macrophage markers, but increased the M1

macrophage markers. In vivo, the lack of IL4R α in myeloid cells caused substantial alteration in cardiovascular remodeling: enhanced cardiac dysfunction post-MI and attenuated cardiac and vascular fibrosis post hypertensive injury. Since macrophages represent one of the major myeloid cell types in the injured myocardium, and the infiltration of neutrophils was not largely changed in MyIL4R α mice, the significant differences in cardiovascular remodeling caused by myeloid-specific IL4R α ablation is likely to be mediated through its effects on macrophages.

It is likely that the deficiency of IL4R α did change the properties of macrophage in vivo, however, the present M1/M2 model we used is not sufficient enough to reveal these changes. This indicates the inadequacy of the M1/M2 dichotomy since the M1/M2 model is based on the in vitro activation of macrophages, which stimulates macrophages with a defined set of factors. This does not resemble anything that occurs in vivo¹¹. Instead of M1 and M2, two polarized extremes, macrophages exist as a wide spectrum that line between M1 and M2. Presently, we lack markers to characterize the intermediates. Current markers only characterize the two extremes, for example TNF α and CD206 are commonly used in flow cytometry to identify M1 and M2 macrophages respectively. The transcriptional profiles of human macrophages display a broad transcriptional range that challenges the M1/M2 paradigm¹¹. Third, stimuli in cardiovascular diseases may activate macrophages that are considerably deviated from the M1/M2 axis.

Based on the rationale above, in order to characterize macrophages from MyIL4R α KO mice in cardiovascular remodeling more broadly, in addition to the current M1 and M2 macrophage markers that are more involved in M2a subset, the genes to be determined can be more extended, such as the genes typically expressed by M2b, M2c and M2d subsets. Additionally, instead of measuring gene expression in the tissue, specifically sort pure macrophage population from injured tissues by flow cytometry and then determine the expression of M1/M2 macrophage related genes by RNA sequencing and qRT-PCR would definitely

provide more information about the role of IL4R α signaling in macrophage polarization during cardiovascular remodeling.

IL4R α signaling in resident and infiltrating macrophages

We have consistently shown in our studies that the expression of certain genes is significantly changed in heart and aorta at basal levels as a result of myeloid IL4R α deletion. However, these differences disappear in the inflammatory state after MI and AngII/Salt-induced hypertensive injury. These genes include BNP, Arg1, TNF α , IL-1 β , MCP-1, IL-6, Nox1 and Nox4 in heart, and Col1A1, MMP2, MMP8, PDGF α and Gal-3 in aorta. This is a wide range of genes involved in a variety of pathophysiological processes such as hypertrophy, inflammation, oxidative stress, fibrosis, and M2 macrophage polarization, which suggests a systemic effect rather than a random event caused by myeloid cells lacking IL4R α . The main difference of myeloid cells in the determined tissues at steady state and those at inflammatory state is that, the macrophages at steady state are resident macrophages while the macrophages upon inflammation are infiltrating macrophages.

Most resident macrophages in steady state originate from the embryonic yolk sac, while macrophages in the inflammatory state are mainly from circulating monocytes derived from bone marrow hematopoietic stem cells, although proliferation of resident macrophages also contributes. The distinct origin of resident and infiltrating macrophages may explain the significant differences in gene expression at basal level that disappear after inflammation. This may also partially contribute to the different responses of MyIL4R α KO mice in terms of cardiac function in two different models: severe acute injury in MI and the more mild hypertensive injury induced by AngII/Salt, because compared with control mice, MyIL4R α mice displayed worse cardiac function after MI, but a more preserved cardiac function in response to hypertension. In MI induced by permanent occlusion, resident macrophages can be replaced by monocyte-derived infiltrating macrophages¹². In hypertensive cardiac injury induced by AngII and high salt, where the injury is more mild and chronic, cardiac macrophages are also replaced by hematopoietic-derived monocytes although it

is possible that a more mild and chronic progression of injury will result in maintaining a macrophage population that originates from local proliferation of the resident macrophage pool.

Although it is suggestive that IL4R α signaling may differentially regulate resident and infiltrating macrophages, the gene expression data that we acquired is all based on analysis of transcripts from cardiac tissue rather than purified macrophages. In order to test our hypothesis, it would be necessary to isolate macrophages from sham and injured cardiac tissue using cell sorting, and then perform RNA sequencing and qRT-PCR to characterize their transcriptional profile, including genes associated with hypertrophy, ROS generation, inflammation progression and fibrosis. This would help to distinguish resident and infiltrating macrophages and to demonstrate the involvement of IL4R α signaling in these two distinct macrophage populations. In addition, CCR2 is currently considered as a marker that is positive in monocyte-derived infiltrating macrophages but negative in yolk sac-derived resident macrophages^{13, 14}, so specifically sort CCR2⁻ and CCR2⁺ cells from control and MyIL4R α KO mice in MI and AngII/salt-induced injury model, and then determine their transcriptional profile can more specifically demonstrate the role of IL4R α signaling tissue resident and monocyte-derived infiltrating macrophages.

The fate of embryonic yolk sac-originated, resident macrophages and bone marrow hematopoietic stem cell-derived infiltrating macrophages after injury and their contribution in the modulation of the post injury inflammation is still unknown. In order to investigate how IL4R α signaling differentially regulates resident and infiltrating macrophages during cardiac injury, lineage tracing experiments could be employed. This would identify changes in the proliferation of resident macrophages and also the recruitment and proliferation of hematopoietic-derived infiltrating macrophages. MyIL4R α KO mice could be crossed to a GFP reporter line and MyIL4R α KO/GFP bone marrow chimeras could be generated to create myeloid IL4R α KO in the resident cardiac macrophage population or in the circulating hematopoietic-derived monocyte/macrophage lineage. We can then trace the number and recruitment

of GFP-labeled resident macrophages or non-GFP-labeled infiltrating macrophages after injury in MyIL4R α KO mice in order to clarify the involvement of IL4R α signaling in the proliferation and recruitment of these two distinct macrophage population. Alternately, the temporally regulated CX3CR1^{CreERT2} Cre line could be used to generate IL4R α knockout in the resident cardiac macrophage population, but not the infiltrating macrophage population. Since the resident cardiac macrophage population is maintained through self-renewal, transient tamoxifen administration will cause IL4R α gene inactivation that will be maintained indefinitely through local proliferation. In contrast, IL4R α gene inactivation in circulating monocytes will be transient since they are continuously replaced by new hematopoietic stem cell-derived monocytes, therefore after 2-4 weeks all circulating monocytes will have wild type IL4R α .

It has been reported that monocytes/macrophage turnover and flux occurs extremely rapidly during MI and these cells are also capable of exiting the heart during inflammation¹⁵. In order to investigate macrophage and monocyte kinetics and whether IL4R α signaling is involved in the modulation of macrophage exit, dioctadecyloxacarbocyanine (DiO) can be used to label tissue-specific resident macrophages. Through intramyocardial injection of DiO, resident macrophages in heart but not circulating cells can be labeled. In order to trace the exit of cardiac resident macrophages during inflammation, we can detect DiO⁺ macrophages in heart, lymph nodes, spleen and bone marrow after injury with flow cytometry, and identify if IL4R α signaling affects macrophage kinetics and the regulation of cardiac resident macrophage exit.

Macrophage-specific transcriptional profile assay and lineage tracing of embryonically-derived resident macrophage and monocyte-derived infiltrating macrophage populations after injury can collectively distinguish the role of IL4R α signaling in these two distinctive macrophage subsets. Furthermore, these future experiments can provide valuable mechanistic information about myeloid IL4R α signaling and identify the contribution of resident and infiltrating macrophages in cardiac remodeling post MI or AngII and high salt.

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