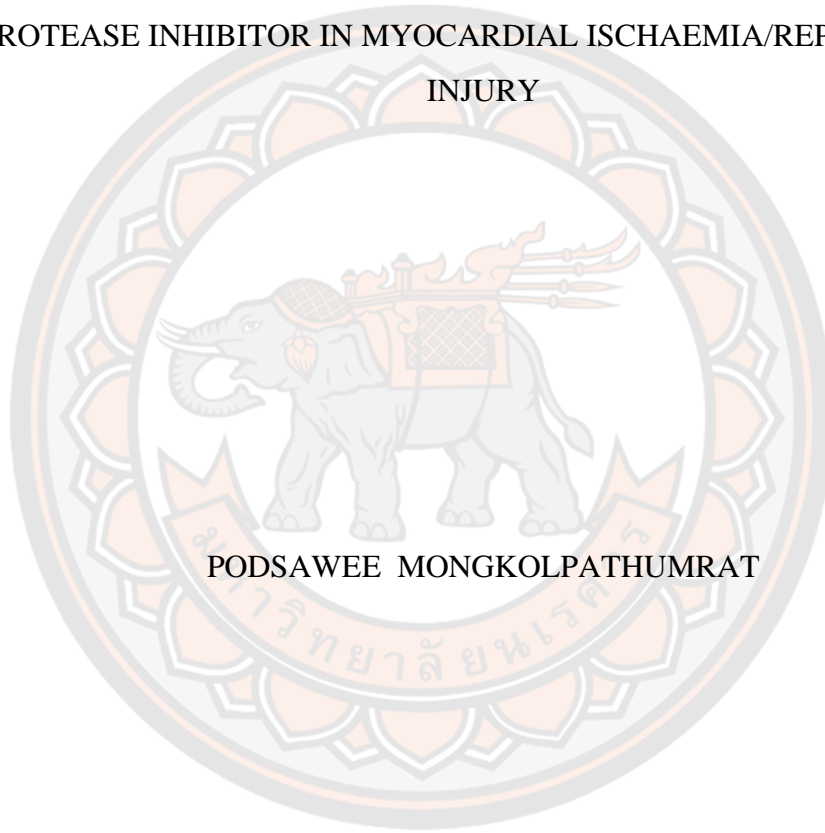




AN *IN VIVO* EFFECT OF RECOMBINANT HUMAN SECRETORY LEUKOCYTE
PROTEASE INHIBITOR IN MYOCARDIAL ISCHAEMIA/REPERFUSION
INJURY



PODSAWEE MONGKOLPATHUMRAT

A Thesis Submitted to the Graduate School of Naresuan University
in Partial Fulfillment of the Requirements
for the Doctor of Philosophy in Biomedical Sciences

2022

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By Podsawee Mongkolpathumrat

has been approved by the Graduate School as partial fulfillment of the requirements for the Doctor of Philosophy in Biomedical Sciences of Naresuan University

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Title AN *IN VIVO* EFFECT OF RECOMBINANT HUMAN SECRETORY LEUKOCYTE PROTEASE INHIBITOR IN MYOCARDIAL ISCHAEMIA/REPERFUSION INJURY

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Keywords Myocardial infarction, Ischaemia/reperfusion, Secretory leukocyte protease inhibitor (SLPI), Post-ischaemic treatment, Cardioprotection, Anti-protease deficient

ABSTRACT

Proteolysis by the protease enzyme aggravates myocardial ischaemia/reperfusion (I/R) injury by expanding the injured area and inducing inflammation. These lead to impaired cardiac function and cardiac structure, which contribute to cardiac remodelling and heart failure. Inhibition of proteases seems to provide therapeutic benefit. Our previous study demonstrated that giving recombinant human secretory leukocyte protease inhibitor (rhSLPI) by means of overexpression of the rhSLPI gene or treatment with recombinant protein of human SLPI provided a cytoprotective effect against I/R injury. Unfortunately, the information mostly came from an *in vitro* and an *ex vivo* experiment with pre-ischaemic treatment. Nevertheless, the roles and consequences of rhSLPI in the post-ischemic period, especially in an *in vivo* model, as well as post-ischaemic cardiac remodelling and hypertrophy have not been intensively investigated. In this study, recombinant human (rh)SLPI was administered intravenously during left anterior descending (LAD) coronary artery ligation and the onset of reperfusion. The results showed that post-ischaemic treatment with rhSLPI could significantly reduce infarct size, lactate dehydrogenase (LDH) and creatine kinase-MB (CK-MB) activity, inflammatory cytokines, and protein carbonyl levels, as well as improve cardiac functions. The

intracellular mechanistic explanation for the cardioprotection is due to inhibition of p38 MAPK phosphorylation, downregulation of Bax, caspase-3 and 8 protein levels, and activation of Akt and ERK1/2 phosphorylation. In summary, this is the first report showing the cardioprotective effects against myocardial I/R injury of post-ischaemic treatments with rhSLPI *in vivo*.

Although the cardioprotective effect of SLPI is proven, it remains unclear whether the cardioprotective effect of SLPI seen in our previous work is due to inhibition of protease enzymes. Therefore, an anti-protease deficient mutant SLPI has been developed to investigate if the cardioprotective effect is dependent upon its anti-protease activity. In this part, recombinant protein of anti-protease deficient mutant SLPI (L72K, M73G, L74G), or mt-SLPI, was intravenously administered to rats after they were subjected to LAD ligation. The results showed that mt-SLPI could significantly reduce cardiac cell death, and intracellular reactive oxygen species (ROS) production against an *in vitro* simulated I/R injury. Furthermore, post-ischaemic treatment of mt-SLPI could significantly reduce infarct size and cardiac biomarkers such as lactate dehydrogenase (LDH) and creatine kinase-MB (CK-MB) activity, improve cardiac functions, attenuate I/R induced-p38 MAPK phosphorylation, and reduce apoptotic regulatory protein levels, including Bax, cleaved-Caspase-3 and total Caspase-8, in rats subjected to an *in vivo* I/R injury. Additionally, the beneficial effect of mt-SLPI was not significantly different from wild-type (wt-SLPI). Thus, anti-protease deficient mutant SLPI could also provide a cardioprotective effect, which could be more clinically beneficial in terms of providing cardioprotection without interfering with basal serine protease activity.

In summary, post-ischemic treatment of recombinant human SLPI could be used as a future novel therapeutic alternative for myocardial I/R injury.

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TABLE OF CONTENTS

	Page
ABSTRACT.....	C
ACKNOWLEDGEMENTS.....	E
TABLE OF CONTENTS.....	F
LIST OF TABLES.....	J
LIST OF FIGURES.....	K
CHAPTER I INTRODUCTION.....	14
Introduction.....	14
Objectives of this study.....	16
Hypothesis.....	16
Scope of the study.....	17
CHAPTER II LITERATURE REVIEWS.....	19
1. Cardiovascular diseases.....	19
1.1 Definition of myocardial ischaemia.....	21
1.2 Ischemic/Reperfusion injury.....	21
1.5 Protease enzymes in I/R injury.....	30
1.6 Inflammation and ischaemia/reperfusion injury.....	33
2 Secretory leukocyte protease inhibitors (SLPI).....	52
2.1 Biological and biochemical property and effects of SLPI.....	52
2.2 Roles of SLPI in physiology and responses.....	55
2.2.1 SLPI in regulating cell proliferation, differentiation, and apoptosis.....	55
2.2.2 Physiology of SLPI in response to infection and inflammation.....	55
2.3 Role of SLPI in non-communicable diseases (NCDs).....	57
2.3.1 SLPI and neurodegenerative diseases.....	57
2.3.2 SLPI in Respiratory disorders.....	58
2.3.3 SLPI in Urology Obstetrics and Gynaecology.....	60

2.3.4 SLPI in Liver diseases	61
2.3.5 SLPI in Kidney diseases	61
2.3.6 SLPI and ocular diseases	62
2.3.7 SLPI in bone, cartilage, and dental disorders	62
2.3.8 SLPI in Cancer	64
2.3.9 SLPI in Metabolic diseases	67
2.3.10 SLPI in Cardiovascular diseases	67
CHAPTER III RESEARCH METHODOLOGY	71
Research Methodology	71
Experimental Animals	74
1. The effect of post-ischaemic treatment of recombinant human SLPI treatment on rat hearts subjected to an <i>in vivo</i> ischaemia/reperfusion.	75
1.1 Experimental group assignment	75
1.2 Surgical preparation of myocardial I/R model in rats	77
1.3 Determination of hemodynamic parameters by Mikro-Tip® pressure catheter for rat (Millar, Houston, TX, USA)	78
1.4 Determination of the area at risk and infarct size	78
1.5 Determination of Serum Creatine Kinase (MB Isoenzyme) and Lactate Dehydrogenase (LDH) Activity	78
1.6 Heart tissue homogenization and protein collection	78
1.7 Determination of protein concentration by Bradford assay	79
1.8 Determination of inflammatory cytokines level by Enzyme-linked immunosorbent assay (ELISA)	79
1.9 Spectrophotometric determination of protein carbonyl (PC) content level	80
1.10 Spectrophotometric determination of Ischaemic modified albumin (IMA) level	81
2. The effect of antiprotease-deficiency of SLPI on ischaemia/reperfusion injury.	83
2.1 Recombinant protein of anti-protease deficient mutant SLPI	83
2.1.1 Production of recombinant mutant forms of SLPI (mt-SLPI)	83
2.1.2 Purification of anti-protease deficient mutant SLPI	84

2.2 Assessment of inhibitory activities of anti-protease deficient mutant by neutrophil elastase activity	84
2.3 Cell culture	85
2.4 An <i>in vitro</i> Hypoxia/Reoxygenation induce cardiac cell death.....	85
2.5 Determination of cell viability by MTT assay	85
2.6 Determination of Intracellular reactive oxygen species (ROS) Production	86
2.7 Experimental animal ethical approval	86
2.8 Experimental group assignment	87
2.9 Surgical preparation of myocardial I/R model in rats	89
2.10 Evaluation of infarct size and area at risk	90
2.11 Determination of serum creatine kinase (MB isoenzyme) and lactate dehydrogenase (LDH) activity	90
2.12 Tissue Homogenate and protein collection	90
2.13 Determination of protein concentration by Bradford assay	91
2.14 Western blot analysis.....	91
Data analysis.....	92
CHAPTER IV RESULTS.....	93
Part 1: Determination of post-ischaemic treatment of recombinant human SLPI treatment on rat hearts subjected to an <i>in vivo</i> ischaemia/reperfusion.	93
1.1 The Animal Body Weight and Heart Weight of Experimental Animals	93
1.2 Effect of Post-Ischemic rhSLPI Treatment on Infarct Size.....	95
1.3 Effect of Post-Ischemic rhSLPI Treatment on Cardiac Biomarkers	97
1.4 Effect of rhSLPI Treatment on LVP in I/R Rat.....	99
1.5 Effect of Post-Ischemic rhSLPI Treatment on Inflammatory Cytokines Level.....	103
1.6 Effect of Post-Ischemic rhSLPI Treatment on Oxidatively cardiac and serum protein carbonylation level	105
1.7 Effect of Post-Ischemic rhSLPI Treatment on Oxidatively cardiac and serum ischaemic modified albumin (IMA) level	106
1.8 Effect of Post-Ischemic rhSLPI Treatment on Signal Transduction Molecules	108

1.9 Effect of Post-Ischemic rhSLPI Treatment on Apoptosis Regulatory Molecules	110
Part 2: The effect of antiprotease-deficiency of SLPI on I/R injury.....	112
2.1 The neutrophil elastase activity of wild-type and mutated SLPI on H9c2 cells.....	112
2.2 Anti-protease deficient SLPI reduced cardiac cell injury and intracellular ROS production in hypoxia/reoxygenation(H/R) condition	114
2.3 Anti-protease deficient SLPI reduced infarct size cardiac biomarkers in an <i>in vivo</i> I/R injury.....	116
2.4 Anti-protease deficient SLPI reduced cardiac biomarkers in an <i>in vivo</i> I/R injury.	118
2.5 Effect of <i>in vivo</i> treatment of anti-protease deficient SLPI on cardiac function parameters in I/R injury	120
2.6 Effect of anti-protease deficient SLPI on signal transduction and apoptosis regulatory molecules	124
CHAPTER V DISCUSSION & CONCLUSION	126
REFERENCES	137
BIOGRAPHY	162

LIST OF TABLES

	Page
Table 1 The number of animals in this study.....	74
Table 2 The baseline parameters of left ventricular pressure (LVP) determined the effect of rhSLPI on the LVP parameters in I/R (baseline).....	100
Table 3 The parameters of left ventricular pressure of ischemic phase determined the effect of rhSLPI on LVP parameters in MI (30 min after ligation).	101
Table 4 The parameters of left ventricular pressure of reperfusion phase determined the rhSLPI effect on LVP parameters in MI (120 min after reperfusion).	102
Table 5 The baseline parameters of left ventricular pressure (LVP) determined the effect of SLPI on the LVP parameters in I/R (baseline).....	121
Table 6 The parameters of left ventricular pressure (LVP) of ischemic phase determined the effect of SLPI on the LVP parameters in I/R (ligation). * $p < 0.05$ vs. sham, # $p < 0.05$ vs. I/R.	122
Table 7 The baseline parameters of left ventricular pressure (LVP) of reperfusion phase determined the effect of SLPI on the LVP parameters in I/R (reperfusion). * $p < 0.05$ vs. sham, # $p < 0.05$ vs. I/R.....	123

LIST OF FIGURES

	Page
Figure 1 The information of heart disease and stroke statistics from World Heart Federation (27).....	20
Figure 2 The concept of lethal reperfusion injury. The infarct size are associated with prolonged ischaemia time that increase infarct size as red dash line. After ischaemic, infarct size are increase until the reperfusion performed. In theoretical, infarct size could limit immediately after performed the reperfusion as green dash line. Infarct, the infarct still increased after reperfusion and stop at the end as black line (33).....	22
Figure 3 Schematic illustrating cellular change during ischaemia (13).....	24
Figure 4 Ion exchanges during ischaemia: 1) excretion of H ⁺ due to pH lowering, 2) deactivation due to loss of ATP, and 3) reduction of Na ⁺ /Ca ²⁺ exchange due to lowered extracellular pH and intracellular accumulation of Na ⁺ (37).....	26
Figure 5 Intrinsic and extrinsic pathways of apoptosis (36).....	28
Figure 6 Schematic representation of the mechanisms of I/R induced changes in cardiac (2).....	32
Figure 7 Neutrophil trafficking to ischemic sites occurs during reperfusion of ischemic tissues and involves 11 distinct steps (76).....	36
Figure 8 p38 MAPKs signalling pathways (107)	42
Figure 9 Targeting the reperfusion injury salvage kinase (RISK) pathway (140).....	45
Figure 10 Mechanism of Ischaemic modified albumin generation (158).....	49
Figure 11 Release kinetics of IMA in relation to standard cardiac biomarkers including cardiac troponin, cTn and natriuretic peptide, BNP (158).....	51
Figure 12 3D structure of SLPI and disulfide bridge (PDB ID: 2Z7F)	54
Figure 13 Schematic representation the previous study in SLPI	70
Figure 14 Schematic representation the research methodology of post-ischaemic treatment of SLPI under I/R injury condition	72
Figure 15 Schematic representation the research methodology of anti-protease deficiency SLPI treatment under I/R injury	73
Figure 16 Schematic diagram of experimental protocol.....	76
Figure 17 Schematic diagram of experimental protocol.....	88

Figure 18 Determination of body weight of experimental animal before performing the surgical procedure of myocardial I/R injury (A), heart weight harvested at the end of the surgery (B) and heart weight to body weight ratio in rats of the study cohort (C).	94
Figure 19 Determination of the percentage of area at risk (AAR) to ventricle volume (V) (A), percentage of infarct size to area at risk (B), (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R).....	96
Figure 20 Determination of the activity of Lactate Dehydrogenase (LDH) (A) and Creatine kinase-MB (CK-MB) (B) (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R).....	98
Figure 21 Determination of effect of post-ischaemic treatment of rhSLPI on cardiac inflammatory cytokines level including IL-1 β (A), IL-6 (B) and TNF- α (C) in the sham group, I/R group, rhSLPI-DI and rhSLPI-OR (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R) (n = 6).....	104
Figure 22 Determination of cardiac(A) and serum(B) protein carbonylation after treated with rhSLPI-DI and rhSLPI-OR (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R) (n = 6).	105
Figure 23 Determination of cardiac (A) and serum (B) ischaemic modified albumin level after treated with rhSLPI-DI and rhSLPI-OR (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R) (n = 6)	107
Figure 24 Determination of rhSLPI on activation of MAPK kinase involved in cell injury and survival in MI rat by Western blot analysis (A). The quantitative analysis for the MAPK phosphorylation was presented for p38 (B), JNK (C), ERK (D) and Akt (E). (* $p < 0.05$ vs. sham). (# $p < 0.05$ vs. I/R) (n = 6).....	109
Figure 25 Determination of rhSLPI on apoptosis regulatory protein levels in MI rat by Western blot analysis (A). The quantitative analysis for the expression was presented for bax (B), caspase-3 (C) and caspase-8 (D) (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R) (n = 6).....	111
Figure 26 Determination of neutrophil elastase activity of wt-SLPI and mt-SLPI, (* $p < 0.05$ vs. control)	113
Figure 27 Determination of percentage of cell viability after treated with wt-SLPI and mt-SLPI (B) (* $p < 0.05$ vs. control).....	113
Figure 28 Determination of percentage of cell viability under H/R condition and treated with wt-SLPI and mt-SLPI (* $p < 0.05$ vs. control) (# $p < 0.05$ vs. H/R)..	114
Figure 29 Determination of intracellular ROS under H/R condition and treated with wt-SLPI and mt-SLPI (* $p < 0.05$ vs. control) (# $p < 0.05$ vs. H/R).....	115

- Figure 30 Determination of the percentage of area at risk(AAR) to ventricle volume(V) (A), percentage of infarct size to area at risk(B) (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R)..... 117
- Figure 31 Determination of the activity of Lactate Dehydrogenase (LDH) (A) and Creatine kinase-MB (CK-MB) (B) (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R). 119
- Figure 32 Determination of the apoptotic regulatory signalling protein level in MI rat by Western blot analysis (A). The quantitative analysis for the expression was presented for p38 MAPK phosphorylation (B), Bax (C), cleaved-Caspase-3 (D) and Caspase-8 (E) (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R) (n = 6)..... 125
- Figure 33 A schematic diagram of the major findings in this study. rhSLPI that was treated in the timing of the post-ischemia duration. rhSLPI could protect the heart from the ischemic condition. The mechanisms for this could be associated with the attenuation of intracellular ROS production, activation of Akt and p38 MAPK phosphorylation, reduction in inflammatory cytokines (TNF- α , IL-1 β and IL-6) and reduction in apoptosis regulatory proteins (Bax, caspase-3, caspase-8)..... 129
- Figure 34 A schematic diagram of the major findings in this study. Both type of wild type and mutant (anti-protease deficient) SLPI could improve cell viability, reduce infarct size and improve cardiac function. These could associate with attenuation of p38 MAPK activation, intracellular ROS production, and activation of apoptotic regulatory signalling proteins, Bax, Caspase-3 and Caspase-8. 133

CHAPTER I

INTRODUCTION

Introduction

Ischaemic Heart Disease is predicted to be the major cause of death among the population around the world in 2030 (1). This phenomenon seems to happen everywhere in the world, not only in developed countries. According to epidemiological data from Thailand, ischaemic heart disease has become one of the leading causes of death in the Thai population (1). The survivors of myocardial infarction can subsequently suffer from heart failure. Therefore, any strategies that prevent or lower the severity of myocardial ischaemia/reperfusion injury can save patients' lives and improve their quality of life.

Ischemia causes cardiac cells to be injured due to a lack of oxygen and nutrients from the blood, as well as the activation of molecular cascades. Reperfusion therapy is the only intervention that allows the blood to perfuse back to the infarct area, such as with angioplasty, coronary bypass surgery, reducing cellular injury and death. However, reperfusion itself could also cause further injury. Altogether, the injury is known as an ischemic/reperfusion (I/R) injury (2). During myocardial ischaemia and reperfusion, various biochemical processes occur, including post-ischaemic inflammation, the production of oxygen radicals, polymorphonuclear cell infiltration, and protease release. These contribute to tissue damage, cellular necrosis, and subsequent functional impairment (3, 4). In particular, the protease enzymes that release from both neutrophils and injured cardiac cells, could potentially aggravate the injury (5). In cardiomyocytes, protease enzymes are basically active, but their actions are regulated by transcription, translation, chaperone molecules, and endogenous inhibitors (2). In I/R injury, these regulatory mechanisms are altered, resulting in an increase in both intracellular and extracellular protease activities (6-11). The proteases present in the myocardium that are known to be involved in I/R injury, include calpain, matrix metalloproteinases (MMPs), and cathepsins (12). In particular, after reperfusion, inflammatory cell infiltration in the injury area led to increased injury area and intracellular structure change by enhancing protease enzyme activity and

chymase (13). Interestingly, this enzyme's effect on intracellular changes more than angiotensin converting enzyme (ACE) approximately 20-fold (14), resulting in contributing to the progression of heart failure by expanding cell injury, cell death, and cardiac remodelling. The inhibition of protease enzyme activities could be considered as a strategy to prevent ischaemic/reperfusion injury (13). Gene expression profiling revealed the 8,734 genes in response to cold ischaemia (CI) and reperfusion (15). Among the identified genes, secretory leukocyte protease inhibitor (SLPI) was thereby identified as a particularly promising candidate for treatment or prevention of I/R injury and post-ischaemic inflammation (16), as well as I/R injury in transplanted heart (17).

Secretory leukocyte protease inhibitor (SLPI) is a 107-amino acid-long protein in the whey acidic protein family (WAP). SLPI is a 12 kDa non-glycosylated cationic protein that is described as an inhibitor of serine proteases such as neutrophil elastase, cathepsin G, tryptase, and chymase (18, 19). The SLPI play roles in various principle areas including antimicrobial agent, controls the processing of inflammatory mediator and protect the host from excessive tissue damage by proteolytic enzyme that release during inflammation, suppress the inflammatory response through transcription factor NF- κ B and control the cell growth cell differentiation and cell apoptosis (20). On the other hand, SLPI can inhibit bacterial and fungal growth and viral infection (21). The previous studies showed that overexpression of human secretory leukocyte protease inhibitor (hSLPI) and treatment with recombinant human SLPI (rhSLPI) provided cardioprotection against an *in vitro* and an *ex vivo* I/R injury (22, 23). It is noteworthy that the cardioprotective effect of SLPI found in those studies was the results from a pre-treatment experimental model. However, the roles and mechanisms of rhSLPI and the consequences in post-ischemic and reperfusion periods, especially in an *in vivo* model have not been studied. Moreover, the cardioprotective effect of SLPI probably be interpreted in the way that SLPI inhibit proteases. Interestingly, the findings from previous studies showed an anti-protease independent effect of SLPI that suppress macrophage response to bacteria lipopolysaccharide (LPS), attenuate caspase-3 activation and DNA degradation through inhibition TNF- α expression (24, 25). However, the requirement of anti-

protease activity of SLPI as cardioprotective agent against ischaemic and reperfusion injury, especially in an *in vivo* model, has never been investigated.

Therefore, this PhD dissertation aims to determine the post-ischemic roles and mechanisms of SLPI and the effect of anti-protease independent SLPI in an *in vivo* experiment. The outcome of this thesis was to provide more clinically relevant information about the therapeutic effect of SLPI, which strengthened the possibility of using SLPI as a therapeutic agent.

Objectives of this study

1. To investigate the effect of recombinant human SLPI on physiological and biochemical function, in rats subjected to *in vivo* ischaemia/reperfusion
2. To determine the anti-protease involvement in cardioprotective mechanisms of recombinant human SLPI against ischaemia/reperfusion

Hypothesis

Aim 1 To investigate the effect of recombinant human SLPI on physiological and biochemical function, in rats subjected to *in vivo* ischaemia/reperfusion

Hypothesis 1: post-ischaemic treatment of rhSLPI improves cardiac function and reduces infarct size in rat heart subjected to *in vivo* ischaemia/reperfusion.

Hypothesis 2: post-ischaemic treatment of rhSLPI reduced I/R induced p38 MAPK activation, activate pro-survival kinases and reduce apoptotic regulatory protein.

Aim 2. To determine the anti-protease involvement in cardioprotective mechanisms of recombinant human SLPI against ischaemia/reperfusion

Hypothesis 1: SLPI increase cell viability and reduce intracellular ROS level in H9c2 cell that subjected to *in vitro* H/R condition in anti-protease independent manner.

Hypothesis 2: SLPI improves cardiac function and reduces infarct size in rat heart subjected to *in vivo* ischaemia/reperfusion in anti-protease independent manner. And apoptotic regulatory proteins.

Scope of the study

The study was determining the effect of secretory leukocyte protease inhibitor (SLPI) and antiprotease deficiency SLPI in ischaemia/reperfusion (I/R) injury *in vivo*. The experiment is divided to 2 parts including

1. To determine the effect of post-ischemic treatment of recombinant human SLPI. An *in vivo* experiment, adult male Wistar rats were used as experimental animal model. The surgery for ischaemia/reperfusion (I/R) injury was generated on left anterior descending (LAD) artery. The recombinant human SLPI was administrated to the rats via intrajugular vein route in different timing including during ligation (DI) and onset at reperfusion (OR). The cardiac physiology was measured and recorded along with the surgery via pressure catheter that canulated through jugular vein and located in left ventricle (LV). At the end of surgery, infract size and area at risk were evaluated by Evan blue and TTC staining. Moreover, blood serum and cardiac tissue were collected for analysis for cardiac injury markers were measured from the blood serum. The cardiac tissues were homogenated and measured apoptotic regulatory protein by Western blot analysis.

2. To determine the cardioprotection effect of antiprotease-deficiency of SLPI, the cardiac myoblast cell line (H9c2) was used for an *in vitro* experiments. The antiprotease-deficiency form of SLPI, generated by site directed mutagenesis by Professor Cichy, was purified and used in this study. Cellular toxicity of anti-protease deficiency mutant SLPI was evaluated in H9c2 cell via MTT assay. The intracellular ROS was measured in H9c2 subjected to an *in vitro* hypoxia/reoxygenation (H/R). For an *in vivo* experiments, adult male Wistar rats were used as experimental animal model. The open-heart surgery and left anterior descending (LAD) artery was performed for simulating myocardial ischaemia/reperfusion (I/R) injury. Rats were treated with recombinant anti-protease deficiency mutant SLPI, as well as wildtype SLPI, at onset reperfusion timing while recording left ventricular pressure (LVP) parameters as cardiac physiology via pressure catheter located in left ventricle. The

infarct size and area at risk , ventricular pressure was determined as physiological parameters. Moreover, blood serum and cardiac tissue were collected for analysis of cardiac injury markers. The cardiac tissues were homogenated and measured apoptotic regulatory protein by Western blot analysis.



CHAPTER II

LITERATURE REVIEWS

1. Cardiovascular diseases

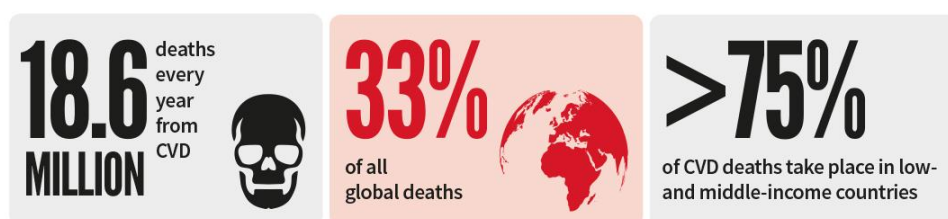
Cardiovascular diseases (CVD) are a group of heart and blood vessels disorders including coronary heart disease, cerebrovascular disease, rheumatic heart disease and other condition. The report from World Health Organization (WHO) address that CVD is leading to cause of the death globally, which taking estimated 17.9 million people, especially heart attack and stroke were accounting to 32% of global death in 2019 (26). The majority of death was found in prematurely people which under 70 years of age. Similarly, the information of world heart federation also shows that CVD is the world's number 1 killer that cause of 18.6 million deaths every year or about 33% of all global death as showed in Figure 1(27). Almost of CVD deaths take place in low and middle-income countries. The most important risk factors of CVD are the unhealthy behaviours including tobacco use, unhealthy diet, obesity, physical activity and harmful use of alcohol. Because of the most common cause of CVDs is a built-up of fatty acid plaque on the inner blood vessel wall that supply the heart and brain, American Heart Association(AHA) and National Institutes of Health suggests the way to keep the heart healthy is to be active, keep a healthy weight, learn about cholesterol, do not smoke and use smokeless tobacco and learn about sugar and diabetes (28).



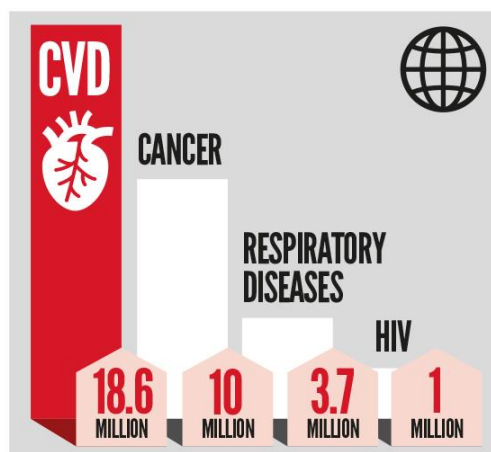
CARDIOVASCULAR DISEASE

THE WORLD'S NUMBER 1 KILLER

Cardiovascular diseases are a group of disorders of the heart and blood vessels, commonly referred to as **heart disease** and **stroke**.



GLOBAL CAUSES OF DEATH



RISK FACTORS FOR CVD



Sources: World Health Organization;
IHME, Global Burden of Disease

info@worldheart.org
www.worldheart.org

f worldheartfederation
t worldheartfed
@ worldheartfederation

Figure 1 The information of heart disease and stroke statistics from World Heart Federation (27).

1.1 Definition of myocardial ischaemia

Myocardial ischaemia is caused from blockade of coronary artery, which supplies the blood and oxygen to heart tissues. The blockade of coronary artery decreased the perfusion of the blood to heart tissue that due to thrombosis, acute alteration of coronary atherosclerotic plaques. The result from loss of oxygen or blood supply to heart tissue not only imbalance oxygen supply and oxygen demand but also altered biochemical mechanism in the heart tissues, especially loss source of ATP production, oxygen, for energy metabolism. A lack of oxygen alters heart tissue to anaerobic metabolism for generate ATP that result in accumulation of hydrogen ions and lactate. The metabolic changes lead to irreversible injury in heart tissues (29). The procedure that reperfusing the blood to ischaemic area is called the reperfusion. The reperfusion aims to stabilize a plaque or prevent a disease progression in patient that was early diagnostic (30). On the other hand, the revascularization was performed in myocardial ischaemic patients which including percutaneous coronary intervention (PCI) and coronary artery bypass graft (CABG) surgery. These procedure aims to reperfusing the effective flow to the ischaemic area that could reduce and limit the expanding of infarct area. However, the reperfusion also has worst effect to heart tissue that result of the re-flow blood to the ischaemic area.

1.2 Ischemic/Reperfusion injury

The Blockade of coronary artery was leading to heart tissue lack of oxygen supply and induce cardiac cell death. The cardiac cell death was associated with time of ischaemia. The prolonged ischaemic time could increase infarct size until all of cardiac tissue as showed in red dash line in Figure 2. After reperfusion from various procedures such as angioplasty, thrombolytic therapy, coronary bypass surgery and cardiac transplant, these are reperfusing the blood to supply ischaemic area again. In the theoretical, reperfusing blood flow could limit the infarct size and cell damage immediately after the flow back to the infarct area as showed in green dash line in Figure 2. On the other hand, the reflow blood is not limit the cell injury and infarct size immediately but there are contribute to cardiac cell injury as called “ischaemic/reperfusion injury (I/R)” after the reperfusion as showed in black line in

Figure 2 (31). Therefore, I/R injury is common problem after various intervention such as angioplasty, cardiovascular surgery and cardiac transplantation (32).

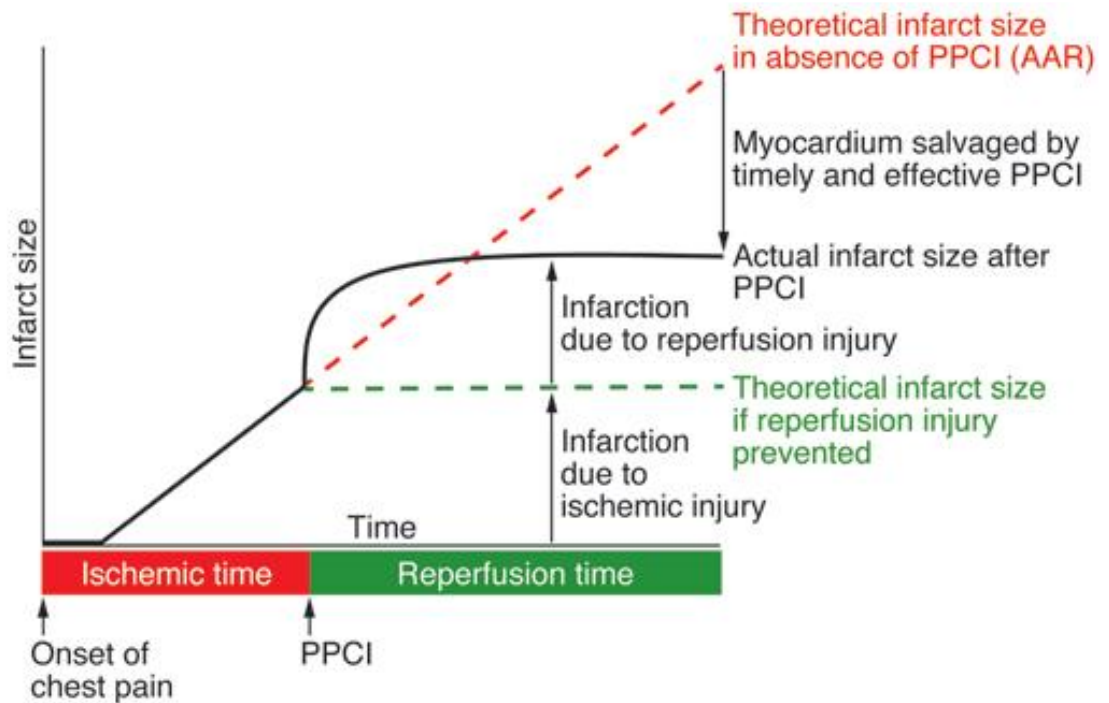


Figure 2 The concept of lethal reperfusion injury. The infarct size are associated with prolonged ischaemia time that increase infarct size as red dash line. After ischaemic, infarct size are increase until the reperfusion performed. In theoretical, infarct size could limit immediately after performed the reperfusion as green dash line. Infarct, the infarct still increased after reperfusion and stop at the end as black line (33).

A few minutes after a reperfusion, ROS is generated by various source The reperfusion is generated ROS burst and develop intracellular Ca^{2+} overload that impairing the recovery of the cardiac function. Although, during myocardial infraction, pH is decreased less than 7.0 that lead to intracellular acidosis but in reperfusion periods, the pH rapidly restored by remove lactate and activate $\text{Na}^+\text{-H}^+$ exchanger as well as $\text{Na}^+\text{-HCO}^-$ symporter. These lead to rapidly shift the intracellular pH that contribute to cardiomyocyte death by cardiomyocyte hypercontracture as shown in Figure 3 (33). The ROS and Ca^{2+} overload can activate and modify the protease activity in the cell. The activation of various protease activity in the heart promote the development of cardiac dysfunction after I/R injury (29).

Intracellular changes in I/R injury

I/R injury was consisting of various mechanism that including programmed cell death, activation of immune response system and intracellular oxidative stress. The numerous pathways and signalling were activated and affect to the heart tissue in both ischaemia and reperfusion duration.

During ischaemia, the beginning of cascade was the impairment of coronary artery that led to lack of blood supply to cardiac tissue. The area of infraction depends on the period that lack of perfusion. After occlusion, the infraction begin in the endocardium and progresses transmurally overtime to epicardium as “wave front” so the duration of occlusion is related to the infarct size (34). Moreover, the ultimate size of myocardium cause from coronary occlusion as called “area at risk” (34). Lack of blood and oxygen supply contribute to stop mitochondrial oxidative phosphorylation from loss the oxygen that is major source to generate the ATP for energy metabolism. Anaerobic glycolysis metabolism is occurred instead of aerobic glycolysis metabolism for generate the energy (Figure 3).

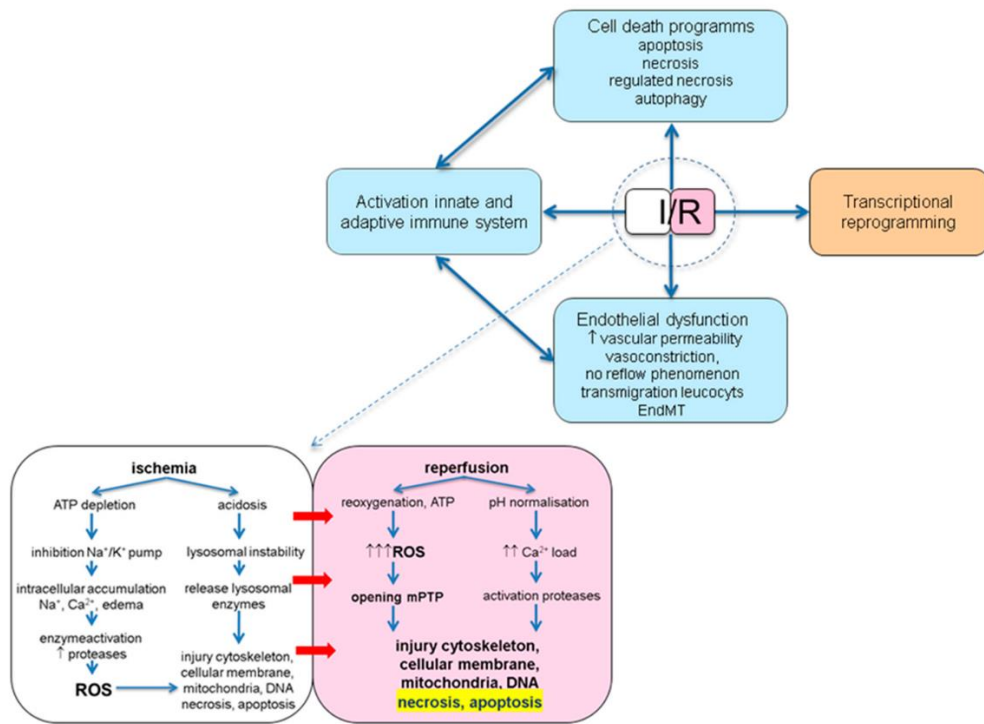


Figure 3 Schematic illustrating cellular change during ischaemia (13)

The major product of anaerobic glycolysis is hydrogen ion and lactic acid that lead to intercellular acidosis (5). Fatty acid is used in mitochondria oxidative phosphorylation instead of glucose. Moreover, the decreasing of intracellular pH leading to inhibit the activity of enzyme in the cell, so the cell needs to remove hydrogen ion from the cell for improve intracellular pH. The hydrogen ion can efflux from the cell by Na^+ , H^+ exchanger (NHE) that remove hydrogen ion from the cell exchange with Na^+ ion. Na^+ influx is contributed to water influx into the cell and lead to cell swelling. In addition, the less energy and ion change also impair the excitation contraction uncoupling and electrical activity. Initially, electrical activity impairment cause from lack of ATP for Na^+ , K^+ -ATPase, which result to Na^+ and Cl^- influx into the cell. The accumulation of Na^+ ion enhance the influx of water into the cell and lead to cell swelling. Moreover, increasing of K^+ efflux from the cell that contributed to ventricular arrhythmia. The decline of ATP is not affected only Na^+ , K^+ -ATPase. Ca^{2+} ATPase (SERCA) also affects from lack of ATP that used ATP for uptake Ca^{2+} ion into sarcoplasmic reticulum (ER) leading to accumulation of Ca^{2+} ion in ER, Ca^{2+} overload so the Ca^{2+} efflux might also regulate by $\text{Na}^+/\text{Ca}^{2+}$ exchanger (NCX) and plasma-membrane Ca^{2+} ATPase (PMCA). The accumulation of Ca^{2+} ion is contributed to ER stress. However, the intracellular Ca^{2+} overload lead to cell death and cell injury (29, 35) (Figure 4). Mitochondria can uptake Ca^{2+} ion by uniporter transporter but size of mitochondrial Ca^{2+} pool is small in normal condition. However, Ca^{2+} also influx and accumulated in mitochondria under pathological condition (5). The accumulation of Ca^{2+} ion in mitochondria can release from different way including reversal uniport transporter permeability of transition pore (PTP) and Na^+/H^+ dependent Ca^{2+} exchanger. Mitochondria is also needing to remove Ca^{2+} ion by Na^+/H^+ dependent Ca^{2+} exchanger, which remove Ca^{2+} ion exchange with influx Na^+/H^+ ion. The influx of Na^+ ion induce water influx into the mitochondria that lead to mitochondria swelling and rupture (36).

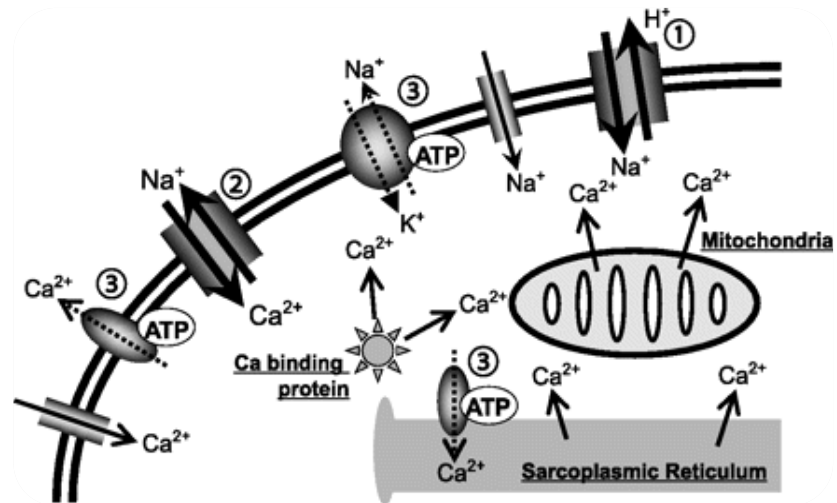


Figure 4 Ion exchanges during ischaemia: 1) excretion of H^+ due to pH lowering, 2) deactivation due to loss of ATP, and 3) reduction of Na^+/Ca^{2+} exchange due to lowered extracellular pH and intracellular accumulation of Na^+ (37).

Outer mitochondria membrane (OMM) rupture is results in mitochondria swelling that release pro-apoptotic mitochondria protein such as cytochrome c and Bcl-2 family proteins (36). Apoptosis is a generally encoded program leading to cell death both of normal development and homeostasis. The characteristic of apoptosis including cell shrinkage, nuclear fragmentation, chromatin condensation and membrane blebbing. These are the result of caspase protease activity. The apoptosis can activation through 2 main pathway including intrinsic and extrinsic pathway that can activate through B cell lymphoma 2 (Bcl-2) protein family both of anti-apoptosis Bcl-2 proteins and pro-apoptotic proteins such as Bcl-2, Bcl-2-associated X protein (BAX) and Bcl-2 antagonist or killer (BAK) (36). The intrinsic pathway can be activated from DNA fragment or ER stress, which is activate BAX and BAK. BAX and BAK activation lead to forming lipid pores on outer OMM and releasing cytochrome c from the intermembrane space (IMS) (38). The releasing of cytochrome c can bind apoptotic protease activating factor -1 (APAF1) that induce changing a conformation of caspase activation platform as apoptosome (39). The recruitment and dimerization of apoptosome activate initiator apoptotic caspase, caspase 9. Caspase 9 cleaved and activated executioner apoptotic caspase, caspase 9 and caspase 7, which lead to cell apoptosis (40). On the other hands, extrinsic pathway can activate by death ligand binding to death receptor, which induce recruitment and dimerization of adaptor protein, FAS-associated death domain protein (FADD). FADD activate initiator caspase, caspase 8 that cleave and activate the executioner caspase, caspase 3 and caspase 7. Then, caspase 3 and caspase 7 can activate a cell apoptosis. In addition, caspase 8 is also activate BAX or BAK through Bcl-2 homology 3 (BH3) interacting domain death agonist (BID) (41)

Mitochondria balance cell apoptosis pathway by activate anti-apoptotic Bcl-2 protein for inhibiting BID and activation of BAX and BAK. Moreover, mitochondria release X-linked inhibitor of apoptosis protein (XIAP) that can inhibit caspase activity both of recruitment of caspase 9, activation of caspase 3 and caspase 7. Whereas, after activation initiator caspase, mitochondria release second mitochondria-derived activator of caspase SMAC and OMI for block the XIAP activity as Figure 5(36).

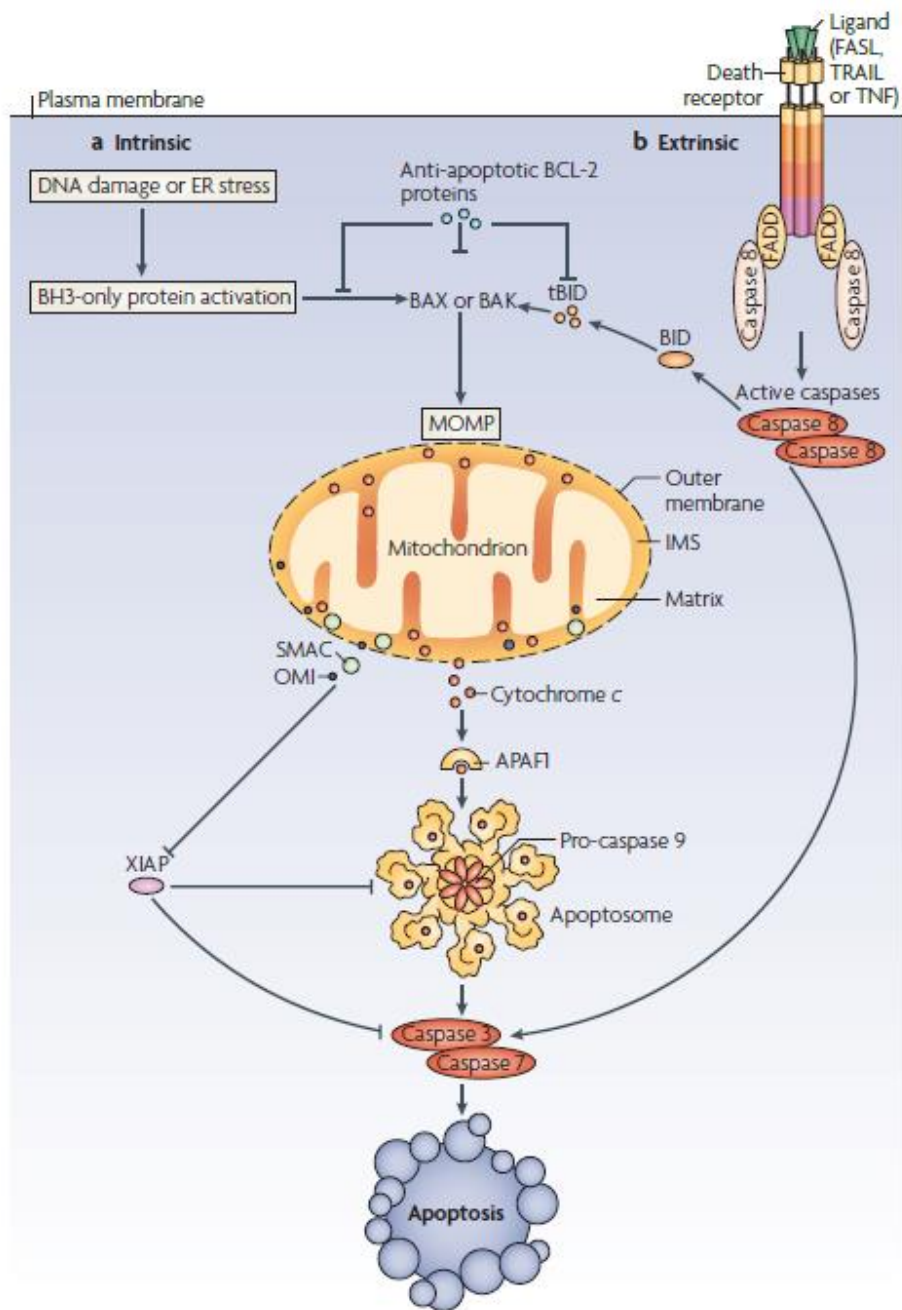


Figure 5 Intrinsic and extrinsic pathways of apoptosis (36).

However, intracellular Na^+ ions accumulation that led to programmed cell death by mitochondria swelling was not only affected from electrical ions imbalance during ischaemia. The other results of ion's imbalances that along with Na^+ ions accumulation was Ca^{2+} accumulation. Ca^{2+} ions accumulation was crucial factors that contribute to myocardial infarction progression because these accumulation led to the activation of Ca^{2+} dependent proteases enzyme such as calpains. Even though calpain still inactive in ischaemic period until normalization pH in reperfusion period and damage to the cells.

Although reperfusion restore blood flow and normalize pH level that contain oxygen and substrate to ischaemia area. The blood flow wash out accumulated H^+ , normalize pH and delivery substrate for aerobic ATP generation (5) (Figure 3). Even reperfusion can reduce infarct size by up to 50 % but reperfusion still be double-edge sword that cause cellular damage (42). Cellular damage from reperfusion was occurred underlying generation of reactive oxygen species (ROS). ROS is lead to calcium overload and opening of mitochondrial permeability transition (MPT), which release cytochrome C, succinate and mitochondrial DNA (mt-DNA). These substances were molecules that could induce cell death through apoptosis, necrosis and activated immune response as damage associated molecular pattern (DAMPs) (13).

1.5 Protease enzymes in I/R injury

Protein is important components of the cell functions. Proteases are the enzyme, which cleave the protein to be the amino acid. Protease can classified as serine, cysteine or threonine protease, aspartic, matrix metalloprotease based on their site of action (43). In pathophysiology of heart diseases is due to the function of various extracellular and intracellular protein, especially, the protease enzyme that cleaved peptide bond (10). The alteration of protease enzyme due to the mechanism underlying the myocardial I/R injury produce oxidative stress, Ca^{2+} overload and pH changing. These can cause altered functioning of various organelle in the cell such as extracellular matrix (ECM), sarcoplasmic reticulum (SR) and mitochondria that also leading to activate protease enzyme and impair contractile ability of the heart cell (10). The alteration of protease enzyme in cardiac tissue can lead to cardiovascular diseases (44). Protease is essential enzyme that play role in homeostasis of extracellular matrix (ECM) by degradation of misfold protein, malfunctional protein and protein turnover (45). The I/R injury increase a protease activity that led to changing of the structure and cell population both of intracellular and extracellular matrix depend on type of protease enzyme (46). The essential protease in the cardiac cell including calpain, cathepsin and matrix metalloproteinase (MMPs) as shown in Figure 6(2).

Calpain is a family of Ca^{2+} -dependent cysteine protease that involve in the proteins structure degradation and cell death pathway (2, 47, 48). Calpain is produced and localized in the cytosol as proenzyme that can be activated by intracellular Ca^{2+} influx (43). However, calpain can be directly activated by phosphorylation at serine 50 through ERK even without calcium influx (49). Family of calpain is including μ -calpain (calpain I), m-calpain (calpain II) and muscle specific calpain. The μ -calpain and m-calpain is highly expressed in the heart (48, 50). Calpain translocation can be induced by Ca^{2+} during ischaemia reperfusion. However, calpain activation only occurred after reperfusion that normalized intracellular pH because intracellular acidosis inhibits calpain activation during ischaemia (47). Moreover, calpain is known to contribute to cardiovascular diseases, since it involved in the degradation of troponin I (TnI), which is component of the actin tropomyosin complex during I/R injury (51). Treatment with specific calpain inhibitor, MDL-28170, could reduce

infarct size (47). Furthermore, the aldehydic calpain inhibitor, calpeptin, improved cardiac function such as ejection fraction (EF) after treated in mouse myocardial infarction model (48).

Cathepsins are lysosomal proteases family that primary protease enzyme found in acidosis environment of lysosome (43). Cathepsin are classified into serine (cathepsin A and G), aspartic (cathepsin D and E) and cysteine cathepsin depend on catalytic activities. Cathepsins is enzyme that function in acidosis environment (52). Therefore, I/R injury alter the phenotype of lysosome to lysosomal autophagy after 40 min of hypoxia that leading to mitochondria degradation (53). Moreover, cathepsin gene expression in the heart is enhanced by angiotensin II (54) However, cathepsin D and L are increase activity in I/R injury and activate MMP that cleavage fibronectin, laminin, type I, IV and XVIII collagen (55, 56).

The matrix metalloproteinase (MMPs) discovered to be crucial tools in tadpole morphogenesis (57). MMPs are endopeptidases that utilize a highly-conserved zinc-binding catalytic centre in order to cleave protein. MMPs can be divided into 5 groups depend on substrate preference including collagenases, gelatinases, stromelysins, matrilysins (58). MMP-2 and MMP-9 are enzyme for degrading type IV collagen that is important major component of basement membrane (58). The MMPs can be activated by high level of ROS during I/R injury (59). In addition, MMP-2 and MMP-9, gelatinase, are found in cardiac myocytes cardiac fibroblast and endothelial cell (60). MMP-2 and MMP-9 have been found increasing activity in myocardial I/R injury (60, 61). Moreover, MMP-2 and MMP-9 is play role in early and late of late matrix remodeling after myocardial I/R injury (61, 62). MMP-2 and MMP-9 are activated both in myocardium and plasma in acute myocardial ischemic/ reperfusion injury patients (60). Furthermore, MMP activity and ECM degradation can be regulated by chymase angiotensin converting enzyme (ACE) at post-translation level (63). Interestingly, the expression level of MMP is elevated in hypertensive models, especially, angiotensin II induced hypertension (64). Moreover, overexpression of MMP-1 is related to accumulation of cardiac fibroblast and cardiac dysfunction and remodeling due to chronic pressure overload (65). Besides, MMP-2 and MMP9 are upregulated in the dilated failing heart and development of cardiac remodeling model (66).

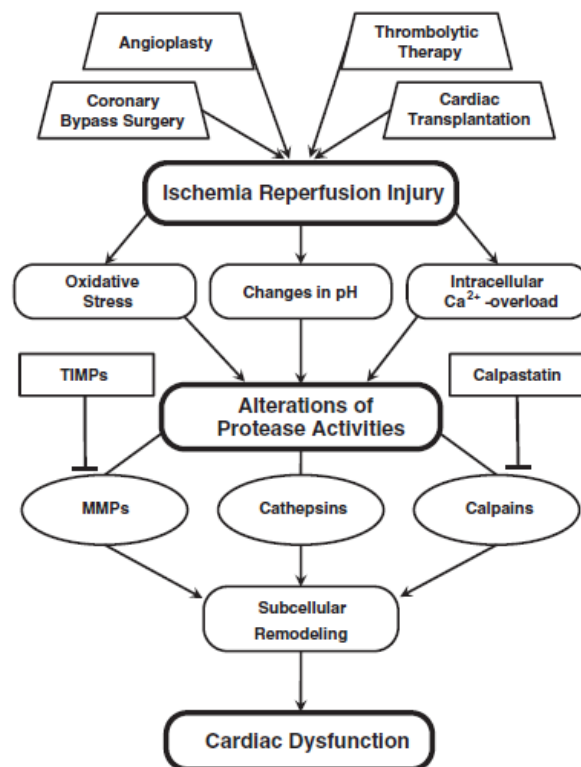


Figure 6 Schematic representation of the mechanisms of I/R induced changes in cardiac (2).

1.6 Inflammation and ischaemia/reperfusion injury

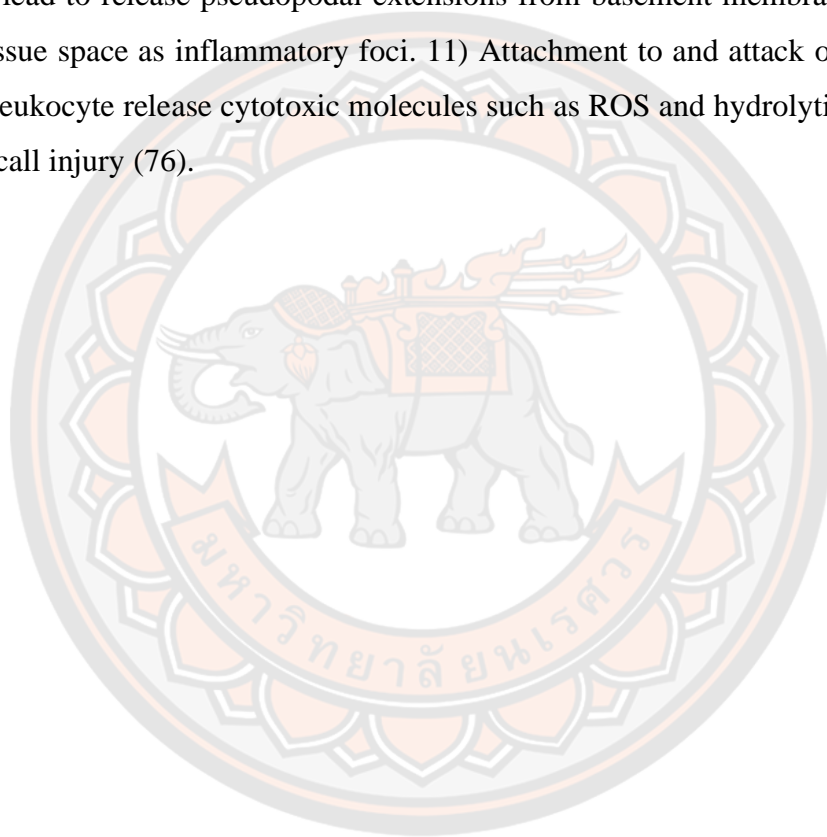
After cell injury in I/R injury, ROS was one of molecules that releasing in injury area. These have potential to directly injury the cells and trigger inflammatory cascade through the induction of cytokines. This activation led to 3 repair overlapping phases that including inflammation, reparative or proliferation and mature phase. Firstly, inflammation phase was the activation of chemokines and cytokines cascade that resulting in recruitment of local infiltration of leukocyte into the infarct area. Second, proliferation phase, mononuclear cell and macrophage was activated and released cytokines and growth factor, which recruit and active myofibroblasts and vascular cells. The activation of myofilament was released extracellular matrix protein that was overlap to last phase. Lastly, maturation phase, reparative fibroblast and vascular cells become apoptosis and cross-linked collagen-based scar was formed (67).

Inflammation in I/R injury is defined as sterile inflammation that the inflammatory response associated with the recognition of releasing endogenous and non-pathogenic signals from damaged cell as DAMPs (13, 68). The endogenous ligands is released from cell death that including high-mobility group box-1 (HMGB1), heat shock proteins (HSPs), S100-proteins and mitochondrial DNAs (mt-DNAs). The releasing of DAMPs activates transmembrane proteins, including toll-like receptors (TLRs) and nucleotide-binding oligomerization domain-like receptor family of cytosolic proteins also known as Nod-like receptors, NLRP3 inflammasome, function as a pattern recognition receptors (PRR), especially TLR2 and 4 that upregulated in tubular epithelial cell in ischaemia (69, 70). The TLRs activation led to recruitment of downstream various adaptor molecules such as TNF-receptor-associated factor, myeloid differentiation primary-response protein 88 (MyD88) and toll-interleukin 1 receptor (TIR) domains that result to activation transcription factors consist of nuclear factor kappa-light-chain-enhancer of activated B cells (NF- κ B) and IFN-regulatory factor -3 (IRF3). These transcription factors regulate pro-inflammatory gene transcription and inflammatory response (71). In addition, NF- κ B can also be activated by free radical, ROS, and cytokines including TNF- α and IL-1 β (72). An important source of preformed and newly synthesized cytokines is mast cell degranulation that usually occurs in ischaemic area (73). The

result of degranulation of mast cell is a rapid release of TNF- α that induce IL-6 for mononuclear cells infiltration. So TLRs activation plays crucial role in trigger of the cytokines cascades and MAPK pathways (74). On other hands, non-pathogenic signals, released from damaged cell in I/R injury, lead to activation of NLRP3 inflammasomes, which are large multiple protein complexes (68). NLRP3 inflammasomes compose of 3 components including a member of the NLRP family proteins, NLRP3, apoptosis-associated speck-like protein, which consist of caspase recruitment domain (ASC) and pro-caspase-1 (75). The consequence of NLRP3 activation is IL-1 β production that is converted by caspase-1. Then, IL-1 β induces the initial pro-inflammatory response and release of other inflammatory cytokines that facilitate the recruitment and activation of inflammatory cells, especially neutrophils and monocytes (68).

The inflammation response to I/R injury is characterized by recruitment of neutrophils and other leukocytes in I/R site (76). The inflammatory response to tissue cause by production and secretion of cytokines, chemokines and proinflammatory cytokines (13). During reperfusion, leukocyte trafficking into ischemic sites by 11 steps (76) as shown in Figure 7 including 1) Margination, neutrophils from capillaries move into larger diameter vascular postcapillary venular segment of microvascular by hydrodynamic forces from blood flow to endothelial wall. 2) Tethering and rolling, neutrophil binding to adhesion molecule that express on activated endothelial cells during I/R injury. 3) Slow rolling, after leukocyte bind to adhesion molecule that enable leukocyte to slow rolling by forming more weak interaction with selectins on endothelial surface. Moreover, surface of leukocyte forming to long nanotubes for tethering and rolling leukocyte. 4) Firm or stationary adhesion, leukocyte develop strong adhesion by integrin-dependent interaction with endothelial ICAM-1 that rolling leukocyte and firming adhesion. 5) Luminal crawling, ICAM-1 activate intracellular signalling that change cytoskeleton and polarization of the cell. Crawling leukocyte move along endothelial cell for explore interendothelial junction that is route for diapedesis of leukocyte. 6) Transendothelial cell migration, leukocyte cross endothelial cell through interendothelial junction and overlaying on basement membrane that express low matrix protein (Pr⁻) deposition. 7) Abluminal crawling, the

diapedesing leukocyte interacting with basement membrane structure by adhesion molecule. 8) Penetration of pericyte gaps and regions of low matrix protein expression in the basement membrane, abluminal crawling leukocyte break the layer at region of low matrix protein deposition in the basement membrane that leading to leukocyte can move through this barrier. 9 and 10) Detachment from the vessel wall and migration through the interstitial matrix, leukocyte migrate into the tissue space that due to detaching from basement membrane components and adhesion molecules. These lead to release pseudopodal extensions from basement membrane and migrate into tissue space as inflammatory foci. 11) Attachment to and attack on parenchymal cells, leukocyte release cytotoxic molecules such as ROS and hydrolytic enzymes that cause cell injury (76).



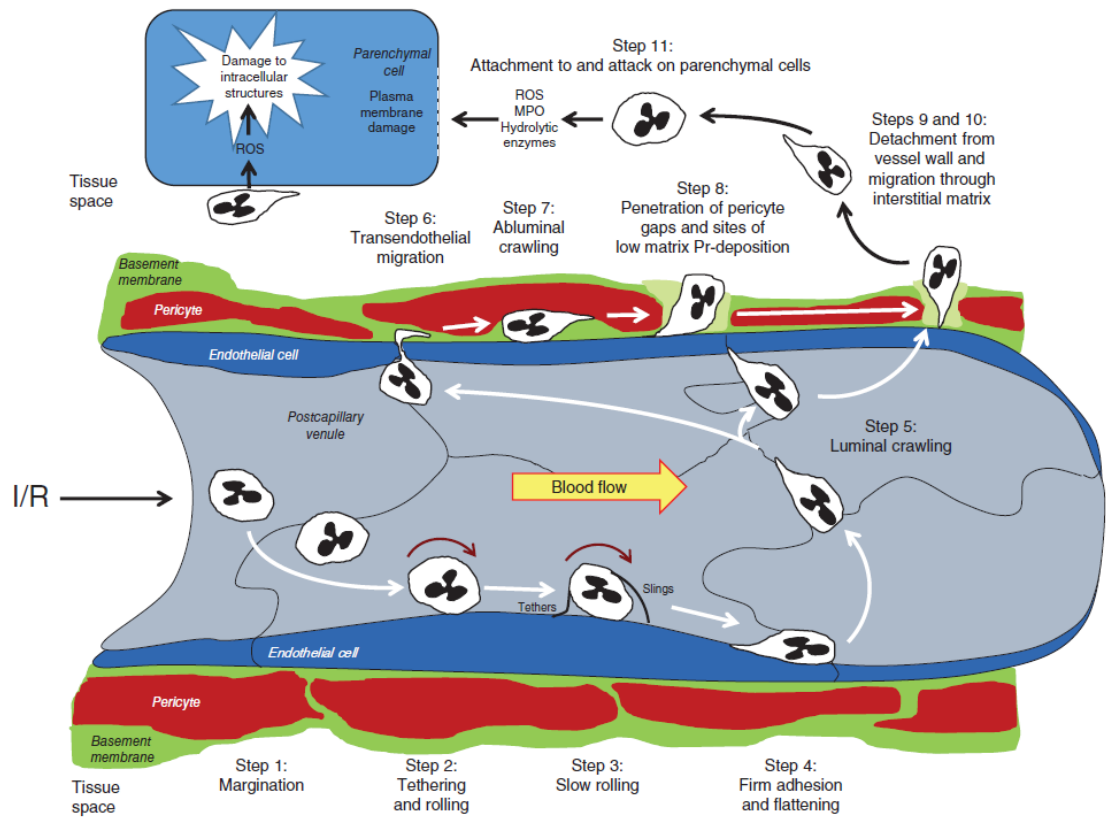


Figure 7 Neutrophil trafficking to ischemic sites occurs during reperfusion of ischemic tissues and involves 11 distinct steps (76).

The inflammation is a key defence mechanism in order to restrict the injured area. However, inflammation is a double-edged sword that contributes to the progression of the disease. Inflammation responses are different depending on diseases, but share some common mediators of inflammation such as interleukin 1 β (IL-1 β), tumour necrosis factor (TNF)- α or IL-6 (77). Moreover, the primary inflammatory cytokines including IL-1 β and TNF- α activate intracellular signalling pathways that are involved in I/R injury, activation of mitogen-activated protein kinase (MAPK) pathway through the Toll-like receptor (TLR)-4, activation through IL-1 receptor or TNF receptor (78). Finally, these activate transcription factors, nuclear factor kappa B (NF- κ B), especially, TNF- α is a potent activator of NF- κ B that leads to releasing amounts of inflammatory cytokines and recruiting neutrophils into injury areas (79).

Inflammatory serine protease inhibitor

Previous studies showed the relationship between ischaemia/reperfusion injury and neutrophil activation that is activated through free radicals, expression of adhesion molecules and inflammatory cytokines (80, 81). Serine proteases are a key of inflammatory response by activated leukocytes and mast cells (82). The attenuation of ischaemia/reperfusion injury could reduce neutrophil activity, free radical scavengers, lipid peroxidation inhibitors, protease inhibitors, leukocyte depletion and adhesion molecules expression inhibitors (80, 81, 83). Previous studies showed that ONO-5046 Na, which is Polymorphonuclear (PMN) elastase inhibitor, could reduce and block PMN elastase activity and limit the inflammatory cascade indirectly on I/R injury in heart transplantation (81). In addition, this inhibitor also attenuated I/R injury in lung and liver (84, 85). In other inhibitors on the same condition, I/R injury in heart transplantation, Sivelestat is a neutrophil elastase inhibitor that also lowers CK-MB, lactate and inflammatory cytokines levels (83). Similarly, the report from M. Kambe *et al.* showed Sivelestat, a neutrophil elastase inhibitor, improves cardiac function after administration at the onset of reperfusion in I/R injury conditions (86).

Not only neutrophil elastase inhibitors, other protease inhibitors also attenuated I/R injury. Matrix metalloproteinase inhibitor, MMP-2-inhibitor-NO-donor hybrid, could improve coronary flow and heart rate against I/R injury conditions. Moreover, the improvement is associated with a reduction of tissue injury and MMP-2

activity (87). Likewise, Krzywonos-Zawadzka and colleagues study showed MMP-2, myosin light chain, and nitric oxide synthase inhibitors improved mechanical heart function by decreased the expression level of iNOS, eNOS and enhance NO synthesis (88). The study of inflammatory serine proteases (ISPs) inhibitor, administered after 30 minutes of ischaemia and 24 hours of reperfusion, showed a reduction in cathepsin G and chymase activity, when compared with control group. IPS inhibitors also reduced myocardial apoptosis, infarct size and improved cardiac function that against to I/R injury (89). The reported from Kolpakov *et al.* showed dipeptidyl peptidase I (DPPI), which is lysosomal enzyme that involved in the ISPs, knock out mice markedly reduce the activity of neutrophil- and mast cell-derived serine protease after 4-week post-MI, when compared with wild type mice. Moreover, lacking of DDPI also improved cardiac contractile function along with promotion of angiogenic cytokines such as vascular endothelial growth factor (VEGF) A and B (90). Determination of creatine kinase and myeloperoxidase activity in myocardium after administration of serine protease inhibitor, aprotinin, in MI rats' model showed that it effectively preserved myocardium from I/R injury, as reduce induction of cardiac myocytes apoptosis even after 24 hours of refusion. Aprotinin also inhibited polymorphonuclear leukocyte-induced myocardial injury from I/R injury (91). Not only neutrophil elastase, cathepsin G is also involved in cardiovascular diseases.

Chymase from mast cell is also important similar to cathepsin G in cardiovascular pathology, especially the activation of angiotensin II pathway that contributed to cardiac remodeling and heart failure (92). Previous study showed that chymase involve in plaque progression and instability in atherosclerosis. After treated with chymase inhibitor, RO5066852, the reduction of spontaneous atherosclerosis and accelerated plaque progression found in the thoracic aorta of apoE^{-/-} mice (93). Similarly, NK3201 was treated 3 days before ligation, the result showed NK3201 was reduced chymase activity without altering Angiotensin Converting Enzyme (ACE) activity (94). NK3201 improved pressure develop and reduced mortality rate 17% (95). In hamster, chymase inhibitor, Suc-Val-Pro-Phep (OPh)₂, was injected into thoracic cavity that result in transforming growth factor β 1 lowering along with reducing density of mast cell. Therefore, chymase inhibitor could attenuate postoperative cardiac adhesion (96). However, the findings from computational study

revealed the putative off-targets for chymase inhibitors were identified through various structural and functional similarity analyses along with molecular docking studies (97, 98). Then, the unpredictable adverse effect of small molecules was concerned that lead to endogenous anti-protease peptide was be alternative choices. The endogenous inhibitor usually express and function in the body which could be safe and reliable.

Signalling in I/R injury

The consequences of reperfusion result in releasing of intracellular death ligands, which induce various intracellular pathways including mitochondrial-mediated apoptosis (99). These transduces the signalling through broad spectrum of death stressors and death receptor that response to the releasing of external stimuli. However, mitochondria-mediated apoptosis is not only pathway that is activated after the opening of the mitochondrial permeability transition pores (mTTP) at the reperfusion time (100). Death receptors signalling, which is induced by releasing death ligand, can promote cell apoptosis pathway and cell survival pathway that enhance cardioprotection pathway. Cell survival pathway is consisting of reperfusion injury salvage kinase (RISK) pathway and survival activating factor enhancement (SAFE) pathway (101). This pathway is regulated by specific ligand binding to cell surface receptors. The important death receptor is members of the tumour necrosis factor (TNF) superfamily that consist of Fas, TNFR1, TRAIL2 (102). The signalling is activated from integral plasma membrane protein binding to FasL, which activate through Fas receptor. Interestingly, Fas receptor is usually express in all type of the cell type but basal FasL expression level is restricted to specific cell types (103). However, Jeremias *et al.* study reported that during ischaemia/reperfusion injury FasL is induced to express in the heart (104). In death receptor details, previous study describes the interaction of ligand and receptor is mediated by homotypic interaction of death-fold motif that is generally binding to the same motif type. Death-fold motif is several varieties of death domain consist of death domains (DD), death effector domain (DED), caspase recruitment domains (CARD) and pyrin domain (PYD). The interaction between TNF- α and TNFR could induce complex I assembly on the cytoplasmic tail of receptor. Downstream of complex I are including cell survival,

apoptosis through TRADD and RIPK1 recruitment. TRADD and RIPK1 recruitment are result in adaptor protein TNF receptor-associated factor 2 and 5 (TRAF2/5) and cellular inhibitor of apoptosis proteins 1 and 2 (cIAP1/2) that attach to lysine 63 (K63)-linked ubiquitin chains. Ubiquitin chains promote the linear ubiquitin chain assembly complex (LUBAC) recruitment that also activate transforming growth factor- β -activated kinase 1 (TAK1) binding proteins 2 and 3 (TAB2/3). TAK1 play crucial role in inhibitor of κ B kinase (IKKs) through NF- κ B upregulation that leading to promote cell survival and inflammation. In addition, TAK1 activation also activate mitogen-activated protein kinase (MAPKs) pathway that provide additional survival pathway (99).

Mitogen-activated protein kinase are a family of heterogeneous serine/threonine kinase, which regulate cell growth, cell proliferation, survival and cell death (76). The intracellular signalling including extracellular signal-regulated kinases (ERKs), c-Jun N-terminal kinases (JNKs) and p38 MAPKs. Furthermore, the all-MAPK pathways are consisting of protein kinase families including MAPK kinase kinases (MKKKs or MAPKKK), MAPK kinases (MKKs or MAPKKs) and MAPKs. MAPKs are activated by dual phosphorylation at tyrosine and threonine residue in a conversed Thr-*Xaa*-Tyr (*Xaa* is any amino-acid) in the activation loop of kinase subdomain VIII. MAPKs can reverse phosphorylation and return to inactivated state. MAPKs is specific catalysed by dual phosphorylation both of Ser/Thr residues that interaction between N-terminal region located on the MAPKKs (105). Cellular stress and cytokines can activate p38 through MAPKKKs, MAPKKs and p38 respectively that leading to cell adaptation and physiology response as shown in Figure 8 (106, 107).

The p38 MAPK was first identified in *Saccharomyces cerevisiae* as protein product of Hog1 (108). The mammalian p38 MAPK consist of 4 isoforms including α , β , γ and δ . The isoform that expresses in the most the cell types is p38 α , which is 38 kDa polypeptide. However, other isoforms were identified by different encoded gens p38 β and p38 γ (as called SAPK3 and ERK6), which express in skeletal muscle and p38 δ (as called SAPK4) that express in testis, pancreas, kidney and small intestine (109). Most stimuli that activate p38 MAPK can also activate JNK. Upstream kinases of p38 MAPK include MEK3 and MEK6, which is activated by upstream MAPKKKs from physical, chemical stress stimuli, inflammatory cytokines such as IL-1 and TNF- α (110). The MEK3/6 can activate p38 MAPK by the phosphorylation at Thr-Gly-Tyr (TGY) in activation loop that specific to p38 MAPK because length of activation loop is different from ERK2 and JNK (111). The p38 MAPK activation could also be activated in leukocytes by various cytokines or extracellular mediator, especially, respiratory burst or apoptosis (112). Moreover, p38 MAPK activation in macrophage and neutrophil are also regulate T-cell differentiation and apoptosis through gamma interferon production (113) as same as in I/R injury. Since those stimuli can activate releasing of ROS, disrupt mitochondria membrane and activate inflammatory response that activate p38 MAPK, JNK and ERK (114). The downstream substrate of

p38 MAPK including MAPKAP-K2 or MAPKAP-K3 (115). These substrates of p38 contribute to subsequent phosphorylation to HSP27 that prevent actin cytoskeleton for cell migration (116). Moreover, these substrate can activate subsequent phosphorylation such as transcription factor ATF2 or SAP1 (107). In addition, p38 MAPK is involve cell death through activated translocated of Bax from cytosol to mitochondria (117). Not only play role in cell death, p38 MAPK have been found to be involved in cell growth, cell differentiation and cell cycle that activated by granulocyte macrophage colony-stimulating factor (GM-CSF), fibroblast growth factor (FGF), erythropoietin, IL-3, IL-2, IL-7, insulin like growth factor (IGF), vascular endothelial growth factor (VEGF) (118-120).

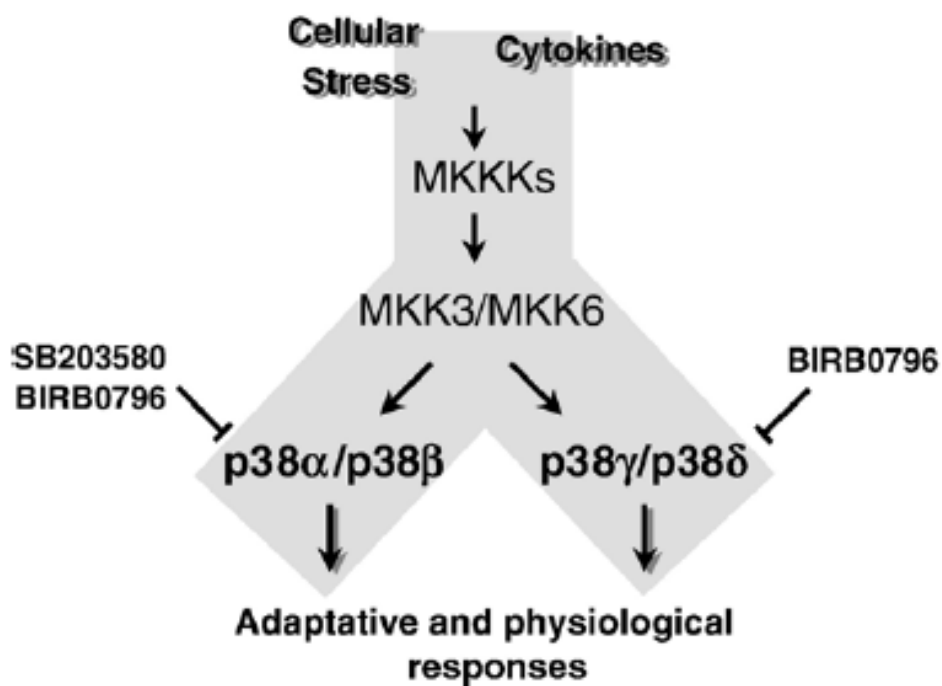


Figure 8 p38 MAPKs signalling pathways (107)

The c-Jun N-terminal kinases (JNKs) were firstly isolated from rat liver that injected with cycloheximide (121, 122). JNKs is activated from G protein-couple receptors, serum and growth factor (122). In mammals, there are 3 different isoforms of JNKs including JNK1, JNK2 and JNK3, which located on 3 different chromosomes. JNK1 and JNK2 are mostly express form that found in various tissues,

but JNK3 is mainly expressed in central nervous system (CNS) neurons, cardiac smooth muscle, and testis (123). JNKs localize from cytoplasm to the nucleus following stimulation. JNK activation, similar to ERK1/2 and p38, requires dual phosphorylation on tyrosine/threonine residues within Thr-Pro-Tyr (TPY). JNK is also recognized to respond to cytokines such as TNF- α and IL-1 (124). JNK signalling plays a major role in cell apoptosis (125). The signalling starts from phosphorylation of MEK4 and MEK7 by MAPKs such as MEKK1-4, MLK2, TAK1 and ASK1 and 2 (122). The substrate of JNKs is N-terminal of transcription factor c-Jun that is phosphorylated on Ser63 and Ser73. JNK can also phosphorylate several transcription factors such as ATF-2, nerve growth factor (NGF), NFAT and STAT (110, 122). Furthermore, JNK can phosphorylate Bcl-2 and Bcl-X_L that is pro-apoptotic activity (126). Previous study showed p-JNK expression level was significantly increased in myocardial injury induced by I/R (127). The overexpression of tumour necrosis factor receptor associated factor -1 (TRAF1) upregulates JNK/p38 cascade that aggravates the development of myocardial I/R injury through inflammation and cardiomyocyte death (128).

On the other hand, the activation of pro-survival proteins that reduce cell death through inhibiting pro-apoptotic cascade against I/R injury by pro-survival proteins called as "Reperfusion injury salvage kinase (RISK) pathway". RISK pathway was first described by Yellon's group in 2002 that showed cardioprotective effect underlying urocortin induction (129). The RISK pathway is a combination of two parallel cascades including PI3K and ERK1/2. The RISK pathway has important concepts that describe the function of this pathway. Firstly, short-term activation of kinases is protective, the activation of pro-survival kinases has a protective effect when acutely activated, whereas chronic activation could be considered to enhance cardiac dysfunction (101, 130). Previous study reported that the alteration of these kinases' activation was regulated by PTEN activation. PTEN was described as a crucial "switch" that regulated these pathways (131). Second concept, this pathway should be activated at the time of early reperfusion for cardioprotective effect. Previously, RISK pathway was demonstrated by activating at two time points underlying ischaemic preconditioning, which includes "trigger phase" and "during the onset of reperfusion". Trigger phase was during the preconditioning cycle at ischaemic

episode. During the onset of reperfusion was early phase of perfusion that related to the opening of mitochondrial permeability transition pore (mPTP). The target of protective effect is activate the pro-survival kinase within the first 15 min of opening mPTP when onset the reperfusion because these was loss the cardioprotective effect activation after 15 min (132). Therefore, common feature of cardioprotective effect is early activation of survival kinase signalling cascades including phosphatidylinositol-3-OH kinase (PI3K)-Akt and p42/44 extracellular signal-regulated kinase (ERK1/2).

Protein kinase B (PKB)/Akt was firstly discovered by three researcher groups in 1991 that reported PKB linked to cell survival pathway (133-135). PKB is activated downstream of phosphatidylinositol-3-OH-kinase (PI3K) signalling cascades through wide range of receptors (136). The phosphorylation of PI3K results in lipids phosphorylated at the 3'-OH position of the inositol head group including predominantly phosphatidylinositol 3,4,5 trisphosphate (PIP₃) and (PI_{3,4})P₂. The activation cause PKB translocated to plasma membrane. Phosphatidylinositol-3-OH-kinase (PI3K) participates in protection against ischaemia/reperfusion injury through serine/threonine kinase, Akt (137). The activation of PI3K/Akt is both of directly phosphorylate the pro-apoptotic protein BAD or indirectly phosphorylate and recruit of distal signalling moieties such as 70-kDa ribosomal protein S6 kinase (p70S6K), p90 ribosomal S6 kinase (p90RSK) (138, 139). The result of BAD phosphorylation is inhibited apoptosis by binding to 14-3-3 sequesters of mitochondria. Moreover, the PI3K/Akt activation is also inhibit the change of BAX conformation that require in translocation to mitochondria as in Figure 9 (140). The consequence of PI3K phosphorylation is a removal of various pro-apoptotic proteins such as BAD, BAX, and p53 from mitochondrial action site. Akt phosphorylation is also inhibit the opening of mPTP that leading to cytochrome *c* releasing from mitochondria and maintain mitochondrial membrane potential by inducing eNOS activation (141).

Protecting the Heart Against Reperfusion Injury:
Targeting the Reperfusion Injury Salvage Kinase (RISK)-Pathway

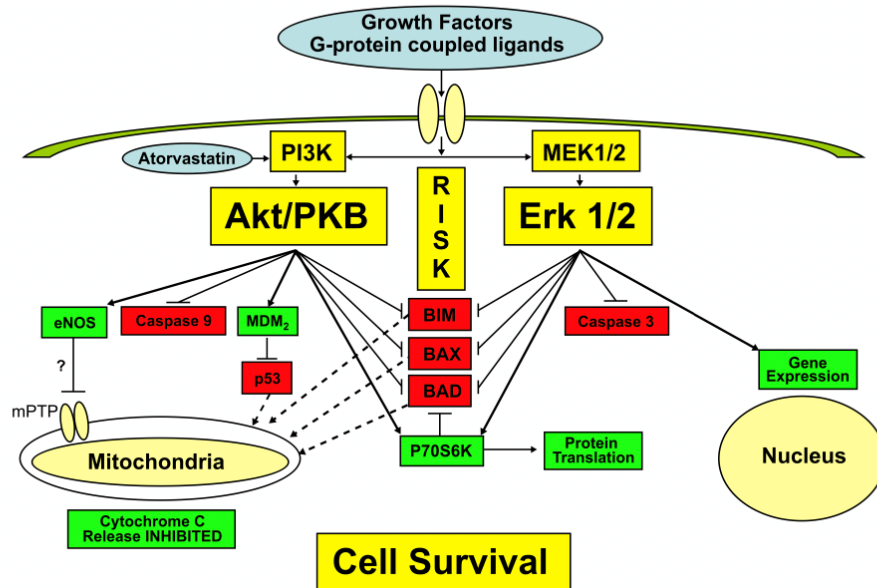


Figure 9 Targeting the reperfusion injury salvage kinase (RISK) pathway (140).



Extracellular signal-regulated kinases (ERKs) are serine/threonine protein kinase, which is classical mitogen kinase cascade including MAPKKKs A-Raf, B-Raf and Raf-1, MAPKKs MEK1 and MEK2, and MAPKs ERK1 and ERK2. ERK1 and ERK2 share 83% amino acid identity and express in various tissues (110). ERK1/2 has relative molecular weight of 42/44 kDa. ERKs is normally located in the cytoplasm. Intracellular and extracellular can induce serine/threonine phosphorylation in the VII region of ERK1/2. The regulation of ERK1/2 is important for maintenance of cell proliferation, growth, development, and differentiation. ERK1/2 is activated by ligand of the heterotrimeric G protein couple receptor and cytokines. Cell surface receptor, tyrosine kinase (RTK) and G protein-coupled receptor activate signals through Raf/MEK/ERK cascade through GTP-binding protein Ras. Active Ras or Ras-GTP transmit signal to downstream effector proteins, serine/threonine kinase Raf. Ras-GTP binds to Raf induce its translocation from the cytoplasm to the cell membrane. Translocation generates transient membrane-associated signal. The activated Raf bind and phosphorylate dual kinase MEK1 and MEK2, which subsequently phosphorylate ERK1/2 within Thr-Glu-Tyr (TEY) in activation loop. Only 5% of activated Ras molecules can induce full ERK1/2 activation (142). The ERK1/2 activation is crucial for translocation into the nucleus, which then subsequently phosphorylates various transcription factors such as STATs, ATF₂, Elk-1, c-Myc, Fos and Jun. In I/R injury, the heart damage can lead to irreversible fatal injuries and death (143). Previous study showed the relationship between ERK1/2 signalling pathway and inflammation in I/R injury (144). The activation of ERK1/2 could downregulate inflammatory cytokines in ameliorates acute myocardial infarction in rats (145). Moreover, ERK1/2 activation was decreased myocardial inflammatory cytokines including TNF- α and IL-1 β that related to reducing of infarction size and releasing of cardiac troponin I (cTnI) through upstream master switch, upregulating early growth response (Egr)-1 (146).

Oxidatively modified protein: Protein carbonylation (PC) and ischaemia modified albumin (IMA) as a marker for I/R injury

Oxidative stress is defined as an imbalance between reactive oxygen species (ROS) and antioxidant molecules (147). ROS is produced in normal physiological condition that play role in various enzyme cascades in cellular metabolic processes. The source of ROS is mitochondria that produce superoxide anion (O_2^-), hydrogen peroxide (H_2O_2) and hydroxyl radical (OH) (148). These ROS can form through electrons leakage from electron transport chain. ROS is important initiator and mediator of many diseases, especially, cardiovascular diseases (149). The continuous and cumulative of ROS is damage both of directly and indirectly all biomolecules including proteins, lipid, DNA and carbohydrate (150). Among biomolecules that oxidatively modified, biomolecule carbonylation is major hallmark of oxidative stress (151). Protein carbonylation was firstly described in 1990 by Levine and Stadman (152). It is recognized as universal marker of oxidative stress that linked to human diseases such as Alzheimer's disease, chronic lung disease, chronic renal failure, diabetes sepsis and ischaemia/reperfusion injury (153). Protein carbonylation is irreversible post-translational modification (PTM) that cause from ROS oxidized amino acids and protein carbonyl groups (154). The products of oxidation, reactive carbonyl group, including high molecular weight (HMW) carbonyl and low molecular weight (LMW). HMW is including aldehyde, keto and lactam groups formed in the targeted biomolecules which is carbonylated phospholipids, proteins and DNA. On other hand, LMW caused by oxidative cleavage reactions, methylglyoxal derived from protein glycooxidation and lipid peroxidation. The accumulation of these product is characteristic of carbonyl stress that is nucleophilic substrates and leading to alteration of biomolecules. Alteration of biomolecules were increase cell toxicity that lead to cell apoptosis (155). Previous studies showed protein carbonyl level was related to the oxidative stress in the cardiovascular diseases. The muscle ischaemia reperfusion injury in rats showed the protein carbonylation level was significantly increased in I/R group that related to xanthin oxidase (XO) and adenosine deaminase (AD). In intermittent hypoxia on oxidative stress induced myocardial damage in mice study showed an increasing in protein carbonyl related to lipid peroxidation an infarct size in intermittent hypoxic injury (156). In addition, plasma protein carbonyl

concentration is also increased in left ventricular hypertrophy (LVH) patient when compared to patient with normal geometry (154). The correlation of protein carbonyl to ATP synthesis in the cardiomyopathy hamster rats and correlation between protein carbonyl content and plasma cardiac troponin (cTnT) was reported (157).

Ischaemic modified albumin (IMA) is an unstable form of human serum albumin (HSA), which is binding site for transition metal ions including cobalt, copper and nickel. Myocardial ischaemia generate number of free radicals, acidosis develops. As myocardial ischaemia could reduce myocardial perfusion, this led to in N-terminal amino acid unstable to binding to copper (Cu^{++}). So, Copper (Cu^{++}) is released from weak binding sites on plasma proteins. Cu^{++} converted to Cu^+ by ascorbic acid in the circulation. Cu^+ reacted to oxygen and produce superoxide radicals (O_2^-). After that, superoxide dismutase (SOD) dismutase the O_2^- forming hydrogen peroxide (H_2O_2) that can degraded by catalase enzyme. The releasing of Cu^{++} ions is scavenged by albumin but tightly bound to the N-terminus. Albumin bounded-copper is damaged by hydroxyl free radicals that remove three N-terminal amino acids and Cu^{++} ions to repeat the mechanism (Figure 10) (158).

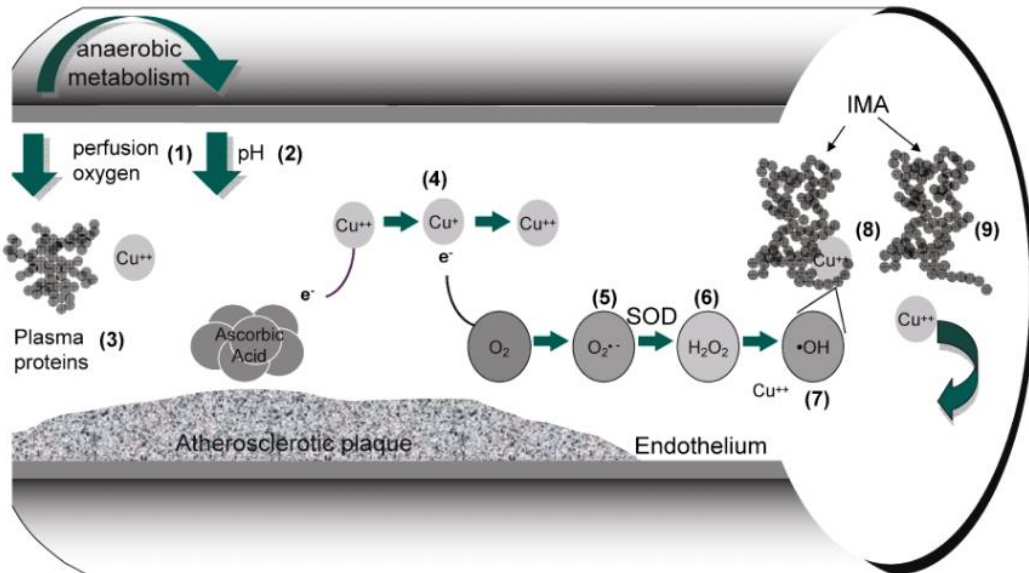
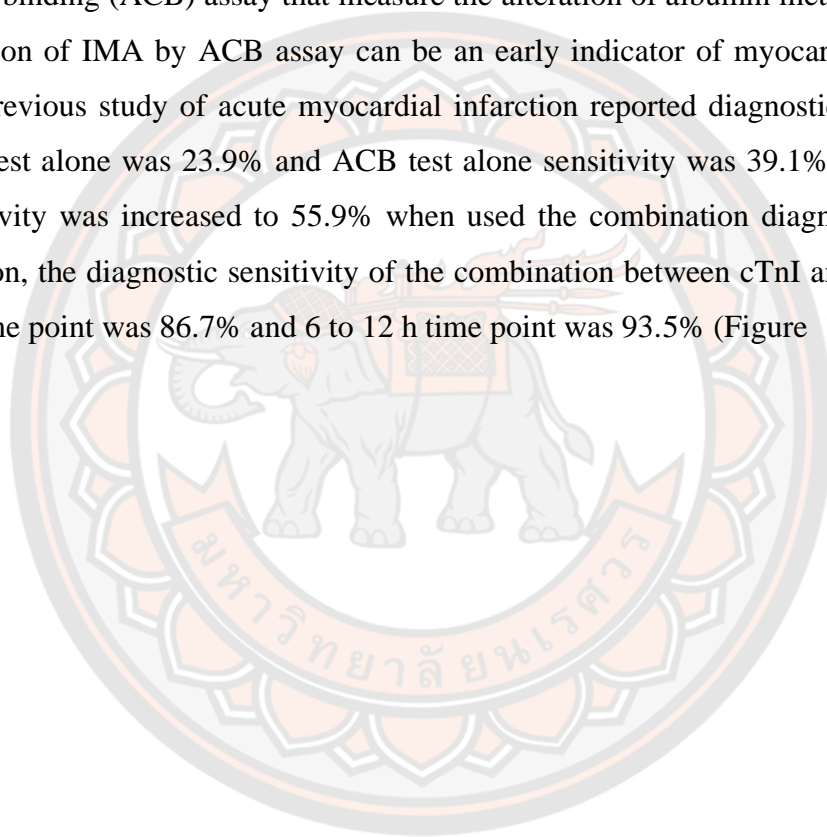


Figure 10 Mechanism of Ischaemic modified albumin generation (158)

The previous report showed the releasing of fatty acid in myocardial ischaemic condition could reduce the ability of albumin to bind to cobalt, by changing conformation of N-terminal region (159), due to conformation change of N-terminal site. Moreover, clinical data showed that plasma IMA level rapid rose in patient after balloon inflation, fall at 6 hours and return to normal level at 24 hours (160). Interestingly, the rise of plasma IMA was occurred earlier than cardiac troponin and natriuretic peptides. Measurement of IMA can be performed by *in vitro* albumin cobalt binding (ACB) assay that measure the alteration of albumin metal binding. The elevation of IMA by ACB assay can be an early indicator of myocardial infarction. The previous study of acute myocardial infarction reported diagnostic sensitivity of cTnI test alone was 23.9% and ACB test alone sensitivity was 39.1% but diagnostic sensitivity was increased to 55.9% when used the combination diagnostic (161). In addition, the diagnostic sensitivity of the combination between cTnI and IMA at 1 to 6 h time point was 86.7% and 6 to 12 h time point was 93.5% (Figure 11).



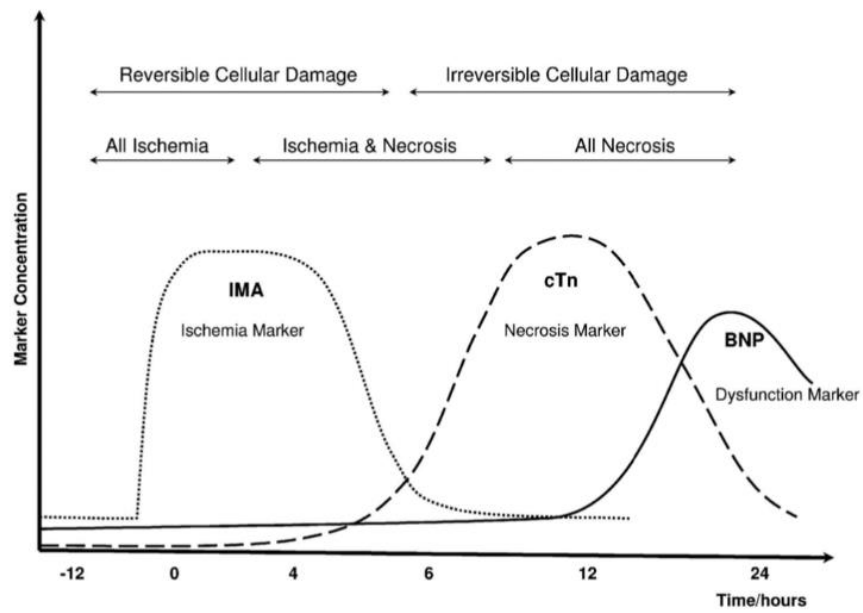


Figure 11 Release kinetics of IMA in relation to standard cardiac biomarkers including cardiac troponin, cTn and natriuretic peptide, BNP (158).

2 Secretory leukocyte protease inhibitors (SLPI)

2.1 Biological and biochemical property and effects of SLPI

The secretory leukocyte protease inhibitor (SLPI) is an 11.7 kDa boomerang-like shape protein non-glycosylate protein (162), containing two whey acidic protein (WAP) domains linked by four disulfide bonds (163) (164). The SLPI is WAP II or C-terminal domain has been known to involve in the protease inhibitory activity (165), which selectively target serine protease enzymes (Figure 12). The protease inhibitory domain resides at residues 67-74 (165), in particular Leu72-Met73- Leu 74 are crucial for antiprotease activity (166). One of the most abundant inflammatory serine proteases is neutrophil elastase (NE). Inhibition of neutrophil elastase (NE) require the association between SLPI and fibronectin or elastin by tissue transglutaminase-2 and plasma factor XIIIa (167). Moreover, SLPI can inhibit cathepsin G, chymase, chymotrypsin, trypsin, and tryptase activity (18, 19, 168, 169), inhibit the production and activity of matrix metalloproteinases (MMPs) (170). The inhibition of serine protease plasmin by SLPI blocks the plasminogen activator through annexin A2 leading to reduced plasmin generation (171).

Although the protease inhibitory activity of SLPI is independent on WAP domain I, the WAP I or N-terminal domain possesses variety of beneficial effects. The WAP I domain is essential for broad-spectrum antimicrobial activity (172-174). SLPI can directly kill microorganisms, including *Staphylococcus aureus*, *Streptococcus pyogenes*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Candida albicans*, and *Aspergillus fumigatus* (172-175). Moreover, SLPI could interfere the human immunodeficiency virus 1 (HIV-1) infection to macrophage by competitively binding to annexin II or scramblase 1 and 4, which are essential binding partner for HIV-1 on T-lymphocytes and macrophages cell membrane (176, 177). In addition, scramblase is a binding partner protein for SLPI involved protein passing through the intracellular (178).

It has been known that SLPI express in various types of cells, including human epithelial cells, immune cells, and fibroblasts (179-181). A high concentration of SLPI was secreted in saliva and mucosal tissue. The concentration of SLPI in the saliva is 30 times higher than in the circulation (182). Human SLPI protein was

encoded from the region of 678 kb on chromosome 20q12-13.2 (164). SLPI mRNA expression is upregulated by several types of pattern recognition receptor ligands, including Toll-like receptors (TLR) ligands (175, 183, 184). Therefore, microorganisms are able to induce SLPI expression from their cell components, including lipopolysaccharide (LPS) of a bacterial cell wall, viral RNA, and parasites (185-188). In addition, SLPI expression in epithelial cells can be stimulated by several types of cytokines including tumor necrotic factor (TNF), interleukin-1 beta (IL-1 β), transforming growth factor alpha (TGF- α), insulin-like growth factor 1 (IGF-1), progesterone, and corticosteroids (189-191). In macrophages, Interferon (IFN) and IL-10 have been shown to upregulate SLPI expression in contrary to IL-6 that found to downregulate the expression of SLPI (192, 193). Interestingly, an observation that IFN- γ can reduce TNF- α and nitric oxide (NO) production in macrophages to tolerance to SLPI (183, 194). Although SLPI known to inhibit NE activity, but NE itself could regulate SLPI expression (195). This information suggested that pro-inflammatory cytokines and cell components regulate SLPI expression.

Although SLPI can inhibit the protease activity, but the protease can also inactivate the SLPI itself. Secreted SLPI can be inactivated by myeloperoxidase-catalyzed oxidation, by activated neutrophils (196). Previous study reported that SLPI could be digested by matrix metalloprotease-9 (MMP-9), which subsequently suppress the protease inhibitory activity of SLPI (197). In another way around, cleaved-SLPI loses its ability to inhibit monocyte MMP-9 synthesis, implying that excessive MMP-9 production can overcome SLPI (175, 197). Similar to the case of MMP-9, chymase is also known to cleave and suppress the protease inhibitory activity of SLPI (18, 198). SLPI can also be digested by cathepsins B, L, and S, which renders their anti-neutrophil elastase function inactive (199). This also cause the reduction of half-life in circulation (200).



Figure 12 3D structure of SLPI and disulfide bridge (PDB ID: 2Z7F)

2.2 Roles of SLPI in physiology and responses

2.2.1 SLPI in regulating cell proliferation, differentiation, and apoptosis

Roles of SLPI in cell proliferation has been well described in cancer model, in which SLPI promotes cell proliferation by transcriptional activation of the cyclin D1, which important regulator of cell cycle progression and activate cell proliferation (20). In addition to activation of cell renewal, anti-apoptotic activity of SLPI has also been reported. SLPI could inhibit TNF- α -induced apoptosis by downregulating pro-apoptotic caspase-3 (24). The evidence of SLPI in several types of cancer has been reported and also mentioned in the latter section in this review article.

2.2.2 Physiology of SLPI in response to infection and inflammation

The anti-microbial activity of SLPI has been known to be dependent on the N-terminal domain of SLPI (201-203), which related to the cationic nature of the SLPI (204) that allow the protein to adhere to and destabilize bacteria's anionic cell membrane (203, 205). Not only destroying the bacterial cell membrane, SLPI can also inhibit the mRNA translation process by interfering the ribosome to access the Shine-Dalgarno region, which prevents initiation of protein synthesis (206, 207). The anti-proteolytic effect of SLPI may not be necessary for it to serve as an LPS inhibitor.

The antibacterial activity has been studied in several microbial models including *E. coli*, *Staphylococcus aureus*, *P. aeruginosa* and *Staphylococcus epidermidis* (208) *Neisseria gonorrhoeae*, group A *Streptococcus*, *Mycobacterium bovis*, and *Mycobacterium tuberculosis* (209-212). Increasing in serum SLPI levels have been reported in human sepsis and experimental endotoxemia. In sepsis patients, the maximal multiple organ failure ratings and serum SLPI concentrations are highly correlated (213). SLPI-deficient animals experienced severe inflammatory responses with elevated serum IL-6 and led to a considerable rise in morbidity and mortality rates. In the absence of SLPI, macrophages, which are the primary LPS responders, produced more IL-6 and high-mobility group (HMG)-1 protein, a late mediator of endotoxin lethality. (20, 214) These results highlighted that SLPI can provide a protective role in septic shock. In addition, studies in animal model suggested that

SLPI may regulate host susceptibility to bacterial infection. SLPI KO mice subjected to cecal ligation and puncture (CLP) were substantially more vulnerable to endotoxin shock and sepsis (214). Study from Nishimura, *et al.* show that SLPI-null mice showed worsen clinical outcomes of lung infection with the intracellular bacterial pathogen mycobacterium (215).

Anti-inflammatory activity of SLPI has been shown in macrophage responses to bacterial lipopolysaccharides (LPS) (216). The predominant pathway of SLPI for regulating anti-inflammation is due to the attenuation of the degradation of the I- κ B (inhibiting factor of NF- κ B) from the ubiquitin-proteasome pathway (217). Following cell activation, I- κ B is quickly destroyed, allowing NF- κ B to enter the nucleus and regulate inflammatory gene transcription (20), consequently reduce the level of inflammatory cytokines. On the other hand, SLPI can inhibit the NF- κ B signalling pathway by entering the cytoplasm and nucleus to compete with the NF- κ B component p65 to associate with the promoter regions of the IL-8, TNF- α (218), IL-10, and IL-1 β (219). Numerous LPS-responsive elements, such as NF- κ B/rel binding sites, are found in the promoters of LPS-inducible genes, such as NO synthase and TNF α (220). The integrins function as co-stimulators of macrophage in response to LPS, which could be blocked by SLPI. This could subsequently interfere signalling activation for LPS-induced NO and TNF- α production (220).

Epithelial cells, which was recognized the bacteria, will release the B-cell activating factor (BAFF) this is a signal to stimulate B lymphocytes (221). B cell will stimulate the NF- κ B to produce the cytokines regulating class switching of antibody such as IgG and IgA. SLPI can attenuate the class switching antibody process by directly eliminating bacteria and inhibiting NF- κ B signalling (221).

The fungicidal activity of SLPI has been shown in metabolically active *Candida albicans* and *Aspergillus fumigatus* (222) in dose-dependent manner. Although the antimicrobial activity of SLPI, similar to other cationic antimicrobial polypeptides, is restricted to circumstances of low ionic strength, its fungicidal activity was at concentrations higher than 1 mM (for *C. albicans*) or 2 mM (for *A. fumigatus*) (222).

The anti-viral activity of could be hypothesized by the evidence of lack of oral HIV-1 transmission and the decreased mother-to-child HIV-1 transmission by the

mother's milk, which may be due to the high concentrations of SLPI in salivary (223). Similar to this, low rates of perinatal HIV-1 transmission have been linked to high quantity of SLPI in vaginal secretions (223). The possibly explanation of reducing HIV-1 transmission by SLPI is due to the interference of viral invading process to target cells, and subsequently limit viral replication (177), which independent to SLPI anti-protease activity. Furthermore, it appears that anti-HIV-1 effect of SLPI require a strong binding of SLPI on monocyte surface molecules or receptors (224). The phospholipid (PL) binding protein annexin A2 (AnxA2) and the phospholipid scramblases 1 and 4 (PLSCR1, PLSCR4) are membrane-associated proteins regulate the membrane phospholipids mobility (177). Annexin A2 has been identified as a receptor for CMV (225) and respiratory syncytial virus (226), and later as a molecule that require for HIV-1 infection (227). SLPI was proved to be a binding partner of AnxA2 and disrupt the HIV-1 binding and invading the macrophage. In addition, PLSCR1 and PLSCR4 interact directly with the CD4 receptor at the cell surface of T lymphocytes, where HIV-1 association is required for infection. Since SLPI can bind to the similar region of cytoplasmic domain of PLSCR1, that require for CD4 receptor binding.

2.3 Role of SLPI in non-communicable diseases (NCDs)

Although roles and effects of SLPI has been studied for decade, but the majority of the evidence was highlighted in infectious and immunity, which has been intensively reviewed by several articles. However, the review literature concerning the roles and effects of SLPI in non-communicable diseases (NCDs) is still required. Here, we collect the information from the published articles and summarized in several disease model.

2.3.1 SLPI and neurodegenerative diseases

Secretory leukocyte protease inhibitor (SLPI) is commonly found in mucosal surfaces including saliva, epithelial cells of respiratory tract and urogenital tract (228, 229). However, SLPI was showed the response to central nervous system (CNS) injury that including cerebral ischemia and spinal cord injury (230, 231). The focal

cerebral ischemia model by unilateral middle cerebral artery occlusion (MCAO) showed the upregulation of SLPI in ipsilateral cortex by cerebral ischemia at 12 to 48 hours and the SLPI level continually increased after 5 days of MCAO (230). Furthermore, overexpression of SLPI significantly lower neurological deficit scores. (230). The neuroprotective effect of SLPI also demonstrated in traumatic CNS injury model that performed moderate contusion injury at T11. The SLPI mRNA express at 1 day after the injury whereas SLPI protein could be observed at 3 days after injury. In addition, administration of recombinant SLPI significantly improved motor function that assessed by Basso Mouse Scale (BMS). Moreover, receiving SLPI could increase tissue sparing, myelin integrity, number of ventral horn neuron and density of serotonergic axons caudal to the lesion (231).

2.3.2 SLPI in Respiratory disorders

In respiratory airway, balance of proteases and anti-proteases were indicated to immune response in inflammatory area, especially in cystic fibrosis (CF). CF cause ineffective innate immunity by transmembrane conductance regulator mutation that impair ion channel and mucociliary clearance. These led to chronic pathogen colonization from *Pseudomonas aeruginosa*, and inflammatory response which located in both of upper and lower airways as reservoirs of infection, so discrimination of pathogen located lead to therapeutic treatment for specific immune compartments. The has been reported the level of proteases and anti-proteases concentration were significantly higher in sputum of CF patients compared to nasal lavage (NL) from healthy subject, as 10-fold of neutrophil elastase (NE) and 5000-fold of SLPI. Furthermore, NE/SLPI ratio in NL was 726-fold higher than sputum, respectively (232). Likewise, NL and sputum of CF patients before and after intravenous (IV) antibiotic therapy, IV antibiotic treatment was significantly promoted on inflammatory response in lower airway but trend to decreased in upper airway. MMP9/TIMP1 and NE/SLPI ratio were significantly higher in sputum when compared to NL. Besides, NE/SLPI ratio was 10-fold higher in NL compared to healthy people. Upper airway was indicated delayed anti-proteases and proteases response to IV-antibiotic therapy than lower airway. Then, changes in microbiological

patterns after treated with antibiotic therapy that associated with changes of protease and antiproteases imbalances (233). For the protease activity in animal model, the clinically significant of SLPI has been reported in genetic modified animal model lacking SLPI expression, the bleomycin was used to develop lung fibrosis model in mice, which found that there was an increase in MMP9 activity in *slpi*^{-/-} mice, which related to an impairment of collagen gene expression but reduce lung fibrosis. In addition, the protease mediated TGF- β activity was increased above their increased in wild-type mice after *slpi*^{-/-} mice treated with bleomycin that impair collagen gene expression but minimal reduction of lung fibrosis so SLPI knockout could not prevent the lung fibrosis development following bleomycin-induced lung injury (234).

Not only, CF was the cause of the shift between protease and anti-protease balance, but also found in chronic obstructive pulmonary disease (COPD) following cigarette smoking. The study of differentiated nasal epithelial cells (NECs) and nasal lavage fluid (NLF) of smokers and non-smokers reported an increase in SLPI level in NECs and NLF from smokers. The interferon-sensitive response element (ISRE) binding sites were one of regulatory sites of SLPI promoter (235). Transcription factors of interferon signalling pathway, STAT1 could regulated SLPI expression in epithelial cells and lungs of *stat1*^{-/-} mice compared to wild-type. This finding showed that SLPI regulation and activity in nasal mucosa were induced by smoking (236).

SLPI was downregulated in both of human and mice of severe asthma (SA) in correlation with poor lung function. This could be due to the upregulation of interferon- gamma (IFN- γ) in chronic inflammatory model. The IFN- γ attenuate SLPI expression in airway epithelial cells could indirectly activate protease activity from of mast cell, which contribute to the severity of involved in increased airway hyperresponsiveness (AHR) in mice (237). SLPI seems to have therapeutic benefits since overexpression of SLPI could ameliorate AHR, and more efficiently when treated in combination with corticosteroids (CS). The effective treatment of severe asthma patient was bronchial thermoplasty (BT) which is an endoscopic therapy targets the smooth muscle in the lungs (238). This technique shows to reduce several gene expression that involve in airway inflammation and remodelling in patients with severe asthma. Interestingly, the results showed the SLPI was observed in patients

who had less than 2 exacerbations post-BT. (239) Similarly, Ano S. et al reported that responsive patients showed SLPI gene upregulation, which suggests that SLPI could potentially be useful for identifying risk of exacerbations post-BT (240).

2.3.3 SLPI in Urology Obstetrics and Gynaecology

In the second trimester of pregnancy, short cervical length (CL) was strong predictor of spontaneous preterm delivery (241). The association between short cervical length (CL) and the level of neutrophil elastase (NE), SLPI, and IL-8 has been reported in cervical fluid. Although only cervical fluid NE level, but not SLPI, show correlated to CL (242), but SLPI and progranulin (PGRN) concentration are positively correlated with inflammatory cytokines in cervical mucus samples from 23-26 weeks of gestation reflecting risk of preterm delivery (PD). The finding from the same study in animal model also showed the similar finding about an increasing in SLPI mRNA expression in pregnant mice treated with progesterone supplement. The overexpression of SLPI exhibit anti-inflammation and results in attenuation of cervical remodelling (243). PD is mostly found as a complication in pregnancies after *in vitro* fertilization (IVF). Serum SLPI level can potentially be the best predictive markers for PD, similar to HE4 and IL-13 (244). SLPI was also measured in menstrual fluids and found as one marker among five factors that moderate intraparticipant agreement, but limited variation exists in the selected proteins in menstrual fluid within and between cohort of women (245). Furthermore, the SLPI level in cervical mucus seem to higher in unexplained infertility patients than control group (246). SLPI is also upregulated in endometrial biopsies from persistent mating-induced endometritis (PMIE) and could potentially be a diagnostic marker with 100% sensitivity and 78% specificity (247).

SLPI is crucial for embryos development and implantation. Correlation between *slpi* mRNA expression and embryos development progression were evaluated after the 8-cell stage. The expression of *slpi* mRNA was lower in *in vitro* than *in vivo* embryos. Correspondingly, *slpi* knockdown by antisense oligonucleotides diminished embryos development speed and implantation rate compared with *slpi* sense-transfected embryos and *in vitro* controls (248).

2.3.4 SLPI in Liver diseases

Acute liver failure (ALF) cause by an exceed of hepatocyte death and innate immune response activation. Acetaminophen-induced ALF (AALF) is mostly found in ALF patient that led to immunoparesis and innate immune response impairment (249). SLPI in hepatic and circulatory concentration were increased in AALF. SLPI also expression in biliary epithelial cell and macrophages in the necrosis area. SLPI was mediated inflammatory response in AALF by modulating monocyte and macrophage function by reducing NF- κ B p65, TNF- α , and IL-6 and preserved IL-10 secretion following LPS challenging (250). Besides, SLPI and IL-6, in plasma of donor, were two candidates of risk-prediction biomarker for organ donor and recipient. It has been reported that SLPI can be used as a predictive marker for liver transplantation(251).

2.3.5 SLPI in Kidney diseases

Acute kidney injury (AKI) was common complication after cardiac surgery. Biomarkers play an important role for early diagnosis of AKI patients. It has been found that serum and urinary SLPI mRNA and protein level significantly increased in AKI patients (252). Urinary SLPI level is strongly corelated with SLPI mRNA level in the kidneys, reflecting organ damage associated to SLPI level (253). In kidney transplantation, SLPI concentration in discarded cold-preserved solution can be used as biomarkers for evaluation of the graft quality in kidney transplantation. The level of SLPI is high in delayed graft function or rejected graft post-transplant patient. In addition, SLPI could discriminate estimated glomerular filtration rate (eGFR) in low-risk patients (254). In patients who developed AKI after thoracoabdominal aortic aneurysm repair (TAAA) showed significantly increase in serum SLPI level. Multivariable logistic regression was also showed significantly related between SLPI level at 12 hours after ICU admission and AKI. The sensitivity and specificity of SLPI detection for AKI prediction was 76.47% and 87.5% , respectively, with the optimal cut-off 70.03 ng/ml at 12 hours after surgery (255). The survival rate of kidney transplantation of deceased donors (DD) was lower than living donors (LD)

(256). Transcriptome analysis from kidney biopsies showed SLPI was 203 fold upregulated in DD when compared to LD, which reflected to early donor injury, acute and adaptive immune response that related to inflammation, cell death, remodelling and fibrosis (257). In ischemia/reperfusion (I/R)-induced AKI mice suggest the potential of renoprotection underlying SLPI and SERPINA3M upregulation which related to apoptosis and inflammation (258).

2.3.6 SLPI and ocular diseases

Cellular and tissue homeostasis were maintained by balance between protease and anti-protease. The protease and antiprotease balance alteration was also involved in ocular diseases especially, keratitis, corneal ulceration and endophthalmitis (259, 260). In *S. aureus* keratitis and epithelial defects of murine model showed high level of MMP-8, IL-1, IL-6, TNF- α and SLPI while undetectable SLPI expression in normal control corneal (261). Similarly, Reviglio *et al.* reported that there is no SLPI express in normal ocular tissues but it can be induced by micro-organism invasion. This study showed, SLPI expression protect rat corneal, vitreous and retina tissue from inflammatory cells that release proteolytic enzyme after invaded by *S. Aureus* endophthalmitis (260, 261).

2.3.7 SLPI in bone, cartilage, and dental disorders

The inflammation and metabolic stress can also result in the bone and cartilage disease especially, osteoarthritis (OA) by upregulating the cartilage destruction (262). Cartilage destruction was caused by the upregulating extracellular matrix degradation enzyme and/or downregulating cartilage extracellular matrix molecules from the inflammation (263, 264). Moreover, OA-associate protease was not only alter the protease enzyme activity but it was regulated by cellular inhibitory molecules which is tissue inhibitor of matrix metalloproteinase (TIMPs) (264). Interestingly, treatment with product of inflammation or metabolic stress in chondrocytes including IL-1 β , HIF-2 α , or ZIP8, showed the upregulation of SLPI in this cell (20, 265). In addition, SLPI is specifically upregulated in OA cartilage and blood serum in both of OA patients and OA mice. These could highlight the application of SLPI as a potential

biomarker of OA (265). Similarly finding also suggests that SLPI is tissue dependent release from intra-articular human OA knee. (266).

Balance between osteoclast and osteoblast regulate osteoporosis. Several factors have been known to involve in bone differentiation and mineralization including, collagen I (Col I), osteocalcin (OCN), and alkaline phosphatase (ALP), dentin saloprotein (DSP), dentin phosphoprotein (DPP), dentin sialophosphoprotein (DSPP), dentin matrix protein- 1 (DMP-1X), and bone sialoprotein (BSP) (267).

Furthermore, pre-treatment osteoblast cells (MC3T3-E1 cells) by recombinant SLPI accelerates the adhesion and migration on Ti surfaces (268), increased cell viability, mineralization, and pre-osteoblasts differentiation. This could be due to SLPI activate upregulation of ALP, DSPP, DMP-1, BSP and Col I (269). Similar findings have been reported in odontoblast-like MDPC-23 cells that pre-treatment with SLPI upregulated gene expression of BSP, OCN, Col I, osteonectin (ON), MMP-2 and MMP-9 but downregulate DSPP.

SLPI show crucial role in odontoblasts and pre-dentin on post-natal (PN) day of mice. SLPI was expressed in odontoblasts and pre-dentin on PN4, under dentin and apical region on PNA10 to PN15 and under layer of odontoblasts and in odontoblasts on PN20. This study hypothesize that SLPI may regulated MMP-2 and -9 in odontoblasts during dentin matrix formation related to differentiation and mineralization (270). In junctional epithelium (JE), Odontogenic ameloblast-associated protein (ODAM) promotes JE-related gene expression, as well as regulate expression of SLPI (271). SLPI was found as key molecules that involving in periodontal tissue homeostasis during biophysical force (BF)-induced tooth movement (BTM) by alveolar bone AB remodelling. SLPI could induce osteoblastogenic genes including runt-related transcription factor 2 (Runx2), RANKL and MCSF expression combined with compression or tension so SLPI could be target molecule for BTM intervention (272). Furthermore, PDL from healthy patients was showed cytoplasmic SLPI expression that negatively correlated to LPS-induced stimulation of IL-6 and MCP-1 (188).

Severe congenital neutropenia (SCN) was haematological disorder that impaired promyelocytic proliferation and maturation with neutrophil count < 500

cells/ μ L (273). In dental pulp cells with SCN showed downregulation of ELANE and SLPI expression that consequently cause the attenuation of cell proliferation, attachment, spreading, colony formation, and wound healing with elevated reactive oxygen species (ROS), apoptosis and inflammation (274).

2.3.8 SLPI in Cancer

In cancer, increased SLPI expression has been reported in several types of cancers. Therefore, SLPI can potentially be an ideal biomarker for diagnosis of cancer. Moreover, elevated level of SLPI also found to be involve in metastasis ability of some cancer cells. In this part, the role of SLPI in different types of cancer will be discussed.

There is high SLPI expression in colorectal cancer tissue. Knockdown of SLPI by siRNA could attenuate cancer cell proliferation, migration and invasion that related to downregulation of AKT signalling (162). Immunohistochemistry study showed upregulation of SLPI is associated with pathologic characteristic of colorectal cancer. This suggests that SLPI could be used an indicator of progression and metastasis in colorectal cancer patients (275).

Pancreatic ductal adenocarcinoma (PDAC) also express high level of SLPI, while SLPI gene silencing showed a significant reduction in cancer cell proliferation, increased the apoptosis, and attenuated cell migration and invasion (276). Pancreatic cancer tissue or cell line (Bxpc-3 and Panc-1 cell) showed high SLPI expression level. Similar to other studies, SLPI gene silencing, by shRNA-SLPI, significantly reduced cell viability, suppress cell proliferation and induced cell apoptosis (277).

In gastric cancer, evaluation of 68 cases of gastric cancer tissue showed high expression of SLPI, which associate with the survival time, clinical classification, and tumour size. An in vitro experiments reviewed that upregulation of SLPI enhance cancer cell proliferation and metastasis through regulating P53, Bcl-2 and Caspase-8 expression (278).

Bioinformatics analysis and confirmation of gene and protein expression showed downregulation of SLPI in breast cancer (BC) tissues. Moreover, SLPI level was also negatively correlated with estrogen receptor (ER) and progesterone receptor

(PR) but positively correlated with IL-17 receptor B (IL17B) expression (279). High SLPI secretion also correlated with the aggressiveness of triple-negative breast cancer (TNBC) 4T1 cell. SLPI secretion associated with spontaneous lung metastasis from 4T1 tumours orthotopically implants in mice and worse outcome patients. Interestingly, SLPI was found physically interacts with the retinoblastoma tumour suppressor protein (Rb) and FoxM1 form to be Rb-FoxM1 complex. This complex released FoxM1 that may activate breast cancer metastasis targeting gene, FoxM1 (280). Comparison of mouse breast cancer cell line 4T1 and its highly metastatic 4T1.2 clone showed that SLPI was a dominant secreted protein that highly expression in both of medium and cell lysates of 4T1.2 cells (281). Pre-treatment of SLPI in murine (F3II) and human (MCF-7) breast tumour cells decreased E-cadherin expression and re-localized to cytoplasm and β -catenin re-localized to the nucleus. Similarly, stable F3II overexpressing SLPI showed disrupted E-cadherin and β -catenin complex that related to increasing of Bax/Bcl-2 ratio and p21 protein level, decreasing of c-Myc protein and Cyclin D1 and Claudin-1 levels (282). This suggests negative effect of SLPI in breast cancer.

Cancer metastasis required intravasate into the lymphatic system or vasculature and extravasate (283). SERPINE2 and SLPI was secreted from polyclonal mouse model which were necessary and sufficient for vascular mimicry and ensure their perfusion by anticoagulant effect. Lung-metastasis relapse patient showed overexpression of SERPINE2 and SLPI, suggesting that these two molecules can promote metastatic progression in human cancer (284). In addition, previous study showed that serum SLPI and SERPRINE2 level was higher in Papillary thyroid cancer (PTC) patient compared to multinodular nontoxic goiter (MNG) and control group (CG) (285). Likewise, results from DNA microarray indicated SLPI could be a potential biomarker for PTC (286).

There was a report showed high SLPI expression in head and neck squamous cell carcinoma (HNSCC) without human papillomavirus (HPV) driven in tumour tissue of smokers higher than non-smokers similar to increasing annexin A2 gene expression level. (287) It has been report that high SLPI expression level was associated with higher risk of HSCC with smoker history (288). Interestingly in oral

squamous cell cancer (OSCC) tissue, only SLPI expression has been found in association with lymph node metastasis, overall survival (OS) and disease-specific survival (DSS) (289). Additionally, SLPI was one of fourteen biomarkers protein candidate from saliva samples of OSCC that showed higher expression. In oropharyngeal cancer (OPC), although the oral gargle SLPI levels was not significantly associated with OPC, but it was associated with tonsillectomy and HPV. Besides, increasing SLPI level was also related to increasing odds of incomplete treatment response (290). SLPI play role in invasion in human gingival carcinoma Ca9-22 cell line (291). SLPI-deleted human gingival carcinoma Ca9-22 (Δ SLPI) cells showed small lamellipodia/dorsal ruffles slower moving in Δ SLPI cells that associated with well-developed intermediate filament bundles in desmosome junction compared to wtCa9-22 cells (292), and exhibit lower migration (293). These studies suggest that SLPI involve in cancer cell migration and invasion.

In contrary to the above information, SLPI downregulation has been reported to correlated with cancer progression. Brushed biopsy samples indicated that SLPI progressive declining trend between healthy normal and oral premalignant lesion tissue (OPMLs) tissue and further decreasing in OSCC lesion tissues. This indicated that reduction of SLPI is correlated with oral cancer progression (294). Similar to oral leukoplakia (OL), which is the most common oral precancerous lesions and be a potential predictive tool for the malignant transformation, immunohistochemical and histological grades is negatively correlated with the SLPI level. An *in vitro* biological effects of SLPI in Human Premalignant Oral Leukoplakia Cell Line (MSK-Leuk 1) and Wayne State University-Head and Neck 4 (WSU-HN4) cell lines was measured showed that SLPI inhibited TNF receptor-associated factor 1 (TRAF1) regulated cell apoptosis (295).

SLPI involved in bladder cancer (BCa) and prostate cancer (PCa) metastasis that altered by androgen response elements (AREs) located at different position in the miR525 precursor promoter. AREs induce vasculogenic mimicry (VM) formation either decrease PCa and increased BCa metastasis through miRNA525p that altered SLPI mRNA expression (296). AR also promote castration-resistant prostate cancer (CRPC) survival and growth, which correlate to higher serum level of SLPI.

Therefore, SLPI promote CRPC cell survival and growth after androgen withdrawal *in vivo* and *in vitro* (297).

The study in gastric cancer (AGS) cell line showed the high level of SLPI, and lipocalin-2 (LCN2). The LCN2 binding with SLPI is mediated by IL-17. Treatment with IL-17 significantly suppress AGS cell proliferation, clone formation, migration, invasion, cell cycle and cell apoptosis by targeting SLPI (298).

2.3.9 SLPI in Metabolic diseases

Metabolic diseases, which is a cluster of conditions that increase risk of heart disease, stroke, and type 2 diabetes, become a major public health issue. Although several studies have been reviewed on pathophysiology of the diseases, but roles and effects of SLPI in metabolic diseases seems not well-known.

The methyl-CpG-binding protein MeCP2 has been identified as proteins that selectively bind methylated DNA (299). The abnormalities methyl-CpG binding protein 2 (Mecp2) can be found in metabolic disorders (300). Obese human and mice showed upregulation of Mecp2 in white adipose tissue (WAT) that consequently bind to SLPI promotor and regulate SLPI expression. (301). In pathway of fatty acid metabolism regulation and lipid accumulation, Fatty acid transport protein 1 (FATP1) has been identified to be involved in lipid metabolic pathway (273). Study in model of FATP overexpression/interference by differentially expressed genes (DEGs) showed that SLPI is a candidate gene controlling fat deposition and fatty acid metabolism (302).

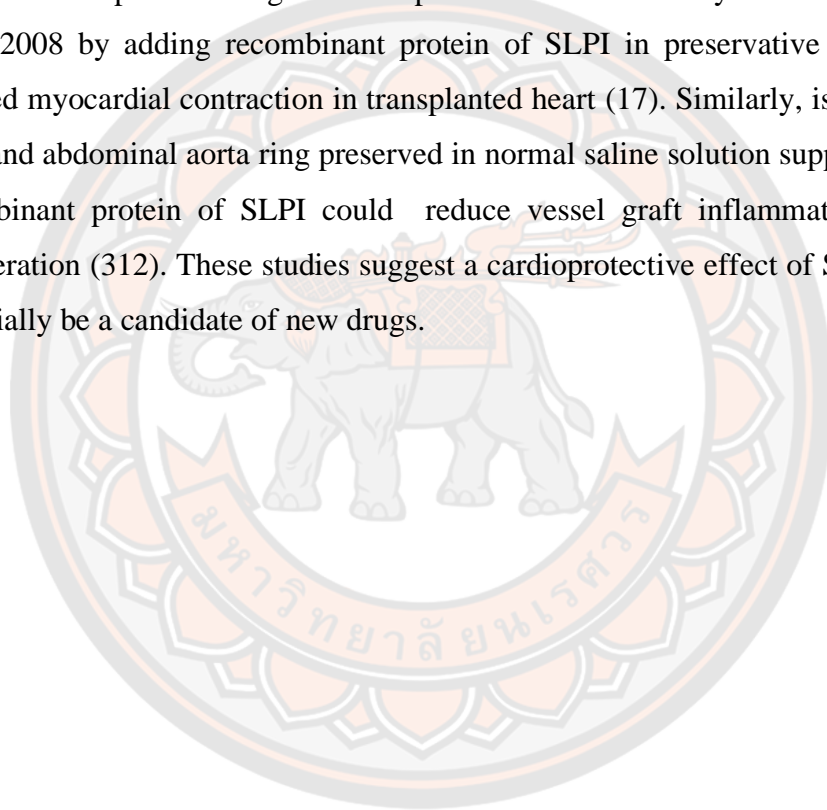
2.3.10 SLPI in Cardiovascular diseases

Cardiovascular diseases (CVDs) are considered as the major cause of global mortality and disability. The pathophysiology as well as candidate to treatment has been intensively studied, however, there are limit number of studies on the roles and effects of SLPI in cardiovascular diseases, particularly ischemic heart disease (IHD).

Protease enzymes cause widespread destruction and have relatively long half-lives in tissue (303). Moreover, an increasing in the activity of proteolytic enzymes such as chymase, matrix metalloproteinases, calpains, cathepsins, and caspases

contribute to the process of cell death, injury (12). Therefore, inhibition of protease activity can therefore be considered as powerful strategies for prevention of ischaemia/reperfusion (I/R) induced tissue injury. The level of serum neutrophil serine proteases (NSPs) inhibitors from coronary artery disease (CAD) and coronary artery ectasia (CAE) patients were significantly increased, particularly α 1-protease inhibitor (PI) and α 2-macroglobin (MG). Whereas SLPI and elafin were not significantly increased in CAE and CAD patient that due to vessel could not a main distribution site for SLPI and elafin (304). In addition, atrial fibrillation (AF) incident and circulating SLPI level is positively correlated in diverse population that related with the circulating level of MMP-2, TIMP-2 and VCAM-1 (305). Several studies in *in vitro* model of myocardial ischaemia reperfusion (I/R) injury, by simulated I/R (sI/R) condition, showed that pretreatment of recombinant human SLPI could reduce cardiac myoblast (H9c2) cell death and attenuate activation of p38 MAPK (23). Similarly, the overexpression of SLPI gene could also reduce cell death and cell injury (23), as well as protect the heart from an *in vivo* I/R injury (306). This could be repetitively showed in isolated adult rat ventricular myocytes (AVRMs) (22) and isolated adult rat cardiac fibroblasts (ARCFs) (307) (Figure 13). The mechanisms are believed to attenuate reactive oxygen species production and apoptosis pathway. The similar findings on cardioprotection effect of SLPI can also be demonstrated in an *ex vivo* (22) and *in vivo* model (308) of I/R injury. Pre-treatment of SLPI or giving during LAD ligation and onset at reperfusion also showed cardioprotective effect against I/R injury. The reduction of infarct size, improvement of cardiac function, reduce intracellular ROS production such as protein carbonyl (PC) and ischaemic modified albumin (IMA), inflammatory cytokines and regulatory apoptotic protein are also intensively studied (308). Interestingly, although the beneficial effects of SLPI is believed to be due to the anti-protease activity, few studies showed that those effect of SLPI might be independent on its anti-protease activity. The study of anti-protease deficiency activity of SLPI as mutant SLPI (L72K, M73G, L74G) can also provide cardioprotection against myocardial I/R injury (309). These data suggested that SLPI has cardioprotective effect in cardiovascular diseases especially, myocardial I/R injury.

Not only for the heart, but SLPI can also provide vasculo-protection on vascular endothelial cell (310) against an in vitro simulated ischemia/reperfusion (sI/R) injury. The similar mechanistic findings have been reported by reducing cell death, intracellular ROS production, attenuation of apoptotic pathway and enhance cell survival pathway. SLPI that derived from vascular endothelial cell could be a angiocine that reduced cardiac cell death(311). Therefore, application of SLPI as a cardio-vasculo protective agent could possible. Previous study from Schneeberger et al, in 2008 by adding recombinant protein of SLPI in preservative solution could restored myocardial contraction in transplanted heart (17). Similarly, isolated thoracic aorta and abdominal aorta ring preserved in normal saline solution supplemented with recombinant protein of SLPI could reduce vessel graft inflammation and tissue degeneration (312). These studies suggest a cardioprotective effect of SLPI and could potentially be a candidate of new drugs.



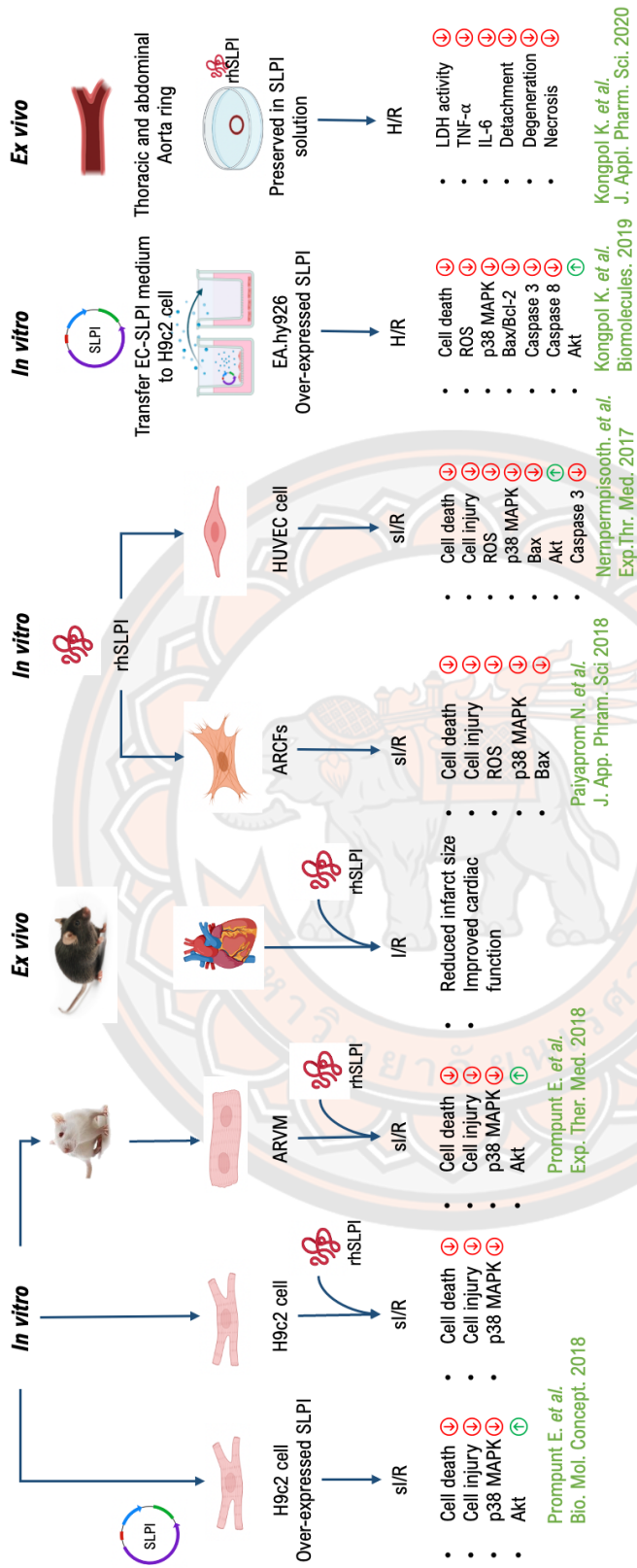


Figure 13 Schematic representation the previous study in SLPI

CHAPTER III

RESEARCH METHODOLOGY

This chapter presents the methodology of this research including material and method. The detail of each topic is described below.

Research Methodology

The conceptual idea of experiment is determining the cardiac physiology and biochemical alteration in Wistar rat model subjected to ischaemia/reperfusion injury. In this PhD dissertation, the study was divided into 2 major parts according to the aim of study, including;

Aim 1 To investigate the effect of recombinant human SLPI on physiological and biochemical function, in rats subjected to *in vivo* ischaemia/reperfusion (Figure 14)

Aim 2. To determine the anti-protease involvement in cardioprotective mechanisms of recombinant human SLPI against ischaemia/reperfusion (Figure 15)

The recombinant human SLPI (rhSLPI) (for aim 1) or anti-protease deficiency mutant of SLPI (for aim 1 and 2) were administered via intrajugular vein. Determination of cardiac physiology and function were measured by end-systolic pressure (ESP), end-diastolic pressure (EDP), dP/dt max, contractility index (CI), dP/dt min, Tau/e, develop pressure (devP) and heart rate (HR). The sensitivity to infarction and area at risk were measured by tissue staining. Moreover, biochemical alterations including MAPK phosphorylation and signalling protein involve in apoptosis such as p38, Akt, ERK1/2, Bax, caspase 3 and caspase 8 were determined by Western blot analysis as in Figure 14 and Figure 15.

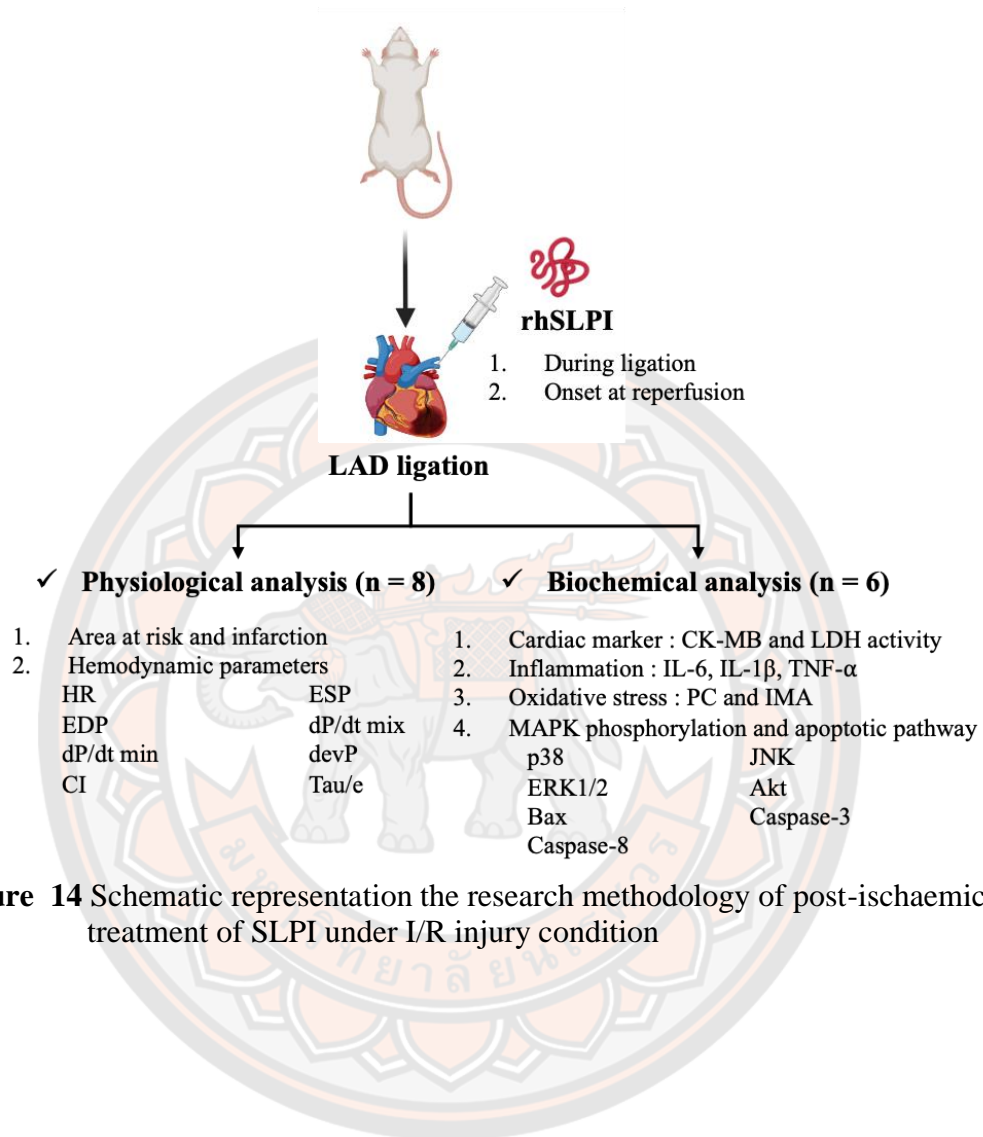


Figure 14 Schematic representation the research methodology of post-ischaemic treatment of SLPI under I/R injury condition

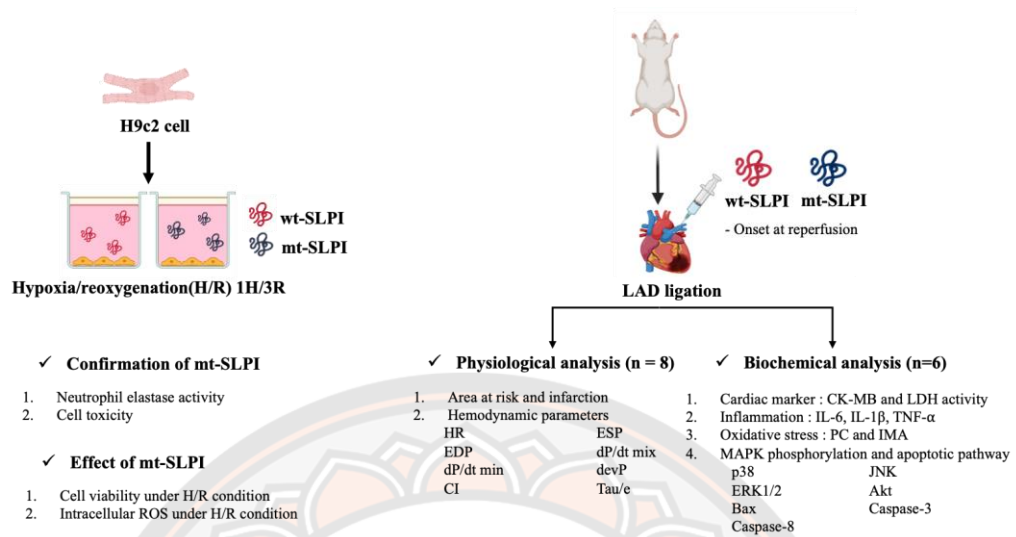


Figure 15 Schematic representation the research methodology of anti-protease deficiency SLPI treatment under I/R injury

Experimental Animals

Adult male Wistar rats weighting 250-300g were purchased from the Nomura Siam International, Thailand. All animals were maintained under environmentally controlled conditions (22 ± 1 °C, 12 h light: dark cycle) Chulalongkorn University Laboratory Animal Centre (CULAC). All protocols used in this study were approved by the Animal Use and Care Committee at Naresuan University (NU-AE620615) and the Institutional Animal Care and Use Committee, Faculty of Veterinary Science, Chulalongkorn University, Thailand (Protocol No.1973025). The overall number of animals was used in this study is shown in Table 1.

Table 1 The number of animals in this study

Experiment aim	Number of animals
1	70
2	70
Total	140

1. The effect of post-ischaemic treatment of recombinant human SLPI treatment on rat hearts subjected to an *in vivo* ischaemia/reperfusion.

To determine the effect of post-ischaemic treatment of recombinant human SLPI treatment on cardiac physiology, functions, and sensitivity to infarction, and intracellular biochemical alterations in rat hearts subjected to an *in vivo* ischaemia/reperfusion Recombinant human SLPI (rhSLPI, Sino Biology Inc., Beijing, China) was diluted in sterile phosphate buffered saline (PBS) and rat was injected through intravenous route with 50 µg of SLPI in 500 µl total solution. The dosage of rhSLPI in this study based on the previous reports in an *in vivo* model (313, 314)

1.1 Experimental group assignment

Schematic diagram of experimental protocol, as shown in . Seventy adults male Wistar rats were used in this study, which were divided into 2 experimental groups. All of animals were performed following experiment protocol that including

- | | |
|----------------|----------|
| 1. Baseline | 30 mins |
| 2. Ligation | 30 mins |
| 3. Reperfusion | 120 mins |

Both of experiments were including 4 animal group which is sham, vehicle, rhSLPI treated at during ligation (rhSLPI-DI) and rhSLPI treated at onset of reperfusion (rhSLPI-OR). Both of treatment group, rhSLPI-DI and rhSLPI-OR, rats were administrated 50 µg rhSLPI at 15 mins of ligation and beginning of reperfusion, respectively. The experiments were including physiological study, forty rats were used (Sham =8, Vehicle = 8, Treatment group =8 x2, 8 rats as spare animals) and biochemical analysis, thirty rat were used (Sham =6, Vehicle = 6, Treatment group =6 x2, 6 rat as spare animals) (Figure 16).

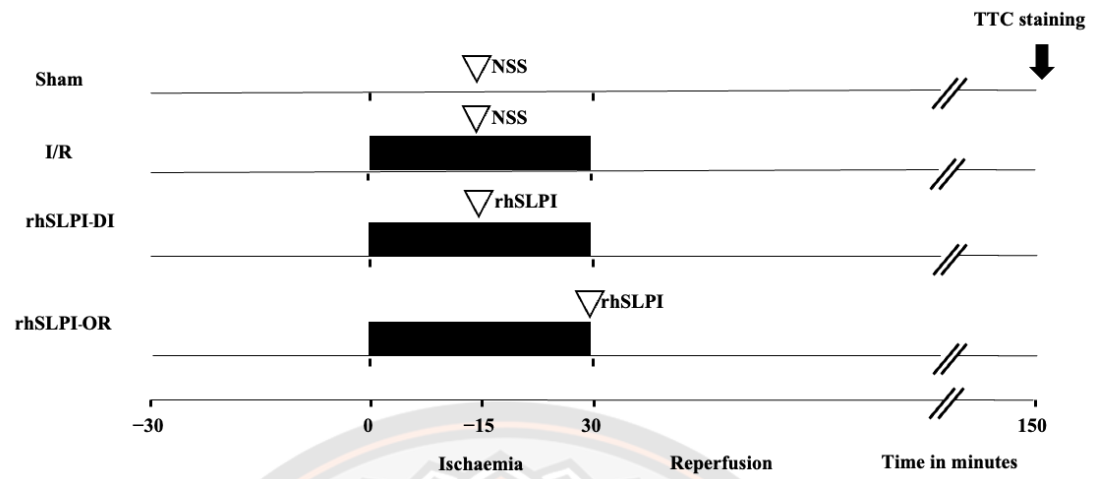
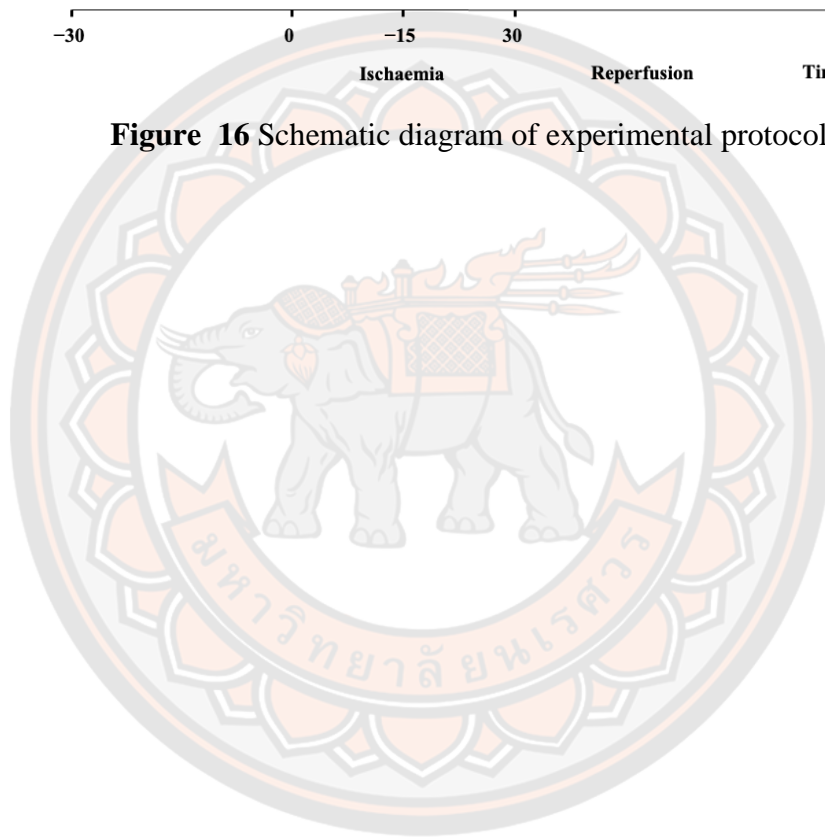


Figure 16 Schematic diagram of experimental protocol



1.2 Surgical preparation of myocardial I/R model in rats

Rats were anesthetized in isoflurane induction chamber followed by tracheotomy for intubation and connected to the rodent ventilator (VentElite, Harvard apparatus, MA, USA). The tidal volume was set at 2.5 mL with a rate of 80 breaths/min. A level of anaesthesia was maintained with isoflurane 1.8-2.0% in 100% oxygen. The body temperature was maintained at 37 °C using warm water heating pump. Lead II electrocardiogram (ECG) was attached to the rat and connected to the ECG amplifier. The carotid artery was cannulated with Mikro-Tip® pressure catheter for rat (Millar, Houston, Texas, USA) for measuring left ventricular pressure (LVP) parameters. The jugular vein was also cannulated fluid-filled catheter for blood collection and rhSLPI administration. Then, left thoracotomy was performed to reveal left coronary artery. A 6-0 synthetic, monofilament, nonabsorbable polypropylene suture was tied around the left anterior descending (LAD) of the left main coronary artery with the PE-50 tube to simulate ischaemic condition. Regional ischaemia was confirmed with an elevation of ST-segment in lead II tracing and faded whitish colour tissue by visual inspection. The ligation was released after 30 min of ischaemia, and the ligation was released by pulling the tube out of the ligation while the suture was remained at the same place. The reperfusion was continued for 120 min. The ECG and LVP were recorded throughout the experiment with an IOX system (IOX 2.10.8.6, EMKA Technologies, Paris, France) and were stored on a hard drive for later analysis with ECG Auto software (ECG Auto 3.5.5.12, EMKA Technologies, Paris, France). The LVP was analysed for end-diastolic pressure (EDP), end-systolic pressure (ESP), develop pressure (devP), and heart rate (HR). The contractility was inferred from the maximum rate of rise of the LVP (dP/dtmax) and contractility index (CI) defined as the dP/dtmax over the pressure at that point. In addition, the lusitropic indices were determined by the maximum rate of fall of the LVP (dP/dtmin) and Tau. At the end of the protocol, the hearts were quickly excised for infarct size assessment.

1.3 Determination of hemodynamic parameters by Mikro-Tip® pressure catheter for rat (Millar, Houston, TX, USA)

After the animal preparation, the pressure-conductance catheter (Millar, Houston, TX, USA) was advanced to record the left ventricular pressure in left ventricle. All hemodynamic parameters were recorded including end-systolic pressure (ESP), end-diastolic pressure (EDP), dP/dt max, contractility index (CI), dP/dt min, Tau/e, develop pressure (devP) and heart rate (HR).

1.4 Determination of the area at risk and infarct size

After the end of the reperfusion protocol, the LAD was re-occluded and 2% (w/v) Evans blue solution (in PBS) was intravenously injected in order to differentiate the area at risk (non-perfused during the coronary occlusion) from the non-ischemic area. At the end of the surgical protocol, the heart was excised, weighed and transversally sliced in 1-mm-thick slices that were subsequently incubated in 1% (w/v) 2,3,5-triphenyl tetrazolium chloride (TTC) at 37 °C for 10 min to define the necrotic myocardium after enhancing the contrast between stained and unstained TTC tissues with a 10% (v/v) formalin (15–20 h) final incubation. The infarct area (TTC-negative) and the non-ischemic area (Evans blue-stained area) were measured by using ImageJ software.

1.5 Determination of Serum Creatine Kinase (MB Isoenzyme) and Lactate Dehydrogenase (LDH) Activity

Serum was collected at the end of the study protocol for determining the level of cardiac biomarkers. The creatine kinase (MB isoenzyme) and lactate dehydrogenase (LDH) activity was analysed by using an automated biochemistry analyser (Cobas c 111 analysers, Roche, Basel, Switzerland).

1.6 Heart tissue homogenization and protein collection

Another set of experiment was performed on another group of rats to assess the biochemical parameters. At the end of the I/R protocol, the heart was rapidly excised, and then the whole ventricular tissue was collected, quickly frozen in liquid nitrogen, and stored at -80°C until analysis. One hundred milligrams of tissue

from each organ were isolated and then homogenised by hand homogeniser on ice. One hundred milligram of heart tissue was homogenized with 1 ml of homogenisation buffer (20 mM Tris HCl pH6.8, 1mM Na₃VO₄, 5 mM NaF and protease inhibitor tables (complete®). Tissue homogenate (100 mg/ml tissue extract) was centrifuged at 14,000 rpm for 10 min at 4°C. The supernatants were collected and frozen for further analysis

1.7 Determination of protein concentration by Bradford assay

Determination of protein concentration was performed by using Bradford reagent (HIMEDIA®). Five microliter of protein extractions were added into 250 µl of Bradford reagent and mixed by pipetting. The reactions were incubated at room temperature for at least 5 min and measured the absorbance at λ595 nm by spectrophotometer. The protein concentration was determined by using bovine serum albumin (BSA) as a standard protein for calculating and normalizing the amount of total protein that used in ELISA method and Western blot analysis at 100 µg and 25 µg, respectively

1.8 Determination of inflammatory cytokines level by Enzyme-linked immunosorbent assay (ELISA)

The ELISA (ABTS ELISA Buffer Kit, Peprotech®) were prepared at room temperature by gentle mixing. Firstly, the 96-well plate was pre-coated by adding 100 µl of 1 µg/ml capture antibody to each well and incubated overnight at room temperature. Next day, the plated was inverted for removing the liquid and blot on the paper towel. After that, the plate was washed with 200 µl washing buffer solution for 4 times. The blocking solution was added into the well for 200 µl and incubated for 1 h. The reactions were washed for 4 times again. One hundred microgram of tissue homogenates were added into the wells and incubated at room temperature for at least 2 h. The plate was washed again and added 100 µl detection antibody and incubated at the room temperature for 2 h. The plate was washed again and 100 µl of Avidin-HRP conjugated 1:2000 was added and incubated at room temperature for 30 min. Then, the plate was washed and 100 µl of ABTS liquid substrate was added into the well and incubate at the room temperature for colour

development. The sample absorbance was measured by spectrophotometer at 405 nm with correction wavelength correction set at 650 nm.

1.9 Spectrophotometric determination of protein carbonyl (PC) content level

Oxidative induction is a key factor leading to cardiac cell death in myocardial ischaemia and ischaemia/reperfusion injury (315), and subsequently resulted in biochemical modifications of some biomolecules such as protein, lipid, and DNA (316). Ischaemia modified albumin (IMA) and Protein Carbonyl (PC) is proteins that are considered as a modified product on the similar basis of oxidative stress induced protein modification and may have diagnostic potential in acute myocardial infarction (316). In this study, the oxidatively modified proteins including IMA and PC were determined in both serum and cardiac tissue homogenate.

Both serum and cardiac tissue protein carbonyl (PC) content level were spectrophotometrically determined by colorimetric DNPH assay, as previously described [24]. Firstly, protein extracts were diluted to 1:10 with phosphate-buffered saline (PBS). Two hundred microliters of diluted protein extractions were added into 800 μ l of 10 mM DNPH in 2.5 M HCl. One millilitre of 20% (w/v) trichloroacetic acid (TCA) was then added and centrifuged at 10,000 \times g for 10 min at 4 °C to precipitate protein. The protein pellet was washed 3 times with 1 ml of 1:1 (v/v) ethanol: ethyl acetate and centrifuged at 10,000 \times g for 10 min at 4 °C. After final washing, the protein pellet was resuspended in 500 μ l of 6 M guanidine hydrochloride and centrifuged at 10,000 \times g for 10 min at 4 °C. The supernatant was collected and measured the absorbance at 370 nm using 6 M guanidine hydrochloride as a blank. The PC content (nmol/mg) was calculated following the procedure used in a previous study (317).

1.10 Spectrophotometric determination of Ischaemic modified albumin (IMA) level

Determination of ischaemic modified albumin was performed by using albumin cobalt binding (ACB) assay, as previously described (317). Two hundred microlitre of serum or cardiac tissue homogenate was added into 50 μ l of 0.1% (w/v) Cobalt chloride and mixed gently. The samples were incubated at room temperature for 10 min for adequate cobalt-albumin binding. Then, fifty microlitre of 1.5 mg/ml dithiothreitol (DTT) was added to colorizing the reaction and incubated at room temperature for 2 min. One millilitre of 0.9% (w/v) Sodium chloride (NaCl) to quench the reaction and absorbance measured at 470 nm. The determination of ischaemic modified albumin was calculated by serum-cobalt blank without DTT as a blank of individual sample.

1.11 Determination of MAPKs phosphorylation and signalling protein involve in apoptosis

Principle of sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE)

Electrophoresis is method for separating protein sample depending on their migration in electrical field. The migration of protein in electrical field is depend on their charge, size, shape and isoelectric point. Normally, protein is formed to be tertiary structure, which has net electrical charge and pH. The protein should be denatured and neutralized by detergent such as sodium dodecyl sulphate (SDS). Then, the neutralized protein was separated by polyacrylamide gel, which depending on only molecular weight. Sodium dodecyl sulphate (SDS), lauryl sulphate, is an anionic detergent, which has a negative charge in a wide pH range when its dissolve in solvent. SDS bind to protein with 1.4g SDS per gram of protein ration for destroying the complex structure of protein. SDS convert the net charge of protein to negative charge in proportion to its length. Polyacrylamide (PAM) is a polymer from polyacrylamide subunit, which usually used in separate biological macromolecules such as protein and nucleic acid. Interestingly, SDS does not interact with proteins that leading to the separation of protein due to the difference of molecular weight.

Western blot analysis is an important technique to detection and analysis of protein. This technique is based on antigen-antibody interaction by specific binding to protein. After protein was separated by SDS-PAGE, the protein should be transfer onto polyvinylidene fluoride developed negative films. Band intensity in difference lane should be compared on relative expression of protein (308).

The heart homogenate was mixed with equal volume of 2X SDS-PAGE sample buffers, containing 10% (v/v) 2-mercaptoethanol and bromophenol blue dye. The sample was boiled for 10 min. A measured 25 µg of protein was loaded into SDS-PAGE polyacrylamide gel electrophoresis gel for separation. Electrophoresis was performed at 120V for 2 h. After separation, proteins were transferred to Immobilon-P membranes (Millipore) using a semi-dry apparatus under an electrical current of 15 mV, for 45 min. Then, membranes were incubated in a 5% (w/v) of dried skimmed milk powder in TBST solution for 1 h with gentle shaking at room temperature. The membranes were incubated with primary antibodies for phosphorylated-Akt (Santa Cruz Biotechnology, Inc., #sc-7985), total-Akt (Santa Cruz Biotechnology, Inc., #sc-8312), phosphorylated p38 (Cell signalling Technology, #9211), total-p38 (Cell signalling Technology, #8690), Bax (Santa Cruz Biotechnology, Inc., #sc-493), Bcl-2 (Santa Cruz Biotechnology, Inc., #sc-492), caspase 3 (Santa Cruz Biotechnology, Inc., #sc-7148) and caspase-8 (Cell signalling Technology, #9476) (All of primary antibodies were diluted at 1:1,000 in 1% (w/v) skimmed milk + TBST buffer) and the horseradish peroxidase-conjugated secondary antibody (goat anti-rabbit (Merck, #AP132P) and rabbit anti-goat (Merck, #AP106P), which was diluted at 1:5,000 in 1% (w/v) skimmed milk + TBST, after the heart protein was separated in SDS-PAGE. The band intensity quantitation was captured and analysed by ChemiDoc XRS+, Image Lab™ 2.0 Software (Bio-Rad Laboratories, Inc.) (318).

2. The effect of antiprotease-deficiency of SLPI on ischaemia/reperfusion injury.

From our previous studies as well as the first part in this dissertation demonstrated the cardioprotection of Secretory Leukocyte Protease Inhibitor (SLPI) against myocardial ischaemia/reperfusion (I/R) injury. Although the beneficial effects of SLPI are believed to be due to the anti-protease activity, few studies show an independent on anti-protease activity of SLPI (319). Furthermore, there are no such evidence confirm that the cardioprotective effects seen from the previous studies is really due to inhibition of the proteases. To answer this research question, the recombinant protein of anti-protease deficient mutant SLPI (L72K, M73G, L74G), which is lack of anti-protease activity, was used to elucidate the cardioprotection in both in vitro of hypoxia/reoxygenation (H/R) and in vivo model of myocardial I/R injury.

2.1 Recombinant protein of anti-protease deficient mutant SLPI

2.1.1 Production of recombinant mutant forms of SLPI (mt-SLPI)

The mutant SLPI plasmid harbouring the substitutions of amino acids that critical for SLPI's antiprotease activity Leu⁷²Lys, Met⁷³Gly, Leu⁷⁴Gly, (L72K, M73G, L74G) was kindly provided by Professor Joanna Cichy, Jagiellonian University, Kraków, Poland. The cDNA encoding mutant SLPI was generated by polymerase chain reaction (PCR), using RNA isolated from human alveolar epithelial cells as a template, and the mutations was generated by site directed mutagenesis. The cDNA containing mutant SLPI from PCR reaction was inserted to pPIC9 expression vector (Life Technologies, Carlsbad, CA, USA) with the addition of a hexahistidine tag and an enterokinase cleavage site to its N terminus (319). The mutant SLPI-pPIC9 was transformed into *Escherichia coli* TOP10. The transformants were screened using colony PCR and corrected plasmid was transformed into *Pichia pastoris* KM71H. Protein expression level was optimized according to manufacturer's instruction (Life Technologies, Carlsbad, CA, USA).

2.1.2 Purification of anti-protease deficient mutant SLPI

A single colony of mt-SLPI was inoculated in Yeast Extract-Peptone-Dextrose (YPD) broth supplemented with 100 µg/mL zeocin and incubated at 30 °C, 250 rpm for overnight. Then, the cell was harvested, re-suspended with Buffered Glycerol Complex Medium (BMGY) broth in a ratio of 1: 10 (v/v) and incubated at 30 °C, 250 rpm. After 16-18 h incubation, the cell was harvested and re-suspended to an OD₆₀₀ of 10 in Buffered Methanol-complex Medium (BMMY) and further incubated at 30 °C, 250 rpm. The final concentration of 1% (v/v) methanol was daily added. After 7 days incubation, the supernatant was collected and loaded onto nickel–nitrilotriacetic acid matrix (Ni²⁺-NTA) affinity chromatography (GE Healthcare, Uppsala, Sweden). The recombinant protein was eluted with stepwise gradient of 50, 100, 150, 250 and 500 mM of imidazole in 50 mM Tris-HCL, pH 8.0 and 300 mM NaCl. The purified protein was confirmed by 10% sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) and Western blot analysis using an anti-His tag antibody.

2.2 Assessment of inhibitory activities of anti-protease deficient mutant by neutrophil elastase activity

The activity of neutrophil elastase (NE) was measured by using neutrophil elastase activity kit was purchased from Abcam (ab204730, Cambridge, UK). The measurement is based on the ability of neutrophil elastase to proteolytically cleave a synthetic substrate in order to release a fluorophore. The neutrophil elastase was preincubated for 10 min with recombinant human SLPI (wild type; wt-SLPI) and anti-protease deficient mutants (mt-SLPI) at 2:1 [SLPI:NE] molar ratio, at 20°C in 0.1 M Tris-HCl (pH 8.0) with 0.5 M NaCl for 1 h. The SLPI-NE mixture and mutant SLPI-NE mixture were added into reaction mix that containing the neutrophil elastase buffer and substrate, while standard NE was used as control. A reaction was incubated at 37 °C for 20 min. Then, the activity was measured with fluorescence microplate reader (EnSpire® Multimode Plate Reader, PerkinElmer, MA, USA) at 380/500 nm (excitation/emission). The activity of neutrophil elastase was expressed as % relative fluorescence units (RFU) of standard NE control and subtract with sample background.

2.3 Cell culture

The rat embryonic cardiomyocyte cell line (H9c2) was purchased from American Type Culture Collection (ATCC, Manassas, VA, USA) as ATCC-CRL1446. Cells were cultured in completed Dulbecco's Modified Eagle Medium (DMEM) supplement with 10% foetal bovine serum and 5000 units/mL of penicillin/streptomycin that were purchased from Gibco (Gibco BRL, Life Technologies, Inc., NY, USA). Cells were maintained in humidified atmosphere 95% air and 5% carbon dioxide at 37 °C.

2.4 An *in vitro* Hypoxia/Reoxygenation induce cardiac cell death

An *in vitro* Hypoxia/Reoxygenation (H/R) protocol was modified from previous study (320). H9c2 cells were seeded into 96 well plated at density of 1.0×10^4 cells/well and left until cell density reached 70–80% confluence under humidified CO₂ incubator. Then, the medium was removed and replaced with 100 µl DMEM without serum and overlaid medium with 200 µL Liquid paraffin. Cells were incubated at 37 °C in a humidified CO₂ incubator for 1 h, then replaced with completed DMEM and incubated for 3 h (reperfusion). After reperfusion, cell viability was determined by MTT assay. The optimized timing was considered as timing that caused 50% cell death, which was used throughout an *in vitro* study.

2.5 Determination of cell viability by MTT assay

MTT(3-[4,5-dimethylthiazol-2-yl]-2,5-diphenyltetrazolium bromide) was purchased from Thermo Fisher scientific. The medium was removed and replaced with 0.5 mg/mL MTT reagent. Cells were incubated with MTT reagent for 4 h in humidified CO₂ incubator. After incubation, the dimethyl sulfoxide (DMSO) was added to solubilize the form-azan crystal. Cell viability was determined using a spectrophotometer at a wavelength of 490 nm, using DMSO as a blank (308).

2.6 Determination of Intracellular reactive oxygen species (ROS)

Production

The determination of intracellular reactive oxygen species (ROS) production was followed by the previous report (22) that using 2',7'-Dichlorofluorescein diacetate (DCFH-DA, Sigma, St. Louis, MO, USA). Briefly, cells were cultured in 96 well plates with DMEM. The culture medium was removed and replaced with 2 μ M DCFH-DA in DMEM without serum in dark room for 24 h at 37 °C. Then, medium was removed and replaced with DMEM without serum and covered with liquid paraffin, which followed by H/R protocol. After incubation, medium was removed and replace with completed DMEM with DCFH-DA and incubated at 37 °C in a humidified CO₂ incubator for 1 h. The intracellular ROS production was measured by using an EnSpire® Multimode Plate Reader (PerkinElmer, MA, USA) with excitation wavelength at 485 nm and emission wavelength at 530 nm.

2.7 Experimental animal ethical approval

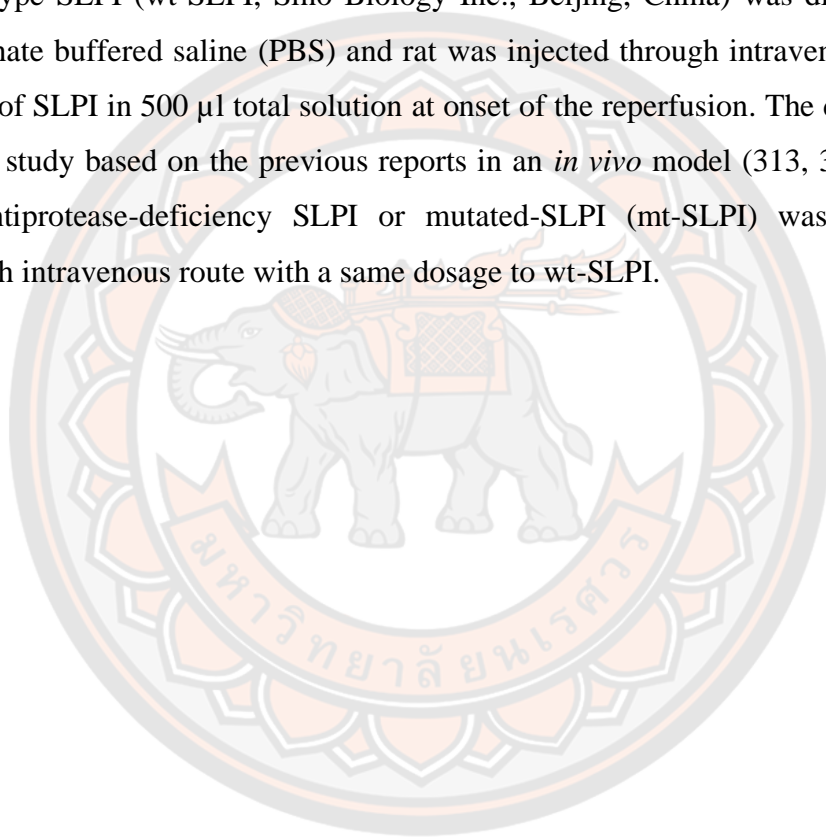
All animal procedures study were performed in accordance with the Guidance on the Operation of the Animals (Scientific Procedures) Act 1986 and the World Health Organization Guidelines for Breeding and Care of Laboratory Animals and approved by the committee of Centre for Animal Research, Naresuan University (NU-AE620615) and Chulalongkorn University Laboratory Animal Centre (CULAC), Protocol No.1973025. All surgery was performed under isoflurane combined with oxygen and all effort were made to minimize pain, suffering, and distress of the animals involved.

A total of 70 adults male Wistar rats (8 weeks old, 200-250 g) were purchased from Nomura Siam International, Bangkok, Thailand, which used for 14 rats in each group. These was divided into 2 subgroups including 8 for infarct size determination and cardiac function, and 6 for biochemical analysis and 14 for spare). Animals were maintained in an environmentally control condition (22°C \pm 1°C, 12:12 h light: dark cycle) at the Chulalongkorn University Laboratory Animal Centre (CULAC), Bangkok, Thailand.

2.8 Experimental group assignment

Schematic diagram of experimental protocol, as shown in Figure 17. seventy adults male Wistar rats were used in this study, which divided into 2 experimental groups.

For physiological study, forty rats were used (Sham =8, Vehicle = 8, Treatment group =8 x2, 8 rats as spare animals). For biochemical analysis, thirty rat were used (Sham =6, Vehicle = 6, Treatment group =6 x2, 6 rat as spare animals). Wild-type SLPI (wt-SLPI, Sino Biology Inc., Beijing, China) was diluted in sterile phosphate buffered saline (PBS) and rat was injected through intravenous route with 50 µg of SLPI in 500 µl total solution at onset of the reperfusion. The dosage of SLPI in this study based on the previous reports in an *in vivo* model (313, 314). Similarly, the antiprotease-deficiency SLPI or mutated-SLPI (mt-SLPI) was administrated through intravenous route with a same dosage to wt-SLPI.



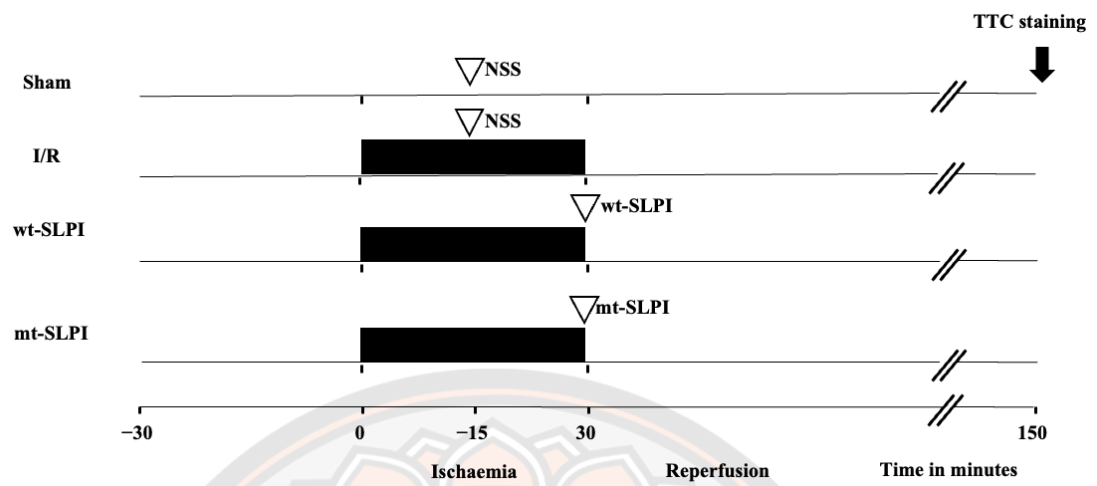
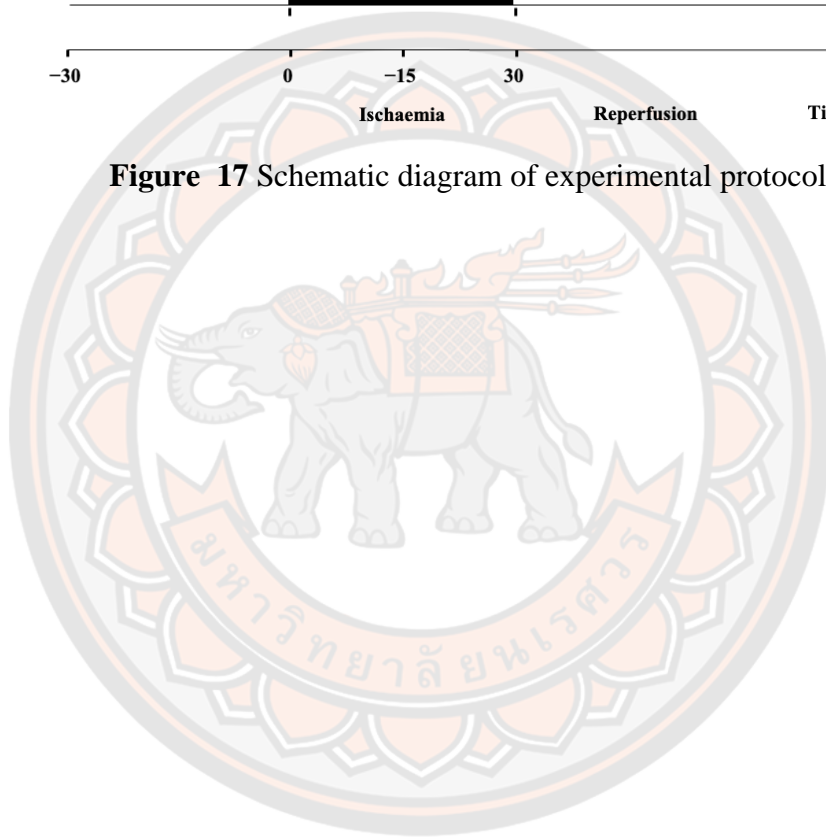


Figure 17 Schematic diagram of experimental protocol



2.9 Surgical preparation of myocardial I/R model in rats

The surgical procedure in this study was performed as described previously (308). Isoflurane induction chamber was used for anesthetized and followed by tracheotomy for intubation and connected to the rodent ventilator (VentElite, Harvard apparatus, MA, USA). The tidal volume was set at 2.5 mL with respiratory rate of 80 breaths/min and maintained with 1.8-2.0% isoflurane in 100% oxygen. The body temperature was maintained with warm water heating pump at 37°C throughout the surgery. Moreover, lead II electrocardiogram (ECG) was monitored by attached to the rat's chest. The carotid artery was cannulated with Mikro-Tip® pressure catheter for rat (Millar, Houston, Texas, USA) for measuring left ventricular pressure (LVP) parameters. Blood samples were collected from fluid-filled catheter that cannulated at jugular vein. In addition, jugular vein cannulation was also used for administering the wt-SLPI and mt-SLPI. Then, left coronary artery was approached through left thoracotomy. Left anterior descending coronary artery (LAD) was tied with 6-0 synthetic, monofilament, nonabsorbable polypropylene suture over the PE-50 tube to simulate ischaemia. After ligation, an ischaemic condition was confirmed with an elevation of ST-segment in Lead II tracing of ECG and visual inspection as faded whitish colour of the epicardium below the ligation. The ligation was released after 30 min of occlusion by pulling the PE-50 out from the ligation while the suture was remained at the same place. The reperfusion was continued until 120 min after the beginning of reperfusion. The LVP was analysed for end-diastolic pressure (EDP), end-systolic pressure (ESP), develop pressure (devP), and heart rate (HR). The contractility was inferred from the maximum rate of rise of the LVP (dP/dt_{max}) and the contractility index (CI) defined as the dP/dt_{max} over the pressure at that point. In addition, the relaxation indices were determined by the maximum rate of fall of the LVP (dP/dt_{min}) and Tau. At the end of reperfusion period, the heart was quickly harvested and performed infarct size and area at risk experiments.

2.10 Evaluation of infarct size and area at risk

The evaluation of infarction and area at risk was performed at the end of surgery reperfusion period by re-occlusion the LAD as described previously (308). The area at risk (non-perfusion area during LAD ligation) was differentiated from non-infarction area by using 2%(w/v) Evans blue solution in PBS that injected via intravenous. Then, heart weight was measured and performed transversely heart slice section to 1 mm-thickness. The heart sections were incubated in 1% (w/v) of 2,3,5-triphenyl tetrazolium chloride (TTC) at 37 °C for 10 min for indicating necrotic myocardium. The sections were enhanced the contrast of tissues section by incubated in 10% (v/v) formalin for 15-20 h. The non-ischaemic area (Evans blue stained area) and infarct area (TTC negative) were blindly groups data and evaluated by using ImageJ software.

2.11 Determination of serum creatine kinase (MB isoenzyme) and lactate dehydrogenase (LDH) activity

At the end of the animal protocol, blood collection was performed and spined down for collecting the blood serum. The levels of biomarkers including creatine kinase (MB isoenzyme) and lactate dehydrogenase (LDH) activity was evaluated and analysed by automate biochemistry analyser (Cobas c 111 analysers, Roche)

2.12 Tissue Homogenate and protein collection

Another set of experimental animals (n = 6 for each group) was subjected to I/R injury, similar to the procedure of the experiment for infarct size determination and cardiac function, and animals were treated wt-SLPI or mt-SLPI. After the surgery, the heart was excised immediately at the end of experiment. The ventricle part was collected and quickly frozen in liquid nitrogen and -80 °C until performed next experiment. One hundred milligrams of ventricle tissue were homogenized in 1 mL of homogenization buffer (20 mM Tris HCl pH 6.8, 1 mM Na₃VO₄, 5 mM NaF and cOmplete™ Protease Inhibitor Cocktail (Merck Millipore, USA)). The tissues were gently homogenized by using hand homogenizer on ice.

Tissue homogenate was then collected and centrifuged at 14000 rpm for 10 min at 4 °C. The supernatant was collected and frozen for further experiment.

2.13 Determination of protein concentration by Bradford assay

Protein concentration was measured by using Bradford reagent (HIMEDIA[®], India). Five microliter of protein extract was mixed with 250 µL of Bradford reagent, which then incubated at room temperature for 5 min and measured at the absorbance at λ 595 nm by spectrophotometer. Protein concentration was calculated and normalized by standard curve that created from bovine serum albumin (BSA). The protein concentration was used for fixing the amount of total protein to 100 µg and 25 µg that using in ELISA and Western blot analysis, respectively.

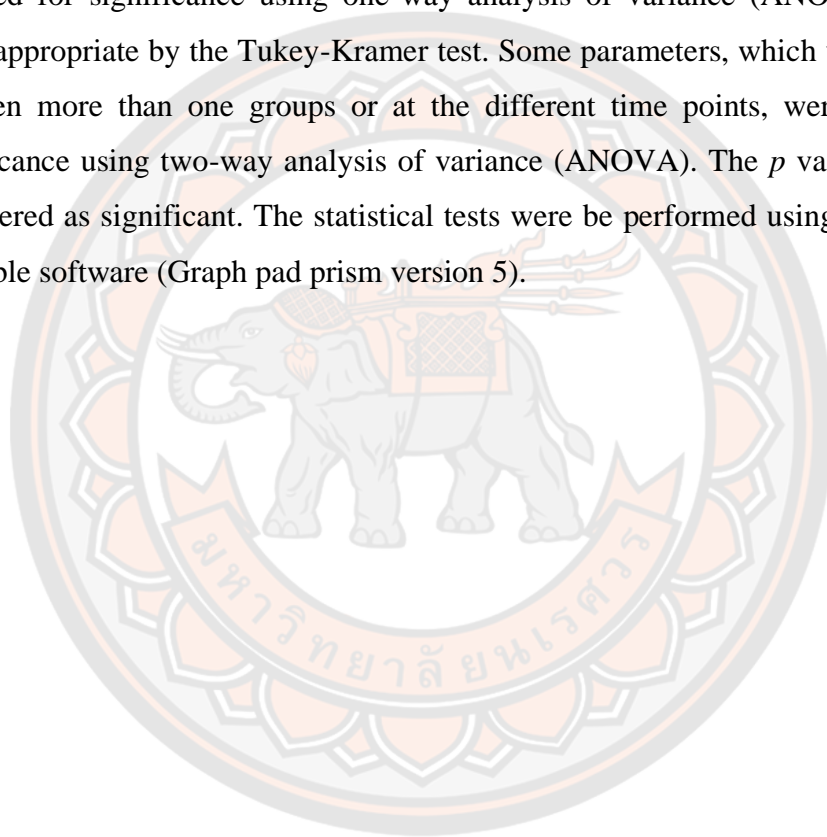
2.14 Western blot analysis

The heart homogenates were mixed with an equal volume of 2×SDS-PAGE sample buffers, containing 10% (v/v) 2-mercaptoethanol and bromophenol blue dye. Then, the samples were boiled for 10 min. Heart homogenate protein was separated on 10 or 12% SDS-polyacrylamide gels and transferred into Immobilon-P membranes (Millipore). Membranes were incubated in 5% (w/v) dried skimmed milk powder in Tris-buffered saline (pH 7.4) containing 0.1% Triton X-100 (TBST) buffer for 1 h at room temperature. After that, membrane were probed overnight at 4 °C with the appropriate primary antibody as follows: phosphorylated p38 (Cell signalling Technology, Danvers, MA, USA, #9211), total-p38 (Cell signalling Technology, Danvers, MA, USA, #8690), Bax (Santa Cruz Biotechnology, Inc., Dallas, TX, USA, #sc-493), cleaved-caspase 3 (Cell signalling Technology, Danvers, MA, USA, #9661) and caspase-8 (Cell signalling Technology, Danvers, MA, USA, #4790), Actin (Cell signalling Technology, Danvers, MA, USA, #4967) (all of the primary antibodies were diluted at 1:1000 in 1% (w/v) skimmed milk + TBST buffer). Then, the membranes were washed and exposed for 1 h at room temperature to horseradish peroxidase-conjugated secondary antibody (goat anti-rabbit (Merck, Darmstadt, Germany, #AP132P) at 1:5000 in 1% (w/v) skimmed milk in TBST buffer. The signal was developed by exposure the membranes with Affinity[®] ECL Western Blot Kit, picogram Grade (Affinity Biosciences, Melbourne,

Australia). The band intensity quantitation was captured and analysed by using ImageQuant™ LAS 500 (GE Healthcare, Chicago, IL, USA).

Data analysis

All experiments were performed in triplicate. Data was processed using SPSS (Statistical Package for Social Sciences) release 13.0 for Windows and reported as mean \pm standard error (SEM). All comparisons involving more than one group was assessed for significance using one-way analysis of variance (ANOVA), followed when appropriate by the Tukey-Kramer test. Some parameters, which were compared between more than one groups or at the different time points, were assessed for significance using two-way analysis of variance (ANOVA). The p value < 0.05 was considered as significant. The statistical tests were performed using commercially available software (Graph pad prism version 5).



CHAPTER IV

RESULTS

The results in this study were divided into 2 parts including

- 1) The determination of post-ischæmic treatment of recombinant human SLPI treatment on rat hearts subjected to an *in vivo* ischaemia/reperfusion.
- 2) The effect of antiprotease-deficiency of SLPI on ischaemia/reperfusion injury.

Part 1: Determination of post-ischæmic treatment of recombinant human SLPI treatment on rat hearts subjected to an *in vivo* ischaemia/reperfusion.

1.1 The Animal Body Weight and Heart Weight of Experimental Animals

The animal body weight was measured before the surgery and heart weight was measured after the end of surgical procedures. The results showed that the body weight of all groups was not significantly different (355.1 ± 8.21 g, 346.2 ± 5.77 g, 362.6 ± 8.544 g and 374.1 ± 10.31 g, $p > 0.05$) (Figure 18A) Similarly, the heart weight of rats in all groups was also not significantly different (0.893 ± 0.03 g, 0.886 ± 0.05 g, 0.960 ± 0.04 g and 0.9335 ± 0.03 g, $p > 0.05$) (Figure 18B). Therefore, the calculated heart weight and body weight ratio (HW/BW) also showed no significant difference in every group (0.0026 ± 0.0006 , 0.0027 ± 0.0009 vs. 0.0026 ± 0.0001 and 0.0025 ± 0.0005 , $p > 0.05$) (Figure 18C).

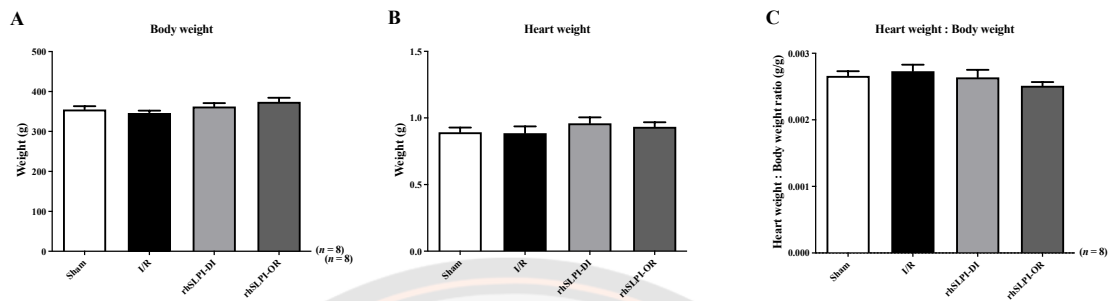
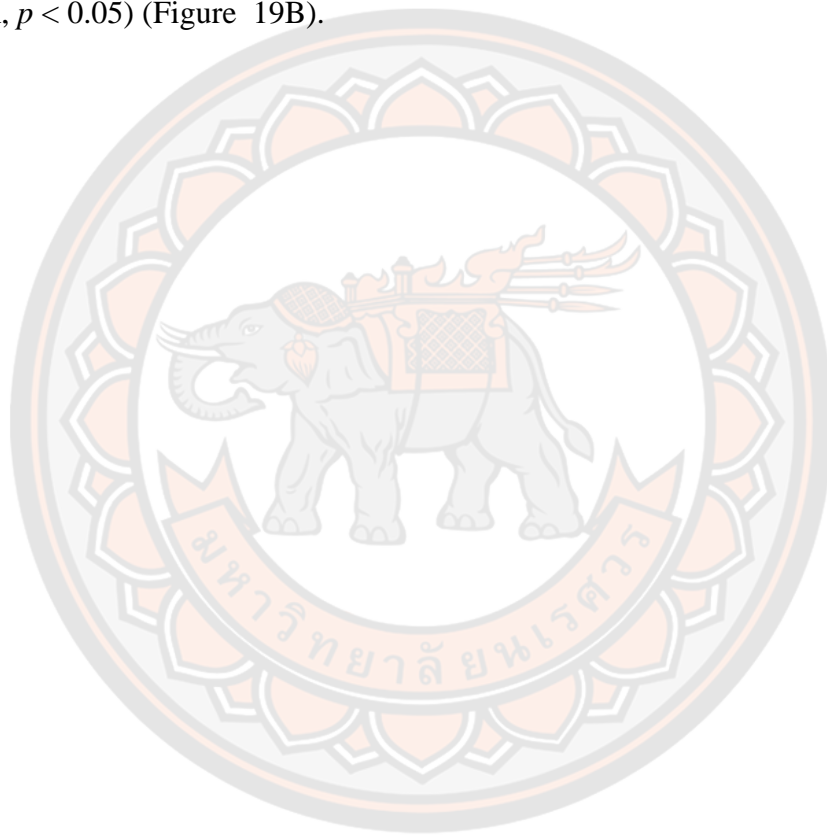


Figure 18 Determination of body weight of experimental animal before performing the surgical procedure of myocardial I/R injury (A), heart weight harvested at the end of the surgery (B) and heart weight to body weight ratio in rats of the study cohort (C).

1.2 Effect of Post-Ischemic rhSLPI Treatment on Infarct Size

First, we confirmed by evaluating the area at risk (AAR) that there was no difference in the I/R injury induced in all rats. Indeed, AAR was 49.38 ± 1.72 , 47.64 ± 3.85 and 46.89 ± 5.93 in I/R, rhSLPI-DI and rhSLPI-OR, respectively (Figure 19A). The results in Figure 20B showed that infarct size (% infarct/AAR) in rats treated by rhSLPI was significantly lower than that of the non-treated I/R group ($34.53 \pm 2.61\%$ for rhSLPI-DI and $31.75 \pm 4.64\%$ for rhSLPI-OR vs. $47.32 \pm 3.83\%$ for I/R, $p < 0.05$) (Figure 19B).



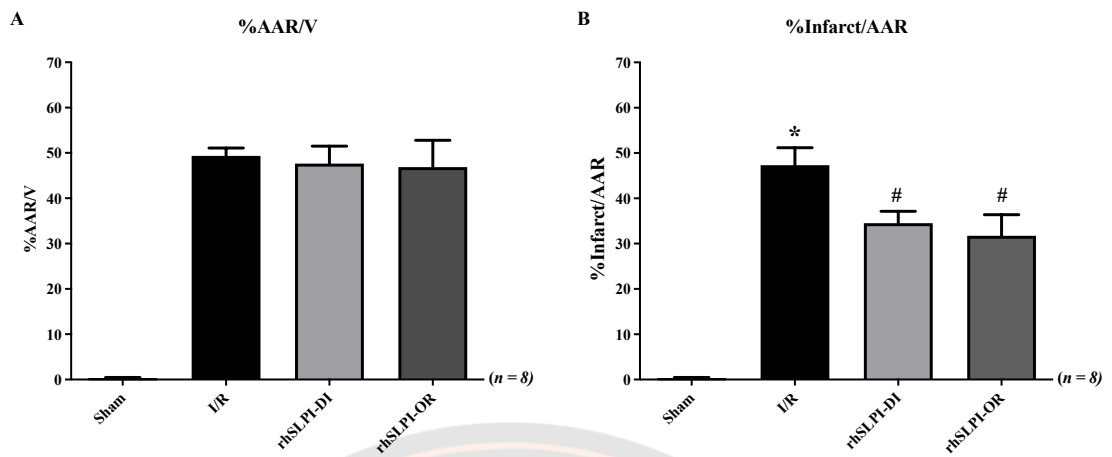


Figure 19 Determination of the percentage of area at risk (AAR) to ventricle volume (V) (A), percentage of infarct size to area at risk (B), (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R)

1.3 Effect of Post-Ischemic rhSLPI Treatment on Cardiac Biomarkers

Serum cardiac biomarkers were assessed by measuring both LDH and CK-MB activity.

The results showed that the LDH activity of the I/R group was significantly higher than that of the sham group (664.9 ± 118.9 vs. 218.4 ± 40.79 unit per litter (U/L), $p < 0.05$) (Figure 20A). Treatment with rhSLPI significantly reduced serum LDH activity in both the rhSLPI-DI group and the rhSLPI-OR group compared to that of the I/R group (363.0 ± 79.91 U/L, 299.8 ± 150.2 U/L vs. 664.9 ± 118.9 U/L, $p < 0.05$) (Figure 20A).

Similarly, for CK-MB activity, values obtained for the I/R group were significantly higher than those of the sham group (203 ± 13.43 U/L vs. 14.8 ± 11.20 U/L, $p < 0.05$) (Figure 20B). Treatment with rhSLPI significantly reduced serum CK-MB activity in both treated groups vs. the I/R group (141.0 ± 5.27 U/L and 138.8 ± 10.08 U/L vs. 203.8 ± 13.41 U/L, $p < 0.05$) (Figure 20B).

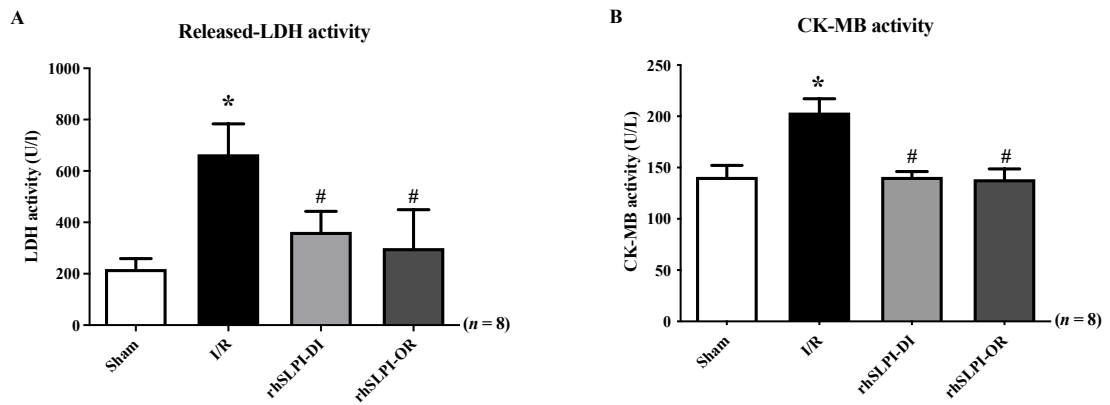
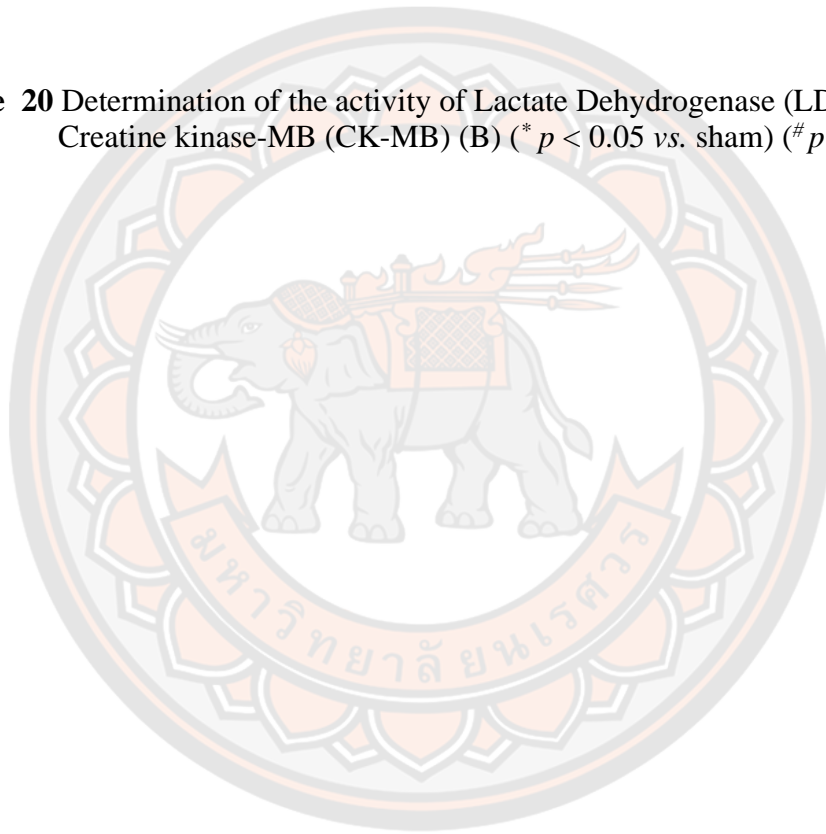


Figure 20 Determination of the activity of Lactate Dehydrogenase (LDH) (A) and Creatine kinase-MB (CK-MB) (B) (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R)



1.4 Effect of rhSLPI Treatment on LVP in I/R Rat

The LVP of the I/R rat was evaluated by using high-fidelity micromanometer catheters placed inside the left ventricular chamber. The results were divided into three phases including at baseline (after stabilization for 30 min prior to LAD ligation), ischemia (30 min after LAD ligation) and reperfusion (at 120 min after reperfusion). At the baseline phase, all of the LVP parameters including the EDP, ESP, dP/dt_{max} , $Ctrl$, dP/dt_{min} , Tau/e , $devP$ and HR were not significantly different when compared among groups (Table 2) The LVP parameters of the ischemic phase (30 min after LAD ligation) are shown in Table 3. The result shows that ischemia induced a reduction in ESP, dP/dt_{max} and $devP$ and an increase in EDP, dp/dt_{min} and Tau/e . Treatment with rhSLPI during ischemia significantly reduced EDP, dp/dt_{min} and Tau/e and increased ESP, dP/dt_{max} and $devP$. The LVP parameters in the reperfusion phase (at 120 min after reperfusion) are shown in Table 4. The result shows ischemia induced a reduction in ESP, dP/dt_{max} and $devP$ and an increase in EDP, dp/dt_{min} and Tau/e . Treatment with rhSLPI both during ischemia and at the onset of reperfusion significantly reduced EDP, dp/dt_{min} and Tau/e and increased ESP, dP/dt_{max} and $devP$.

Table 2 The baseline parameters of left ventricular pressure (LVP) determined the effect of rhSLPI on the LVP parameters in *IR* (baseline).

Parameters	Group			
	Sham (<i>n</i> = 8)	<i>IR</i> (<i>n</i> = 8)	rhSLPI-DI (<i>n</i> = 8)	rhSLPI-OR (<i>n</i> = 8)
EDP (mmHg)	4.87 ± 0.53	4.23 ± 0.16	4.43 ± 0.53	4.75 ± 0.29
ESP (mmHg)	113.8 ± 6.34	104.80 ± 9.31	119.2 ± 15.30	118.9 ± 17.25
dp/dt _{max} (mmHg/s)	5233 ± 359.2	5071 ± 391.1	6113 ± 575.4	5470 ± 287.1
Ctrl	100.5 ± 2.02	106.9 ± 5.59	99.73 ± 7.59	100.4 ± 6.0
dp/dt _{min} (mmHg/s)	-4989 ± 383.2	-4526 ± 487.1	-5627 ± 831.8	-5116 ± 362.6
Tau/e (ms)	10.18 ± 0.21	11.03 ± 0.43	9.67 ± 0.83	9.34 ± 0.73
devP (mmHg)	109.4 ± 5.40	108.1 ± 9.85	115.8 ± 16.75	109.8 ± 12.96
HR (bpm)	431.5 ± 18.09	426.9 ± 20.09	416.4 ± 10.04	437.8 ± 13.66

**p* < 0.05 vs. sham, # *p* < 0.05 vs. *IR*

Table 3 The parameters of left ventricular pressure of ischemic phase determined the effect of rhSLPI on LVP parameters in MI (30 min after ligation).

Parameters	Group		
	Sham (n = 8)	I/R (n = 8)	rhSLPI DI (n = 8)
EDP (mmHg)	5.36 ± 0.40	8.63 ± 1.55 *	3.65 ± 0.46 #
ESP (mmHg)	111.8 ± 10.1	81.81 ± 9.69 *	131.2 ± 9.08 #
dp/dt _{max} (mmHg/s)	5072 ± 725.1	3547 ± 415.7 *	5983 ± 373.3 #
Ctrl	97.63 ± 5.21	101.5 ± 6.60	100.6 ± 2.55
dp/dt _{min} (mmHg/s)	-4185 ± 206.6	-3139 ± 93.69 *	-5646 ± 701.1 #
Tau/e (ms)	10.11 ± 0.46	12.38 ± 1.05 *	10.04 ± 0.37 #
devP (mmHg)	106.9 ± 9.78	83.47 ± 7.72 *	126.7 ± 12.82 #
HR (bpm)	429.3 ± 19.13	405.3 ± 24.52	390.1 ± 15.31
			rhSLPI-OR (n = 8)
			7.29 ± 0.18
			101.8 ± 17.0
			4520 ± 541.0
			80.88 ± 21.69
			-4565 ± 590.5
			8.744 ± 0.22
			105.5 ± 8.85
			421.2 ± 12.75

* $p < 0.05$ vs. sham, # $p < 0.05$ vs. I/R.

Table 4 The parameters of left ventricular pressure of reperfusion phase determined the rhSLPI effect on LVP parameters in MI (120 min after reperfusion).

Parameters	Group			
	Sham (n = 8)	I/R (n = 8)	rhSLPI-DI (n = 8)	rhSLPI-OR (n = 8)
EDP (mmHg)	5.85 ± 0.60	7.63 ± 0.08 *	2.871 ± 0.19 #	4.084 ± 0.60 #
ESP (mmHg)	105.6 ± 6.65	82.74 ± 6.63 *	111.1 ± 10.01 #	94.47 ± 8.80 #
dp/dt _{max} (mmHg/s)	4509 ± 527.4	2836 ± 373.4 *	4739 ± 466.8 #	4458 ± 376 #
Ctrl	91.27 ± 5.79	94.41 ± 9.65	90.42 ± 2.79	72.85 ± 20.30
dp/dt _{min} (mmHg/s)	-4890 ± 569.3	-2418 ± 669.7 *	-4127 ± 244.6 #	-3990 ± 264.3 #
Tau/e (ms)	11.24 ± 0.53	14.83 ± 3.58	9.73 ± 0.54	8.754 ± 1.37
devP (mmHg)	104.4 ± 7.40	80.96 ± 7.25	96.28 ± 4.08	95.51 ± 6.61
HR (Bpm)	408.5 ± 20.81	373.9 ± 42.74	402.7 ± 6.47	410.3 ± 10.92

* $p < 0.05$ vs. sham, # $p < 0.05$ vs. I/R.

1.5 Effect of Post-Ischemic rhSLPI Treatment on Inflammatory Cytokines Level

Excessive inflammation has been described as one of the pathophysiological mechanisms that occurs in myocardial I/R injury and plays a key role in inducing cell death. In this study, the cardiac inflammatory cytokines level including IL-1 β , IL-6 and TNF- α was measured by ELISA. The results show that there was a marked increase in the cardiac IL-1 β level in the I/R group vs. the sham group (309.3 ± 32.45 ng/mL vs. 221.4 ± 16.91 ng/mL, $p < 0.05$) (Figure 21A). The rhSLPI treatment at reperfusion was able to drastically decrease the IL-1 β level while rhSLPI treatment during ischemia was not. There was no difference in the I/R group vs. sham for the cardiac levels of IL-6 and TNF- α (IL-6: 332.1 ± 16.72 ng/mL vs. 328.9 ± 11.45 ng/mL, and TNF- α : 256.7 ± 18.68 ng/mL vs. 229.9 ± 5.02 ng/mL, $p < 0.05$) (Figure 21B,C). However, post-ischemic treatments with rhSLPI significantly reduced the cardiac IL-6 level when compared to the I/R group (267.3 ± 18.34 ng/mL vs. 332.1 ± 16.73 ng/mL, $p < 0.05$) (Figure 21B). Interestingly, the results show that cardiac IL-1 β , IL-6 and TNF- α levels in the rhSLPI-OR group were significantly lower than the I/R group (Figure 21A-C).

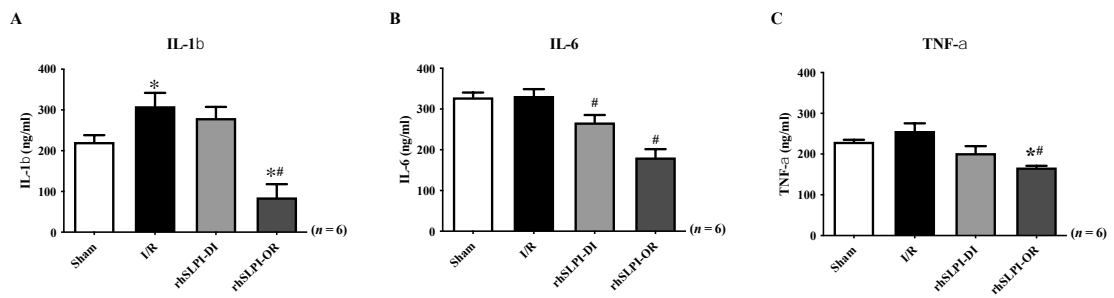
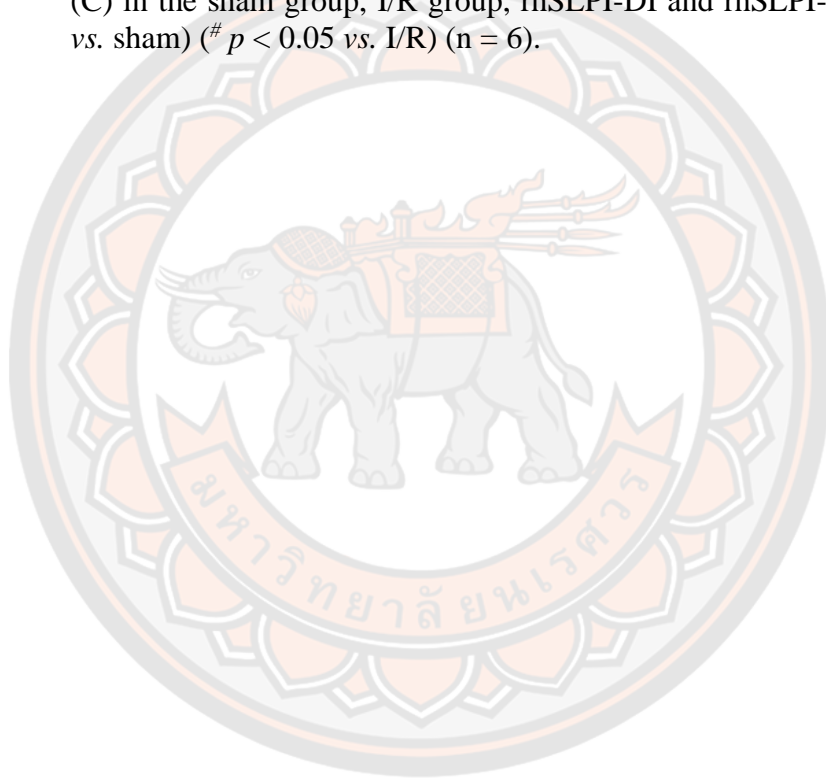


Figure 21 Determination of effect of post-ischaeamic treatment of rhSLPI on cardiac inflammatory cytokines level including IL-1 β (A), IL-6 (B) and TNF- α (C) in the sham group, I/R group, rhSLPI-DI and rhSLPI-OR (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R) (n = 6).



1.6 Effect of Post-Ischemic rhSLPI Treatment on Oxidatively cardiac and serum protein carbonylation level

The result shows that cardiac PC content levels in the I/R group were significantly higher than those of the sham group (cardiac PC: 70.75 ± 2.40 nmol/mg vs. 43.70 ± 0.78 nmol/mg, and serum PC: 3.66 ± 0.15 vs. 2.95 ± 0.31 , $p < 0.05$) (Figure 22A,B). Treatment with rhSLPI in rhSLPI at reperfusion was significantly lower than that of the I/R group (49.08 ± 75.70 nmol/mg vs. 70.75 ± 2.40 nmol/mg, $p < 0.05$) (Figure 22A). In addition, the result shows that the serum PC content level in rhSLPI-DI and rhSLPI-OR was significantly lower than that of the I/R group (3.25 ± 0.04 nmol/mg and 3.04 ± 0.11 nmol/mg vs. 3.66 ± 0.15 nmol/mg, $p < 0.05$)

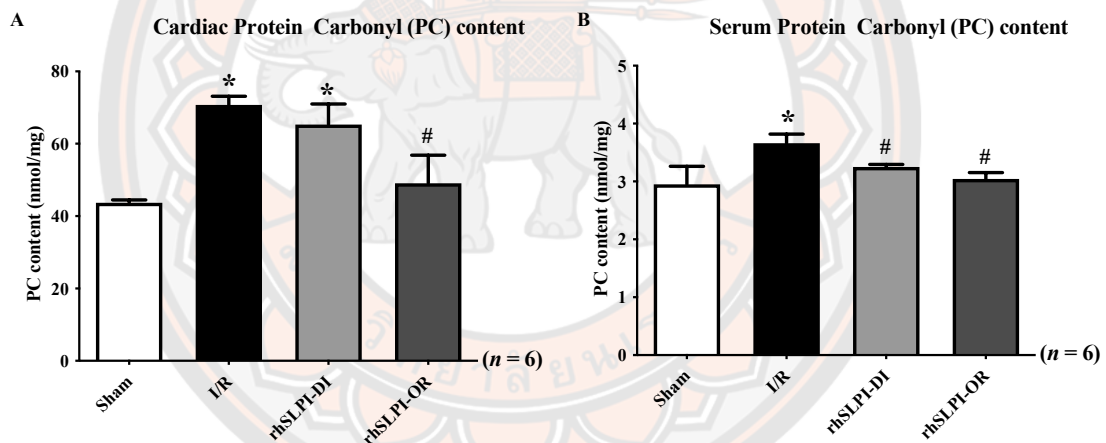
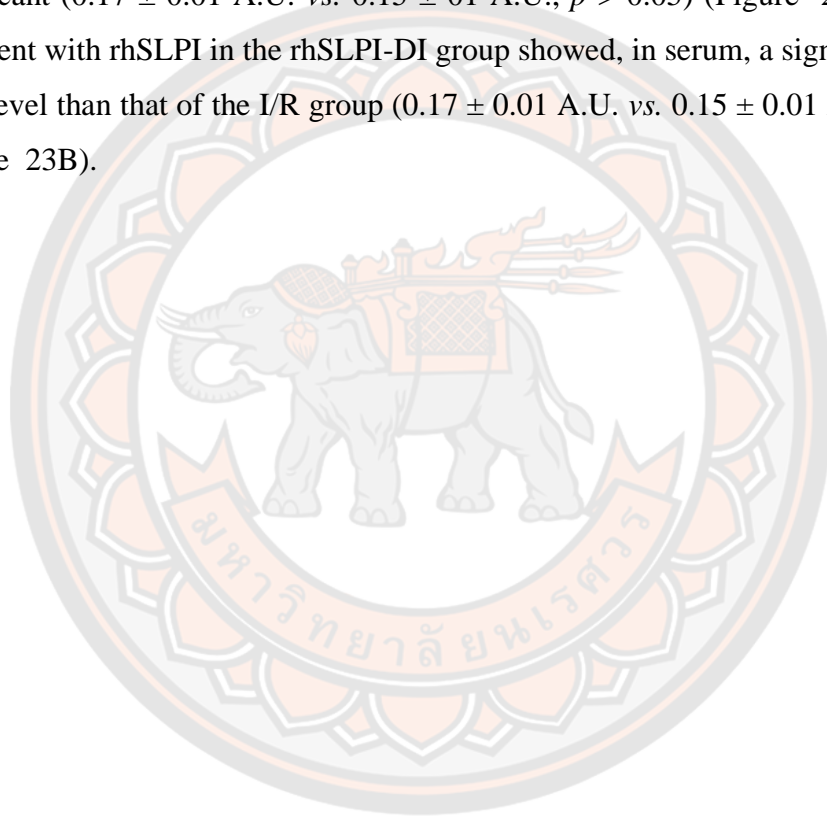


Figure 22 Determination of cardiac(A) and serum(B) protein carbonylation after treated with rhSLPI-DI and rhSLPI-OR (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R) (n = 6).

1.7 Effect of Post-Ischemic rhSLPI Treatment on Oxidatively cardiac and serum ischaemic modified albumin (IMA) level

In addition, the results show that the cardiac IMA level in I/R, rhSLPI DI and rhSLPI-OR groups was significantly higher than that of the sham group (0.24 ± 0.04 , 0.24 ± 0.03 and 0.24 ± 0.03 arbitrary unit (A.U.) vs. 0.16 ± 0.01 A.U., $p < 0.05$) (Figure 23A). However, the serum IMA level of the I/R group showed a trend to be greater than the sham group, but this was not statistically significant (0.17 ± 0.01 A.U. vs. 0.15 ± 0.01 A.U., $p > 0.05$) (Figure 23B); however, treatment with rhSLPI in the rhSLPI-DI group showed, in serum, a significantly lower IMA level than that of the I/R group (0.17 ± 0.01 A.U. vs. 0.15 ± 0.01 A.U., $p < 0.05$) (Figure 23B).



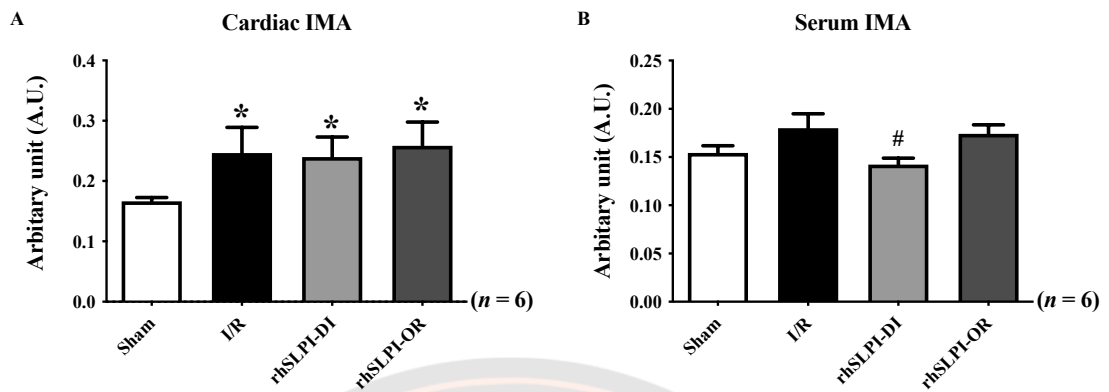


Figure 23 Determination of cardiac (A) and serum (B) ischaemic modified albumin level after treated with rhSLPI-DI and rhSLPI-OR (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R) ($n = 6$)

1.8 Effect of Post-Ischemic rhSLPI Treatment on Signal Transduction Molecules

To determine the effect of rhSLPI in signal transduction on the organ level response to myocardial ischemia/reperfusion injury, Western blot analysis was performed on the heart homogenate protein. The results show that there was a significant activation of p38 MAPK and JNK phosphorylation in the I/R group, when compared to the sham group (p38 MAPK: 1.07 ± 0.18 vs. 0.50 ± 0.07 , and JNK: 0.23 ± 0.012 vs. 0.14 ± 0.01 , $p < 0.05$) (Figure 24A-C). Similarly, ERK and Akt phosphorylation was significantly lower in the I/R group, when compared to the sham group (ERK: 0.26 ± 0.04 vs. 0.39 ± 0.03 , and Akt: 0.41 ± 0.07 vs. 0.74 ± 0.15 , $p < 0.05$) (Figure 24A,D,E). In post-ischemic rhSLPI treatment groups, showed that rhSLPI could significantly reduce p38 MAPK activation (0.57 ± 0.06 and 0.49 ± 0.09 vs. 1.07 ± 0.18 , $p < 0.05$) (Figure 24B). In contrast, rhSLPI could enhance JNK, ERK and Akt phosphorylation when compared with the I/R group (0.28 ± 0.01 vs. 0.23 ± 0.01 , 0.54 ± 0.09 vs. 0.26 ± 0.04 and 0.77 ± 0.06 vs. 0.41 ± 0.07 , $p < 0.05$).

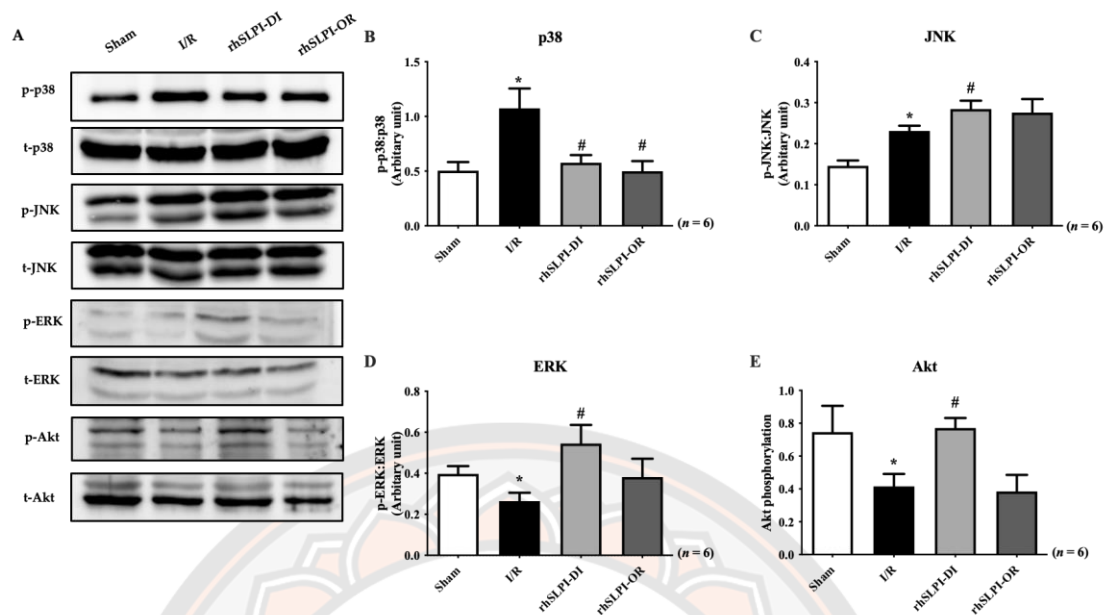
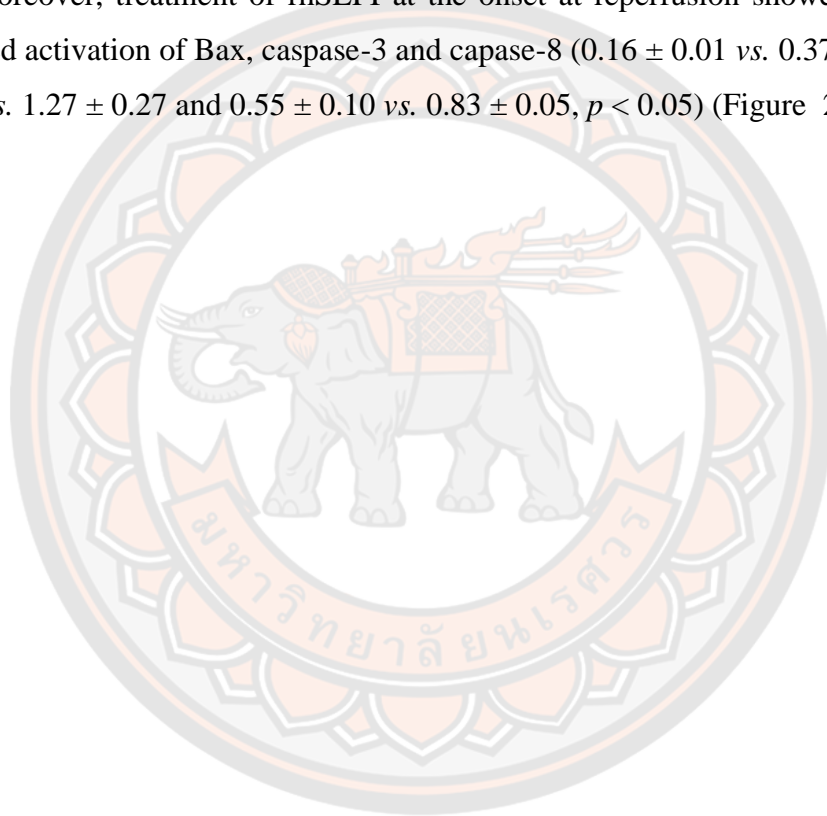


Figure 24 Determination of rhSLPI on activation of MAPK kinase involved in cell injury and survival in MI rat by Western blot analysis (A). The quantitative analysis for the MAPK phosphorylation was presented for p38 (B), JNK (C), ERK (D) and Akt (E). (* $p < 0.05$ vs. sham). (# $p < 0.05$ vs. I/R) (n = 6)

1.9 Effect of Post-Ischemic rhSLPI Treatment on Apoptosis Regulatory Molecules

To determine the effect of rhSLPI on apoptosis regulatory molecules on the organ level response to myocardial ischemia/reperfusion injury, the results show that there was a significant increase in Bax, caspase-3 and caspase-8 levels of the I/R group, when compared to the sham group (Bax 0.37 ± 0.03 vs. 0.11 ± 0.02 , caspase-3 1.27 ± 0.27 vs. 0.45 ± 0.08 and caspase-8 0.83 ± 0.05 vs. 0.36 ± 0.04 , $p < 0.05$) (Figure 25A-D). Moreover, treatment of rhSLPI at the onset at reperfusion showed significantly reduced activation of Bax, caspase-3 and caspase-8 (0.16 ± 0.01 vs. 0.37 ± 0.03 , 0.35 ± 0.04 vs. 1.27 ± 0.27 and 0.55 ± 0.10 vs. 0.83 ± 0.05 , $p < 0.05$) (Figure 25B-D).



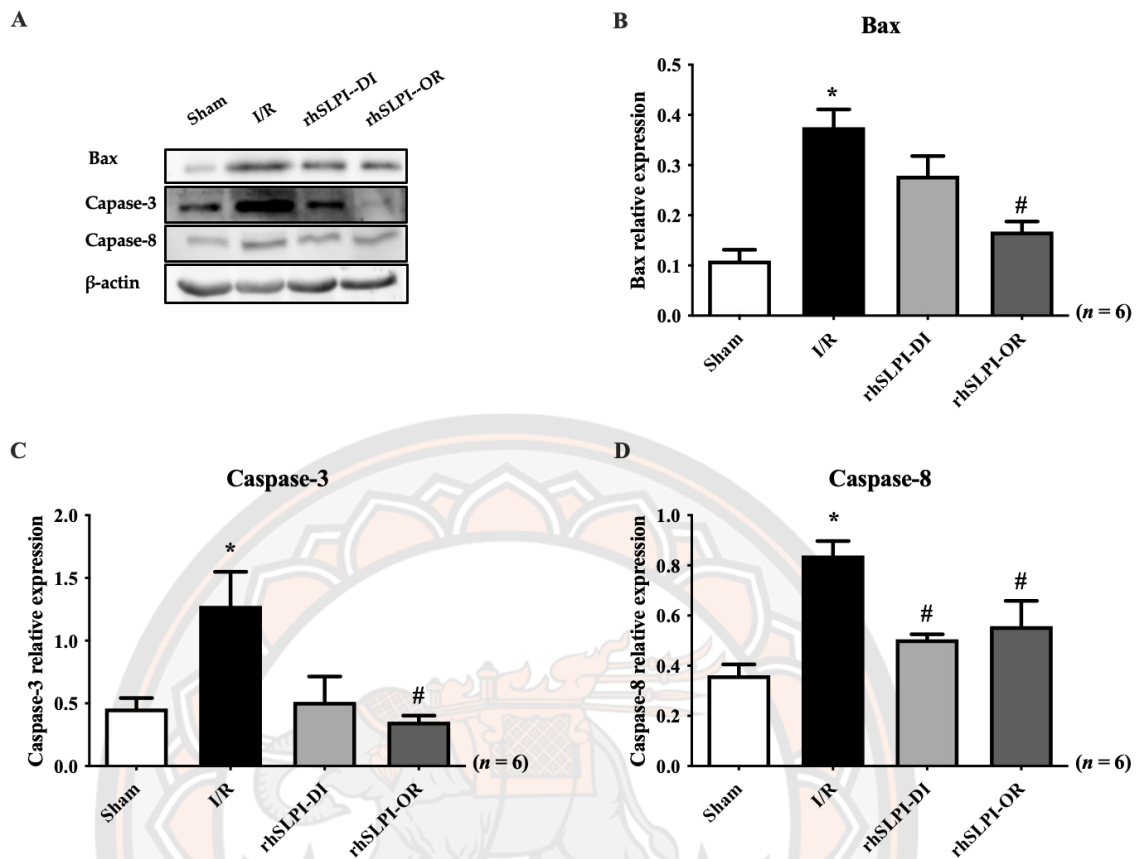
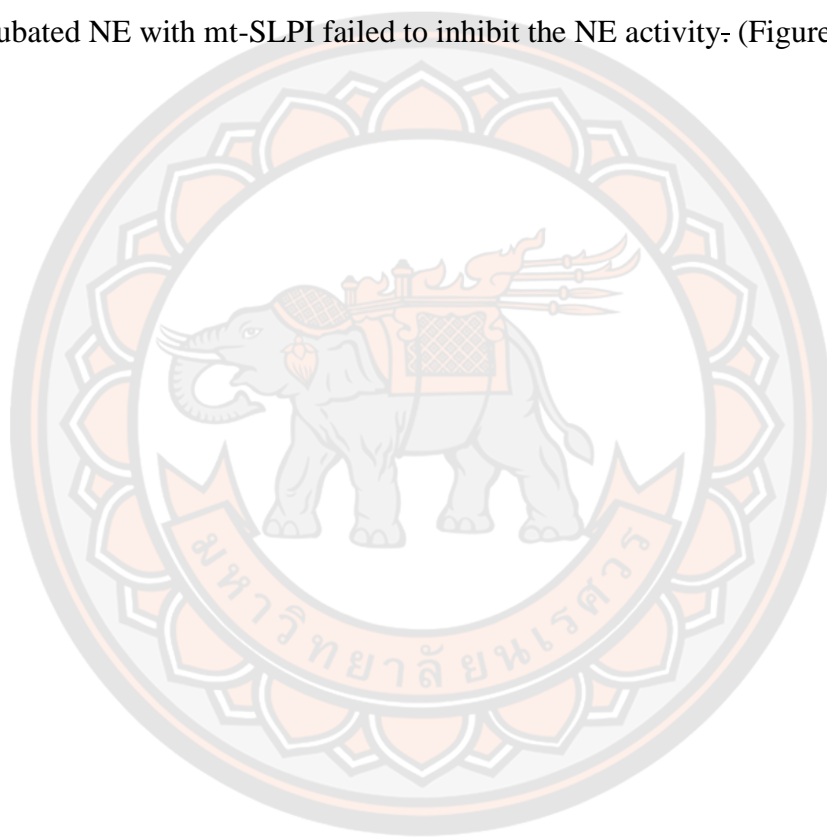


Figure 25 Determination of rhSLPI on apoptosis regulatory protein levels in MI rat by Western blot analysis (A). The quantitative analysis for the expression was presented for bax (B), caspase-3 (C) and caspase-8 (D) (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R) (n = 6).

Part 2: The effect of antiprotease-deficiency of SLPI on I/R injury.

2.1 The neutrophil elastase activity of wild-type and mutated SLPI on H9c2 cells

The neutrophil elastase activity of wild-type(wt) and mutated(mt) SLPI were measured by fluorometric technique. The results showed that the enzymatic activity of NE was significantly inhibited when preincubated with wt-SLPI to $22.0 \pm 2.51\%$ RFU when compared to that of control ($p < 0.05$), whereas preincubated NE with mt-SLPI failed to inhibit the NE activity:- (Figure 26).



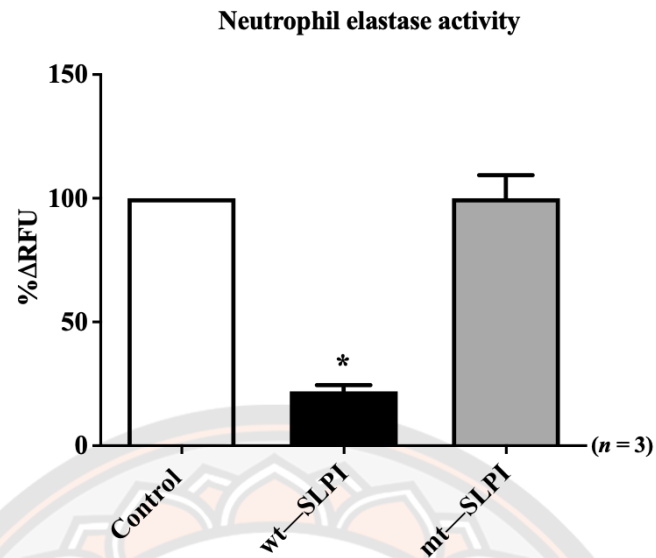


Figure 26 Determination of neutrophil elastase activity of wt-SLPI and mt-SLPI, (* $p < 0.05$ vs. control)

Then, both of wt-SLPI and mt-SLPI were treated to H9c2 and was determined for cellular toxicity. The results showed that there was not significantly difference in cell viability when cells exposed to both of wt-SLPI and mt-SLPI in comparison to those of control group (100 ± 2.44 and 100 ± 5.29 vs. 101.1 ± 2.03 , $p > 0.05$) (Figure 27).

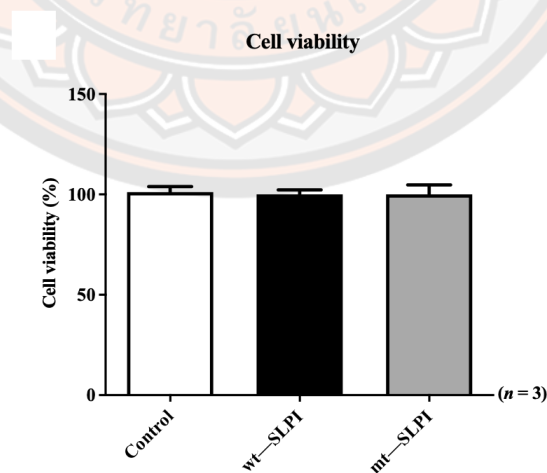


Figure 27 Determination of percentage of cell viability after treated with wt-SLPI and mt-SLPI (B) (* $p < 0.05$ vs. control)

2.2 Anti-protease deficient SLPI reduced cardiac cell injury and intracellular ROS production in hypoxia/reoxygenation(H/R) condition

An *in vitro* cardioprotective effect of mt-SLPI was performed against hypoxia/reoxygenation(H/R) condition. The result showed that mt-SLPI significantly increased cell viability when compared with H/R group (83.38 ± 3.57 vs. 70.05 ± 2.93 , $p < 0.05$), which was comparable to wt-SLPI (83.16 ± 2.85 vs. 70.05 ± 2.93 , $p < 0.05$) (Figure 28).

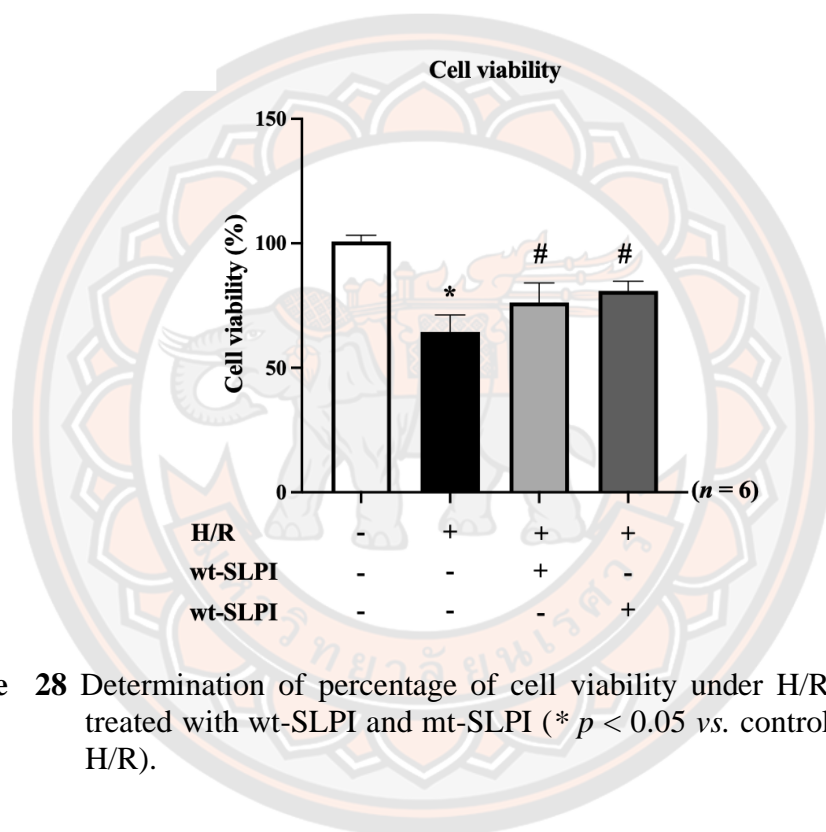


Figure 28 Determination of percentage of cell viability under H/R condition and treated with wt-SLPI and mt-SLPI (* $p < 0.05$ vs. control) (# $p < 0.05$ vs. H/R).

The intracellular ROS level was also determined. The results showed that treatment with both of wt-SLPI and mt-SLPI could significantly reduce intracellular ROS level when compared with H/R group (2,488,000 and 2,425,000 vs. 2,941,000 Arbitrary unit (A.U.), $p < 0.05$) (Figure 29)

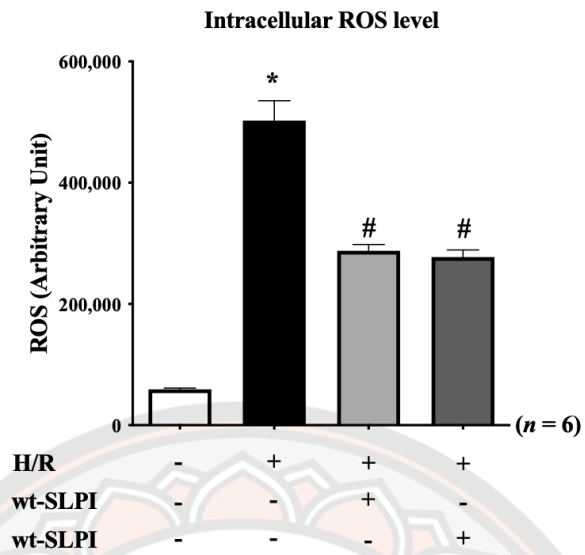


Figure 29 Determination of intracellular ROS under H/R condition and treated with wt-SLPI and mt-SLPI (* $p < 0.05$ vs. control) (# $p < 0.05$ vs. H/R).

2.3 Anti-protease deficient SLPI reduced infarct size cardiac biomarkers in an *in vivo* I/R injury.

There were not significantly difference in % area at risk (AAR) in I/R injury group and both treated groups (Figure 30A). Results in Figure 30B showed that infarct size (% infarct/AAR) in rats treated with both of wt-SLPI and mt-SLPI was significantly lower than that of I/R group (31.75 ± 4.64 , 41.60 ± 1.98 vs. 52.65 ± 4.23 , $p < 0.05$).



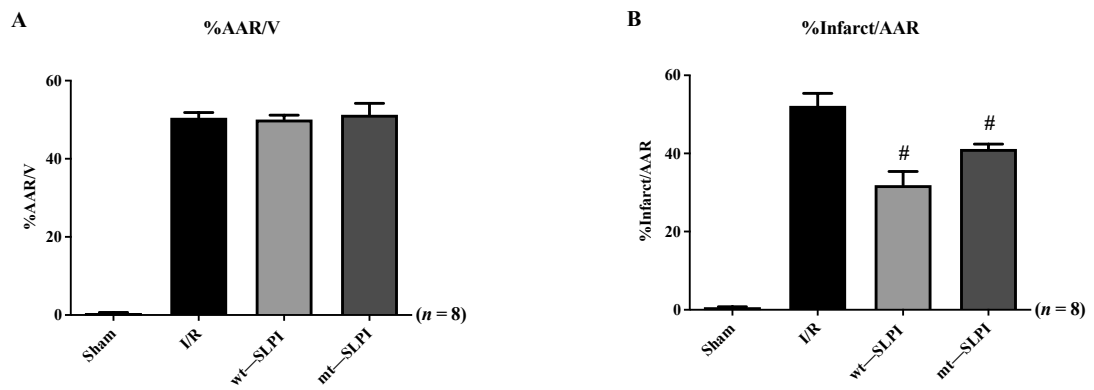
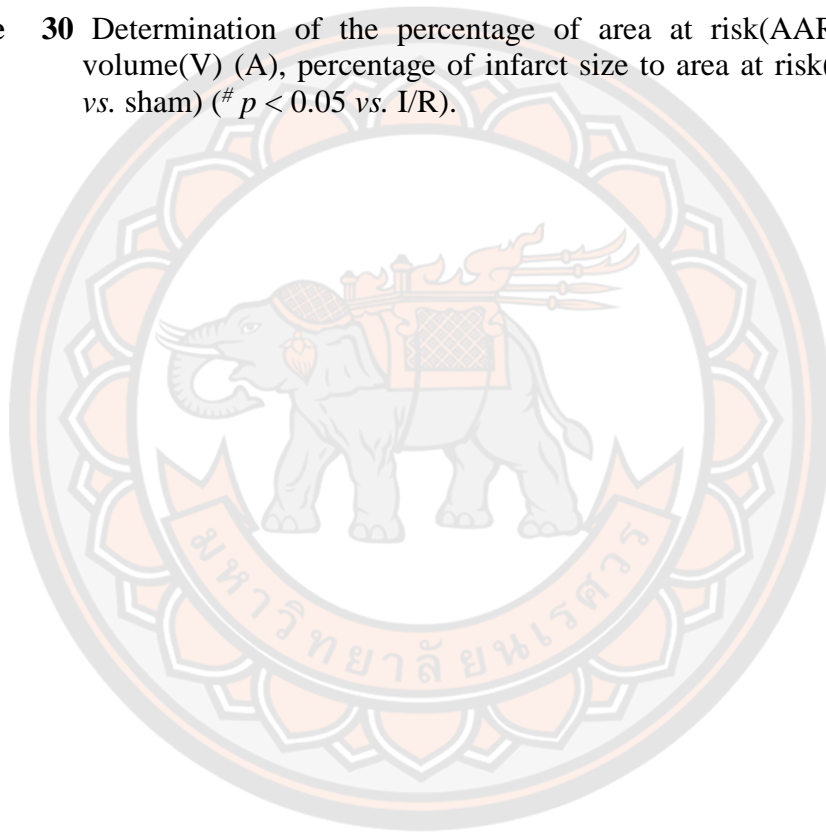


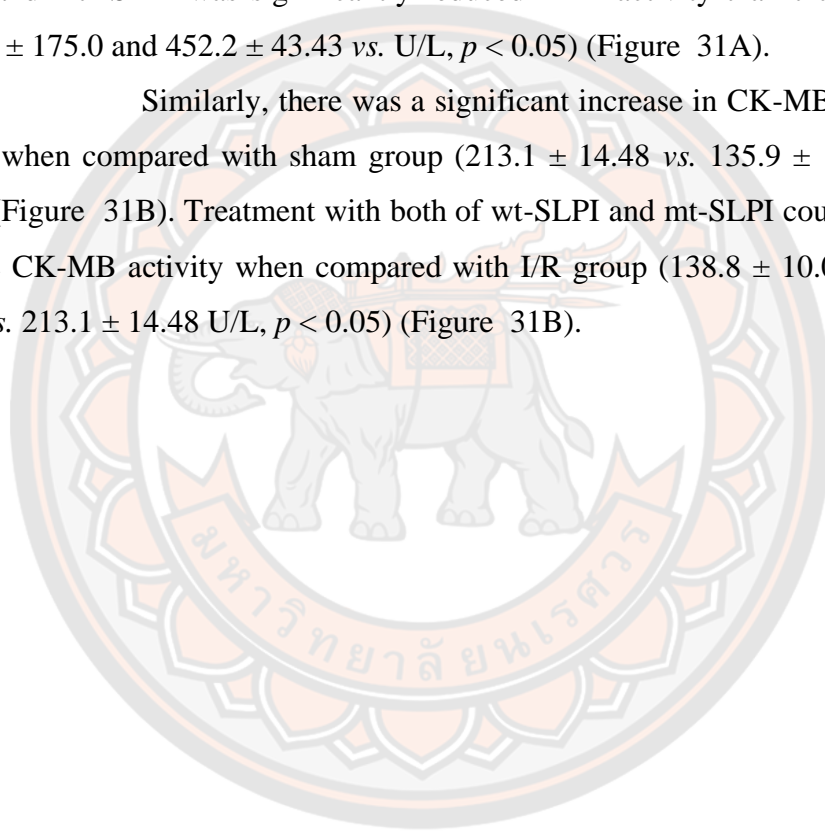
Figure 30 Determination of the percentage of area at risk(AAR) to ventricle volume(V) (A), percentage of infarct size to area at risk(B) (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R).



2.4 Anti-protease deficient SLPI reduced cardiac biomarkers in an *in vivo* I/R injury.

Cardiac biomarkers including LDH and CK-MB activity were measured from serum collected at the end of study protocol. The results showed that LDH activity of the I/R group was significantly higher than sham group (785.3 ± 162.1 vs. 187.8 ± 30.12 U/L, $p < 0.05$) (Figure 31A). Treatment group both of wt-SLPI and mt-SLPI was significantly reduced LDH activity than that of I/R group (364.5 ± 175.0 and 452.2 ± 43.43 vs. U/L, $p < 0.05$) (Figure 31A).

Similarly, there was a significant increase in CK-MB activity in I/R group when compared with sham group (213.1 ± 14.48 vs. 135.9 ± 11.42 U/L, $p < 0.05$) (Figure 31B). Treatment with both of wt-SLPI and mt-SLPI could significantly reduce CK-MB activity when compared with I/R group (138.8 ± 10.08 and 122.5 ± 7.34 vs. 213.1 ± 14.48 U/L, $p < 0.05$) (Figure 31B).



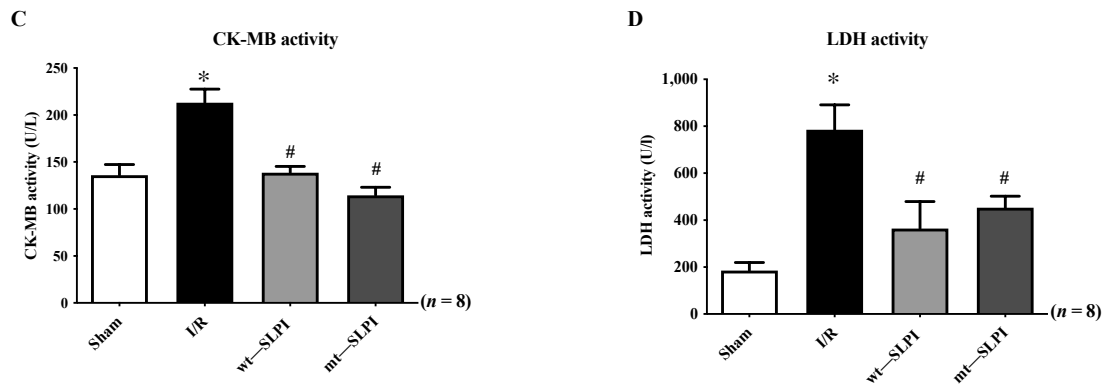
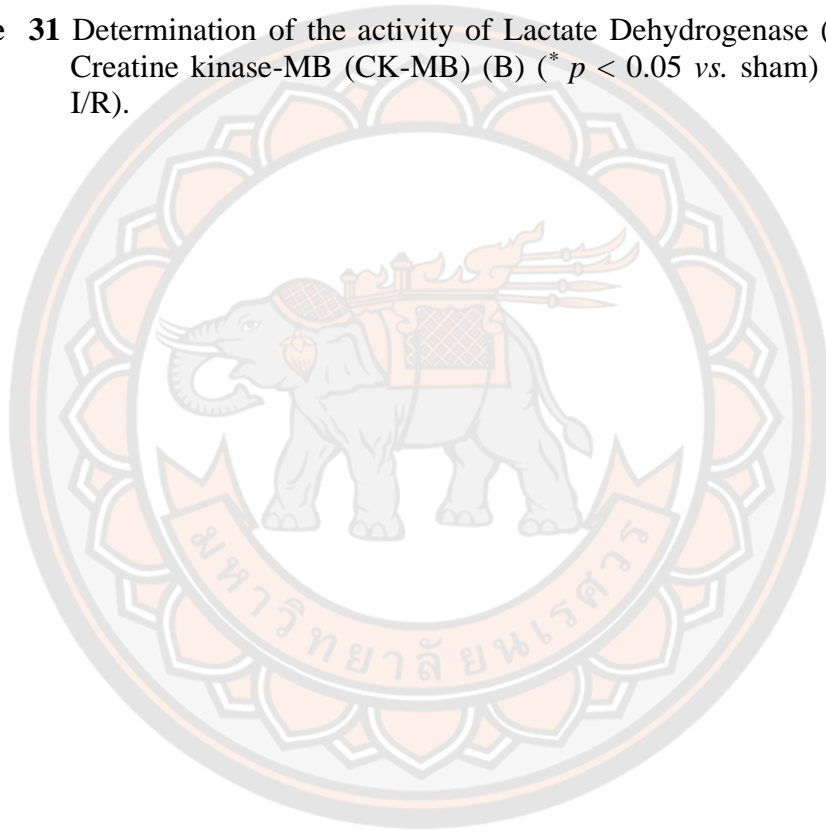


Figure 31 Determination of the activity of Lactate Dehydrogenase (LDH) (A) and Creatine kinase-MB (CK-MB) (B) (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R).



2.5 Effect of *in vivo* treatment of anti-protease deficient SLPI on cardiac function parameters in I/R injury

The left ventricular pressure (LVP) parameters were measured, and the data was collected by high-fidelity micromanometer catheters placed inside the left ventricular chamber. The results of LVP were divided into 3 phases according to the surgery processes including baseline (after stabilization for 30 min prior to LAD ligation), ischemia (30 min after LAD ligation) and reperfusion (at 120 min after reperfusion). At the baseline phase, all of LVP parameters including EDP, ESP, dP/dt_{max} , CI, dP/dt_{min} , Tau/e, devP and HR were not significantly different among groups (Table 5) At the ligation phase (30 min after LAD ligation), the ischaemia induced the reduction of ESP, dP/dt_{max} , devP and increased EDP, dP/dt_{min} and Tau/e in I/R, wt-SLPI, and mt-SLPI group when compared with sham group (Table 6). At the reperfusion phase, the I/R injury induced the reduction of ESP, dP/dt_{max} , devP and increase of EDP, dP/dt_{min} and Tau/e when compared with sham group. After treatment with wt-SLPI, the results showed wt-SLPI could increase ESP, dP/dt_{max} , devP and reduced EDP, dP/dt_{min} and Tau/e when compared with I/R group (Table 7). Whereas, mt-SLPI treatment could reduce only EDP parameter when compared with I/R group.

Table 5 The baseline parameters of left ventricular pressure (LVP) determined the effect of SLPI on the LVP parameters in I/R (baseline).

Parameters	Group			
	Sham (n=8)	I/R (n=8)	wt-SLPI (n=8)	mt-SLPI (n=8)
EDP (mmHg)	5.07 ± 0.73	4.37 ± 0.12	4.70 ± 0.21	4.23 ± 0.20
ESP (mmHg)	118.7 ± 5.63	112.7 ± 7.15	122.2 ± 18.42	110.6 ± 6.17
dp/dt _{max} (mmHg/s)	4958 ± 328.00	4778 ± 367.30	5709 ± 226.00	4973 ± 662.60
Ctrl	101.5 ± 2.47	104.4 ± 6.49	105.9 ± 3.29	103.6 ± 6.28
dp/dt _{min} (mmHg/s)	-4668 ± 295.00	-4884 ± 466.70	-4935 ± 444.20	-4938 ± 336.00
Tau/e (ms)	10.32 ± 0.23	10.63 ± 0.24	8.657 ± 0.35	10.17 ± 0.11
devP (mmHg)	113.8 ± 4.41	116.2 ± 7.92	119.1 ± 11.59	110 ± 6.38
HR (bpm)	447.8 ± 11.13	438.3 ± 21.36	450.3 ± 7.02	450.2 ± 16.01

Table 6 The parameters of left ventricular pressure (LVP) of ischemic phase determined the effect of SLPI on the LVP parameters in I/R (ligation). * $p < 0.05$ vs. sham, # $p < 0.05$ vs. I/R.

Parameters	Group		
	Sham (n=8)	I/R (n=8)	wt-SLPI (n=8)
EDP (mmHg)	5.24 ± 0.28	10.10 ± 0.52*	7.14 ± 0.10*
ESP (mmHg)	118.1 ± 11.26	90.83 ± 5.02*	118.2 ± 4.65*
dp/dt _{max} (mmHg/s)	5517 ± 810.00	3244 ± 403.20*	4902 ± 332.20*
Ctrl	99.86 ± 6.67	96.03 ± 4.80	107.8 ± 10.72
dp/dt _{min} (mmHg/s)	-4267 ± 124.30	-3108 ± 61.71*	-3689 ± 466.10*
Tau/e (ms)	9.713 ± 0.35	12.87 ± 1.20	8.686 ± 0.16
devP (mmHg)	113 ± 6.84	79.55 ± 9.42*	113.6 ± 4.69*
HR (bpm)	444.5 ± 16.51	423.9 ± 20.68	432.4 ± 7.72
			mt-SLPI (n=8)
			6.72 ± 0.65*
			102.5 ± 8.37*
			4454 ± 426.50*
			99.14 ± 4.15
			-3405 ± 496.40*
			10.94 ± 0.46*
			96.51 ± 7.19*
			447.4 ± 9.24

Table 7 The baseline parameters of left ventricular pressure (LVP) of reperfusion phase determined the effect of SLPI on the LVP parameters in I/R (reperfusion). * $p < 0.05$ vs. sham, # $p < 0.05$ vs. I/R.

Parameters	Group			
	Sham (n=8)	I/R (n=8)	wt-SLPI (n=8)	mt-SLPI (n=8)
EDP (mmHg)	6.20 ± 0.70	7.66 ± 0.06 *	4.22 ± 0.43 #	4.99 ± 0.52 #
ESP (mmHg)	109.7 ± 7.41	74.21 ± 7.09 *	104.5 ± 3.43 #	79.91 ± 8.71
dp/dt _{max} (mmHg/s)	4872 ± 541.80	2688 ± 419.70 *	4437 ± 484.60 #	3390 ± 338.10
Ctrl	95.09 ± 6.07	80.05 ± 9.02	91.06 ± 11.58 #	93.65 ± 3.34
dp/dt _{min} (mmHg/s)	-5330 ± 510.10	-2252 ± 477.30 *	-3854 ± 585.90 #	-2922 ± 292.50
Tau/e (ms)	10.97 ± 0.64	15.94 ± 4.40 *	8.131 ± 1.58 #	12.57 ± 0.40
devP (mmHg)	106.6 ± 5.04	76.47 ± 8.06 *	101.1 ± 4.98 #	86.59 ± 6.40
HR (bpm)	425 ± 18.01	411.6 ± 26.03	417.9 ± 10.07	411.8 ± 10.92

2.6 Effect of anti-protease deficient SLPI on signal transduction and apoptosis regulatory molecules

The signal transduction that response to myocardial ischemia/reperfusion injury in the presence and absence of wt-SLPI and mt-SLPI at the onset of reperfusion was determined by Western blot analysis. The results showed that there was a significantly activation of p38 MAPK in I/R group when compared with sham group (1.07 ± 0.18 vs. 0.50 ± 0.07 , $p < 0.05$) (Figure 32A). Treatment of both wt-SLPI and mt-SLPI at the onset of reperfusion could significantly reduce phosphorylated p38 MAPK when compared with I/R group (0.49 ± 0.09 and 0.50 ± 0.09 vs. 1.07 ± 0.18 , $p < 0.05$). Similar results were observed in apoptotic regulatory pathway including Bax, caspase-3 and caspase-8. The results showed that I/R injury significantly increased pro-apoptotic proteins level when compared with sham group (Bax: 0.28 ± 0.04 vs. 0.11 ± 0.02 , cleaved-Caspase-3: 0.49 ± 0.06 vs. 0.24 ± 0.02 , Caspase-8: 0.79 ± 0.03 vs. 0.39 ± 0.03 , $p < 0.05$) (Figure 32B, C and D). Treatment of both wt-SLPI and mt-SLPI significantly reduced the pro-apoptotic proteins level when compared with I/R group (Bax: 0.10 ± 0.02 and 0.15 ± 0.01 vs. 0.28 ± 0.04 , cleaved-Caspase-3: 0.32 ± 0.04 and 0.35 ± 0.09 vs. 0.49 ± 0.06 Caspase-8: 0.46 ± 0.03 and 0.46 ± 0.03 vs. 0.79 ± 0.03 , $p < 0.05$) (Figure 32B, C and D).

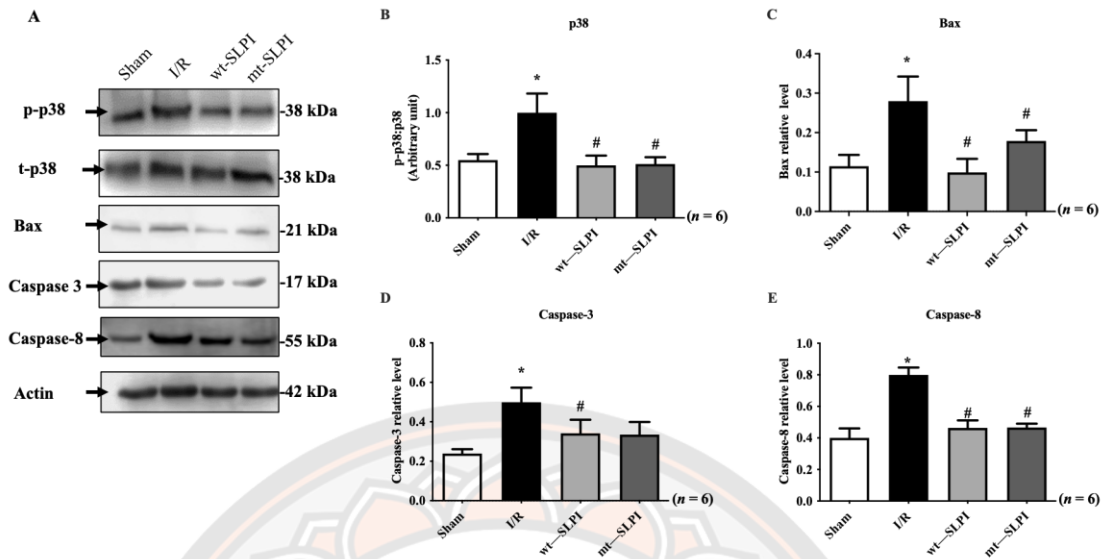


Figure 32 Determination of the apoptotic regulatory signalling protein level in MI rat by Western blot analysis (A). The quantitative analysis for the expression was presented for p38 MAPK phosphorylation (B), Bax (C), cleaved-Caspase-3 (D) and Caspase-8 (E) (* $p < 0.05$ vs. sham) (# $p < 0.05$ vs. I/R) ($n = 6$)

CHAPTER V

DISCUSSION & CONCLUSION

In the present study, we demonstrated, for the first time, the cardioprotective effect of recombinant human secretory leukocyte protease inhibitor (rhSLPI) administered as a post-ischemic treatment in an *in vivo* rat model of myocardial I/R injury. The major findings of this study are that post-ischemic treatment with rhSLPI induced a reduction in infarct size, cardiac inflammatory cytokine levels and the production of oxidatively modified proteins and an improvement in cardiac function. Furthermore, rhSLPI treatment could be associated with the attenuation of apoptosis regulatory signalling, such as p38 MAPK, Bax, caspase-3 and caspase-8, and the activation of the cell survival proteins Akt and ERK by phosphorylation.

Proteases are crucial for the maintenance of cellular homeostasis through the destruction of adversely misfolded or malfunctioning proteins, extracellular matrix (ECM) degradation and activation of cellular processes (7, 11). In cardiomyocytes, protease enzymes are basically active but counterbalanced by their endogenous inhibitors in order to finely control their action (2). During myocardial I/R injury, the regulatory mechanisms are altered, and results in a large increase in both intracellular and extracellular protease activities (6-11). The leukocyte-derived inflammatory serine proteases (ISPs), both from neutrophil- and mast cell-derived serine proteases, such as calpain, matrix metalloproteinases (MMPs) and cathepsins, have been reported to be involved in cardiac injury (7). Alterations of protease activity not only cause cardiac cell injury and death but also result in subcellular cardiac remodeling and the loss of cardiac functions. Therefore, inhibition of protease activity can, therefore, be considered as a powerful strategy for preventing the expansion of injured tissue as well as the progression of cardiac remodeling and hypertrophy.

A strategy to inhibit protease activity, by using chymase inhibitor monotherapy, has been studied in several models, such as rodents, dogs and pigs, which provide similar information on reducing infarct size (94, 321-323). In addition, implementation of a dual-inhibitor (cathepsin and chymase inhibitor, DCCI) also

showed reduced infarction size (324). This evidence convinces the cardioprotective potential of serine protease inhibition against myocardial I/R injury. One of the concerning issues is that the protease inhibitors reported in those previous studies were small molecule chemical inhibitors. The findings from a computational study revealed the existence of chymase inhibitors of putative off-targets that were identified through various structural and functional similarity analyses as well as with molecular docking studies (97). This is a warning for possible adverse effects in the case of small molecule inhibitors. Alternatively, using broad endogenous anti-protease peptides, which are normally expressed and function in the body, could provide more reliable results and safety. Secretory leukocyte protease inhibitor (SLPI) is an endogenous anti-serine protease protein that is normally expressed in several mucous tissues. Several studies described its pharmacological properties including antimicrobial and antiviral (325), as well as anti-inflammatory (326) and anti-apoptotic activities (327). Our study demonstrates that the post-ischemic administration of rhSLPI as early as possible, even during ischemia, could reduce infarct size and improve cardiac function.

The ischemic condition impairs cardiac function by reducing hemodynamic parameters for both the systolic and diastolic functions. Treatment with rhSLPI either after the coronary ligation (during ischemia) or at the onset of reperfusion improved hemodynamic functions. This result correlates with reduced infarct size. An *in vivo* post-ischemic treatment with rhSLPI, injected at both time points, could significantly reduce infarct size. This finding is similar to that of our previous studies in both *in vitro* and *ex vivo* models of global ischemia (22, 23). The dose of rhSLPI in the present study (50 µg per 350 g body weight) is comparable to that used in our previous study (1000 ng/mL) which also provided cardioprotective effects (22).

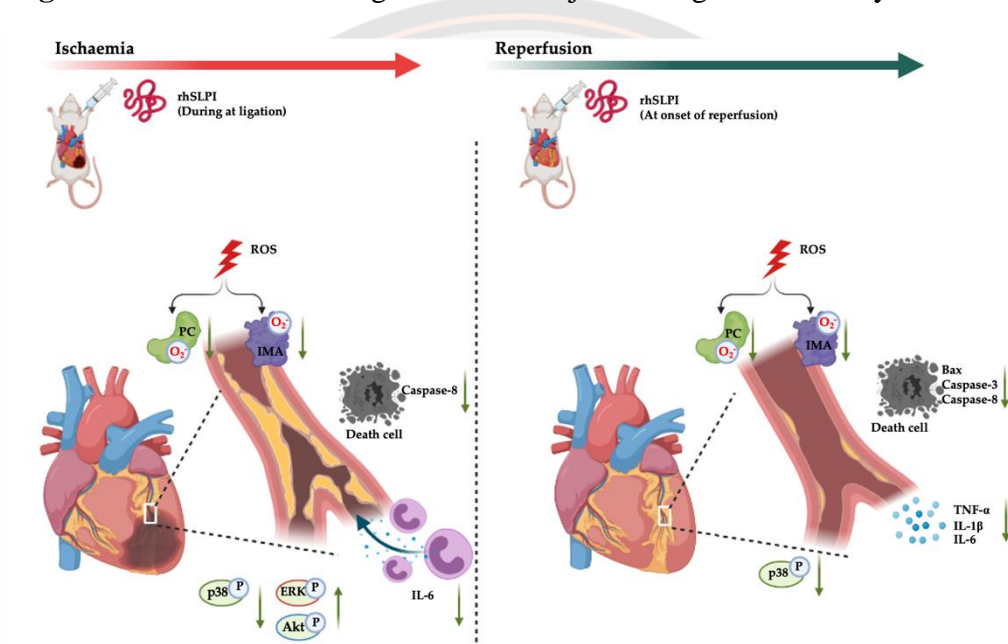
Reactive oxygen species (ROS) are one of the detrimental components of I/R injury (328). ROS play a major role in inducing cell injury and cell death via directly damaging cell membranes and, indirectly, through the recruitment of inflammatory cells and activation of the pro-apoptotic pathways (147). It has been reported that SLPI could reduce intracellular ROS production in an *in vitro* simulated ischemia/reperfusion injury (22, 23, 307, 310, 311). In this study, the assessment of antioxidative stress was performed by determining the oxidatively modified products,

PC and IMA. It has been reported that PC was increased in patients with acute myocardial infarction (329) and heart failure (330). In addition, the IMA level was elevated in patients with acute coronary syndrome in all subgroups, including non-ischemic chest pain (NICP), unstable angina (UA) or myocardial infarction (MI) (331). Therefore, PC and IMA could be cardiac biomarkers for assessing the oxidative stress in myocardial I/R models. In this study, rhSLPI could reduce oxidative stress by lowering the protein carbonyl content level in both cardiac tissue and serum, which could explain the beneficial effect toward infarct size reduction. However, it seems that IMA levels were slightly modified by rhSLPI treatment. It is possibly due to the lower sensitivity of IMA in terms of modification its in terms of being a diagnostic marker. The previous study showed that, in comparison with PC, IMA showed lower diagnostic sensitivity and area under the receiver operating characteristic (ROC) for the diagnosis of non-ST elevation myocardial infarction patients (332).

One of the possible major effects leading to decreased cardiac injury, for the post-ischemic rhSLPI treatment, is the ability to reduce reperfusion-induced inflammation. Accordingly, the results of the present study show that post-ischemic rhSLPI treatment could reduce production of inflammatory cytokines IL-1 β , TNF- α and IL-6. The anti-inflammatory effect of SLPI was demonstrated in the present study, corroborating the results obtained by Jin et al. showing that SLPI reduced inflammatory cytokines in activated macrophages (183, 333). The attenuation of inflammation, as well as the decrease in the infarct size, could also be associated with the reduction in p38 MAPK phosphorylation in the rhSLPI-treated groups. Although p38 MAPK and JNK are both major signalling pathways known to be involved in the inflammatory response and cardiac cell death in I/R injury (334), post-ischemic treatment with rhSLPI could only reduce p38 MAPK phosphorylation, not JNK. Our previous report also demonstrated *in vitro* that rhSLPI treatment showed an association with pro-survival kinase activation, i.e., protein kinase B (PKB) or Akt (22, 23). Akt is a serine/threonine protein kinase, which is involved in survival pathways similar to p44/p42 MAPK and ERK1/2. Similar to our previous findings, our study here demonstrates that an *in vivo* post-ischemic treatment of rhSLPI could restore Akt and ERK1/2 phosphorylation, which consequently attenuates apoptosis regulatory molecules, e.g., Bax, caspase-3 and caspase-8. Taken together, the findings

of our present study are consistent with our previous reports, using both an *in vitro* and an *ex vivo* study model. Indeed, rhSLPI treatment induced cardioprotection by reducing infarct size, by attenuating cardiac inflammation and oxidative stress and by its association with the regulatory molecules involved in cell death and injury, in order to finally result in an improved cardiac function (Figure 33).

Figure 33 A schematic diagram of the major findings in this study. rhSLPI that was



treated in the timing of the post-ischemia duration. rhSLPI could protect the heart from the ischemic condition. The mechanisms for this could be associated with the attenuation of intracellular ROS production, activation of Akt and p38 MAPK phosphorylation, reduction in inflammatory cytokines (TNF- α , IL-1 β and IL-6) and reduction in apoptosis regulatory proteins (Bax, caspase-3, caspase-8).

The result of rhSLPI post-ischaemic treatment showed the potential of a cardioprotective effect in *in vivo* model that improved the cardiac function, and reduce infarct size, cardiac markers, inflammation and apoptotic regulatory proteins. The cardioprotective effect of SLPI was believed to result of anti-protease activity. However, the mechanism of rhSLPI have not been clearly that due to anti-protease activity or direct effect of SLPI. Then, this is *the first study* to show the cardioprotective effect of anti-protease deficient SLPI in both an *in vitro*

hypoxia/reoxygenation in cardiac cells and administered as post-ischaemic treatment in a rat model subjected to an *in vivo* myocardial I/R injury. The major findings are that the mutant form of SLPI (mt-SLPI) containing triple substitutions of amino acids critical for SLPI's antiprotease activity (L72K, M73G, L74G) could reduce cell death, infarct size, cardiac injury markers, and improved cardiac functions, by attenuating intracellular signalling molecules involved in cell death, including p38 MAPK, Bax, and Caspase-8.

In a myocardial ischaemia/reperfusion injury, the level of protease enzymes activity level increased for both intracellular and extracellular cardiac cells in order to maintain homeostasis of cellular structure by degrading of damaged proteins (12). Normally, protease enzymes play a crucial role in producing and degrading proteins in order to recycle dysfunctional and damaged proteins in the cell (43). The myocardial injury during ischaemia contributes to the accumulation of activated neutrophils in the injury area. The accumulation of activated neutrophil leads to tissue injury as result of releasing of cytotoxic cytokines including inflammatory cytokines and proteases enzymes which eventually results in cell death (335). Moreover, after reperfusion, these were attributed to more activated reactive oxygen species (ROS), inflammatory cytokines, and the accumulation of neutrophils (22, 324). Increasing in ROS and inflammatory cytokines levels triggered the recruitment and infiltration of neutrophils and mast cells, which released serine proteases including cathepsin, calpain and matrix metalloproteinase (MMP), which are key mediators involved in cardiovascular diseases progression (336). The post-MI patients showed an increased level of protease enzyme in serum which is related to growth factors levels which is connected to the fibrosis development (337, 338). Therefore, the protease enzyme that plays a crucial role in the development and progression of cardiovascular diseases. In addition, an imbalance of protease activity as well as protease inhibitors in the cell were contributed to cardiac cell injury and the changing the structure of cardiac tissue as cardiac remodelling or cardiac hypertrophy (12). Therefore, the inhibition of serine protease enzymes has therapeutic potential and applications to prevent the progression of cardiac remodelling or heart failure after myocardial infarction.

The protease enzyme inhibitory strategy has been shown to provide a therapeutic potential to reduce cardiac cell death, injury, and remodelling in several

study models (339-342), which also include the study from our study on SLPI. SLPI have been proved to reduce cardiac cell death in ischaemia/reperfusion injury, which is believed to reduced reactive oxygen species, attenuated cell stress signalling, and enhanced cell survival pathway, which subsequently attenuated the apoptotic regulatory pathways (22, 23, 307, 308, 310-312). This evidence suggests that inhibition of protease activity could be a major contributing mechanism explaining the therapeutic potential of SLPI. However, the direct effect of SLPI itself, regardless of its anti-protease activity, has also been demonstrated.

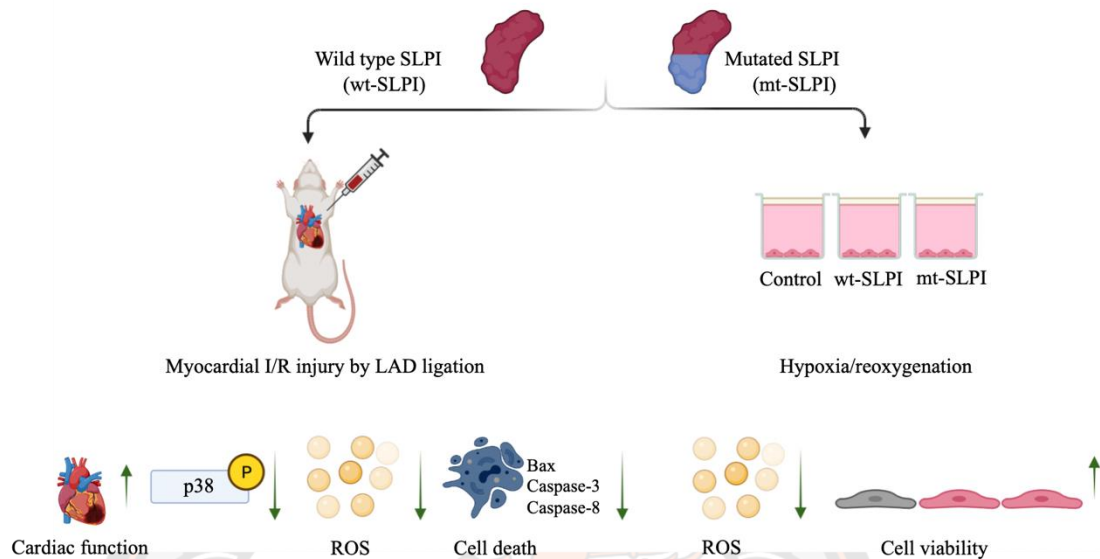
It is well known that the central role of the protease inhibitory effect of SLPI located at Leu⁷²-Met⁷³ residues (343). However, the mechanism of the direct effect of SLPI as well as intracellular signal transduction downstream of SLPI stimulation is still unclear. Mutation of the critical amino acids that govern SLPI anti-protease activity have been implemented and the results were interpreted in such a way that losing the ability to inhibit serine protease could not affect the beneficial effect of SLPI, particularly on anti-HIV infection and anti-inflammation (319, 325). Yet, anti-protease activity deficient SLPI has never been investigated with cardiovascular diseases, particularly myocardial ischaemia/reperfusion injury. Our study demonstrates, as first evidence on the cardiovascular model, that anti-protease activity deficient SLPI treatment in post-ischaemic condition could reduce infarct size, cardiac biomarkers, inflammatory cytokines and improve cardiac function (Figure 34).

Anti-protease deficient SLPI (L72K, M73G, L74G) has been generated and studies have been conducted with an immunological study model (319). The potential mechanism of anti-protease deficient SLPI was intracellular interaction and competing binding of SLPI to p65 which prevented the activation of NF- κ B and resulted in reduced of TNF- α and IL-8 production (344). In addition, SLPI binding partners have been identified, association of SLPI with a calcium dependent phospholipid binding membrane Annexin A2 (AnxA2) enhanced AnxA2 phosphorylation (227), which consequently mediates Akt-survival pathway activation (345). Besides, SLPI can bind to phospholipid cellular receptors-scramblases 1 and 4 which resulted in inhibition of HIV-1 infection (177). Scramblases can bind to onzin, the c-Myc transcription factor. The association of scramblases and onzin could interact with Akt and Mdm2, inhibit p53, and lead to inhibiting cell apoptosis (346).

The information indicates that SLPI could have a direct effect signalling without anti-protease activity by binding to molecules involved in the survival pathway. Although the anti-protease independent mechanism of SLPI against cell death has been reported, the mechanism related to cardioprotection still requires elucidation.

Serine proteases constitute the most numerous groups of proteases, accounting for 40% of them, and they are prevalent in many physiological functions, both normal and disease-related functions (347-349). Inhibition of serine proteases also interferes with physiological homeostasis. The anti-protease independent effect of SLPI in this current study in the context of myocardial I/R injury, which could point out the “*Direct Effect*” of SLPI on cardioprotection. Implementation of anti-protease deficient recombinant-SLPI could be more clinically beneficial in terms of providing cardioprotection without interfering with basal serine protease activity. Therefore, further investigation of anti-protease deficient recombinant-SLPI in a more clinical related study should be performed since our findings convinced that it would provide very useful information. Since the half-life of SLPI after administration is short, approximately 60 min in the circulation (200), any strategies to prolong the half-life of SLPI, increase its stability, or to offer a more efficient delivery method required investigation. A previous study using chimeric protein of SLPI-Cementoin fusion protein found that it could successfully enhance the biological activity of SLPI (350). Therefore, chimeric of anti-protease deficient SLPI-Cementoin has an interesting potential to enhance the physiological activity of anti-protease deficient recombinant-SLPI.

Our study demonstrates, for the *first time*, that rhSLPI treatment after coronary artery occlusion and treatment of anti-protease deficient recombinant SLPI



protein in an *in vivo* rat model. rhSLPI and anti-protease deficient recombinant SLPI protein could reduce cardiac cell injury in an *in vitro* hypoxia/reoxygenation, reduced infarct size, and improve the cardiac function in rats subjected to an *in vivo* myocardial I/R injury. Our findings suggested that SLPI could provide cardioprotection without anti-protease activity.

Figure 34 A schematic diagram of the major findings in this study. Both type of wild type and mutant (anti-protease deficient) SLPI could improve cell viability, reduce infarct size and improve cardiac function. These could associate with attenuation of p38 MAPK activation, intracellular ROS production, and activation of apoptotic regulatory signalling proteins, Bax, Caspase-3 and Caspase-8.

Limitation of this study

There are some limitations in the current study that need to be addressed. The major source of protease secretion in myocardial I/R injury is from inflammatory cells in the heart. There are some limitations in the current study that need to be addressed. The major after reperfusion, particularly neutrophils (3). In this study, cardiac tissue inflammatory source of protease secretion in myocardial I/R injury is from inflammatory cells in the cytokines were measured from a ventricular tissue

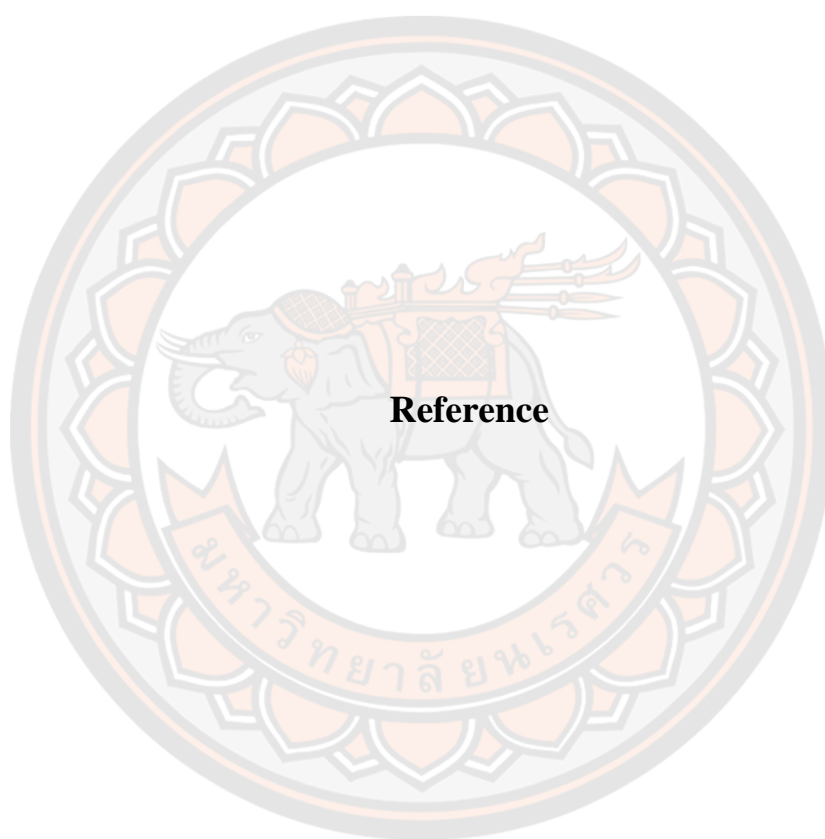
homogenate, which is believed to heart after reperfusion, particularly neutrophils (3). In this study, cardiac tissue inflammation contains a certain number of leukocytes in the cardiac tissue. Therefore, the inflammatory cytokines were measured from a ventricular tissue homogenate, which is believed cytokines level shown in this study is actually from both ventricular tissue and residence leukocytes. The immunohistochemistry on the ventricular tissue section to determine or quantify infiltrated inflammatory cells needs to be investigated. Furthermore, assessment of protease activity, particularly cathepsin G and chymase, from ventricular tissue extract should also be performed by an *in vitro* cleavage of a fluorescent peptide substrate (324). It is noteworthy that although our current study showed that treatment of rhSLPI could reduce p38 MAPK phosphorylation and activate Akt/ERK phosphorylation, this evidence could not provide a direct proof that SLPI protects the heart from I/R injury through those signalling pathways. The findings from this study, as well as the previous reports, could only suggest the association of those cell survival pathways with the protective effect of SLPI. Therefore, abolishing the protection, by using inhibitors of both pathways, could confirm the involvement of cell survival pathways on cardioprotection. In part of anti-protease deficiency SLPI, the consequences of I/R injury included both cell injury in addition to cellular inflammation and immune responses, which are known to be involved in the disease progression (68). The inflammatory cytokines level, leukocytes infiltration, and response of protease enzymes which secreted from infiltrate leukocytes, in the presence of mutant SLPI treatment, should be investigated. As discussed previously concerning the direct effect of SLPI in association with the binding partners, such as Annexin A2, scramblases 1 and 4. This information will provide more mechanistic insight about the cardioprotective effect of SLPI.

Design of future studies

It is also suggested that, for further investigation, the association between SLPI and those candidates' binding partners in myocardial I/R injury are challenging. Moreover, the effect of long-term treatment of rhSLPI in myocardial infarction and post-myocardial infarction cardiac remodeling and heart failure progression should be assessed to provide the useful data before moving forward to clinical trials.

The SLPI mechanism was not clearly investigated. However, previous studies showed the binding protein partner of SLPI, Annexin A2, which was upregulated along with SLPI expression in human smoking mucosa samples from squamous cell carcinoma of the head and neck (HNSCC) (351). The binding between Annexin A2 and SLPI prevented human papillomavirus (HPV) infection by competitively binding with Annexin A2 against HPV. Furthermore, an HIV-1 infection study found that SLPI binding to Annexin A2 heterotetramer (A2t) on the macrophage surface, including A2 and S100A10, impairs productive HIV-1 infection. However, the mechanism has not been determined. Annexin A2 antibody inhibited HIV-1 infection, whereas A2t inhibitor did not (352). Other SLPI binding partner binding protein was phospholipid scramblases 1 and 4 which were cellular receptors for regulating inner and outer plasma membrane movement (177). SLPI could disrupt the binding between CD4 and scramblase receptors because the results showed SLPI binding to scramblase receptor 1 on the same region with CD4 of HIV-1 that can modulating the association between scramblase receptors and CD4 (177).

Previous studies showed that SLPI was discovered to have a rapid clearance rate in both human plasma and urine. SLPI is normally eliminated through glomerular filtration, then reabsorption and degradation in tubular cells, and in the 2-6 h interval, the estimated half-life of SLPI in plasma is 120 minutes (200). Besides, SLPI is inactivated by enzyme that is secreted from respiratory tract such as cathepsin (353). Thus, transportation of SLPI to target organ is new challenge. Therefore, any strategies to improve the stability and extend the half-life of SLPI in system, could provide greater therapeutic benefit. Several advantages of nanoparticles for peptide drug carriers have been listed, for example reducing the enzymatic digestion and aggregation of peptide drugs, increasing the transmembrane absorption. Therefore, fabrication of nanoparticle encapsulated rhSLPI and its efficiency for I/R injury need to be investigated.



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