IN VITRO & *IN VIVO* ANTI-ADIPOGENIC EFFECTS OF A STANDARDIZED QUASSINOID COMPOSITION FROM *EURYCOMA LONGIFOLIA*

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FACULTY OF MEDICINE UNIVERSITY OF MALAYA KUALA LUMPUR

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IN VITRO & IN VIVO ANTI-ADIPOGENIC EFFECTS OF A STANDARDIZED QUASSINOID COMPOSITION FROM *EURYCOMA LONGIFOLIA*

ABSTRACT

Dysregulation of adipocyte metabolism often leads to metabolic dysfunction and obesity. Comorbidities of obesity up-surge the medical risk factors in modern days society. Eurycoma longifolia Jack (EL) is an herbal medicinal plant native to South-East Asian countries, widely known as 'Tongkat Ali.' Bioactive compounds of EL were previously shown to reduce omentum fat mass and oestradiol-induced fatty uterine adhesion in rats. However, the exact role of EL in the modulation of adipogenesis remains to be investigated further. Therefore, this study sought to investigate the effects of a standardized quassinoids composition of EL (SQEL) on the adipogenesis of 3T3-L1 preadipocyte cells and in high-fat-diet-induced obese C57BL/6J mice. The 3T3-L1 cells were induced to differentiate and treated with various concentrations of SQEL (0-100 μ g/mL) for 8 days. Oil Red O staining and intracellular triglyceride quantification assay were performed to determine the effect of SQEL on adipogenic differentiation and cytosolic triglyceride accumulation in 3T3-L1 cells. In addition, the effect of SQEL on lipolysis was also examined by quantifying glycerol released by mature adipocytes treated with SQEL at various concentrations. The mRNA and protein expressions of adipogenic markers were measured using qRT-PCR and immunoblot analysis, respectively. Similarly, C57BL/6J mice were fed with normal and high-fat diet and given 5 mg/kg and 10 mg/kg (i.p) of SQEL for 12 weeks. Weekly food intake and body weight were measured throughout the treatment period. Oral glucose tolerance and intraperitoneal insulin tolerance tests were conducted on the 12th week of the study. At the end of treatment, blood serum was collected for measurement of serum lipids. Epididymal and perirenal fat pads and liver were excised, weighed and used for

histological studies. SQEL significantly inhibited adipogenesis and reduced intracellular accumulation of lipids in adipocytes. Moreover, the mRNA expression of major adipogenic transcription factors (PPARy and C/EBPa) and markers (FAS, LPL and KLF15) were reduced while Sirt1 and FoxO3 proteins were upregulated during the initial stage of differentiation. On the other hand, SQEL also increased lipolysis by elevating glycerol production and reducing intracellular triglycerides in mature adipocytes. In addition, SQEL suppressed body weight gain and decreased epididymal and perirenal fat pad mass in both the normal and high-fat diet fed mice. Moreover, accumulation of fat in the liver and size of adipose tissue were found reduced with SQEL treatment in high-fat diet mice. SQEL treatment also induced energy expenditure in adipose tissue of mice on HFD by elevating the expression of thermogenic genes, AMPK and PGC-1a. Furthermore, SOEL also improved glucose intolerance and decreased elevated total cholesterol and triglyceride in mice fed with high-fat diet. These novel findings suggest that SQEL has an anti-adipogenic effect and could be explored as an alternative pharmacologic agent inhibiting cellular differentiation of pre-adipocytes for the prevention of obesity.

Keywords: Eurycoma longifolia; Adipogenesis; Energy homeostasis; Lipolysis; Obesity

KESAN-KESAN *IN VITRO & IN VIVO* ANTI-ADIPOGENIK KOMPOSISI QUASSINOID YANG DISERAGAMKAN DARIPADA *EURYCOMA LONGIFOLIA*

ABSTRAK

Masalah regulasi metabolisma adiposit menyebabkan disfungsi metabolik dan obesiti. Obesiti pula meningkatkan risiko masalah kesihatan di kalangan masyarakat moden. Eurycoma longifolia Jack (EL) ialah tumbuhan ubatan herba dikenali sebagai Tongkat Ali yang kebayakanya terdapat di negara-negara Asia Tenggara. Dalam kajian terdahulu, sebatian bioaktif daripada EL didapati boleh mengurangkan jisim lemak omentum dan berlemak teraruh daripada estradiol pemendapan rahim dalam tikus. Walaubagaimanapun, fungsi EL di dalam modulasi adipogenesis masih belum dikaji. Oleh sebab itu, kajian ini dilakukan untuk mengkaji kesan komposisi guassinoids yang diseragamkan (SQEL) dalam adipogenesis dengan menggunakan sel-sel pra-adiposit 3T3-L1 dan model tikus obes C57BL/6J yang diinduksikan oleh diet berlemak tinggi. Sel-sel 3T3-L1 telah didorong untuk diferensiasi dan dirawat dengan SQEL dalam pelbagai kepekatan (0-100 µg/mL) selama 8 hari. Ujian pewarnaan Oil Red O dan pengkuantitian trigliserida intraselular telah dilakukan untuk mengenalpasti kesan SQEL keatas proses adipogenesis dalam sel-sel 3T3-L1. Tambahan pula, kesan SQEL dalam adipolisis juga diperiksa dengan mengukur kandungan gliserol yang dihasilkan oleh selsel adiposit matang yang dirawat dengan SQEL dalam pelbagai kepekatan. Selain itu, profil mRNA dan protein berkaitan dengan proses adipogenik juga diukur dengan mengunakan kaedah reaksi rantai polimerase transkripsi membalik dan analisis imunoblot. Tikus C57BL/6J diberi diet biasa dan diet berlemak tinggi dan juga diberikan 5 mg/kg dan 10 mg/kg (i.p) SQEL selama 12 minggu. Pengambilan makanan dan berat badan diukur setiap minggu sepanjang tempoh rawatan. Ujian toleransi glukosa oral dan toleransi insulin intraperitoneum dijalankan pada minggu ke-12. Pada akhir rawatan,

serum darah dikumpulkan untuk pengukuran lipid serum. Pad lemak epididimal dan perirenal dan hati dikeluarkan, ditimbang dan digunakan untuk kajian histologi. Kajian ini membuktikan bahawa SQEL menghalang proses adipogenesis, mengurangkan pengumpulan lipid intraselular dan kandungan trigliserida dalam adiposit dengan ketara. Selain itu, expresi mRNA faktor transkripsi (PPARy dan C/EBPa) dan penanda utama adipogenik (FAS, LPL dan KLF15) dikurangkan malah ekspresi protein Sirt1 dan FoxO3 ditingkatkan pada peringkat awal pembezaan sel pra-adiposit. Seterusnya, SQEL juga meningkatkan lipolisis dengan meningkatkan pengeluaran gliserol dan mengurangkan trigliserida intraselular dalam adiposit matang. Di samping itu, SQEL juga menindas peningkatan berat badan dan menurunkan jisim pad lemak epididimal dan perirenal di dalam kedua-dua model tikus yang diberi makan diet biasa dan berlemak tinggi. Selain itu, pengumpulan lemak di dalam hati dan saiz tisu adiposa dapat dikurangkan dengan rawatan SQEL dalam model tikus yang diberi diet berlemak tinggi. Rawatan SQEL juga menginduksi penggunaan tenaga dalam tisu adipos tikus yang diberi diet berlemak tinggi dengan meningkatkan ekspresi gen-gen termogenik, AMPK dan PGC-1a. Tambahan pula, SQEL membaikpulih intoleransi glukosa dan menurunkan jumlah kolesterol dan trigliserida dalam tikus yang diberi diet berlemak tinggi. Penemuan novel ini menunjukkan bahawa SQEL mempunyai kesan anti-adipogenik dan berpotensi sebagai ejen farmakologi alternatif yang menghalang pembezaan sel-sel pra-adiposit untuk pencegahan obesiti.

Kata kunci: Eurycoma longifolia; Adipogenesis; Homeostasis tenaga; Lipolisis; Obesiti

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TABLE OF CONTENTS

Abst	ract		.iii
Abs	trak		v
Ack	nowledg	ements	vii
Tabl	e of Cor	ntentsv	'iii
List	of Figur	es	xii
List	of Table	2Sx	civ
List	of Symb	ools and Abbreviations	xv
List	of Appe	ndicesx	cix
CHA	APTER	1: INTRODUCTION	1
CHA	APTER	2: LITERATURE REVIEW	5
2.1	Adipod	cytes	5
	2.1.1	Origin of Adipocytes	5
	2.1.2	Adipogenesis	5
	2.1.3	In vitro Models of Adipogenesis	6
	2.1.4	Hormonal Inducers of Adipogenesis	7
2.2	Transc	riptional Regulation of Adipogenesis	8
	2.2.1	Peroxisome Proliferator-Activated Receptor γ	10
	2.2.2	CCAAT/Enhancer Binding Proteins	11
2.3	Adipog	genic Proteins	12
	2.3.1	Fatty Acid Synthase	12
	2.3.2	Lipoprotein Lipase	13
	2.3.3	Fatty-Acid-Binding Proteins	14
	2.3.4	Kruppel-Like Factor 15	15

2.4	Signaling Pathways Involved in Adipogenesis						
	2.4.1	Insulin Signaling Pathway	16				
	2.4.2	AMP-activated Protein Kinase (AMPK) Pathway	17				
	2.4.3	Mitogen-Activated Protein Kinase (MAPK) Pathway	18				
	2.4.4	Wnt Signaling Pathway	19				
	2.4.5	Sirtuin1 Signaling Pathway	20				
2.5	Develo	pment of adipose tissues and obesity	22				
	2.5.1	White Adipose Tissue	23				
	2.5.2	Brown Adipose Tissue	24				
2.6	Obesity	,	25				
	2.6.1	Insulin Resistance	26				
2.7	Managi	ng Obesity and Related Complications	27				
2.8	Synthet	ic anti-obesity drugs	29				
2.9	9 Naturally-derived Anti-adipogenic/Obesity Drugs						
2.10) Eurycoma longifolia Jack						
	2.10.1	Medicinal uses of <i>Eurycoma longifolia</i>	36				
	2.10.2	Chemical Constituents	37				
		2.10.2.1 Eurycomanone	38				
	2.10.3	Standardized Quassinoids composition from Eurycoma longifolia	39				
2.11	Rationa	le for the study	39				
СНА	PTER 3	3: METHODOLOGY	41				
3.1	Prepara	tion of the Standardized Quassinoids composition from Eurycon	ma				
	longifo	lia (SQEL)	42				
3.2	Mainter	nance and Propagation of 3T3-L1 cells	43				
3.3	Differe	ntiation of 3T3-L1 cells	44				
3.4	Cell via	bility and Cytotoxicity	45				

3.5	Oil Red	d O Staining	46
3.6	Triglyc	eride Quantification Assay	47
	3.6.1	Extraction of Intracellular Triglyceride from Matured Adipocytes	47
	3.6.2	Protein Quantification	47
	3.6.3	Quantification of Triglyceride	48
3.7	Lipolys	sis Assay	49
3.8	Immun	oblotting Analysis	51
	3.8.1	Preparation of Cell Lysates	51
	3.8.2	Preparation of Protein Sample	51
	3.8.3	Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis	(SDS-
		PAGE)	52
3.9	Quantit	tative Real-Time Polymerase Chain Reaction (qRT-PCR)	52
	3.9.1	RNA Extraction	52
	3.9.2	cDNA Synthesis	53
	3.9.3	mRNA Expression	54
3.10	Animal	l Experiments	56
	3.10.1	Oral Glucose Tolerance Test	57
	3.10.2	Intraperitoneal Insulin Tolerance Test	58
	3.10.3	Serum Biochemistry	58
	3.10.4	Liver and Fat Tissues Histological Analysis	58
	3.10.5	Fat Tissues qRT-PCR Analysis	59
3.11	Statisti	cal Analysis	61
CHA	PTER	4: RESULTS	62
4.1	Cytoto	xicity effect of SQEL and eurycomanone	62
4.2	SQEL	and eurycomanone inhibit adipogenesis of 3T3-L1 cells	65
4.3	SQEL	and eurycomanone reduce lipogenesis and induce adipolysis	68

4.4	SQEL and eurycomanone reduce the expression of adipogenesis-associated						
	proteins and genes in 3T3-L1 cells70						
4.5	SQEL suppresses body weight gain in C57BL/6J mice73						
4.6	SQEL improves impaired glucose tolerance but not insulin sensitivity in C57BL/6J						
	mice76						
4.7	SQEL reduces adipose tissue mass in C57BL/6J mice						
4.8	Effects of SQEL treatment on fat accumulation in the liver and adipose tissue						
	hypertrophy in C57BL/6J mice						
4.9	Effects of SQEL treatment on lipid profile and fasting blood glucose in C57BL/6J						
	mice						
4.10	SQEL treatment increases the mRNA levels of AMPK and PGC-1 α in adipose						
	tissues of C57BL/6J mice						
CHAPTER 5: DISCUSSION							
CHA	PTER 6: CONCLUSION						
6.1	Conclusion						
6.2	Limitations of the study and future direction						
Refe	rences						
List o	of Publications and Papers Presented						
Appe	ndix						

LIST OF FIGURES

Figure 2.1: Determination and differentiation of adipocytes
Figure 2.2: Differentiation from preadipocyte to mature adipocyte and the transcriptional control at different stages of adipogenesis
Figure 2.3: White and brown adipose tissue specimen stained with hematoxylin and eosin.
Figure 2.4: <i>Eurycoma longifolia</i> plant
Figure 3.1: Summary of the methods
Figure 3.2: The bioactive ingredients of SQEL
Figure 3.3: Biosystem StepOne TM Plus PCR cycling program
Figure 3.4: Animal study group segregation
Figure 3.5: Summary of the animal study
Figure 4.1: Effects of SQEL and eurycomanone on the viability of 3T3-L1 preadipocytes.
Figure 4.2: Effects of SQEL and eurycomanone on the viability of differentiating preadipocytes and matured adipocytes
Figure 4.3: Adipogenic inhibitory effects of SQEL and eurycomanone in 3T3-L1 cells.
Figure 4.4: SQEL and eurycomanone inhibit the intracellular triglyceride accumulation and induce lipolysis in matured adipocytes
Figure 4.5: Effects of SQEL and eurycomanone on the expression of adipogenic markers in differentiating cells
Figure 4.6: Effects of SQEL treatment on body weight of C57BL/6J mice74
Figure 4.7: Effects of SQEL treatment on food consumption of C57BL/6J mice75
Figure 4.8: Effects of SQEL treatment on glucose and insulin sensitivity of C57BL/6J mice
Figure 4.9: Effects of SQEL treatment on the adipose tissue development in C57BL/6J mice

Figure 4.10: Effects of SQEL treatment on the adipose and liver tissue mass in C57BL/6J
mice
Figure 4.11: Effects of SQEL treatment on adipose and liver tissues in C57BL/6J mice.
Figure 4.12: Effects of SQEL and eurycomanone on the mRNA expression of AMPK and
PGC-1α in adipose tissues of C57BL/6J mice

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LIST OF TABLES

Table 2.1: BMI classification.	26
Table 2.2: Examples of common synthetic anti-obesity drugs.	30
Table 2.3: Potential phytochemicals for the treatment of obesity	32
Table 2.4: Traditional uses of Eurycoma longifolia.	37
Table 3.1: Media formulations.	45
Table 3.2: Triglyceride Reaction Mix.	49
Table 3.3: Glycerol Reaction Mix	50
Table 3.4: Composition of DNA Elimination Mix.	54
Table 3.5: Composition of Reverse-transcription Mix.	54
Table 3.6: Composition of PCR mix	55
Table 3.7 Forward and Reverse primers.	60
Table 3.8 Composition of PCR mix	60
Table 4.1: Effect of SQEL treatment on blood serum parameters in C57BL/6 mice	85

LIST OF SYMBOLS AND ABBREVIATIONS

↑	:	increase
\downarrow	:	decrease
°C	:	degree Celsius
a.u	:	arbitrary unit
x g	:	gravitational force
kg/m ²	:	kilograms by the square to height in meters
AAALAC	:	Association for Assessment and Accreditation of Laboratory
		Animal Care International
Abs	:	Absorbance
ACC	:	Acetyl-CoA carboxylase
Akt	:	protein kinase B
AMM	:	adipocyte maintenance medium
AMP	:	adenosine monophosphate
AMPK	:	AMP-activated protein kinase
ANOVA	:	Analysis of variance
aP2	:	adipocyte protein 2
APC	:	adenomatous polyposis coli
ATCC	:	American Type Culture Collection
BAT	÷	brown adipose tissue
BMI	:	body mass index
BSA	:	bovine serum albumin
BW	:	body weight
C/EBPa	:	CCAAT-enhancer-binding protein alpha
C/EBPβ	:	CCAAT-enhancer-binding protein beta
С/ЕВРб	:	CCAAT-enhancer-binding protein delta
cDNA	:	complementary DNA
cm	:	centimeter
CO^2	:	carbon dioxide
CoA	:	co-enzyme A
CREB	:	cAMP response element-binding protein
DM	:	differentiation medium
DMEM	:	Dulbecco's Modified Eagle Medium

DMSO	:	Dimethyl sulfoxide
DNA	:	Deoxyribonucleic acid
DTT	:	Dithiothreitol
EL	:	Eurycoma longifolia Jack
ERK	:	extracellular signal-regulated kinases
et al	:	ea alia (and another people)
Eu	:	eurycomanone
FABPs	:	fatty-acid-binding proteins
FAS	:	fatty acid synthetase
FoxO	:	Forkhead box
FoxO3	:	Forkhead box O3
FZD	:	frizzled
g	:	gram
GLUT4	:	glucose transporter 4
GSK3β	:	glycogen synthase kinase 3-β
HCl	:	hydrochloric acid
HDL	:	high-density lipoprotein
HFD	:	high-fat diet
HPLC	:	high performance liquid chromatographic
i.p	:	intraperitoneal
IC50	:	half maximal inhibitory concentration
IPITT	÷	intraperitoneal insulin tolerance test
IR	:	insulin receptor
IRS	:	insulin receptor substrate
Iso	:	isoproterenol
IU	:	international unit
JNKs	:	c-Jun amino-terminal kinases
kcal	:	kilocalorie
kg	:	kilogram
KLF15	:	Kruppel-like factor 15
L	:	liter
LD50	:	half-maximal lethal dose
LDL	:	low-density lipoprotein
LEF/TCF	:	lymphoid-enhancer-binding factor/T-cell-specific transcription
		factor

LPL	:	lipoprotein lipase
LRP5/6	:	low-density-lipoprotein-receptor-related protein-5 or -6
m	:	meter
Μ	:	molar
MAPK	:	mitogen-activated protein kinases
MDI	:	isobutyl-methyl-xanthine/dexamethasone/insulin
mg	:	milligram
mL	:	milliliter
mM	:	millimolar
mMol	:	millimolar
mRNA	:	messenger RNA
MSCs	:	mesenchymal stem cells
mTOR	:	mammalian target of rapamycin
MTT	:	3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide
NADPH	:	Nicotinamide adenine dinucleotide phosphate
ND	:	normal diet
NDC	:	non-differentiated control
NF	:	nuclear factor
nM	:	nanomolar
nm	:	nanometer
NP-40	:	Nonidet P-40
0.g	:	oral garvage
OGTT	:	oral glucose tolerance test
p38	:	p38 MAPK
PAGE	:	Polyacrylamide Gel Electrophoresis
PBS	:	phosphate buffered saline
РСМ	:	pre-adipocyte culture medium
PGC-1a	:	PPAR- γ coactivator 1 α
PI3K	:	phosphoinositide 3-kinase
РКА	:	protein kinase A
PPARγ	:	peroxisome proliferator-activated receptor gamma
PPRE	:	peroxisome proliferator response elements
PRDM16	:	PR domain-containing16
qRT-PCR	:	quantitative real-time polymerase chain reaction
RIPA	:	Radioimmunoprecipitation assay

RNA	:	Ribonucleic acid
rpm	:	revolutions per minute
RXR	:	Retinoid X receptor alpha
SDS	:	Sodium Dodecyl Sulfate
SEM	:	standard error of mean
Sf	:	sulforaphane
Sirt1	:	Sirtuin 1
SMRT	:	silencing mediator of retinoid and thyroid hormone receptors
SQEL	:	standardized quassinoids composition of EL
TBS-T	:	Tris-buffered saline - tween 20
TSC2	:	tuberous sclerosis complex 2
TZDs	:	Thiazolidinediones
UCP1	:	uncoupling protein-1
v/v	:	volume/volume
VC	:	vehicle control
V	:	volt
w/v	:	weight/volume
w/w	:	weight/weight
WAT	:	white adipose tissue
μL	:	microliter
μΜ	:	micromolar
μm	:	micrometre

LIST OF APPENDICES

Appendix A: Preparation of Chemicals and Reagents	148
Appendix B: List of Antibodies	154
Appendix C: List of Primers in RT ² Profiler PCR Array	155
Appendix D: Standard Curve for Protein Quantification Kit	157
Appendix E: Standard Curve for Triglyceride Quantification Kit	158
Appendix F: Standard Curve for Glycerol Quantification Kit	159
Appendix G: Composition of normal diet and high-fat diet	160

CHAPTER 1: INTRODUCTION

Adipocytes are a crucial cellular constituent of fat tissues that play a key role in modulating energy homeostasis and lipid metabolism (Unger et al., 2010). These fat cells are responsible for the accumulation of lipid molecules during energy excess and metabolizing it in the events of energy demand (Ali et al., 2013). Adipogenesis is a cellular differentiation process whereby fibroblastic pre-adipocytes turn into adipocytes in the event of caloric overabundance (Hausman et al., 2001; Sarjeant & Stephens, 2012). Uncontrolled adipogenesis leads to overgrowth of adipose tissues which then enhances buildup of the fatty tissue mass and eventually contributes to the development of obese condition (Fruhbeck et al., 2001). The alarming rise in the prevalence of obesity is observed among people from both developed and developing nations (Zang et al., 2013). In addition, obesity underpins the development of many other serious metabolic diseases such as type 2 diabetes mellitus, hypertension and cardiovascular diseases that possess higher mortality rate (He et al., 2013). As adipogenesis facilitates the progression of obesity, various studies have focused on inhibiting adipocytic differentiation, downregulating lipogenesis and enhancing lipolysis as strategies in preventing the development of obesity (Dave et al., 2012; He et al., 2013; Inafuku et al., 2013; Park et al., 2012; Song et al., 2013).

Interestingly, adipogenesis is a tightly regulated multi-step process which comprises the activation of several transcriptional factors. These transcription initiators are responsible for regulating the expression of adipogenesis-specific genes that lead to the development of adipocyte phenotype. Major adipogenic transcription factors such as CCAAT/enhancer-binding protein β (C/EBP β), peroxisome proliferator-activated receptor γ (PPAR γ), and CCAAT/enhancer-binding protein α (C/EBP α) play a crucial role in coordinating this complex cellular differentiation (Rosen & MacDougald, 2006; White & Stephens, 2010). C/EBP β is expressed upon adipogenic induction and switches on the promoters of the genes encoding PPAR γ and C/EBP α which then activates the expression of adipogenic genes such as fatty acid binding protein (aP2), fatty acid synthetase (FAS) and lipoprotein lipase (LPL) that promotes the progression of adipocytic differentiation (Cristancho & Lazar, 2011; Farmer, 2006).

Earlier studies have demonstrated that PPAR γ alone is enough for adipocyte differentiation (Tontonoz *et al.*, 1994) and its induction is significantly increased during adipogenesis development (Chawla *et al.*, 1994) suggesting that PPAR γ functions as the lead regulator of pre-adipocyte differentiation and therefore, its down-regulation is considered important to suppress adipogenesis. Several lines of evidence suggest that PPAR γ could be down-regulated via numerous signaling pathways. Interestingly, AMP-activated protein kinase (AMPK) pathway suppressed adipogenesis by down-regulating the expression of PPAR γ (He *et al.*, 2013; Huang *et al.*, 2011). In addition, mitogenactivated protein kinases (MAPK) pathway is also involved in the regulation of adipogenesis by phosphorylating PPAR γ , thereby inducing its degradation that suppresses the downstream expression of adipogenic genes (Bost *et al.*, 2005; Zang *et al.*, 2013). Furthermore, studies have found that phosphoinositide 3-kinase/protein kinase B (PI3K/Akt) pathway (Park *et al.*, 2012) and Akt-tuberous sclerosis complex 2-mammalian target of rapamycin (Akt-TSC2-mTORC) pathway (Zhang *et al.*, 2009) also influence PPAR γ expression via insulin signaling in adipogenesis.

Nevertheless, the activity of transcription factors is also regulated at numerous stages through protein acetylation by both acetylase and deacetylase. The histone deacetylase sirtuin 1 (Sirt1) possesses significant roles in a variety of biological processes including adipogenesis. It was reported that the suppression of PPAR γ activity by Sirt1 impaired

adipogenesis and induced lipolysis in matured adipocytes (Picard *et al.*, 2004). Earlier evidence showed that overexpression of Sirt1 attenuates adipocyte differentiation by reducing the expression of PPAR γ and C/EBP α in 3T3-L1 cells (Picard *et al.*, 2004). Similarly, reduced Sirt1 levels promote PPAR γ acetylation and C/EBP α activity, which leads to adipocyte differentiation (Qu *et al.*, 2016). Conversely, the inhibitory effect of PPAR γ on Sirt1 activity (Han *et al.*, 2010) and modulation of Sirt1 expression by C/EBP α during adipogenesis (Jin *et al.*, 2010) indicate Sirt1 could be regulated by adipogenic transcription factors as well. Hence, improving our understanding of the molecular mechanisms in adipogenesis could pave ways for the identification of therapeutic targets against metabolic diseases that are quickly becoming global concerns.

Health awareness programs promoting the practices of a healthy lifestyle, healthy dietary habits and increasing physical activities are highly advocated in the management of obesity. These together with pharmacological therapy may provide additional benefit in ameliorating comorbidities and promoting adherence to behaviour modifications, which in turn may improve physical functions for greater physical activity (Apovian *et al.*, 2015). Currently, several prescriptive anti-obesity drugs can be used to suppress appetite, reduce lipid absorption and enhance fat oxidation for weight management of obese individuals (Padwal & Majumdar, 2007). However, poor efficacy and serious side effects of those drugs have led to their withdrawal from the market leaving only a handful of drugs that can be consumed for the said purpose.

In recent years, the use of naturally-derived compounds for the pharmacological management of obesity has received much attention from the scientific community. Several flavonoids commonly present in herbal plants were reported to possess significant anti-adipogenic effects and these include luteolin (Kwon *et al.*, 2016), isorhamnetin

(Zhang *et al.*, 2016), butein (Wang *et al.*, 2017), delphinidin (Rahman *et al.*, 2016). Hence, exploring phytochemicals as an alternative source to identify and develop safe and effective anti-adipogenic agent for managing obesity remains an interesting option.

Eurycoma longifolia Jack (EL), typically known as 'Tongkat Ali' is a popular tropical plant classified under Simaroubaceae family and native to Southeast Asia countries. Its raw crude powder is widely used as an additive in canned energy drinks and coffee mixtures, as well as generally consumed as a health supplement in the form of capsules. The root of this plant is a popular traditional medication for fever after birth, boils, ulcer wound healing treatment and also acts as energy booster among men (Low et al., 2013). Quassinoids which include the pure compound, eurycomanone found in EL were reported to have biological activities such as anti-plasmodial, anti-cancer, pro-fertility and aphrodisiac activities in males (Bhat & Karim, 2010). Moreover, the effects of EL in the role of adipogenesis were shown indirectly by the reduction of omentum fat mass (Solomon et al., 2014) and its synergistic effect in combination studies with other bioactive compounds in body weight management (Talbott, 2007). However, to date, there is limited information on the effects of EL-derived quassinoids in adipogenesis including the mechanisms involved. Thus, the present study aims to investigate the potential lipid modulation effects of a standardized quassinoids enriched-fraction (SQEL) and eurycomanone of Eurycoma longifolia in adipocytes and in high-fat diet-induced obese mice.

CHAPTER 2: LITERATURE REVIEW

2.1 Adipocytes

2.1.1 Origin of Adipocytes

Adipocytes are the key cellular components of adipose tissue that function as energy storage depot, heat insulator and as a protective layer for many important body organs. They originate from pluripotent mesenchymal stem cells (MSCs) that are capable of developing into several cell types including adipocytes, myocytes, chondrocytes and osteocytes (Covas *et al.*, 2008; Lin *et al.*, 2010).

2.1.2 Adipogenesis

Adipogenesis is a developmental process in which mesenchymal stem cell differentiates into preadipocyte, which then differentiates to become adipocyte (Figure 2.1) (Ali *et al.*, 2013). This process involves a series of well-defined steps including commitment, recruitment and proliferation and terminal differentiation. During the commitment phase, the pluripotent stem cells are committed to differentiate towards adipocyte lineage; hence losing the potential to differentiate into other cell types (Otto & Lane, 2005). As a result, preadipocytes are formed. Next, the preadipocytes proliferate and expand their numbers, known as recruitment and proliferation phase will undergo growth arrest phase after which mitotic clonal expansion is initiated. During this process, the growth-arrested preadipocytes will undergo one more round of DNA replication and cell division which leads to the clonal expansion of the committed cells (Rangwala & Lazar, 2000). The DNA replication step at this stage is crucial to switch on key transcriptional factors which regulate the terminal differentiation of adipocytes.

Terminal differentiation is the final phase where preadipocytes acquire characteristics of matured adipocytes which are non-dividing, lipid-filled and morphologically round. The matured adipocytes actively secrete proteins for lipid synthesis and have enhanced insulin sensitivity (Rosen & MacDougald, 2006). Henceforth, the adipocytes could perform many biological functions as an energy reserve and specialized endocrine cells. To date, adipogenesis is one of the most intensively studied developmental processes due to the availability of good experimental cell culture models of adipocyte differentiation (Ali *et al.*, 2013).



Figure 2.1: Determination and differentiation of adipocytes. Adapted and modified from (Fève, 2005).

2.1.3 In vitro Models of Adipogenesis

Several cellular models are used to study adipogenesis and adipocyte function *in vitro*. The first group of the cellular model system comprises of pluripotent fibroblasts such as 10T1/2, BALB/c-3T3, RCJ3.1, and CHEF/18 fibroblast cell lines that can differentiate into myocytes, chondrocytes and adipocytes (Sarjeant & Stephens, 2012). However, low proliferative capacity and inconsistent differentiation potential during passaging limit the use of primary preadipocytes for the said purpose (Fève, 2005). Therefore, the alternative source of preadipocytes to study the mechanism of adipogenesis are now mainly derived from transgenic mice (Valet *et al.*, 2002). Fibroblast-like preadipocytes derived from these animal models including 3T3-L1, 3T3-F422A, 1246, Ob1771, TA1, and 30A5 that can differentiate into adipocytes are now commonly used to study adipogenesis in a laboratory setting (Sarjeant & Stephens, 2012).

Among these, 3T3-L1 and 3T3-F422A are well-characterized preadipocytes cell lines and widely used to study adipocyte biology *in vitro*. Todaro and Green first isolated 3T3 cells (Green & Meuth, 1974). These cells were obtained from 17 to 19-day-old Swiss 3T3 mouse embryos via clonal isolation (Green & Kehinde, 1979). They are highly preferred because of their capacity to develop a homogeneous mature adipocytes population which is biochemically and morphologically indistinguishable from adipocytes *in situ*. This cell line can be passaged with minimal fall in differentiation potential and is sensitive towards lipogenic and lipolytic drug treatment (Ali *et al.*, 2013; Sarjeant & Stephens, 2012). Moreover, the confluent fibroblastic 3T3 cells can undergo differentiation to become lipid-filled and round-shaped adipocytes when stimulated appropriately using hormonal inducer for *in vitro* study (Green & Kehinde, 1975).

2.1.4 Hormonal Inducers of Adipogenesis

Post-confluent preadipocytes require a suitable mixture of adipogenic inducing agents to initiate adipogenesis. There are various mixtures of adipogenesis hormonal inducers developed based on the origin of preadipocyte cell lines and the differentiation protocols (Gregoire *et al.*, 1998; Hwang *et al.*, 1997). Nevertheless, the standard adipogenesis differentiation inducer mixture that is widely in use is isobutyl-methyl-

xanthine/dexamethasone/insulin (MDI) which was discovered by (Student et al., 1980). The isobutyl-methyl-xanthine is a non-competitive phosphodiesterase inhibitor which elevates intracellular cAMP level and activates protein kinase A by phosphorylation and eventually activates cAMP response element-binding protein (CREB) to initiate adipogenesis (Essayan, 2001; Farmer, 2006). Then, the phosphorylated CREB initiates the expression of adipogenic transcription factors (Birsoy et al., 2008). In addition, dexamethasone is a well-known artificial glucocorticoid analogue that binds and activates glucocorticoid receptor and hence activates transcription factors of adipogenesis at the early stages of differentiation (Lee et al., 1991). However, it may exert inhibitory effect if added at the later stage of the differentiation process, indicating that the effects of hormones are only required during the induction phase of adipogenesis (Caprio et al., 2007). On top of that, the presence of insulin is utmost important throughout adipogenesis (induction and maintenance) since insulin signaling is crucial for proliferation and differentiation of preadipocytes (Ailhaud, 1982). Insulin is the peptide hormone that also suppresses lipolysis and support lipogenesis by promoting glucose uptake for the synthesis of triglycerides in adipocytes (Chen et al., 2016).

2.2 Transcriptional Regulation of Adipogenesis

The differentiation of preadipocytes to adipocytes is highly regulated by a network of transcription factors that direct the expression of key adipogenic proteins responsible for the maturation of adipocytes (Farmer, 2006). The peroxisome proliferator-activated receptor γ (PPAR γ), and the CCAAT/enhancer binding proteins (C/EBPs) such as C/EBP α , β and δ are the main regulators of adipogenesis. *In vitro* induction of adipogenesis by hormonal cocktail activates the expression of C/EBP β and C/EBP δ (Ramji & Foka, 2002). C/EBPs tend to accumulate within 24 hours of adipogenesis induction and initiate mitotic clonal expansion. Subsequently, the glycogen synthase kinase-3 β and mitogen-activated protein kinase (MAPK) phosphorylate and activate

C/EBP β which then together with C/EBP δ induces the expression of PPAR γ and C/EBP α (Tang *et al.*, 2005). PPAR γ and C/EBP α are the two principal transcription factors that regulate the entire process of adipogenic differentiation in mammalian cells (Lefterova & Lazar, 2009). Following their expressions, both PPAR γ and C/EBP α cross activate each other by a positive feedback mechanism and also transactivate a huge group of downstream target genes that determine the fate of adipocytes (Elberg *et al.*, 2000). The accumulated C/EBP α on the day 2 of differentiation stage is phosphorylated by cyclin D3 protein which leads to the inhibition of cell proliferation to facilitate the final differentiation stage of adipogenesis (Wang *et al.*, 2006). Figure 2.2 summarizes the transcriptional control of adipogenesis at different stages of preadipocyte differentiation.



Figure 2.2: Differentiation from preadipocyte to mature adipocyte and the transcriptional control at different stages of adipogenesis. C/EBP β together with C/EBP δ induces the expression of PPAR γ and C/EBP α during the early phase of adipogenesis. Heterodimerization of RXR with PPAR γ enables the DNA binding of PPAR γ which then induces the expression of adipocyte-specific genes in matured adipocytes. Retinoid X receptor alpha; Adapted and modified from (Esteve, 2014).

2.2.1 Peroxisome Proliferator-Activated Receptor y

Peroxisome Proliferator-Activated Receptor γ (PPAR γ) is a member of ligandactivated transcription factors which binds to the target gene promoter to activate gene transcription of proteins involved in various biological processes including energy metabolism, cell proliferation and inflammation (Kersten, 2002). PPAR γ forms a heterodimer with retinoid X receptor (RXR) which enables DNA binding at PPAR γ target genes through interactions with PPAR γ -response element (Tontonoz & Spiegelman, 2008).

PPARy1 and PPARy2 are the two protein isoforms of PPARy which are expressed as a result of splicing and alternate promoter usage (Zhu et al., 1995). Although both PPARy1 and PPARy2 are plentifully expressed in adipose tissues, inactivation of PPARy2 in 3T3-L1 cells blocks adipogenic differentiation while PPARy1 had no effect on adipogenesis (Ren et al., 2002). Moreover, selective PPARy2 deficiency impairs the development of white adipose tissue, reduces lipid accumulation and down-regulates the expression of adipogenic genes in mice (Zhang et al., 2004). This suggests that PPARy2, not PPARy1, plays the regulatory role in adipogenesis. Emerging evidence has demonstrated that PPARy is the master regulator of adipogenesis whereby its absence impairs the capability of preadipocytes to differentiate into adipocytes (Barak et al., 1999; Rosen et al., 1999). Rosen et al. further showed that ectopic expression of C/EBPa in embryonic fibroblast cells lacking PPARy prevents the cells to differentiate (Rosen et al., 2002) while Wu *et al.* showed overexpression of PPAR γ 2 in C/EBP α -null embryonic fibroblast cells restores adipogenesis (Wu et al., 1999). These studies conclusively reveal that PPAR γ 2 is the significant transcriptional regulator of adipogenesis and that C/EBP α may co-regulate the expression of PPAR γ 2. In addition, the failure of PPAR γ -deficient transgenic mice to form adipose tissue further confirms the necessity of PPAR γ for the development of adipocytes both in vitro and in vivo (Barak et al., 1999). Moreover,

deactivation of PPAR γ in mature adipocytes induces insulin resistance through the downregulation of genes related to insulin signaling, lipolysis and free fatty acid intake (Gray *et al.*, 2006; Tamori *et al.*, 2002). In addition, it was shown PPAR γ hyperactivity in mice impairs obesity-induced insulin resistance while PPAR γ deletion, particularly in fat, muscle or liver, eventually leads to hyperlipidemia, hyperglycemia, or hyperinsulinemia (He *et al.*, 2003; Hevener *et al.*, 2003; Norris *et al.*, 2003). Similarly, human subjects with a dominant-negative mutation in the gene encoding PPAR γ (*PPARG*) showed potential to develop lipodystrophy and insulin resistance (Agarwal & Garg, 2002).

The presence of a ligand is important for PPARy to repress and activate the target genes. PPAR ligand includes fatty acids, prostaglandins and oxidized phospholipids (Kersten, 2002). Some naturally occurring PPAR agonists including 9, 10-dihydroxyoctadecenoic acid and 15-deoxy-D(12, 14)-PGJ(2) have been reported to promote inhibiting osteogenesis adipogenesis while (Lecka-Czernik al., 2002). et Thiazolidinediones (TZDs) are well-known synthetic ligands of PPARy and functions as insulin sensitizers in the treatment of type 2 diabetes. TZDs have demonstrated glucoselowering and improvement of insulin sensitivity in insulin-resistant animal models and patients (Evans et al., 2004). Additionally, rosiglitazone also stimulates adipogenesis in human mesenchymal stem cells (Benvenuti et al., 2007).

2.2.2 CCAAT/Enhancer Binding Proteins

The CCAAT/Enhancer Binding Proteins (C/EBPs) belong to a family of basic leucine zipper transcription factors, where C/EBP α , β and δ are the members that are well established in adipogenesis. C/EBPs are not adipocyte-specific proteins. They are also expressed in other body tissues including liver, lung, adrenal gland and placenta (Birkenmeier *et al.*, 1989; Yeh *et al.*, 1995). Interestingly, C/EBP β and δ have been found

expressed mainly during the early phase of adipogenesis while C/EBP α expression overrides in the later stage of differentiation (Cao *et al.*, 1991) (Figure 2.2). This is exemplified in embryonic fibroblasts isolated from C/EBP β and δ deficient mice that are unable to differentiate upon hormonal induction and eventually fails to express PPAR γ , C/EBP α and other adipogenic markers (Tanaka *et al.*, 1997). This suggests that *in vitro* adipocyte differentiation requires the activation of C/EBPs and PPARs that sequentially leads the transcriptional cascade for the maturation of adipocytes. However, an *in vivo* study has reported that transactivation of PPAR γ and C/EBP α can take effect in the absence of C/EBP β and δ while severely impairing the adipocyte development (Tanaka *et al.*, 1997). Therefore, it can be concluded that the presence of C/EBP β and δ is crucial for complete maturation of adipocytes both *in vitro* and *in vivo*.

2.3 Adipogenic Proteins

As the positive feedback loop of PPAR γ and C/EBP α kick-starts adipogenesis, several pro-adipogenic proteins such as fatty acid synthase (FAS), lipoprotein lipase (LPL), fatty-acid-binding proteins (FABPs) and Kruppel-like factor 15 (KLF15) are actuated for the establishment of matured adipocytes.

2.3.1 Fatty Acid Synthase

Fatty acid synthase (FAS) is the primary enzyme involved in *de novo* lipogenesis. FAS is responsible for the elongation of long-chain fatty acids for the synthesis of triglycerides via esterification with glycerol-3-phosphate (Ruderman *et al.*, 1999). Fatty acid synthesis takes place predominantly in the liver and adipose tissues. In adipocytes, FAS extends the short-chain malonyl CoA by condensation with acetyl-CoA to form long-chain fatty acids such as palmitoyl-CoA and stearoyl-CoA. Since FAS promotes fatty acid synthesis and fat accumulation, several studies have demonstrated its significant role in the development of adipocytes and obesity (Berndt *et al.*, 2007; Kovacs *et al.*, 2004; Kumar

et al., 2002). Therefore, this key lipid metabolizing enzyme found abundantly in adipose tissue is a potential drug target to attenuate excess fat storage. In fact, inhibition or downregulation of this protein has been shown to reduce adipocyte differentiation, lipid synthesis and activate fat oxidation and energy expenditure in a transgenic mouse model (Lenhard, 2011). For example, it was shown that FAS inhibition by a potent inhibitor of fatty acid synthase, C57 significantly reduces the body weight of obese mice by suppressing food intake (Kumar *et al.*, 2002). Likewise, it was shown that inhibition of FAS by another inhibitor of FAS, tannic acid in 3T3-L1 pre-adipocytes impairs adipogenesis, represses intracellular lipid accumulation and downregulates mRNA levels of FAS and PPARγ (Fan *et al.*, 2013).

2.3.2 Lipoprotein Lipase

Lipoprotein lipase (LPL) is a glycoprotein synthesized in parenchymal cells and is mainly found in adipose and muscle tissues (Bouvy-Liivrand *et al.*, 2014). LPL is an extracellular lipid-lysing enzyme that is responsible for the hydrolysis of lipids. This is essential to facilitate the rapid clearance of lipid load by releasing free fatty acids from circulating triglycerides for adipose and skeletal muscle tissue uptake. The lipolytic function of LPL is highly controlled by several cofactors. The apolipoprotein C-II in plasma activates while apolipoprotein C-III inhibits the lipolytic activity of LPL (Kinnunen *et al.*, 1977; Schoonjans *et al.*, 1999). Insulin has also been shown to regulate the activity of LPL during adipogenesis in 3T3-L1 cells (Semenkovich *et al.*, 1989). Interestingly, PPAR response element is found in human LPL promoter site and PPAR γ agonist upregulates the mRNA level of LPL in 3T3-L1 preadipocytes suggesting that PPAR γ could be the upstream regulator of this lipolytic enzyme (Schoonjans *et al.*, 1996). Furthermore, increased expression of PPAR γ during adipogenesis also elevates the expression of LPL and promotes lipid accumulation in adipocytes (Naowaboot *et al.*, 2014). In addition, reduced LPL activity is associated with coronary artery disease while the increased activity may lead to hypotriglyceridemia due to the imbalanced distribution of fatty acids (Schneider *et al.*, 2002).

The circulation of free fatty acids within the body could be altered by the variation in the tissue-specific expression pattern of LPL (Preiss-Landl *et al.*, 2002). LPL also has a gatekeeping role in directing the lipid deposition in other tissues (Greenwood, 1985). Free fatty acids are moved into adipose tissue for storage in the event of increased ratio of adipose tissue to muscle LPL activity which is common in obese individuals while the direction of the free fatty acid flow is reversed from the storage to oxidation in muscle if the above ratio is switched the other way around (Kern, 1997). Hence, the activity of LPL is boosted in muscles and fat tissues of individuals who are physically active and obese, respectively (Kern, 1997).

2.3.3 Fatty-Acid-Binding Proteins

Fatty-acid-binding proteins (FABPs) are carrier proteins with high affinity for saturated fatty acids, unsaturated fatty acids and eicosanoids. They facilitate the entry of fatty acids across the plasma membrane, distribute fatty acids within the cell, determine fatty acids storage compartments, regulate fatty acid metabolic enzyme activity and protect the enzymes and membrane from detergent-like effects of fatty acids (Vogel Hertzel & Bernlohr, 2000). FABPs are comprised of nine family members and expressed in various tissues including liver, intestine, heart, lungs, brain and testis. Among the nine members, FABP4 is predominantly expressed in adipocytes and macrophages. The FABP4 also known as 14-15 kDa size adipocyte lipid-binding protein (ALBP) and adipocyte protein 2 (aP2). It is estimated that 3% of the total soluble cellular protein is composed of aP2 in 3T3-L1 cells (Coe & Bernlohr, 1998). Chronic exposure to high extracellular lipids can elevate aP2 level in adipocytes, indicating that fatty acid exposure regulates aP2 expression (Veerkamp & Van Moerkerk, 1993). A previous research

finding has shown that FABP4-deficient mouse preadipocytes displays elevated PPAR γ expression and enhances adipogenesis compared to wild-type cells (Garin-Shkolnik *et al.*, 2014). This group also demonstrated that FABP4 induces proteasomal degradation of PPAR γ by stimulating ubiquitination and hence, suggests that FABP4 negatively regulates adipogenesis by downregulating PPAR γ in adipocytes (Garin-Shkolnik *et al.*, 2014). FABPs also build up fatty acid pool in the cytoplasm to increase substrate availability for lipid metabolizing enzymes such as glycerol-3-phosphates or hormone-sensitive lipase (Haunerland & Spener, 2004). In addition, FABP4 also directly interact with hormone-sensitive lipase and participate in lipolysis by transporting the free fatty acids generated after hydrolysis of triglycerides (Shen *et al.*, 1999).

2.3.4 Kruppel-Like Factor 15

Kruppel-like factors (KLFs) are members of zinc-finger transcription factors which are crucial regulators of adipose tissue development. The presence of highly conserved Cys2/His2 zinc fingers in triplets is a unique feature of the KLF family (Bieker, 2001). The three zinc fingers at the carboxyl-terminal allow KLFs to bind at GC- and CACCCboxes of DNA for transactivation (Turner & Crossley, 1999). Among all KLF member, KLF 15 is abundantly expressed in adipose, kidney, liver, heart and skeletal muscle tissues and is involved in adipogenesis (Uchida *et al.*, 2000). Mori and coworkers showed that the expression of KLF 15, which is a downstream effector of C/EBP β or C/EBP δ increases at day 6 of adipogenesis in 3T3-L1cells (Mori *et al.*, 2005). However, inhibition of KLF 15 could impair PPAR γ , C/EBP α , aP2, or glucose transporter 4 (GLUT4) expression while its overexpression could raise PPAR γ during an earlier stage of differentiation (Wu & Wang, 2013). Apart from this, overexpression of KLF 15 in adipocytes could also initiate adipocyte maturation and modulates gluconeogenesis by increasing GLUT4 expression (Gray *et al.*, 2002). On the other hand, reduced KLF 15 expression was formerly observed in adipose tissue of diet-induced obese mice while KLF15^{-/-} mice are prevented from high fat diet-induced insulin resistance and also suffered from hypoglycemia after an overnight fast (Gray *et al.*, 2007; Sartoretto *et al.*, 2008). Therefore, these findings are suggestive of possible central role attributed to KLF15 in modulating glucose and lipid metabolism.

2.4 Signaling Pathways Involved in Adipogenesis

Adipogenic differentiation involves the commitment of numerous cellular signaling pathways to control PPAR γ and C/EBP α , the key regulators of adipogenesis. Extensive studies on fat cell biology have unveiled several signaling pathways that play an important regulatory role in this differentiation process. These pathways include insulin signaling, adenosine monophosphate (AMP)-activated protein kinase (AMPK), mitogen-activated protein kinase (MAPK), Wnt signaling, and histone deacetylase Sirtuin 1 (Sirt1) signaling pathways.

2.4.1 Insulin Signaling Pathway

Insulin is required throughout preadipocytes differentiation and hence insulin signaling is crucial for adipogenesis. Although the regulation of glucose and lipid metabolism is the ultimate role of insulin, it also regulates the growth and differentiation of adipose tissue (Shaham *et al.*, 2008). Insulin performs its biological role by docking to the insulin receptor (IR), a tyrosine kinase that will be phosphorylated and activated upon insulin binding. Furthermore, insulin receptor substrate (IRS) proteins act as the bridging molecule connecting IR activation to downstream kinase cascades for the activation of several pathways including phosphatidylinositol 3-kinase PI3K and MAPK pathways (Fritsche *et al.*, 2008; Mi *et al.*, 2015)

It has been reported that the inhibition of insulin-dependent IR activation during the early phase of adipogenesis prevents the activation of PI3K/AKT pathway and blocks the differentiation in 3T3-L1 preadipocytes (Kwon *et al.*, 2012). Moreover, mice adipose
tissue lacking IR have reduced fat mass and levels of C/EBP α , further revealing the significance of insulin signaling to sustain the physiological functions of adipocytes (Blüher *et al.*, 2002). Similarly, in IRS-1and IRS-2 double-deficient mouse embryonic fibroblast cells, adipogenesis is severely impaired together with reduced expression of PPAR γ , C/EBP α and its downstream adipogenic markers (LPL and FABP) (Miki *et al.*, 2001). Numerous antiadipogenic agents were reported to regulate the cellular differentiation of adipocytes via insulin-mediated signaling pathways, indicating the importance of IRS proteins in mediating insulin signaling that governs adipogenesis-associated downstream signaling pathways (Liu *et al.*, 2014; Mi *et al.*, 2015; Yoon *et al.*, 2013; Zang *et al.*, 2013).

2.4.2 AMP-activated Protein Kinase (AMPK) Pathway

AMP-activated protein kinase (AMPK) is an energy metabolic sensor and regulator that is involved in energy balance including food intake and calorie expenditure. Impairment of AMPK in energy homeostasis leads to metabolic disorders and cardiovascular diseases (Lage *et al.*, 2008). Elevated AMP: ATP ratio in the event of metabolic stress induced by a drop in cellular ATP level activates AMPK. In addition, AMPK is allosterically activated by AMP to monitor energy balance within the cell by restoring AMP: ATP ratio via modulating metabolic process that produces or consumes ATP in various body tissues (Kahn *et al.*, 2005).

Interestingly, AMPK is a key regulator of lipid metabolism. AMPK phosphorylates and modulates several regulatory enzymes participating in sterol and fatty acid syntheses such as hydroxymethyl-glutaryl-CoA reductase and acetyl-CoA carboxylase (ACC) (Hadie & Carling, 1997). The upregulation of phosphorylated AMPK α increases ACC activity and reduces PPAR γ , C/EBP α and FAS expression and leads to the inhibition of adipogenesis (He *et al.*, 2013; Kim *et al.*, 2014). On the contrary, suppression of AMPK α

phosphorylation could also reduce the expression of adipogenic transcription factors and eventually impairs cellular differentiation in 3T3-L1 cells suggesting that AMPK plays contradicting roles in modulating adipogenesis (Choi et al., 2015). Activated AMPK not only induces fatty oxidation but also inhibits fatty acid synthesis by reducing the malonyl-CoA levels during physical activities in muscles, liver and hypothalamus (Kahn et al., 2005; López et al., 2007). Moreover, AMPK also attenuates lipolysis by impairing protein kinase (PKA)-mediated hormone-sensitive lipase (HSL) activation А and phosphorylating HSL as observed previously in adipocytes (Dagon et al., 2006; Sullivan et al., 1994). However, cAMP-mediated activation of AMPK leads to activation of lipolysis in 3T3-L1 adipocytes (Yin et al., 2003). Mice fed a high-fat diet lacking both AMPK α 1 and AMPK α 2 have increased fat mass as compared with its wild-type (Villena et al., 2004; Zhang et al., 2012). Interestingly, AMPK could favor adipogenesis via different signaling pathways such as extracellular signal-regulated kinase (ERK) pathway, Akt/mTOR signaling and Wnt/β-catenin pathway (Kim et al., 2012; Pantovic et al., 2013; Zhao et al., 2011). In addition, AMPK signaling is modulated by several compounds such as apigenin, ursolic acid and indole-3-carbinol which are also reported to inhibit adipogenesis and stimulate lipolysis via 3T3-L1 cells (Choi et al., 2014; He et al., 2013).

2.4.3 Mitogen-Activated Protein Kinase (MAPK) Pathway

The extracellular signal-regulated kinases (ERKs) 1 and 2; c-Jun amino-terminal kinases (JNKs) 1, 2 and 3; and p38 MAPK (p38) α , β , γ , and δ are MAPKs mainly involved in coordinating intracellular signaling pathway in cellular proliferation and differentiation (Jeffrey *et al.*, 2007). Numerous studies have elucidated the role of MAPKs in adipogenesis. The involvement of ERK in adipocyte differentiation was first demonstrated through the overexpression of Ras, a potent activator of ERK pathway which leads to adipogenesis in 3T3-L1 preadipocyte cells (Benito *et al.*, 1991). Moreover,

Sale *et al.* have confirmed that ERKs are required for adipogenic differentiation of preadipocytes (Sale *et al.*, 1995). However, it is shown that ERK-mediated phosphorylation of PPAR γ impairs its transcriptional activity and blocks adipogenesis, suggesting that ERK could play both positive and negative regulatory roles in modulating adipocyte differentiation (Camp & Tafuri, 1997). On the other hand, *in vivo* study with ERK1 deficient mice on the high-fat diet showed reduced adiposity and decreased insulin resistance (Bost *et al.*, 2005). Besides this, inhibition of p38MAPK during the early phase of adipogenesis could impair C/EBP β phosphorylation and its transactivation activity leading to reduced adipose cell formation. On top of that, mice lacking JNK1 were prevented from HFD-induced weight gain and have improved insulin sensitivity while JNK phosphorylation inhibition promotes adipogenesis in 3T3-L1 cells (Hirosumi *et al.*, 2002; Liu *et al.*, 2014).

2.4.4 Wnt Signaling Pathway

Wnts are glycoproteins that bind to frizzled (FZD) transmembrane receptors to initiate a tightly preserved signaling pathway that possesses a crucial role in regulating several biological processes including cell proliferation and differentiation (Logan & Nusse, 2004). This signal transduction takes place in two ways; either through canonical (β catenin dependent) or non-canonical (β -catenin independent) pathways (Strutt, 2003; Veeman *et al.*, 2003). In the canonical pathway, β -catenin is the main transcriptional activator for the transactivation of Wnt target genes. In the absence of Wnt, cytoplasmic β -catenin is engaged to a degradation complex composed of Axin and adenomatous polyposis coli (APC), which allows phosphorylation by casein kinase I and glycogen synthase kinase 3- β (GSK3 β) and eventually leads to ubiquitination and proteasomal degradation. However, in the presence of Wnt, the binding of Wnt to FZD receptors and low-density-lipoprotein-receptor-related protein-5 or -6 (LRP5/6) co-receptors inactivates the degradation complex and subsequently induces hyperphosphorylation of β -catenin. The activated β -catenin translocates to the nucleus and binds to lymphoidenhancer-binding factor/T-cell-specific transcription factor (LEF/TCF) family of transcription factors to activate Wnt target genes (Christodoulides *et al.*, 2009).

Interestingly, Wnt signaling specifically through the canonical pathway has been reported to inhibit adipogenesis *in vitro*. Initiation of Wnt signaling leads to dysregulation of the cell cycle, blocked mitotic clonal expansion, impaired PPAR γ and C/EBP α expression and eventually inhibits adipogenic differentiation in 3T3-L1 preadipocytes (Ross *et al.*, 2002). Moreover, disruption of intracellular Wnt signaling by overexpression of Axin or dominant-negative TCF4 in 3T3-L1 preadipocytes activates adipogenesis (Ross *et al.*, 2000). Besides this, the expression of a Wnt signaling activator, Wnt10b was found elevated in preadipocytes and declined upon induction of adipogenesis (Bennett *et al.*, 2002). However, ectopic expression of Wnt10b stabilizes β -catenin and impairs adipogenesis in 3T3-L1 preadipocytes (Krishnan *et al.*, 2006). On the other hand, FABP4-mediated Wnt10b expressing transgenic mice showed reduced total body fat, improved sensitivity towards glucose and insulin as well as prevented from HFD-induced adipose tissue accumulation (Longo *et al.*, 2004).

2.4.5 Sirtuin1 Signaling Pathway

Sirtuins (Sirts) are histone deacetylases, known to regulate numerous physiological processes including inflammation, cellular senescence, proliferation, and metabolism. Although seven mammalian sirtuin proteins (Sirt1-Sirt7) have been discovered, Sirt1 is the most well-studied human sirtuin protein (Chung *et al.*, 2010). Sirt1 is a nuclear protein that plays a crucial regulatory role in cellular metabolic and physiological processes by its deacetylase activity on histones and non-histone proteins which include nuclear factor (NF)- κ B, FOXO3, p53, PPAR γ , PPAR- γ coactivator 1 α (PGC-1 α), and endothelial nitric oxide synthase (eNOS) (Yang & Sauve, 2006). In addition, Sirt1 also modulates

adipogenesis and lipolysis. Sirt1 inhibits transactivation of PPAR γ by interacting with nuclear receptor co-repressor and silencing mediator of retinoid and thyroid hormone receptors (SMRT), which then reduces adipogenesis and induces lipolysis (Picard *et al.*, 2004). However, the absence of Sirt1 in adipocytes promotes PPAR γ hyperactivity and hence increases adipocytes differentiation (Picard *et al.*, 2004). On top of that, adipocyte-specific Sirt1 knock-out mice on HFD exhibited increased adipocyte hypertrophy and reduced sensitivity towards glucose and insulin (Mayoral *et al.*, 2015). It has been reported that overexpression of Sirt1 reduces the mRNA levels of C/EBP α , C/EBP δ and aP2 in 3T3-L1 preadipocytes further proving that Sirt1 negatively regulates adipocyte differentiation (Mayoral *et al.*, 2015).

Interestingly, numerous studies have reported Sirt1 inhibits adipogenesis through nucleocytoplasmic signaling modulation of FoxO1 (Lai et al., 2012; Lee et al., 2017; Tseng et al., 2011). Sirt1 binds and deacetylates FoxO1 at three residues within the DNA binding domain to promote nuclear entry (Daitoku et al., 2004; van der Heide & Smidt, 2005). Upon nuclear translocation, FoxO1 binds to peroxisome proliferator response elements (PPRE) then interferes with DNA occupancy of PPARy and inhibits its transcriptional activity thereby impairs gene expression of adipogenic markers which is essential for the maturation of adipocytes (Armoni et al., 2006; Wang & Tong, 2009). On the other hand, FoxO1 acetylation in the absence of Sirt1 promotes adipogenesis in 3T3-L1 preadipocytes by increasing the expression of adipogenic transcription factors (Ahn et al., 2013). However, acetylation of FoxO1 promotes its phosphorylation by PI3K/Akt pathway that initiates nuclear export to the cytoplasm and eventually ubiquitination followed by proteasomal degradation (Matsuzaki et al., 2005). Therefore. phosphorylation of FoxO1 transactivates PPARy and induces adipogenesis in 3T3-L1 cells (Daitoku et al., 2011).

2.5 Development of adipose tissues and obesity

Vertebrates store excess calories in the form of lipids in adipocytes and hence the building up of fat cells leads to the formation of adipose tissues in the body. Adipose tissues possess a crucial role in regulating the levels of free fatty acid and triglycerides in circulation, however, excessive accumulation results in promoting the progression of obesity. It has been shown that adipose tissue development is mediated either by hyperplasia or hypertrophy of adipocytes (Wolfram *et al.*, 2006). An increase in the adipocyte size upon continuous lipid accumulation is termed as hypertrophy (Christodoulides *et al.*, 2009).

Adipocyte hypertrophy is associated with reduced insulin sensitivity which is a risk factor for developing type 2 diabetes even in lean individuals (Arner *et al.*, 2010). In addition, individuals with hypertrophic obesity are more susceptible to poorer metabolic profile as compared to those with hyperplastic obesity (Hoffstedt *et al.*, 2010). A short-term weight gain study in lean men showed that adipocytes size increased significantly following weight gain, yet adipocytes number remain unchanged (Salans *et al.*, 1971). Furthermore, several other reports also confirm that significant reduction in adipose tissue as a result of weight loss is mediated by the decrease in the adipocytes size and not due to a decrease in adipocytes number (Häger *et al.*, 1978; Spalding *et al.*, 2008). Generally, there are two types of adipose tissue, white adipose tissue (WAT) and brown adipose tissue (BAT) that play important regulatory roles in energy homeostasis (Figure 2.3).



Figure 2.3: White and brown adipose tissue specimen stained with hematoxylin and eosin. WAT specimen shows a single large lipid vacuole in each white fat cell. BAT specimen shows granular cytoplasm containing mitochondria and multiple fat vacuoles. Adapted and modified from (van Marken Lichtenbelt *et al.*, 2009).

2.5.1 White Adipose Tissue

The white adipose tissue is composed of 25% of human body weight and its main role is to store energy in the form of lipids in the event of calorie abundant and act as an energy source during calorie deprivation. The fatty acids are stored in a large unilocular lipid droplet that occupies over 90% of the cell volume leaving very minimal space for other cellular organelles (Figure 2.3). It has been reported that approximately 60 to 80% of WAT cells are not homogenously mature adipocytes, but vascular stroma cells composed of preadipocytes, macrophages, stem cells, and endothelial cells (Tchoukalova *et al.*, 2004). In addition, WAT also serves as a thermal insulator and mechanical shock absorber for internal body organs (Trayhurn, 2007). Excessive accumulation of WAT has been involved in the development of obesity-related disorders. However, the distribution of fat is considered more important than its total amount in determining the risk of obesityassociated diseases. Adipose tissues accumulation in the upper body (abdominal fat) is mainly associated with the development of metabolic diseases (Goossens, 2017). Interestingly, WAT has metabolic (lipogenesis, fatty acid oxidation, and lipolysis) and endocrine (production of adipokines) functions (Boudina & Graham, 2014). Moreover, WAT is also recognized as a crucial endocrine organ that secretes various adipokines (cytokines produced by adipocytes) such as leptin, adiponectin, tumor necrosis factor- α , interleukin-6, and resistin to modulate appetite, calorie expenditure, sensitivity towards insulin, inflammation and coagulation (Hauner, 2005). Therefore, the involvement of these secretory hormones in overall metabolic regulation is also directly linked to the development of obesity and its comorbidities.

2.5.2 Brown Adipose Tissue

The brown adipose tissue is an energy-expending and heat producing fat tissue found abundant in hibernating animals and infants that helps in maintaining body temperature. In contrast to WAT, brown adipocytes contain multilocular lipids in small-vesicles, central nucleus and numerous mitochondria which is attributed to the brown colour of BAT (Cinti, 2009) (Figure 2.3). Brown adipose tissue is distributed throughout the cervical, supraclavicular, axillary, paravertebral, mediastinal, and upper abdominal areas to warm the blood supply to important body organs (Wehrli *et al.*, 2007). The multiple small cytosolic lipids serve as fuel for oxidative phosphorylation and heat production that is predominantly controlled by high-density mitochondria in the BAT (Feldmann *et al.*, 2009). The ultimate role of BAT is to dissipate energy via heat production and this is mediated by the mitochondrial transmembrane protein, uncoupling protein-1 (UCP1) that consequently increases fatty acid oxidation as well as induces thermogenesis (Klingenberg, 1999; Mattson, 2010). It was previously shown that chronic cold exposure prevents diet-induced obesity in mice by boosting thermogenesis of BAT via UCP1 activation (Ma *et al.*, 2012).

2.6 Obesity

Obesity has become a global epidemic and hence considered as a major public health issue in both developed and developing countries. Earlier, obesity was prevalent among adults regardless of their genders, however, the worldwide incidence of childhood obesity has also increased dramatically in recent years (Sabin & Kiess, 2015). There are several factors that contribute to the development of obesity such as high intake of energy-dense foods, reduced physical activity, sedentary lifestyle, modern transportation and rapid urbanization (Jeffery & Utter, 2003). Obese individuals are highly susceptible to serious non-communicable diseases such as type 2 diabetes, cardiovascular disease, osteoarthritis, dyslipidemia and some cancers in which elevates the rate of obesity-mediated mortality and morbidity (Garg *et al.*, 2014; Martin-Rodriguez *et al.*, 2015).

Obesity is caused by impaired energy balance when calorie intake surpasses total calorie spent which is mediated by the basal level of metabolism, physical activities and thermogenesis (Hill *et al.*, 2012). Excess calorie intake with physical inactivity promotes energy storage in the form of lipids and leads to the expansion of adipose tissue. Over a period of time, abnormal or excessive fat accumulation in the body eventually end up with increased body weight and leads to the obese condition. Several methods to measure body fat have been identified which includes skinfold measurement, waist circumference and body mass index (BMI) (Pi-Sunyer, 2002). Among them, BMI is a widely used method to classify overweight and obesity in adults. By definition, BMI is the ratio of kilograms by the square to height in meters (kg/m^2) of a person. Asian individuals with BMI \geq 23 are overweight while those with BMI \geq 27.5 are classified as obese (Deurenberg *et al.*, 1998; Ko *et al.*, 2001). It has been reported that Asians are prone to type 2 diabetes, hypertension, and dyslipidemia at lower levels of BMI which has a greater degree of obesity compared with Caucasians (Zaki *et al.*, 2010). The WHO has projected that in 2030, Malaysia would have a 164% increase in total number of diabetics compared to the

patient population recorded three decades ago (Mafauzy, 2006). Hence, obesity has become a major clinical and public health issue that threatens to surpass already expended healthcare services in Malaysia. Table 2.1 shows the classification breakdown of BMI in details.

BMI (kg/m ²)	Classification
< 18.5	Underweight
18.5 - 22.9	Normal
23.0 - 27.5	Overweight
> 27.5	Obese

 Table 2.1: BMI classification. Adapted from (Organization, 2017).

2.6.1 Insulin Resistance

Insulin resistance is a condition of reduced sensitivity of insulin-target tissues such as muscle, adipose and liver tissues as well as other body tissues towards insulin regardless of its normal or elevated level in the blood (Perseghin *et al.*, 2003). Insulin sensitivity is determined by body fat distribution. Studies on obese human subjects have shown that increased visceral but not subcutaneous adipose tissue mass contributes to the development of insulin resistance (Group & Group, 2003; McLaughlin *et al.*, 2011). Furthermore, abdominal fat is considered more lipolytic than subcutaneous fat, and it also hinders the antilipolytic action of insulin, which makes it highly important in causing insulin resistance, and increases the risk of developing diabetes (Roden *et al.*, 1996). Inflammation and hyperinsulinemia are important obesity-mediated risk factors for insulin abnormalities (Ye, 2013). The secretion of pro-inflammatory cytokines by adipose tissue-resident immune cells, mainly by macrophages facilitates the obesity-induced inflammation (Lee & Lee, 2014). As a result, the insulin signaling pathway in adipocytes

and hepatocytes is repressed through inhibition of IRS-1, reduction of PPAR γ activity as well as stimulation of lipolysis (White, 2002; Ye, 2008).

Hyperinsulinemia, a condition of elevated fasting plasma insulin as a consequence of either increased insulin production or reduced insulin clearance may also contribute to insulin resistance in obese people (Ye, 2007). Overproduction of insulin in transgenic mice and an overdose of insulin in human has resulted in hyperinsulinemia and subsequently lead to insulin resistance (Shanik et al., 2008). Insulin-mediated metabolic pathways such as glucose transport, glycogen synthesis and anti-lipolysis are severely impaired under the condition of insulin resistance which is also highly associated with the development of hypertension, type 2 diabetes, dyslipidemia and fatty liver diseases (Bray, 2004). In adipose tissue, reduced insulin sensitivity attenuates insulin-stimulated glucose uptake and anti-lipolytic effect of insulin thereby impairs the physiological functions of adipocytes (Hardy et al., 2012). Dietary modification, calorie restriction and enhanced physical activity among obese people have been shown to reduce weight as well as improve insulin sensitivity (Murphy et al., 2011). In addition, weight loss promoting drugs such as orlistat and sibutramine have also resulted in better glycemic control in parallel with body weight reduction in diabetic obese patients (McNulty et al., 2003; Miles et al., 2002). Furthermore, in vivo studies have demonstrated that boosted exercise in a high-fat-diet-induced obese rat resulted in inflammatory suppression in the liver, muscle and adipose tissues on par with enhanced insulin signaling (Oliveira et al., 2011).

2.7 Managing Obesity and Related Complications

The main therapeutic approach in managing the prevalence of obesity and its comorbidities such as cardiovascular diseases is by weight management. Obese individuals can achieve significant weight reduction at individual-level through their diet and lifestyle modification as well as by switching to available pharmacological intervention and surgery (Health, 1995; Wing *et al.*, 2001). A balance between calorie intake and expenditure is a must for weight management and hence, calorie restriction is one of the popular approaches for weight-loss in the obese subject (Hill *et al.*, 2012; Wadden *et al.*, 2012). Moreover, limiting calorie to ~ 1100 kcal/day promotes weight reduction, decreased liver lipid content, improved insulin sensitivity in skeletal muscle and liver as well as reduced basal glucose production rate in obese patients (Kirk *et al.*, 2009). A prior study has shown that dietary modification such as consuming more vegetables, fruits, whole grains, nuts, and yogurt negatively correlate with long-term weight gain, however, resulted otherwise in subjects consuming more junk foods, sugar-sweetened beverages, processed meats and fast food (Mozaffarian *et al.*, 2011).

In addition, implementing physically active lifestyle also contributes to the prevention of weight gain or induces weight loss. Active lifestyle in combination with diet management produces better results in obtaining and maintaining healthy body weight. A prior study in sports medicine has recommended that at least 150-250 minutes/week of moderate physical activities for overweight and obese individuals since it is associated with overall health improvement, long-term weight loss and prevention of weight regain when accompanied by dietary control (Donnelly *et al.*, 2009). In this regard, several other studies have shown that obese patients whom regularly engage in moderate to highintensity physical exercise have reduced BMI, percentage body fat and hepatic steatosis, better glycemic control, as well as improvement in the cardiovascular health, insulin resistance and lipid profile (Bluher *et al.*, 2014; Ho *et al.*, 2012; Khoo *et al.*, 2015; Little *et al.*, 2014; Monteiro *et al.*, 2015; Oh *et al.*, 2014; Rock *et al.*, 2014).

On the other hand, obesity surgeries such as liposuction and bariatric surgery are also being practised as an alternative weight reduction method especially in a morbidly obese subject who are unable to withstand weight loss by nonsurgical means and suffers from obesity-related comorbidities. Bariatric surgery has resulted in significant weight reduction, reduced the incidence of type-2 diabetic mellitus, reduced elevated blood pressure, cardiovascular diseases and improved serum lipid parameters in patients with severe obesity (Douglas *et al.*, 2015; Milone *et al.*, 2015). In addition, large-volume liposuction in extremely obese subjects reveals a positive improvement in plasma insulin, blood glucose level, insulin sensitivity, cardiovascular risk and blood pressure associated with weight loss (Boriani *et al.*, 2014; Hunstad, 1996; Narsete *et al.*, 2012). However, gastrointestinal ulceration, incisional and internal herniation and nutritional deficiency while thromboembolism, dehiscence, wound infections and seromas can be caused by bariatric surgery and liposuction in morbidly obese individuals (Eldar *et al.*, 2011; Narsete *et al.*, 2012). In addition to adopting a healthy diet, lifestyle modification and obesity surgery, the pharmacological intervention also has been proven successful in the management of obesity and its associated diseases, although some drugs are with limited efficacy or serious adverse effects.

2.8 Synthetic anti-obesity drugs

Weight-loss can be enhanced with medication, though several BMI criteria need to be met by an obese individual before receiving anti-obesity pharmacotherapies. Generally, obese patients with BMI >30kg/m² or BMI of 27 kg/m² accompanied by obesity-related co-morbidities are qualified to be prescribed with anti-obesity drugs (Apovian *et al.*, 2015). Nevertheless, obese subjects on weight-loss pharmacotherapies require long-term commitment towards the prescribed medications as many individuals are subjected to weight-regain upon withdrawal. Furthermore, patients consuming these daily medications also must be aware of the cost and possible side effects. Historically, the main class of synthetic drugs used for weight-reduction in obese population is appetite suppressor and gastrointestinal lipase inhibitor which respectively target to reduce food intake and fat absorption. However, there are several other potential weight-loss drugs that are currently in the development phase. These drugs target central neuropeptide signaling, monoamine neurotransmission, intestinal peptide signaling, pancreatic hormone signaling, and adipose tissue hormone signaling (Colon-Gonzalez *et al.*, 2013). Table 2.2 shows commonly prescribed synthetic drugs for weight management in obese subjects and its associated adverse effects.

Drug	Mode of action	Side effects	References
Phentermine*	Noradrenalin	Headache,	(Smith et al., 2013)
(Fastin)	releaser	hypertension,	(Bain et al., 2014)
	Appetite	insomnia,	
	suppressant	dizziness,	
		palpitation, dry	
		mouth and	
		constipation	
Fluoxetine (Prozac)	Serotonin reuptake	Nervousness	(Ward et al., 1999)
	inhibitor	Mood depression	(Arnold et al.,
	Reduce food intake		2002)
Sibutramine*	Norepinephrine and	Headache,	Li et al., 2005)
(Meridia)	serotonin reuptake	insomnia, dry	(Luque & Rey,
	inhibitor	mouth and	2002)
	Satiety inducer	constipation	(García-Morales et
	Increase	Risk of myocardial	al., 2006)
	thermogenesis	infarction and	
		stroke in the long	
		run	
Rimonabant*	Cannabinoid-1	Nausea, anxiety,	(Leite et al., 2009)
(Acomplia)	receptor antagonist	joint pain, and	(Backhouse et al.,
	Induce lipolysis	diarrhoea	2012)
	and fatty acid	Increase VLDL	
	oxidation	secretion	
Orlistat (Xenical)	Gastric and	Diarrhoea,	(Sahebkar et al.,
	pancreatic lipase	flatulence,	2017)
	inhibitor	bloating,	(Mannucci et al.,
	Reduces dietary fat	abdominal pain and	2008)
	absorption	oily stool	(Sahebkar et al.,
	Improves		2017)
	dyslipidemia		

 Table 2.2: Examples of common synthetic anti-obesity drugs.

Note: *Withdrawn from the market due to life-threatening adverse effects

2.9 Naturally-derived Anti-adipogenic/Obesity Drugs

The pharmacological methods to address obesity are losing popularity since the presently available anti-obesity drugs have considerable serious adverse effects, prone to tolerance and only provide short-term weight loss. Therefore, there is still a need to find novel, safe and cost-effective therapeutic approaches although several possible targets to treat obesity have been recently discovered (Mayer et al., 2009). Traditionally employed herbal based medicines have been very popular worldwide in recent years due to their natural origin, nutraceutical properties and acknowledgement by national health authorities (Who, 2013). In recent years, studies of natural products including crude extracts and isolated natural pure compounds have provided evidence for their preventive and therapeutic potentials in the management of obesity (Vermaak et al., 2011). Several bioactive compounds abundantly found in medicinal plants, fruits and vegetables have been proven to inhibit adipogenesis, induce lipolysis and prevent the development of obesity in vitro, in vivo as well as in obese human subjects (Kim et al., 2015; Song et al., 2013; Wang et al., 2014). The ability to modulate adipose tissue functions by phytochemicals underscores the potential of these molecules for the development of novel phytotherapeutic approaches for obesity treatment (Table 2.3).

Phytochemical	Bioactive	Effects	References
	compound		
	(Source)		
Polyphenols	Ferulic acid	↓ high fat diet-induced	(Son <i>et al.</i> , 2010)
	(plant cell wall)	obesity, serum	(Naowaboot et al.,
		triglyceride and	2016)
		cholesterol level in mice	
		\downarrow insulin resistance and	
		serum leptin levels in	0
		obese mice	
	Resveratrol	↓ adipogenesis	(Baile <i>et al.</i> , 2011)
	(skin of grapes,	\downarrow the expression of	(Fischer-Posovszky
	blueberries,	adipogenic transcription	<i>et al.</i> , 2010)
	raspberries,	factors and genes	
	mulberries)	\uparrow lipolysis and inhibit	
		lipogenesis	
		\downarrow lipid accumulation in	
		matured adipocytes	
		↑ insulin sensitivity	
	Curcumin	\downarrow lipid accumulation and	(Pongchaidecha et
. ((Turmeric)	plasma free fatty acid	al., 2009)
•		levels in high-fat diet	(Alappat & Awad,
		induced obese rat	2010)
		Regulates lipid	
		metabolism ↓ intracellular	
		lipid accumulation	
Flavonoid	Quercetin	↓ adipogenic	(Ahn et al., 2008)
	(plant pigment	differentiation via AMPK	(Jung et al., 2013)
	in onions,	pathway in 3T3-L1 cells	
	apples, Ginkgo	↓ hepatic triglyceride	
	biloba)	accumulation and	
		dyslipidemia in obese	
		mice	

Table 2.3: Potential phytochemicals for the treatment of obesity.

Table 2.3, continued

Alkaloids	Capsaicin	↓ body weight gain and	(Joo et al., 2010)
	(a spicy	adipose tissue size in	(Reyes-Escogido
	component of	high-fat diet fed the rat	Mde et al., 2011)
chilli pepper)		↓ obesity-induced	
		inflammation, metabolic	
		disorders, and liver	
		diseases	
	Ephedrine	Suppress appetite	(Astrup et al.,
	(Ephedra plant)	↑ energy expenditure via	1995)
		thermogenesis	(Carey et al., 2015)
		↓ total body fat, visceral	
		fat Improves blood	
		pressure in obese subjects	
	Caffeine	↓ body weight and fat	(Xu et al., 2015)
	(Coffee beans,	accumulation	(Liu et al., 2015)
	tea-leaves,	Improves blood lipid	
	cocoa beans)	levels	
		↓ serum leptin levels in	
		high-fat diet fed rats	
	5	Induce lipolysis in	
		matured adipocytes	
	Nicotine	Promotes body weight	(Seoane-Collazo et
	(tomato, potato,	reduction and appetite	al., 2014)
	eggplant)	suppression	(Lakhan &
		↑ thermogenesis in brown	Kirchgessner,
		adipose tissue in obese	2011)
		rats	
		Improves glucose	
		homeostasis, insulin	
		sensitivity	
		↓ adipose tissue	
		inflammation	

Terpenoids Abscisic acid Improves glucose (Guri et al., 2007) (Guri et al., 2008) (plant hormone) tolerance and obesityinduced inflammation in diabetic obese mice PPARy agonist that improves sensitivity towards insulin ↓ infiltration of adipose tissue macrophages Carotenoids (Lobo et al., 2010) ↓ adipocyte (bright red, differentiation and (Gammone & D'Orazio, 2015) orange and hypertrophy yellow plant Improves insulin pigments) resistance \ blood glucose levels by regulating cytokine secretions from adipose tissue Lycopene \downarrow leptin, resistin and (Luvizotto *et al.*, (red pigment plasma IL-6 levels in diet-2013) found in fruits induced obese rats (Agarwal & Rao, and vegetables) ↓ risk of cardiovascular 2000) diseases by inhibition of LDL oxidation and lipid peroxidation Organosulfur Ajoene \downarrow cholesterol synthesis (Cartea & Velasco, (garlic) and improves blood 2008) (Yang *et al.*, 2006) pressure Regulate fat cell number through the apoptosis induction

Table 2.3, continued

Sulforaphane	Inhibit adipogenesis	(Choi et al., 2014)
(cruciferous	\downarrow adipocyte hypertrophy,	(Zhang <i>et al.</i> , 2016)
vegetables like	hepatic triglyceride	
broccoli and	accumulation in vitro and	
cabbages)	in vivo	
	Induce adipocytes	
	browning, lipolysis and	
	fatty acid oxidation in	
	3T3-L1 cells	
Diosgenin	Improve dyslipidemia by	(Uemura et al.,
(tubers of	decreasing the hepatic	2011)
Dioscorea wild	lipid content in diabetic	(Szabo <i>et al.</i> , 2018)
yam)	mice	
	↓ obesity-induced	
	endothelial dysfunction	
	and improves blood	
	pressure in obese rats	
Protodioscin	↓ serum triglyceride,	(Wang et al., 2010)
(puncture wine	cholesterol and LDL	
and fenugreek)	levels ↑ HDL levels	
	Sulforaphane (cruciferous vegetables like broccoli and cabbages) Diosgenin (tubers of Dioscorea wild yam) Protodioscin (puncture wine and fenugreek)	SulforaphaneInhibit adipogenesis(cruciferous↓ adipocyte hypertrophy,vegetables likehepatic triglyceridebroccoli andaccumulation <i>in vitro</i> andcabbages) <i>in vivo</i> Induce adipocytesbrowning, lipolysis andfatty acid oxidation in3T3-L1 cellsDiosgeninImprove dyslipidemia by(tubers ofdecreasing the hepaticDioscorea wildlipid content in diabeticyam)mice↓ obesity-inducedendothelial dysfunctionand improves bloodpressure in obese ratsProtodioscin↓ serum triglyceride,(puncture winecholesterol and LDLand fenugreek)levels ↑ HDL levels

Note: ↑= increase; ↓= decrease

2.10 Eurycoma longifolia Jack

Eurycoma longifolia Jack (EL) also known as Tongkat Ali (Figure 2.4) is a tropical medicinal plant classified under the order of Geranial's, genus of *Eurycoma* and family of Simaroubaceae. It is a flowering plant which grows up to 15-18 m in height and commonly found in lowland tropical forest floor up to 500 m above sea level. The leaves of this plant are about 20-40 cm long and it has 2–3 cm long ovoid-shaped green fruit which will turn dark brown after ripening (Bhat & Karim, 2010).



Figure 2.4: Eurycoma longifolia plant.

Retrieved from http://chengailimfruittrees.blogspot.my/2014/05/tongkat-ali.html

Moreover, this plant grows well in the presence of partially shady and well-drained soil with adequate water supply (Bhat & Karim, 2010). Typically, it may take up to 25 years for complete maturation of Tongkat Ali plant before it can be harvested (Keng, 1987). Tongkat Ali plant is indigenous to South East Asian countries and is found with various local names based on the place and country it belonging to. Other than Tongkat Ali, this evergreen plant is also locally known as Long Jack, Malaysian Ginseng, Natural Viagra, Setunjang Bumi, Pasak Bumi, Payung Ali, Penawar Pahit, Tongkat Ali Hitam, Cay ba Binh, Ian-don, and Jelaih especially in countries like Malaysia, Indonesia, Vietnam, Cambodia, Myanmar and Thailand (Rehman *et al.*, 2016).

2.10.1 Medicinal uses of *Eurycoma longifolia*

Eurycoma longifolia is an important medicinal plant and has always been a significant traditional remedy used mainly in South-East Asian countries. Almost all the parts of the plant are used traditionally for various medicinal purposes (Table 2.4).

Plant parts	Traditional Uses	References
Leaves	Washing itches	(Ang et al., 2001)
Fruits	Curing dysentery	(Ang et al., 2001)
Bark	As a vermifuge	(Ang et al., 2001)
Taproots	Treat high blood pressure	(Kuo <i>et al.</i> , 2004)
Root bark	Treatment of diarrhoea and fever	(Kuo <i>et al.</i> , 2004)
		(Perry & Metzger, 1980)
	Aches, ageing, aphrodisiac, antibiotic,	(Sobri et al., 2007)
	appetite stimulant, cancer, diabetes, fever,	(Chan et al., 1989)
	high blood pressure, jaundice, cachexia,	(Darise et al., 1982)
Roots	dropsy, malaria, osteoporosis, sexual	(Mohd Effendy et al.,
	dysfunction, androgen deficiency, glandular	2012)
	swelling, energy tonic and general health	(Kuo <i>et al.</i> , 2004)
	supplement	(Ang et al., 2001)
		(Jamal, 2006)

Table 2.4: Traditional uses of Eurycoma longifolia.

Nowadays, EL is primarily consumed in the form of raw crude powder, capsuled powder, additives in teas, coffees or energy drinks (Bhat & Karim, 2010). Due to the various traditional benefits of EL, many scientific studies have been performed to prove the above-mentioned healing potentials which also pave the way for the isolation of its many bioactive compounds.

2.10.2 Chemical Constituents

EL is rich in various classes of bioactive compound, such as quassinoids, alkaloids, triterpene-type tirucallane, squalene derivatives and phytosterols. Nevertheless, the bitter tasting quassinoids are the major chemical constituent abundantly found in the root of EL. Quassinoids are a group of highly oxygenated triterpenes which is mainly isolated from the plants of Simaroubaceae family and this group of bioactive compounds has gained much attention due to the dynamic pharmacological properties (Guo *et al.*, 2005b).

Eurycomanone, eurycomanol, laurycolactones, eurycomalactone, eurycomalides, longilactone, and eurycolactone are the major isolated quassinoids from EL that have shown various pharmacological effects including antimalarial, anticancer, antiplasmodial, anti-inflammatory and aphrodisiac activities in both *in vitro* and *in vivo* studies (Ang *et al.*, 1995; Chan *et al.*, 1989; Chan *et al.*, 1992; Low *et al.*, 2013; Tran *et al.*, 2014; Wong *et al.*, 2012).

2.10.2.1 Eurycomanone

Eurycomanone is one of the well-studied quassinoids that is predominantly found in the root of EL plant. It was found that the composition of eurycomanone in ethanolic, nbutanolic- and aqueous-based fractions of EL varies, hence Lethal Dose 50 and effective doses are different among the fractions. However, the aqueous-based fractions of EL are the safest among the others with the highest LD50 value of >3000 mg/kg while the nbutanol fraction is the most toxic due to the presence of eurycomanone. A pharmacokinetic study has reported eurycomanone to possess poor oral bioavailability, high volume of distribution and shorter biological half-life (Low et al., 2005). Eurycomanone is a cytotoxic bioactive compound found in EL and it has shown cytotoxicity effects on a panel of human cancer cell lines including, breast, colon, fibrosarcoma, lung, melanoma, prostate, liver and leukemia by modulating cell cycle arrest and apoptotic pathways (Kardono et al., 1991; Tong et al., 2015; Zakaria et al., 2009). In another *in vivo* study, eurycomanone is reported to enhance spermatogenesis through phosphodiesterase and aromatase inhibition in steroidogenesis suggesting the aphrodisiac property of EL root extract is due to the presence of eurycomanone (Low et al., 2013). Furthermore, eurycomanone also showed a potent antimalarial effect against P. falciparum strains that have developed resistance towards chloroquine treatment (Chan et al., 2004; Miller et al., 1986). Besides, the derivative of eurycomanone has been

identified as a potent NF- κ B inhibitor and this signifies the potential use of EL to treat or prevent inflammatory diseases (Tran *et al.*, 2014).

2.10.3 Standardized Quassinoids composition from Eurycoma longifolia

The standardized quassinoids composition from Eurycoma longifolia (SQEL) was prepared from the roots of EL by Low and colleagues (Low et al., 2011). Previously, a toxicity study showed SQEL possess LD_{50} of >2000 mg/kg in rats suggesting that any dose administered below than this is safe in rodent experiments (Low *et al.*, 2014). The pharmacokinetic study showed eurycomanone has lower bioavailability and poor membrane permeability (Ahmad et al., 2018; Low et al., 2005). In a previous study, the author claimed that oral treatment was less effective than the intraperitoneal injection in investigating the anti-tumor effect of EL extract on tumor xenograft model (Al-Salahi et al., 2014). Therefore, administration of SQEL using intraperitoneal injection is preferred as per used in other studies (Al-Salahi et al., 2013; Low et al., 2013; Tong et al., 2015). Interestingly, SQEL was shown to enhance spermatogenesis, improve endothelial dysfunction, possess antiangiogenic activity and anticancer effect on human prostate (LNCap) and leukemic (K-562) cancer cells in previous studies (Al-Salahi et al., 2013; Al-Salahi et al., 2014; Low et al., 2013; Tong et al., 2015). Nevertheless, further studies are still warranted to identify other beneficial uses of SQEL, including its potential antiadipogenic effects.

2.11 Rationale for the study

The involvement of EL in energy metabolism has been shown previously by the reduction of blood glucose in streptozotocin-induced hyperglycemic rats supplemented with aqueous extracts of EL for 10 days (Husen *et al.*, 2004). In addition, treatment with EL root extracts also improved insulin sensitivity by enhancing insulin-induced glucose uptake in 3T3-L1 cells (Lahrita *et al.*, 2015). Moreover, the effects of EL in the role of

adipogenesis were shown indirectly by the reduction of body weight and omentum fat mass in normal-diet-fed rats given aqueous EL extract for 2 weeks (Solomon *et al.*, 2014). On top of that, EL in combination studies with other bioactive compounds has shown a synergistic effect in body weight management (Talbott, 2007). Although EL is widely consumed as an energy drink to enhance overall well-being, its effect on lipid metabolism specifically on adipocyte differentiation is yet to be unveiled. Therefore, this study sought to elucidate the role of SQEL and eurycomanone on anti-adipogenic mechanisms in 3T3-L1 cells and high-fat-diet-induced obese mice. The specific objectives are as follow:

- 1. To investigate the effect of SQEL and eurycomanone on the differentiation of preadipocyte cells.
- 2. To determine the effect of SQEL and eurycomanone on adipogenic genes and proteins.
- 3. To study the anti-adipogenic effect of SQEL in HFD-induced obese mice.

CHAPTER 3: METHODOLOGY



Figure 3.1: Summary of the methods.

3.1 Preparation of the Standardized Quassinoids composition from *Eurycoma longifolia* (SQEL)

The water-soluble standardized quassinoids composition from Eurycoma longifolia in powder form was extracted from the root of the plant according to the methods by (Low et al., 2011) and provided by Professor Kit-Lam Chan, Universiti Sains Malaysia for this study. Briefly, the air-dried powdered roots (15 kg) of the EL were extracted with 6×4 L of 95% methanol for 6 days at 60°C. The combined methanol extract upon evaporation to dryness under partial vacuum produced a dark brown residue of 450 g (3% w/w). The residue was then chromatographed on a pre-packed Diaion HP 20 (Mitsubishi Chemical, Tokyo, Japan) resin column. The chosen guassinoid-rich fraction, SQEL was derived by elution with a gradient of H₂O-MeOH mixtures (1:0 to 0:1) at decreasing polarity (Low et al., 2013), and subsequently dried under partial vacuum to 45 g (10% w/w of crude extract). The SQEL contains $14.49 \pm 0.26\%$ of eurycomanone, $7.39 \pm 0.17\%$ epoxyeurycomanone, $0.72 \pm 0.06\%$ 13,21-dihydroeurycomanone and $9.54 \pm 0.22\%$ w/w eurycomanol as quantified by high performance liquid chromatographic (HPLC) analysis (Al-Salahi et al., 2013; Low et al., 2013). These guassinoids were isolated and their purified structures (> 95%) were identified and confirmed following the protocol described previously (Teh et al., 2011; Teh et al., 2010; Teh-Murugaiyah, et al., 2011). The purity of the compounds was determined with Empower 2 workstation software (Waters, Milford, MA, USA) operated in a Waters Delta Prep HPLC system equipped with a Waters 2996 photodiode array detector. The chemical structures of major quassinoids in SQEL are as illustrated in Figure 3.2.



Figure 3.2: The bioactive ingredients of SQEL.

The pure compound, eurycomanone was purchased and its purity (> 96%) was verified using HPLC (Chengdu Biopurify Phytochemicals Ltd., Chengdu, China). A stock solution of 100 mg/mL SQEL and 25 mg/mL eurycomanone was prepared with dimethyl sulfoxide (DMSO) under the sterile condition and aliquoted in 1.5 mL sterile centrifuge tubes and kept at -20°C till further use.

3.2 Maintenance and Propagation of 3T3-L1 cells

Mouse 3T3-L1 preadipocyte cells (ATCC[®] CL-173TM) were obtained from American Type Culture Collection (ATCC, USA) and cultured in 75 cm² sterile tissue culture flasks containing pre-warmed complete DMEM and incubated in a humidified atmosphere of 5% CO₂ at 37°C. The culture medium was replenished every 2 days and the cells were sub-cultured upon reaching 85-90% confluency. Briefly, the culture medium was removed from the flask completely and cells were washed with 10 mL of sterile 1X PBS. Then, 1 mL 1X 0.25% trypsin/EDTA (Biowest, USA) were added to the flask, shaken gently and incubated at 37°C for 5 minutes or until cells began to detach. Thereafter, the

flask was tapped gently and 9 mL of complete DMEM was added to inactivate the trypsin. Next, cells were re-suspended by aspiration and the cell suspension was transferred to a 15 mL centrifuge tube then centrifuged at 200 x g for 5 minutes. The supernatant was discarded and the cell pellet re-suspended in 1 mL of complete DMEM. Then, 100 μ L of the cell suspension was transferred to a new culture flask with fresh pre-warmed complete DMEM. Cell passage number was recorded and monitored continuously. The cells were discarded at passage 12 and new cells were revived. For cell seeding, a total number of cells were counted. Ten microliter cell suspension was mixed with an equal volume of 0.4% trypan blue satin (Gibco, USA) and added to a haemocytometer counting chamber and viewed under the microscope. Cell number was estimated according to the following formula:

Average cell number x 2 x 10^4 = number of cells/mL

A prior dilution was made to get the final cell number needed for cell seeding according to the culture flask used.

3.3 Differentiation of **3T3-L1** cells

3T3-L1 pre-adipocyte cells were seeded at the optimal density (2000 cells/well) and maintained in pre-adipocyte culture medium (PCM) for 48 hours by incubating at 37°C and 5% CO₂. Then, the confluent pre-adipocytes were induced to differentiate in differentiation medium (DM) for two days. This medium was replaced with adipocyte maintenance medium (AMM) and used to maintain the culture for three days and then changed every three days (Tian *et al.*, 2017). The media formulations are as described in Table 3.1.

Medium	Formulation		
Pre-adipocytes Culture Medium	Complete DMEM		
Differentiation Medium	Complete DMEM, 0.5 mM 3-isobutyl-1-		
	methylxanthine, 1 μM dexamethasone and 10 $\mu g/mL$		
	insulin		
Adipocyte Maintenance Medium	Complete DMEM and 10 µg/mL insulin		

Table 3.1: Media formulations.

3.4 Cell viability and Cytotoxicity

Cell viability and cytotoxicity of SQEL and eurycomanone were determined by 3-(4,5dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay. In MTT assay, the number of viable cells is directly proportional to the reduction amount of tetrazolium salt that forms purple colour formazan crystals (Mosmann, 1983). Cells were cultured in 96well plate at an optimum density (2000 cells/well). After 24 hours, they were either treated with vehicle control or SQEL (0.4 – 100 µg/mL) or eurycomanone (0.4 – 100 µg/mL) in PCM for 72 hours. The viability of the differentiating pre-adipocytes was assessed by treating the 2 days post-confluent cells with SQEL (12.5 – 100 µg/mL) and eurycomanone (3.1 – 25 µg/mL) in DM for 48 hours.

To study the effects of SQEL and eurycomanone on the viability of matured adipocytes, 2 days post-confluent cells were induced to differentiate for 8 days as mentioned previously and treated with SQEL ($12.5 - 100 \mu g/mL$) and eurycomanone (3.1 – 25 $\mu g/mL$) in PCM for 48 hours. Then, 2 mg/mL of MTT in 1X PBS were added to each well and incubated for 3 hours at humidified atmosphere of 5% CO₂ at 37°C. The cell culture medium was removed, followed by the addition of 100 μL of DMSO and then

mixed at 300 rpm for 15 minutes. Absorbance reading was measured at 570 nm by using a multilabel microplate reader (Hidex ChameleonTM, Finland). The effect of SQEL and eurycomanone on cell viability of 3T3-L1 pre-adipocytes, differentiating pre-adipocytes and matured adipocytes were determined as the percentage of cell viability by using the formula below: -

% Cell viability =
$$\frac{Abs (Treated - Blank)}{Abs (DMSO Control - Blank)} \times 100\%$$

The half maximal inhibitory concentration (IC_{50}) was determined using GraphPad Prism software version 6.0 (GraphPad Software Inc., San Diego, CA).

3.5 Oil Red O Staining

Oil Red O staining was performed as described previously by (Chen *et al.*, 2015). Briefly, 3T3-L1 cells were seeded in 96-well plates at the optimal density (2000 cells/well) and allowed to achieve 100% confluence for 2 days. Then, cells were induced to differentiate as described previously and treated with vehicle control or SQEL (0.4 – 100 μ g/mL) or eurycomanone (0.4 – 100 μ g/mL) for 8 days. At the end of the treatment, the culture medium was removed and cells were fixed with 4% paraformaldehyde for 30 minutes. Cells were washed five times with 1X PBS and two times with distilled water and then stained for 1 hour with 0.36% Oil Red O solution. The dye solution was removed and cells were fixed was removed and cells were for every 5 minutes interval. Then, stained lipid droplets were viewed under a microscope and the Oil Red O dye retained in cells was extracted with isopropanol and quantified by absorbance readout at 485 nm using the multilabel microplate reader (Hidex ChameleonTM, Finland). The percentage inhibition of adipogenesis was calculated using the formula below: -

3.6 Triglyceride Quantification Assay

3.6.1 Extraction of Intracellular Triglyceride from Matured Adipocytes

Cells were induced to differentiate as described above and treated with vehicle control or SQEL (12.5 – 100 µg/mL) or eurycomanone (3.1 - 25 µg/mL) or sulforaphane (0.9 µg/mL) for 8 days. Sulforaphane (0.9 µg/mL) was used as assay positive control (Choi *et al.*, 2012). At the end of treatment, the culture medium was removed and cells were washed two times with 1X PBS. Next, the cells were scraped gently and homogenized with 5% NP-40 solution (Tian *et al.*, 2017). Some cell homogenate was centrifuged at 15000 x g and 4°C for 10 minutes and the supernatant was collected and stored at -80°C for protein quantification while the remaining homogenate was used for triglyceride extraction. The remaining cell homogenate was heated to 100°C for 5 minutes or until it turns cloudy by dry block thermostat (Biosan, Latvia) and cooled to room temperature (25 \pm 2°C) and this process was repeated twice. Lastly, the homogenate was collected and stored at -80°C to be used for triglyceride containing supernatant was collected and stored at -80°C to be used for triglyceride quantification assay.

3.6.2 Protein Quantification

Total protein content in cell homogenate was quantified using DC^{TM} Protein Assay kit (Bio-Rad, USA) following the manufacturer's instruction. Briefly, the cell lysates were diluted 5-fold with distilled water and 5 µL were added to a flat bottom 96 well plate. Another set of samples was prepared for generating a standard curve by adding 5 µL of BSA standards whereby the 0 mg/mL well acts as assay blank. Subsequently, 25 µL of reagent A (1 mL reagent A + 20 µL reagent S) was added to each well. Then, 200 µL of reagent B was added to each well and the plate was agitated gently for 5 seconds. Bubbles were removed (if there is any) with a clean pipette tip and the plate was incubated in dark at room temperature $(25 \pm 2^{\circ}C)$ for 15 minutes. Lastly, the absorbance readout at 620 nm was measured using the multilabel microplate reader (Hidex ChameleonTM, Finland). Standard and sample well readings were subtracted with blank reading. BSA Standard curve, Abs 620 nm versus BSA Standard concentration (mg/mL) was plotted and the linear equation y = mx + c was determined using GraphPad Prism software version 6.0 (GraphPad Software Inc., San Diego, CA) to calculate the sample protein concentration. Sample protein concentration was calculated using the formula below: -

Protein concentration $(\mu g/\mu L)$ = Protein amount from standard curve $(mg/mL) \times Df$

Df, dilution factor

3.6.3 Quantification of Triglyceride

were quantified using triglyceride Intracellular contents the Triglyceride Quantification Kit (BioVision, USA) following the manufacturer's protocol. Briefly, the cell lysates were diluted 10-fold with distilled water and 50 µL/well was added in triplicate into a flat bottom 96 well plate. Then, 40 µL of 1 mM triglyceride was mixed with 160 μ l triglyceride assay buffer to prepare 0.2 mM triglyceride standard. Then, 0, 10, 20, 30, 40, 50 µl of the 0.2 mM triglyceride standard solution were added in duplicate into a series of wells and volume adjusted to 50 µl/well with triglyceride assay buffer to generate 0, 2, 4, 6, 8, 10 nM/well of triglyceride standard solution. The 0 nM well was used as assay blank. Then, 2 µl of lipase was added to blank and each standard and sample well, mixed and incubated for 20 minutes at room temperature ($25 \pm 2^{\circ}$ C). After that, 50 μ l/well triglyceride reaction mix were prepared as Table 3.2 and added to each well.

Triglyceride Reaction Mix	Volume (µl)
Triglyceride Assay Buffer	46
Triglyceride Probe	2
Triglyceride Enzyme Mix	2

 Table 3.2: Triglyceride Reaction Mix.

The assay plate was incubated in dark at room temperature $(25 \pm 2^{\circ}C)$ for 60 minutes. Lastly, the absorbance readout at 570 nm was measured using the multilabel microplate reader (Hidex ChameleonTM, Finland). Standard and sample well readings were subtracted with blank reading. The triglyceride standard curve, abs 570 nm versus triglyceride (nM) was plotted and the linear equation y = mx + c was determined using GraphPad Prism software version 6.0 (GraphPad Software Inc., San Diego, CA) to calculate the sample triglyceride concentration. Normalized sample triglyceride concentration was calculated using the formula below: -

Triglyceride concentration =Triglyceride amount from standard curve (nM) x Df
$$(nM/\mu g/\mu L)$$
Protein concentration ($\mu g/\mu L$)

Df, dilution factor

3.7 Lipolysis Assay

3T3-L1 cells were induced to differentiate as mentioned above. Then, the matured adipocytes were treated with vehicle control or SQEL ($12.5 - 100 \mu g/mL$) or eurycomanone ($3.1 - 25 \mu g/mL$) or isoproterenol ($2.1 \mu g/mL$) for 48 hours. Isoproterenol was used as a positive control for release of glycerol from triglycerides (Rondini *et al.*, 2017). The culture medium was collected at the end of the treatment. The collected medium was kept at -20°C until it was used for glycerol quantification. The extent of

lipolysis induced by the treatment was determined by quantifying the released glycerol into the medium using a Glycerol Quantification Kit (BioVision, USA) according to the manufacturer's instructions. Briefly, the collected media were diluted 10-fold with glycerol assay buffer and added 50 μ L/well into a flat bottom 96 well plate. In addition, the 10-fold diluted culture medium was added as a blank for media. Ten microliters of 100 mM glycerol standard mixed with 990 μ l glycerol assay buffer to prepare 1 mM glycerol standard solution. After that, 20 μ L of 1 mM glycerol standard solution was further diluted with 180 μ l glycerol assay buffer to get 100 μ M working glycerol standard concentration. Then, 0, 2, 4, 6, 8 and 10 μ l of the 100 μ M glycerol standard were added in duplicate into a series of wells and volume adjusted to 50 μ l/well with glycerol assay buffer to generate 0, 0.2, 0.4, 0.6, 0.8, 10 nM/well of glycerol standard solution. The 0 nM well was used as blank for glycerol standard. Then, 50 μ l/well glycerol reaction mix was prepared as Table 3.3 and added to each well.

Glycerol Reaction Mix	Volume (µl)
Glycerol Assay Buffer	46
Glycerol Probe	2
Glycerol Enzyme Mix	2

Table 3.3: Glycerol Reaction Mix.

The assay plate was mixed gently for 5 seconds and incubated in dark at room temperature $(25 \pm 2^{\circ}C)$ for 60 minutes. Finally, the absorbance readout at 570 nm was measured using the multilabel microplate reader (Hidex ChameleonTM, Finland). Standard and sample well readings were subtracted with their respective blank readings. The glycerol standard curve, abs 570 nm versus glycerol (nM) was plotted and the linear equation y = mx + c was determined using GraphPad Prism software version 6.0 (GraphPad Software Inc.,

San Diego, CA) to calculate the sample glycerol concentration. Sample glycerol concentration was calculated using the formula below: -

Glycerol concentration (nM) = Glycerol amount from standard curve $(nM) \times Df$

Df, dilution factor

3.8 Immunoblotting Analysis

3.8.1 Preparation of Cell Lysates

3T3-L1 cells were washed twice with cold 1X PBS. Then, 100 μ L/well of complete RIPA lysis buffer was added to 6 well plates. The plate was tilted several times to allow the RIPA lysis buffer to completely cover the cell surface and kept on ice for 10 minutes. Next, the lysed cells were scraped with a cell scraper and the cell lysates were harvested in pre-chilled 1.5 mL microcentrifuge tubes. Lastly, the tubes were centrifuged at 15 000 x g and 4°C for 30 minutes. Then, the fat cake (top layer) was removed and the clear cell lysates (middle layer) were collected in new pre-chilled 1.5 mL microcentrifuge tubes. The total protein concentration of the cell lysates was quantified with *DC*TM Protein Assay Kit (Biorad, USA) as described previously in section 3.6.2.

3.8.2 **Preparation of Protein Sample**

The 5X protein sample loading buffer solution containing 0.25 M Tris-HCl, pH 6.8, 10% SDS, 30% (v/v) glycerol, 10 mM DTT, 0.05% (w/v) bromophenol blue was prepared, aliquoted into 1.5 mL centrifuge tube and stored in -20°C until further use. The frozen 5X protein sample loading buffer solution was thawed at room temperature ($25 \pm 2^{\circ}$ C) prior to use. An equal amount of protein was mixed with 5X protein sample loading buffer solution in a ratio of 4:1 then denatured at 100°C for 10 minutes by using a dry block thermostat (Biosan, Latvia). The protein loading samples were cooled to room

temperature ($25 \pm 2^{\circ}$ C) before proceeding to sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE).

3.8.3 Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis (SDS-PAGE)

Protein samples (15-20 µg) were separated by SDS-PAGE for 2 hours at 110V and then transferred to a polyvinylidene difluoride membrane for 2 hours at 110V (Millipore, USA). The membranes were then blocked with 3% bovine serum albumin solution (0.3 g BSA + 1X TBS-T solution) (Santa Cruz, USA) at room temperature ($25 \pm 2^{\circ}$ C) for 1 hour. Following washing with TBS-T, the membranes were incubated with the primary antibodies against PPAR γ (1:1000), C/EBP α (1:1000), FAS (1:4000), Sirt1 (1:1000), FoxO3a (1:1000) and β -actin (1:20 000), overnight at 4°C. The next day, the membranes were washed five times with 1X TBS-T solution, five minutes each at room temperature ($25 \pm 2^{\circ}$ C). The membranes were then incubated with respective horseradish peroxidaseconjugated secondary antibodies (DAKO, Denmark) for 2 hours at room temperature ($25 \pm 2^{\circ}$ C). The bands were visualized with enhanced chemiluminescence (GE, UK) and exposed to X-ray film (Fujifilm, Japan). Densitometric analysis was performed using Image Studio Lite version 4.0.21 (LI-COR Biosciences) software. The protein levels were normalized to the housekeeping protein and expressed relative to the vehicle control.

3.9 Quantitative Real-Time Polymerase Chain Reaction (qRT-PCR)

3.9.1 RNA Extraction

Total RNA from 3T3-L1 cells was extracted using the RNAeasy Mini Kit (Qiagen, Germany) according to the manufacturer's protocols. The cells were washed with 1X PBS and harvested by trypsinization. Then, the cell pellet was washed again with 1X PBS and lysed by adding 350 μ L of buffer RLT and vortexed for 1 min. Next, 350 μ L of 70% ethanol (v/v) is added to the lysate and mixed well by pipetting up and down several times. Approximately 700 μ L of the sample was transferred into a RNeasy spin column
with a 2 mL collection tube and centrifuged at 8000 x g and room temperature $(25 \pm 2^{\circ}C)$ for 15 seconds. After that, the flow through was discarded and the sample was washed with 700 µL of buffer RW1 by resting for 1 min and then centrifuged at 8000 x g and room temperature $(25 \pm 2^{\circ}C)$ for 15 seconds. The flow-through was discarded and the sample was washed twice with 500 µL of buffer RPE by centrifuging at 8000 x g and room temperature $(25 \pm 2^{\circ}C)$ for 15 seconds and 2 minutes. Then, the spin column was centrifuged at top speed for 1 minute to flush away any remaining buffer and then transferred to a 1.5 mL collection tube. Lastly, 30 µL of RNase-free water was added to the column membrane and then centrifuged at 8000 x g and room temperature $(25 \pm 2^{\circ}C)$ for 1 minute to elute the RNA. The collected RNA sample was stored at -80°C until further use.

3.9.2 cDNA Synthesis

Total RNA concentration and purity were determined using the NanoDropTM 2000/2000c Spectrophotometer (Thermo Scientific, USA). RNase-free water was used as a blank. The RNA sample with an optical density 260/280 ratio greater than 1.8 (good RNA quality) was accepted and used for cDNA synthesis (Manchester, 1996). The cDNA was synthesized from 250 ng of total RNA by using the RT² First Strand Kit (Qiagen, Germany) according to the manufacturer's procedures. The reagents in the kit were thawed and briefly spun for 10-15 seconds prior to use. Then, the DNA elimination mix was prepared as Table 3.4, incubated at 42°C for 5 minutes and immediately placed on ice for 1 minute.

Component	Amount (µL)	
RNA (250 ng)	Variable	
Buffer GE	2	
RNase-free water	Variable	
Total volume	10	

Table 3.4: Composition of DNA Elimination Mix.

After that, the 10 μ L of DNA elimination mix was added to the reverse-transcription mix (Table 3.5) and mixed gently by pipetting. The mixture was incubated at 42°C for 15 minutes and then incubated at 95°C for 5 minutes to stop the reaction. Lastly, 91 μ L of RNase-free water added to the reaction, mixed gently by pipetting and then placed on ice to proceed with the RT-PCR protocol.

Component	Amount (µL)
5X Buffer BC3	4
Control P2	1
RE3 Reverse Transcription Mix	2
RNase-free water	3
Total volume	10

Table 3.5: Composition of Reverse-transcription Mix.

3.9.3 mRNA Expression

The mRNA expressions of adipogenic genes were determined on a custom RT² Profiler PCR Array (APPENDIX C) using SYBR Green qPCR Mastermix according to the manufacturer's instructions (Qiagen, Germany). The PCR components were prepared as summarized in Table 3.6.

Component	Amount (µL)
2X RT ² SYBR Green Mastermix	12.5
cDNA synthesis reaction	1
RNase-free water	11.5
Total volume	25

 Table 3.6: Composition of PCR mix.

The PCR mix (25 μ L/well) was added into the array plate. Then, the plate was tightly sealed with an optical adhesive film, centrifuged at 1000 x g for 1 minutes and placed on a thermal cycler. PCR amplification was performed in a 96-well format Real-time PCR (Biosystem StepOneTM Plus, Applied Biosystems, USA) thermal cycler inclusive of melt curve in PCR cycling program (Figure 3.3). The relative mRNA transcription levels were determined following the 2^{- $\Delta\Delta$}C_t method (Schmittgen & Livak, 2008).



Figure 3.3: Biosystem StepOneTM Plus PCR cycling program.

3.10 Animal Experiments

Six weeks old C57BL/6J male mice with uniform body weight were housed in individually ventilated cages under a controlled laboratory environment with 12 hours of the light-dark cycle in the AAALAC International accredited animal facility at the Department of Pharmacology, Faculty of Medicine, University of Malaya. Animal experimentation was performed according to the study protocol approved by the Institutional Animal Care and Use Committee, Faculty of Medicine, University of Malaya (Ethics Reference Number: 2016-170302/PHAR/R/DB). The animals were randomly divided into 4 experimental groups (n=8 for each group) respectively for normal diet and high-fat diet feeding groups as illustrated in Figure 3.4.



Figure 3.4: Animal study group segregation.

Normal diet (ND) group were fed with rodent maintenance diet (#1324, Altromin, Germany) and high-fat diet (HFD) group were fed with rodent high-fat diet (60% kcal fat) (C1090-60, Altromin, Germany) and water *ad libitum* for 12 weeks (Brandt *et al.*, 2018; Gao *et al.*, 2018). Both diet groups received 0.9% saline, 5 mg/kg and 10 mg/kg of SQEL via intraperitoneal route (i.p) while 10 mg/kg orlistat was given via oral route (o.g)

once every two days for 12 weeks (Al-Salahi *et al.*, 2013; Al-Salahi *et al.*, 2014; Low *et al.*, 2013; Tong *et al.*, 2015). Weekly food intake and mice body weight were measured. Prior to sacrifice at week 12, oral glucose tolerance test (OGTT) and intraperitoneal insulin tolerance test (IPITT) were performed. At the end of the treatment period, all mice were fasted for 6 hours and sacrificed by carbon dioxide inhalation. The liver, epididymal and perirenal white adipose tissues from all groups were excised, weighted and some were fixed in 10% formalin for histopathology. Blood samples from the animals were collected via cardiac puncture and serum was separated and stored at -20°C for biochemical analysis. Summary of the animal study is illustrated in Figure 3.5.



Figure 3.5: Summary of the animal study.

3.10.1 Oral Glucose Tolerance Test

Fasting blood glucose level was measured in all animals at 6 hours post-fasting via tail prick using an Accu-check® glucometer (Roche Diagnostics, Germany). Glucose (2 g/kg) was then administered via oral gavage and blood glucose was measured again at time points of 30, 60, 90 and 120 minutes post-gavage (Gao *et al.*, 2018). The area under

the curve of glucose level was calculated using GraphPad Prism software version 6.0 (GraphPad Software Inc., San Diego, CA).

3.10.2 Intraperitoneal Insulin Tolerance Test

Fasting blood glucose level was measured in all animals at 5 hours post-fasting via tail prick using an Accu-check® glucometer (Roche Diagnostics, Germany). Then, 0.75 IU/kg insulin was injected intraperitoneally and blood glucose was measured again at 15, 30, 60, 90 and 120 minutes post-injection (Gao *et al.*, 2018). The area under the curve of glucose level was calculated using GraphPad Prism software version 6.0 (GraphPad Software Inc., San Diego, CA).

3.10.3 Serum Biochemistry

Collected sera were sent to Haematology & Biochemistry Clinical Laboratory, Veterinary Laboratory Service Unit, Faculty of Veterinary Medicine, University Putra Malaysia to determine the total cholesterol and serum triglycerides levels using Dimension® Xpand® Plus clinical chemistry system (SIEMENS Healthcare Diagnostics Inc.).

3.10.4 Liver and Fat Tissues Histological Analysis

Liver and fat tissues were fixed in 10% buffered formalin, dehydrated and embedded in paraffin. Tissue sections of 4 μ m thick were stained with hematoxylin and eosin to examine the morphology. Photomicrographs were taken using bright field LEICA DM 2000 microscope with LEICA ICC50 HD camera (Leica Microsystems, Germany). The mean diameter of the imaged adipocytes was measured using the ImageJ software with Adiposoft plugin at auto mode (Galarraga *et al.*, 2012). The Adiposoft application was calibrated to identify cells with diameter range (20-200 μ m) and measuring the scale of 0.95 μ m/pixel.

3.10.5 Fat Tissues qRT-PCR Analysis

Total RNA from fat tissues was extracted using the RNAeasy Mini Kit (Qiagen, Germany). The frozen fat tissue was thawed on ice for 10 minutes. Then, 5 µL of QIAzolTM Lysis Reagent (Qiagen, Germany) was added per mg of fat tissue and incubated for 10 minutes at room temperature $(25 \pm 2^{\circ}C)$. Fat tissues were homogenised by using T10 basic ULTRA-TURRAX[®] (IKA Labortechnik, Malaysia) homogenizer and incubated at room temperature $(25 \pm 2^{\circ}C)$ for 5 minutes. After that, 0.2 µL of chloroform was added per µL of tissue homogenate, vortexed for 15 seconds and incubated for 3 minutes at room temperature $(25 \pm 2^{\circ}C)$. Then, the tissue homogenate was centrifuged at 12000 x g and 4°C for 15 minutes. Thereafter, the clear top layer of homogenate was collected in 1.5 mL microcentrifuge tubes then equal volume of 70% (v/v) of ethanol was added and vortexed for 15 seconds. Approximately 700 µL of the sample was transferred into a RNeasy spin column with a 2 mL collection tube and centrifuged at 8000 x g and room temperature $(25 \pm 2^{\circ}C)$ for 15 seconds. After that, the flow through was discarded and the sample was washed with 700 µL of buffer RW1 by resting for 1 min and then centrifuged at 8000 x g and room temperature ($25 \pm 2^{\circ}$ C) for 15 seconds. The flowthrough was discarded and the sample was washed twice with 500 µL of buffer RPE by centrifuging at 8000 x g and room temperature $(25 \pm 2^{\circ}C)$ for 15 seconds and 2 minutes. Then, the spin column was centrifuged at top speed for 1 minute to flush away any remaining buffer and then transferred to a 1.5 mL collection tube. Lastly, 30 µL of RNasefree water was added to the column membrane and then centrifuged at 8000 x g and room temperature $(25 \pm 2^{\circ}C)$ for 1 minute to elute the RNA. The collected RNA sample was stored at -80°C until further use. cDNA was synthesized from 250 ng of total RNA as described previously at section 3.9.2. The mRNA expressions of AMPK and PGC-1a genes were determined according to the procedure described at section 3.9.3 by using the primers listed in Table 3.7.

Table 3.7 Forward and Reverse primers.

Gene	Forward	Reverse	
AMPK	CTCAGTTCCTGGAGAAAGATGG	CTGCCGGTTGAGTATCTTCAC	
PGC-1a	AGCCGTGACCACTGACAACGAG	GCTGCATGGTTCTGAGTGCTAAG	
B-actin	CTGTCCCTGTATGCCTCTG	ATGTCACGCACGATTTCC	
GAPDH	GTGCAGTGCCAGCCTCGTCC	CAGGCGCCCAATACGGCCAA	

The PCR components were prepared as summarized in Table 3.8 and 10 μ L/well was added into the 0.2 mL low profile eight tube strips (ExtraGene, Taiwan). Then, the tube was centrifuged at 300 x rpm for 1 minutes and placed on a thermal cycler. PCR amplification was performed and the relative mRNA transcription levels were determined as defined previously at section 3.9.3.

Component	Amount (µL)
2X RT ² SYBR Green Mastermix	5
cDNA synthesis reaction	1
Forward & Reverse primers	2
RNase-free water	2
Total volume	10

Table 3.8 Composition of PCR mix.

3.11 Statistical Analysis

All the data are expressed as a mean \pm standard error of mean (SEM) from n number of experiments. Student's t-test was performed for comparison between two groups. Comparison for more than two groups was analysed by one-way ANOVA followed by Bonferroni's multiple comparison tests using Graph Pad Prism (Version 6.0, Graph Pad Software Inc., San Diego, CA). A p-value < 0.05 was considered to be statistically significant.

CHAPTER 4: RESULTS

4.1 Cytotoxicity effect of SQEL and eurycomanone

Potential cytotoxicity of both SQEL and eurycomanone on preadipocytes was evaluated using MTT assay before proceeding to study the adipogenesis effects of SQEL and eurycomanone. Eurycomanone exerted greater cytotoxicity to 3T3-L1 cells with an IC₅₀ value of $70.8 \pm 11.7 \mu g/mL$ compared to SQEL with an IC₅₀ value of $160.3 \pm 36.7 \mu g/mL$ (Figure 4.1). Hence, the concentration range of $12.5 - 100 \mu g/mL$ for SQEL and $3.1 - 25 \mu g/mL$ for eurycomanone were chosen for subsequent experiments. The chosen concentrations of SQEL and eurycomanone were further tested for potential cytotoxicity during the differentiation of pre-adipocytes and in the mature adipocytes, respectively. Both SQEL and eurycomanone were not cytotoxic to both the differentiating pre-adipocytes and matured adipocytes even at the highest tested concentration (Figure 4.2 A&B).



Figure 4.1: Effects of SQEL and eurycomanone on the viability of 3T3-L1 preadipocytes. The viability of 3T3-L1 preadipocytes treated with SQEL and eurycomanone $(0.4 - 100 \ \mu\text{g/mL})$ for 72 hours. The cell viability was determined by comparing with vehicle control (100%) and media blank (0%) by MTT reduction assay. Data are presented as the mean \pm SEM of three independent experiments performed in triplicate.



Figure 4.2: Effects of SQEL and eurycomanone on the viability of differentiating preadipocytes and matured adipocytes. (A) The viability of differentiating and (B) matured 3T3-L1 cells treated with SQEL ($12.5 - 100 \mu g/mL$) and eurycomanone ($3.1 - 25 \mu g/mL$) for 72 hours. The cell viability was determined by comparing with vehicle control (100%) and media blank (0%) by MTT reduction assay. Data are presented as the mean \pm SEM of three independent experiments performed in triplicate. Sf, sulforaphane and Iso, isoproterenol.

4.2 SQEL and eurycomanone inhibit adipogenesis of 3T3-L1 cells

The potential anti-adipogenic effects of SQEL and eurycomanone in 3T3-L1 cells were assessed in the differentiating pre-adipocytes concurrently treated with SQEL (12.5 – 100 μ g/mL) and eurycomanone (3.1 - 25 μ g/mL) for 8 days. Microscopic inspection of the Oil Red O staining revealed a concentration-dependent reduction in the number of cells with stained lipid droplets following treatment with SQEL and eurycomanone compared to the control untreated cells (Figure 4.3A). Moreover, SQEL and eurycomanone treatment dose-dependently inhibited adipogenesis, thus validating the previous result (Figure 4.3B). Eurycomanone exerted stronger adipogenic inhibitory effect compared to SQEL as shown by 85% inhibition even with 25 μ g/mL eurycomanone treatment while only 73% inhibition at 100 μ g/mL SQEL concentration. The inhibition by SQEL and eurycomanone is comparable to the inhibition with sulforaphane, the positive control that attained 95% inhibition (Figure 4.3B). Since the anti-adipogenic effect of SQEL and eurycomanone was achieved at the concentrations that did not exert cytotoxicity, both have effectively inhibited adipogenic differentiation in 3T3-L1 cells (Figure 4.3B).



Figure 4.3: Adipogenic inhibitory effects of SQEL and eurycomanone in 3T3-L1 cells. (A) Oil Red O staining of differentiating 3T3-L1 cells treated with increasing concentrations of SQEL ($12.5 - 100 \mu g/mL$) and eurycomanone ($3.1 - 25 \mu g/mL$). Lipids accumulation in cells (dark brown stain) was photographed at 50x magnification after Oil Red O staining, scale bar: 200 µm. The accumulated dye was quantified as absorbance readout at 485 nm wavelength. (B) Adipogenesis inhibition by SQEL and eurycomanone.

Sulforaphane (0.9 μ g/mL) was used as assay positive control. The percentage of adipogenesis inhibition was determined as the absorbance relative to that of vehicle control cells. Data are presented as the mean ± SEM of three independent experiments performed in triplicate, (*p< 0.05, **p< 0.01 and ***p< 0.001 versus vehicle control). NDC, non-differentiated control; VC, vehicle control, 0.5% DMSO and Sf, sulforaphane.

67

4.3 SQEL and eurycomanone reduce lipogenesis and induce lipolysis

Cytosolic lipid accumulation is the most prominent marker of adipogenesis and its quantification is used to assess the extent of *in vitro* adipocyte differentiation. Treatment of the differentiating 3T3-L1 cells with sulforaphane, the assay positive control for a period of 8 days reduced triglyceride accumulation (Figure 4.4A). Similarly, SQEL and eurycomanone treatment at various concentrations significantly and dose-dependently reduced triglyceride accumulation (Figure 4.4A). This further confirms that both the compounds inhibit adipogenesis. Triglycerides are hydrolyzed to form free fatty acids and glycerol in the event of energy demand, a metabolic process called lipolysis. Glycerol content hence indicates the degree of lipolysis in mature adipocytes. SQEL and eurycomanone significantly induced glycerol production in a dose-dependent manner after 48 hours of treatment in the matured adipocytes (Figure 4.4B). Isoproterenol, the assay positive control compound treatment for the same period has elevated the amount of glycerol released from matured adipocytes (Figure 4.4B). The increase in glycerol production was accompanied by a significant dose-dependent reduction in triglycerides contents at the concentrations that did not cause toxicity to matured adipocytes (Figure 4.4B).

4.4).



Figure 4.4: SQEL and eurycomanone inhibit the intracellular triglyceride accumulation and induce lipolysis in matured adipocytes. (A) Intracellular triglycerides content in the differentiating cells. Triglycerides levels were quantified with Triglyceride Quantification Kit and the amount (nM) was normalized to protein content ($\mu g/\mu L$) of the cells. Sulforaphane (0.9 $\mu g/m L$) was used as assay positive control. (B) Lipolysis in matured adipocytes. Matured adipocytes were treated with increasing concentrations of SQEL (12.5 – 100 $\mu g/m L$) and eurycomanone (3.1 – 25 $\mu g/m L$) in DMEM for 48 hours. Culture media collected were used to quantify the amount of glycerol produced with Glycerol Quantification Kit and (C) intracellular triglycerides upon lipolysis were quantified. Isoproterenol (2.1 $\mu g/m L$) was used as assay positive control. Data are presented as the mean \pm SEM of three independent experiments performed in triplicate, (*p< 0.05, **p< 0.01 and ***p< 0.001 versus vehicle control). NDC, non-differentiated control; VC, vehicle control, 0.5% DMSO; Sf, sulforaphane and Iso, isoproterenol.

4.4 SQEL and eurycomanone reduce the expression of adipogenesis-associated proteins and genes in 3T3-L1 cells

Adipogenesis is tightly regulated by the chronological activation of numerous transcription factors including PPARy and C/EBPa. These transcription factors are expressed immediately upon the induction of pre-adipocyte differentiation to activate the expression of a down-stream adipogenic-specific protein such as fatty acid synthase (FAS). Hence, the effect of SQEL and eurycomanone on the regulation of adipogenesisassociated proteins and genes in differentiating 3T3-L1 cells harvested on day 2 of differentiation was studied. The protein expressions of both PPARy and C/EBPa were significantly reduced after SQEL and eurycomanone treatments (Figure 4.5 A&B). Among the PPAR γ isomers (PPAR γ 1 and PPAR γ 2), the protein expression of PPAR γ 2 was reduced by two-fold by SQEL and eurycomanone treatments (Figure 4.5 A&B). Similarly, the protein expression of FAS was also reduced to half-fold after 2 days of SQEL and eurycomanone treatment (Figure 4.5 A&B). Nevertheless, sulforaphane treatment in differentiating cells for 48 hours has increased PPARy1, PPARy2, C/EBPa and FAS protein expression as compared to the vehicle control (Figure 4.5 A&B). Moreover, the mRNA expression of PPARy decreased with eurycomanone treatment while both SQEL and eurycomanone significantly reduced the mRNA level of C/EBPa by two-fold in the differentiating cells (Figure 4.5C). In addition, the mRNA levels of lipoprotein lipase (LPL) and Kruppel-Like Factor 15 (KLF15) which are positively regulated by PPARy were significantly reduced with SQEL and eurycomanone treatment as compared to the vehicle control (Figure 4.5C). Interestingly, significant upregulation by two-fold in the protein and mRNA expression of Sirtuin1 (Sirt1) was observed in the differentiating cells treated with SQEL and eurycomanone (Figure 4.5 A-C). Similarly, the protein expression of FoxO3 also two-fold increased by the same treatment in 3T3-L1 cells (Figure 4.5 A&B).



Figure 4.5: Effects of SQEL and eurycomanone on the expression of adipogenic markers in differentiating cells. (A&B) Protein and (C) mRNA expressions of adipogenic markers in differentiating pre-adipocytes. Intensities of the PPARy1, PPARγ2, C/EBPα, Sirt1, FoxO3a and FAS protein bands were normalized to those of βactin and relative protein expressions of the treated samples were obtained by comparing the normalized protein bands intensity to that of the vehicle control. Ct values of PPAR γ ,

C/EBP α , LPL, KLF15 and Sirt1 were normalized to those of actin and GAPDH and relative mRNA expressions of the treated samples were obtained by comparing to that of the vehicle control. Data are presented as the mean \pm SEM, of three independent experiments performed in triplicate, (*p< 0.05, **p< 0.01 and ***p< 0.001) versus vehicle control. NDC, non-differentiated control; VC, vehicle control, 0.5% DMSO; Eu, eurycomanone; Sf, sulforaphane and a.u; arbitrary unit.

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4.5 SQEL suppresses body weight gain in C57BL/6J mice

Anti-obesity effect of SQEL was evaluated in the high fat diet (HFD)-induced obese C57BL/6J mice. The body weight of mice fed with normal diet (ND) increased gradually with the highest weight of 30.94 ± 0.45 g observed at week 12 (Figure 4.6A). Whereas, the body weight of the mice fed with HFD increased drastically with the highest weight of 39.56 ± 1.23 g at week 12 (Figure 4.6B). Mice fed with HFD demonstrated 62% body weight gain compared to mice on ND which only gained about 28% of weight (Figure 4.6C), although there was no significant difference in their food intake (Figure 4.7 A&B). Interestingly, the mice groups that received 5 mg/kg and 10 mg/kg SQEL for the same study period showed significantly lower percentages of body weight gain with both types of diet, but higher weight reduction in mice fed with HFD than ND (Figure 4.6C). Mice on ND and received 5 mg/kg and 10 mg/kg SQEL have gained 11% and 16% of weight respectively (Figure 4.6C). However, HFD-fed mice received the same treatment respectively gained weight up to 31% and 26% which was similar to the percentage weight gain by saline control mice on ND (Figure 4.6C). The reduction in weight gain of both ND and HFD fed mice groups was comparable to mice given standard drug orlistat that respectively gained only 17% and 4% of weight compared to their initial body weight (Figure 4.6C).



Figure 4.6: Effects of SQEL treatment on body weight of C57BL/6J mice. Weekly body weight (A&B) and (C) percentage body weight gain of mice group fed with normal diet and high-fat diet treated with 5 mg/kg SQEL and 10 mg/kg SQEL for 12 weeks. The percentage body weight gain was calculated by comparing the initial and final body weight. Data are presented as the mean \pm SEM, n=7-8 (*p< 0.05, ** p<0.01 and ***p< 0.001 versus the respective control (0.9% saline) and ###p< 0.001 for high-fat diet versus normal diet 0.9% saline group.



Figure 4.7: Effects of SQEL treatment on food consumption of C57BL/6J mice. Weekly food intake (A&B) of mice group fed with normal diet and high-fat diet treated with 5 mg/kg SQEL and 10 mg/kg SQEL for 12 weeks. Data are presented as the mean \pm SEM, n=7-8.

4.6 SQEL improves impaired glucose tolerance but not insulin sensitivity in C57BL/6J mice

Prior to sacrifice on week 12, mice were subjected to OGTT and IPITT to study the effect of SQEL treatment on glucose and insulin sensitivity. The time course plasma glucose level curve and the area under the curve of glucose which indicates the total glucose amount within a specified period of time was plotted. Impaired glucose tolerance was observed in the HFD fed mice group compared to the ND fed group (Figure 4.8A). Significantly lower glucose intolerance observed in the ND fed mice group supplemented with 5 mg/kg and 10 mg/kg SQEL as well as in the HFD fed mice group treated with 10 mg/kg SQEL compared to its respective saline control mice group (Figure 4.8B). Orlistat treatment has significantly reduced glucose intolerance in both the ND and HFD fed mice on both ND and HFD with and without SQEL treatment (Figure 4.8C). However, orlistat treatment significantly improved insulin sensitivity in mice group given HFD (Figure 4.8D).



Figure 4.8: Effects of SQEL treatment on glucose and insulin sensitivity of C57BL/6J mice. (A) Oral glucose tolerance curve and its (B) area under the curve and (C) insulin tolerance test curve and its (D) area under the curve of mice group fed with

normal diet and high-fat diet treated with 5 mg/kg SQEL and 10 mg/kg SQEL for 12 weeks. Data are presented as the mean \pm SEM, n=7-8 (*p< 0.05, ** p<0.01 and ***p< 0.001 versus the respective control (0.9% saline) and ^{###}p< 0.001 for high-fat diet versus normal diet 0.9% saline group.

4.7 SQEL reduces adipose tissue mass in C57BL/6J mice

At the end of 12th week, mice were fasted for 6 hours and euthanized by carbon dioxide asphyxiation. The epididymal and perirenal fat pads and livers were harvested and weighed. Saline or SQEL-treated ND fed mice possessed smaller epididymal fat pad compared to those fed with HFD (Figure 4.9). SQEL treatment has impaired the development of epididymal fat in mice on HFD (Figure 4.9). Moreover, in the HFD fed mice group treated with SQEL, epididymal and perirenal fat pad mass was reduced significantly compared to its saline control (Figure 4.10 A&B). The decrease in fat mass was comparable with the reduction seen with standard anti-obesity drug orlistat (Figure 4.10 A&B). An unanticipated finding was noted, whereby, the ND fed mice possessed 5.0 ± 0.11 g/100 g BW of liver weight, which is significantly higher as compared to mice fed with HFD that only have 3.89 ± 0.05 g/100 g BW of liver weight in 12 weeks (Figure 4.10C). However, there was an insignificant reduction in the liver weight of mice fed with ND and treated with SQEL for the same period (Figure 4.10C). On the other hand, SQEL treatment in mice fed with HFD showed a significant increase in liver weight to $4.72 \pm$ 0.05 and 5.28 \pm 0.33 g/100 g BW at respective dose when compared to its saline control (Figure 4.10C). However, SQEL-mediated increase in liver weight of mice on HFD was not significantly higher than the liver weight of ND fed saline control mice (Figure 4.10C). The mice group on orlistat treatment and consumed HFD only exhibited a very mild reduction in their liver weight (Figure 4.10C).



Figure 4.9: Effects of SQEL treatment on the adipose tissue development in C57BL/6J mice. Epididymal fat pads of mice on normal and high-fat diet treated with 0.9% saline, 5 mg/kg SQEL, 10 mg/kg SQEL and 10 mg/kg orlistat for 12 weeks. White arrows indicate epididymal fat pads. Scale bar: 2.06 cm.



Figure 4.10: Effects of SQEL treatment on the adipose and liver tissue mass in C57BL/6J mice. Normalized weights of (A) epididymal fat, (B) perirenal fat and (C) liver of mice on normal and high-fat diet treated with 0.9% saline, 5 mg/kg SQEL, 10 mg/kg SQEL and 10 mg/kg orlistat for 12 weeks. Data are presented as the mean ± SEM, n=7-8. (**p< 0.01 and ***p< 0.001) versus respective control (0.9% saline) and $^{\#\#}p$ < 0.001 versus normal diet 0.9% saline.

4.8 Effects of SQEL treatment on fat accumulation in the liver and adipose tissue hypertrophy in C57BL/6J mice

Hepatic steatosis as indicated by the presence of numerous fat globules was observed in the liver histological section of the saline group mice consumed HFD compared to the ND fed group (Figure 4.11A). Moreover, fat globules were absent in the SQEL-treated mice fed with ND (Figure 4.11A). Interestingly, a significant reduction in the number of fat globules was observed in the SQEL treated HFD fed mice when compared to the saline control group of the HFD mice (Figure 4.11A). Similarly, a significant increase in the size of adipocyte was observed in the saline group of the HFD fed mice compared to the saline group of the ND fed mice (Figure 4.11B). The average adipocyte diameter of the saline control mice group on HFD and ND was $82.22 \pm 5.4 \ \mu m$ and $64.98 \pm 3.75 \ \mu m$ respectively. Nevertheless, the adipose tissue diameter of 10 mg/kg SQEL-treated mice group fed with HFD was reduced to $71.88 \pm 3.84 \ \mu m$ in which significantly lower when compared to the saline control mice group (Figure 4.11C) and appeared phenotypically similar to those of mice on ND and orlistat-treated mice fed HFD (Figure 4.11B). These findings demonstrated that SQEL significantly reduced the accumulation of lipid in the liver and adipose tissue hypertrophy in C57BL/6J mice.



Figure 4.11: Effects of SQEL treatment on adipose and liver tissues in C57BL/6J mice. H&E-stained histological images of (A) liver and (B) adipose tissues and (C) adipose tissue size of mice on normal and high-fat diet treated with 0.9% saline, 5 mg/kg SQEL, 10 mg/kg SQEL and 10 mg/kg orlistat for 12 weeks. Data are presented as the mean \pm SEM, n=7-8. (*p< 0.05 and ** p<0.01) versus respective control (0.9% saline) and ^{###}p< 0.001 versus normal diet 0.9% saline. The presence of lipid globules in the mice livers is indicated by black arrows. Magnification: 400x (A) & 100x (B). Scale bar: 50 µm (A) & 200 µm (B).

4.9 Effects of SQEL treatment on lipid profile and fasting blood glucose in C57BL/6J mice

After 12 weeks of SQEL treatment, mice fasted for 6 hours, euthanized by carbon dioxide asphyxiation and blood was withdrawn through cardiac puncture. Serum was separated, stored at -20°C and sent for lipid profiling to study the effects of SQEL treatment on lipid metabolism. Serum total cholesterol level was elevated in mice fed with HFD compared to those on ND (Table 4.1). A slight increase in triglyceride level was observed in mice fed with HFD compared to those on ND (Table 4.1). A slight increase in triglyceride level was observed in mice fed with HFD compared to those on ND but it was not significant (Table 4.1). Treatment with SQEL significantly decreased the total cholesterol and triglyceride levels in mice fed with ND and HFD as observed similar to the orlistat-treated group compared to their respective diet saline control (Table 4.1). Saline control mice fed HFD have higher fasting glucose compared to mice consumed ND. However, SQEL treatment has reduced the fasting glucose level in both ND and HFD fed mice group although the reduction was not significant (Table 4.1).

	Normal diet (Mean ± SEM)			
Parameter	0.9 % Saline (n=8)	5 mg/kg SQEL (n=8)	10 mg/kg SQEL (n=8)	10 mg/kg Orlistat (n=7)
T. Cholesterol (mMol/L)	3.51 ± 0.07	$3.09\pm0.12^{\texttt{a}}$	2.84 ± 0.19^{b}	$2.67\pm0.19^{\texttt{b}}$
Triglyceride (mMol/L)	2.53 ± 0.16	$1.92 \pm 0.12^{\texttt{a}}$	$1.66\pm0.11^{\circ}$	$1.37\pm0.08^{\mathfrak{c}}$
Fasting blood glucose (mMol/L)	8.2 ± 0.44	7.78 ± 0.37	7.76 ± 0.61	8.66 ± 0.63
	High-fat diet (Mean \pm SEM)			
Parameter	0.9 % Saline (n=8)	5 mg/kg SQEL (n=8)	10 mg/kg SQEL (n=8)	10 mg/kg Orlistat (n=7)
T. Cholesterol (mMol/L)	7.13 ± 0.37 †	$4.89 \pm 0.40^{\circ}$	$5.11 \pm 0.23^{\circ}$	$4.83\pm0.28^{\circ}$
Triglyceride (mMol/L)	2.69 ± 0.20	2.26 ± 0.17	2.45 ± 0.19	$1.68\pm0.15^{\text{b}}$
Fasting blood glucose (mMol/L)	9.41 ± 0.48	9.03 ± 0.36	8.38 ± 0.36	9.35 ± 0.29

Table 4.1: Effect of SQEL treatment on blood serum parameters in C57BL/6 mice.

Lipid profile and blood glucose of mice given normal diet and high-fat diet and treated with 0.9% saline, 5 mg/kg SQEL, 10 mg/kg SQEL and 10 mg/kg orlistat for 12 weeks. Data are presented as the mean \pm SEM, n=7-8, ^ap< 0.05, ^bp< 0.01 and ^cp< 0.001 versus control (0.9% saline) and [†]p< 0.0001 versus 0.9% saline of normal diet.

4.10 SQEL treatment increases the mRNA levels of AMPK and PGC-1α in adipose tissues of C57BL/6J mice

PGC-1 α possess important role in regulating the mitochondrial biogenesis that stimulates energy expenditure. AMPK is an energy sensor that modulate the expression of PGC-1 α by extracellular signaling in controlling metabolism (Cantó & Auwerx, 2009). Since SQEL treatment has reduced the mice body weight independent of total calorie intake, the possible involvement of mitochondrial biogenic gene expression was studied in adipose tissues of C57BL/6J mice. The mRNA levels of both AMPK and PGC-1 α were increased in mice fed ND compared to mice on HFD (Figure 4.12 A&B). Treatment with SQEL at 10 mg/kg dose significantly elevated the mRNA levels of AMPK and PGC-1 α by half-fold in mice group fed with HFD as well as in the orlistat-treated group (Figure 4.12 A&B). The AMPK mRNA expression increased in SQEL and orlistat treated mice group on ND, but it was not significant when compared to its saline control group (Figure 4.12A). SQEL treatment reduced the mRNA level of PGC-1 α in mice fed ND when compared to its saline control group (Figure 4.12B). However, the PGC-1 α mRNA level

86



Figure 4.12: Effects of SQEL and eurycomanone on the mRNA expression of AMPK and PGC-1 α in adipose tissues of C57BL/6J mice. mRNA expressions of (A) AMPK and (B) PGC-1 α in adipose tissue of mice on normal and high-fat diet treated with 0.9% saline, 5 mg/kg SQEL, 10 mg/kg SQEL and 10 mg/kg orlistat for 12 weeks. Ct values of AMPK and PGC-1 α were normalized to those of beta-actin and GAPDH and relative mRNA expressions of the treated samples were obtained by comparing to that of the vehicle control. Data are presented as the mean ± SEM, n=7-8. (*p< 0.05 and ** p<0.01) versus respective control (0.9% saline) and *p< 0.05 and **p< 0.01 versus normal diet 0.9% saline.

CHAPTER 5: DISCUSSION

Quassinoids are bioactive constituents of bitter principles from the plants belonging to the Simaroubaceae family. Their broad biological properties have attracted much attention from the scientific community. Various quassinoids isolated from Simaroubaceous plants possess antimalarial, anti-inflammatory, anti-tumor, anti-cancer and anti-parasitic effects (Guo *et al.*, 2005a; Jiwajinda *et al.*, 2002). *Eurycoma longifolia* Jack is a plant classified under the same family and is well-known as a traditional herb used for the treatment of various ailments. Six major quassinoids can be found in the root of this plant which includes, eurycomanone, 13,21-dihydroeurycomanone, $13\alpha(21)$ epoxyeurycomanone, 14,15 β -dihydroxyklaineanone, eurycomalactone, and longilactone (Han *et al.*, 2015). In recent years, natural products have been receiving notable attention as alternative sources to develop safe and effective drugs for weight management. To date, there are various dietary phytochemicals including polyphenols, alkaloids, terpenoids, organosulfur and phytosterols that have been reported to possess anti-obesity effects (Mohamed *et al.*, 2014). However, the effects of quassinoids in adipogenesis and the underlying mechanisms involved remain to be investigated.

In the present study, the anti-adipogenic effect of a quassinoids composition (SQEL) and the pure compound eurycomanone from *Eurycoma longifolia* Jack was investigated. Therefore, SQEL that contains enriched quassinoids (Low *et al.*, 2013) and the commercially available purified eurycomanone were used in this study. In addition, sulforaphane, an isothiocyanate compound found in cruciferous plants that were previously shown the anti-adipogenic effect was used as a positive control in this study (Choi *et al.*, 2012). Fibroblast-like preadipocytes including 3T3-L1, 3T3-F422A, 1246, Ob1771, TA1, and 30A5 cells are able to differentiate into adipocytes and derived from transgenic mice (Sarjeant & Stephens, 2012). The 3T3-L1 cell is one of the best cellular
models widely used to study *in vitro* adipocyte differentiation due to their capacity to develop a homogeneous mature adipocytes population, minimal drop in differentiation potential and better sensitivity towards lipogenic and lipolytic drug treatment (Ali *et al.*, 2013; MacDougald & Lane, 1995; Sarjeant & Stephens, 2012). Pre-adipocytic 3T3-L1 cells are committed to adipocyte differentiation via intracellular lipid accumulation upon hormonal induction (Rosen & MacDougald, 2006). Interestingly, adipogenesis and accumulation of lipid droplets are directly associated with the development of obese condition (Gregoire *et al.*, 1998). A flavonoid treatment has impaired cellular lipid accumulation in 3T3-L1 adipocytes as well as significantly decreased subcutaneous white adipose tissue weight in mice (Inafuku *et al.*, 2013). In another study, adipogenesis and body weight gain were prevented respectively in 3T3-L1 cells and high-fat diet induced obese mice with blueberry extract treatment (Song *et al.*, 2013). Thus, inhibiting adipogenic differentiation may prevent adipocyte hypertrophy and reduce its lipid content as shown previously by several findings (Inafuku *et al.*, 2013; Park *et al.*, 2012; Song *et al.*, 2013).

Prior to the study on the adipogenic inhibitory effects of SQEL and eurycomanone in 3T3-L1 cells, potential cytotoxicity effects of both the compounds were first ascertained. The chosen concentrations of SQEL and eurycomanone were not cytotoxic to the differentiating adipocytes, however, significantly inhibited adipogenesis by reducing the accumulation of cytosolic lipid in differentiating 3T3-L1 cells. Hence, the anti-adipogenic effect shown by these compounds was independent of non-specific cell toxicity. In this study, the pure compound, eurycomanone was found to have greater *in vitro* anti-adipogenic effect compared to the purified aqueous SQEL that contains about 32% quassinoids including 14% of eurycomanone.

Lipolysis is the catabolic process of triglyceride breakdown into free fatty acids and glycerol in adipocytes (Lass *et al.*, 2011). This is an important energy homeostatic process whereby; the free fatty acids are taken up by other body tissues to be utilized for β -oxidation and subsequent ATP generation in the event of energy demand (Kolditz & Langin, 2010). As lipolysis is a critical factor to reduce the amount of stored lipid in adipocytes, it can be one of the effective therapeutic targets to combat obesity. Interestingly, both SQEL and eurycomanone induced lipolysis in mature adipocytes and resulted in an increase in glycerol content but reduced intracellular triglycerides at the concentration that did not exert cytotoxicity. This finding is consistent with a previous study whereby, eurycomanone isolated from the powdered root of EL enhanced glycerol release and reduced lipid accumulation without cytotoxic effects in mature 3T3-L1 adipocytes (Lahrita *et al.*, 2017). The same study also elucidated that the lipolytic effects of eurycomanone are mediated by the direct activation of PKA, a potent activator of lipid hydrolyzing enzyme, hormone-sensitive lipase (Lahrita *et al.*, 2017).

Adipogenesis is a highly controlled process governed by a complex network of transcription factors. Cultured pre-adipocytes will proliferate to achieve growth arrest phase and begin to express the transcription initiator proteins PPAR γ and C/EBP α upon adipogenic induction by a cocktail of hormones (Farmer, 2006; Gregoire *et al.*, 1998). PPAR γ and C/EBP α are key adipogenic transcription factors that initiate the expression of pro-adipogenic markers for the phenotypical establishment of matured adipocyte (Moseti *et al.*, 2016; Rosen, 2005). Nonetheless, several earlier reports have shown that down-regulation of PPAR γ and C/EBP α are corrected adipocyte maturation and triglyceride accumulation in 3T3-L1 cells (Inafuku *et al.*, 2013; Ono & Fujimori, 2011). Comparably, SQEL and eurycomanone treatment have also significantly reduced the protein expression of PPAR γ and C/EBP α during the early stage of differentiation in 3T3-L1

cells. In the current study, SQEL and eurycomanone treatment for 48 hours reduced the expression of both PPAR γ isomers but significant changes were observed only in PPAR γ 2 protein expression. Zhu and colleagues have reported that PPAR γ is expressed in two isoforms: PPAR γ 1 and PPAR γ 2 as a result of splicing and using alternate promoter (Zhu *et al.*, 1995). However, PPAR γ 2 is the isoform that plays the regulatory role in adipogenesis while PPAR γ 1 has no effect in adipogenic differentiation (Ren *et al.*, 2002). This suggests that the down-regulation of PPAR γ 2 has a significant implication on adipocyte differentiation. Surprisingly, sulforaphane treatment resulted in the up-regulation of PPAR γ expression during the early stage of adipogenesis but significantly reduced terminal differentiation and triglyceride accumulation in 3T3-L1 cells suggesting that the compound may reduce the expression of PPAR γ in the later stage of adipogenic differentiation. These results are in agreement with a previous report whereby, significant suppression of PPAR γ expression was observed only after 6 days of sulforaphane treatment in differentiation medium (Choi *et al.*, 2012).

On the other hand, PPAR γ and C/EBP α are also responsible for the expression of adipocyte-specific genes including FAS, LPL and KLF15 which are involved in the formation of mature adipocytes (Farmer, 2006). FAS regulates *de novo* lipogenesis from acetyl-CoA, malonyl-CoA, and NADPH and is abundantly expressed in adipose tissue, liver, and lung (Ranganathan *et al.*, 2006). An earlier study showed that the rate of FAS synthesis is increased during the early phase of adipogenic differentiation which is attributed to the deposition of cytoplasmic lipid in 3T3-L1 cells (Student *et al.*, 1980). In addition, LPL, an early marker for adipogenesis was found to be elevated in adipocytes (Vu *et al.*, 2012). Furthermore, the DNA-binding transcriptional regulator, KLF15 is also induced during adipogenesis to increase the PPAR γ 2 gene promoter activity and its inhibition blocked differentiation in 3T3-L1 cells (Mori *et al.*, 2005). Findings from the

present study showed that the expression of FAS protein, mRNA expression levels of LPL and KLF15 were significantly downregulated in 3T3-L1 cells treated with SQEL and eurycomanone compared to vehicle control cells. Therefore, the reduction of adipogenic-specific genes and protein expression is directly contributed by the suppression of PPAR γ and C/EBP α transcription factors. This finding suggests that SQEL and eurycomanone inhibit differentiation of pre-adipocytes and lipid accumulation in matured adipocytes by inhibiting the expression of adipogenic transcriptional factors and their downstream target proteins.

In addition to PPAR γ and C/EBP α that play a pivotal role in the transcriptional control of adipocyte differentiation in vitro, earlier reports have identified the involvement of metabolic regulatory factors such as sirtuin (Sirt) proteins in adipogenesis (Cho et al., 2009). The activation of Sirt1 has been shown to impair adipocyte formation while its inhibition leads to adipocyte hyperplasia and eventually promotes the expression of adipogenic markers (Backesjo et al., 2006). The upregulation of Sirt1 protein during the early stage of adipogenesis, could reduce the expression of PPARy and inhibit adipocyte maturation (Kim et al., 2015). In addition, Mayoral and colleagues have demonstrated that Sirt1 knock-out mice on high-fat diet displayed PPARy hyperactivity and eventually leads to adjocyte hypertrophy (Mayoral et al., 2015). Moreover, the overexpression of Sirt1 was also previously shown to block triglyceride accumulation in 3T3-L1 cells (Imamura et al., 2017), suggesting that Sirt1 could be the upstream regulator of adipogenic transcription factors PPARy and C/EBPa in modulating adipogenesis. In an earlier study, the nuclear entry of Sirt1 was reported to reduce the expression of PPAR γ and its downstream adipogenic proteins which then inhibits 3T3-L1 adipocyte differentiation (Wang et al., 2016). Picard and colleagues have shown that Sirt1 blocks adipogenesis by repressing the transactivation of PPAR γ upon binding to the PPAR γ cofactors (repression domain 1 and CBF/Su(H) interaction domain) in 3T3-L1 cells

(Picard et al., 2004). In addition, an increased Sirt1 expression during adipogenesis also promotes deacetylation of PPAR γ which then impairs PPAR γ transcriptional activity and obstructs adipogenesis in 3T3-L1 cells (Kim et al., 2015). In the present study, the mRNA and protein expression of Sirt1 during the early phase of adipogenesis was significantly upregulated together with down-regulation of PPARy, C/EBPa and other adipogenicassociated markers by SQEL and eurycomanone treatment. FoxOs are key regulators of metabolism in insulin-sensitive tissues such as liver, adipose, and muscle cells (Gross et al., 2008). Overexpression of FoxO1 and FoxO3a suppress adipogenesis in 3T3-L1 cells by down-regulating PPARy and C/EBPa (Lai et al., 2012; Nakae et al., 2003). Comparably, the protein expression of FoxO3a was dramatically elevated along with suppression of key adipogenic transcription factors by SQEL and eurycomanone treatment in differentiating 3T3-L1 cells. It is known that Sirt1 is the upstream regulator of FoxOs in adipogenic inhibition, the finding from the present study is suggestive of the possible involvement of Sirt1/FoxO3a/PPARy signaling in SQEL and eurycomanonemediated adipogenesis inhibition in 3T3-L1 cells. It is shown that several phytochemicals including agrimol B, fisetin, xanthigen and resveratrol, were also shown to inhibit adipogenesis via Sirt1/PPARy or Sirt1/FoxO/PPARy signaling pathway (Costa et al., 2011; Kim et al., 2015; Lai et al., 2012; Wang et al., 2016).

Several reports have shown the correlation between adipogenesis and the development of obese condition (Nishimura *et al.*, 2007; Spiegelman & Flier, 1996). This is because the number of adipocytes in a given fat mass increases in obesity due to the uncontrolled adipogenesis that contributes to the formation of new adipocytes from precursor cells (Hausman *et al.*, 2001; Tchoukalova *et al.*, 2004). Studies on human have shown that higher fat intake is accompanied by body weight gain and eventually can lead to obesity and other related comorbidities. Rodent is suitable models to study both the mechanistic and therapeutic aspects of obesity since they are susceptible to weight gain upon feeding with HFDs in a relatively short duration (Buettner *et al.*, 2007). Most rodents on obesogenic diet readily become obese, however, inbred mouse strain such as C57BL/6J mice are more prone to obesity when given HFDs (Rossmeisl *et al.*, 2003). Moreover, the HFD-induced obese C57BL/6J mice also develop features of obesity-associated diseases such as hypertriglyceridemia, hyperglycemia, insulin resistance and hepatic steatosis supporting the suitability of this mice strain as an experimental rodent model of metabolic syndrome (Fernandes-Santos *et al.*, 2009; Fraulob *et al.*, 2010). Although dietary intake of 60 kcal% fat in a human would be physiologically irrelevant, the said diets are generally used to enhance weight gain in rodents (Jiang *et al.*, 2009; Johnston *et al.*, 2007). Thus, obesity-related disease models can be established quickly for pre-clinical interventional studies in a shorter period of time.

There has been a growing number of phytochemicals including curcumin, rutin and clerodane diterpene that has been shown to inhibit the progression of adipogenesis in 3T3-L1 cells as well as obesity in C57BL/6J mouse model (Beg *et al.*, 2015; Choi *et al.*, 2006; Ejaz *et al.*, 2009). In the present study, SQEL treatment not only decreased the weight of epididymal and perirenal adipose tissues but has also reduced the adipose tissue size of mice on HFD. This shows that the development of epididymal and perirenal adipose tissues was reduced in the presence of SQEL, possibly due to the inhibitory effect of triglyceride accumulation in fat cells as demonstrated by the inhibition of adipogenesis and cytosolic lipid accumulation *in vitro*. These findings hence, suggest that SQEL-mediated suppression of body weight gain in mice consumed high-fat diet was due to the reduction in adipose tissue size and weight.

Interestingly, body weight gain was prevented in SQEL treated-mice without caloric restriction which is on par with other previous studies that showed weight gain in animal models could also be prevented without the suppression of food intake (Beg *et al.*, 2015;

Inafuku et al., 2013; Sharma et al., 2017; Song et al., 2013). This then suggests that SQEL may regulate body weight gain by enhancing calorie expenditure. It is shown that increased calorie expenditure could be mediated through the action of peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PGC-1a) (Gao et al., 2009). PGC-1a is a transcriptional coactivator and an inducer of transcription factors involved in cellular energy metabolism and also acts as a master regulator of mitochondrial biogenesis (Cantó & Auwerx, 2009). Overexpression of PGC-1a in white adipocytes leads to upregulation in the expression of mitochondrial respiratory chain proteins and metabolic enzymes involved in fatty acid oxidation (Tiraby et al. 2003). Moreover, a previous study has demonstrated the reduction of body weight gain in mice which was mediated by an increase in energy expenditure and fatty acid oxidation was through the actions of PGC-1a on butyrate supplementation (Gao et al., 2009). Furthermore, adipose tissue-specific deletion of PGC-1 α in mice has resulted in severe weight gain, increase in circulating lipids, insulin resistance, impaired glucose homeostasis along with reduced expression of genes modulating lipid metabolism and fatty acid uptake in adipose tissues (Kleiner et al., 2012). Nevertheless, the mRNA expression of PGC-1a was also diminished in adipose tissue of mice on HFD compared to those on low-fat diet for 6 weeks (Cummins et al. 2014). Similarly, in the present study, mice fed with HFD had significantly lower mRNA level of PGC-1a when compared to ND fed mice group. Nonetheless, other studies have demonstrated the involvement of the adenosine monophosphate-activated protein kinase (AMPK) in increased calorie expenditure in mice models (Choi et al., 2017; Kudo et al., 2015). AMPK has been shown to regulate PGC-1a and mitochondrial biogenesis in several tissues, including adipose tissues (Gaidhu et al., 2009). AMPK regulates energy metabolism by stimulating the interaction between PGC1a and PRDM16 resulting in increased mitochondrial biogenesis, thermogenesis, and energy expenditure (Zhang et al., 2016). Another study further demonstrated that AMPK could increase the expression of Sirt1 and enhance mitochondrial biogenesis through PGC1 α (Fernandez-Marcos & Auwerx, 2011). Interestingly, SQEL treatment has elevated the mRNA expression of AMPK and PGC1 α in adipose tissue of mice fed HFD. This finding suggests that SQEL could also alter the energy balance through an increased calorie expenditure via AMPK- PGC1 α signaling in white adipose tissue in preventing weight gain among mice on HFD.

Hyperglycemia and insulin resistance are strongly associated with obesity. Prior studies have shown that C57BL/6J mice fed with high-fat diet have elevated blood glucose level (Winzell & Ahren, 2004) and an anti-obesity compound treatment has improved glucose tolerance (Chen et al., 2017). Results from this study show that the development of glucose intolerance in HFD mice was significantly inhibited by 12 weeks of SQEL treatment. Even though the time-course of glucose clearance in HFD fed saline control mice was delayed compared to that of the ND fed mice, SQEL also improved glucose clearance significantly in mice on a normal diet. Insulin is the key regulator of adipocyte morphology whereby it promotes the differentiation of pre-adipocytes into adipocytes and stimulates lipogenesis as well as inhibiting lipolysis in mature adipocytes (Kahn & Flier, 2000). Adipocytes are one of the cell types that are more sensitive to insulin and hence impaired response towards insulin signaling on metabolism and glucose transport in adipose tissue will lead to insulin resistance in obese individual (Kahn & Flier, 2000). However, the attempt to elucidate the effect of SQEL treatment on insulin sensitivity could not be accomplished since insulin resistance was not observed in both ND and HFD fed mice groups, likely due to a shorter study period. Previously, significant insulin resistance was observed in mice fed with HFD for 16 weeks (Fraulob et al., 2010) and targeted mutagenesis or transgenesis of genes required for insulin action and insulin secretion in mice (Nandi et al., 2004) would yield better animal model to be used for studies on insulin resistant. As PPARy activation has been shown to induce the expression of a number of genes involved in the insulin signaling cascade (Leonardini *et al.*, 2010) inhibition of PPAR γ by SQEL treatment could have led to the lack of effect on insulin sensitivity in normal although glucose intolerance was reduced.

Histological analysis of liver sections of HFD fed mice revealed the accumulation of abundant lipid droplets compared to mice on ND, a prominent sign of hepatic steatosis strongly associated with obesity (Fabbrini *et al.*, 2010). Liver sections of SQEL treated mice fed with ND exhibited normal histology similar to orlistat treatment. Moreover, mice on HFD supplemented with SQEL significantly attenuated the progression of fatty liver disease evidenced by a drastic reduction in the number of lipid droplets in the liver. On the other hand, liver histology of mice received SQEL did not show any sign of inflammation or cytotoxicity, suggesting that increased liver weight was not attributed to liver damage. Interestingly, these findings are comparable to the effects of orlistat treatment in preventing the development of steatohepatitis in obese individuals (Harrison *et al.*, 2003) and indicate that SQEL can intensely suppress the pathological sign in the liver.

Hypertriglyceridemia and hypercholesterolemia are associated with increased risk for obesity as there is a significant correlation between impaired lipid metabolism and obesity (Eisinger *et al.*, 2014; Subramanian & Chait, 2012). Therefore, the effects of SQEL treatment in the regulation of lipid metabolism were studied in both normal and high-fat diet consumed mice. Previously, it was shown that C57BL/6J mice on the obesogenic diet had elevated levels of serum triglycerides and cholesterol compared to those on ND (Beg *et al.*, 2015; Song *et al.*, 2013). However, in the present study, serum total cholesterol but not triglyceride levels were significantly higher in mice fed with HFD compared to those on ND. Nevertheless, decreased level of circulating triglycerides and insignificant change in serum triglycerides have also been found in C57BL/6J mice fed with HFD compared

to mice fed with standard diet previously (Eisinger *et al.*, 2014; Ji *et al.*, 2014). Moreover, high-fat consumption or reduced carbohydrate intake could lessen triglyceride production and/or induce triglyceride clearance that eventually lowers circulating level of triglycerides in obese mouse model (Guo *et al.*, 2009). Results from the present study demonstrated that SQEL treatment reduces both total cholesterol and triglycerides levels in mice regardless of the types of diet given. These outcomes indicate that SQEL modulates triglyceride and cholesterol metabolism both in normal and obese mice.

CHAPTER 6: CONCLUSION

6.1 Conclusion

Adipogenesis dysregulation has been associated with the development of fat tissue mass that leads to obesity, a public health issue owing to its high prevalence, morbidity and mortality. Despite the advancement in pharmacotherapy and other non-pharmacological methods advocated to combat this serious health concern, unsatisfactory outcome and serious side effects warrant the search for a novel and/or alternative phytomedicine for the treatment of obesity. The current study is an effort to investigate the potentials of naturally derived bioactive compounds, SQEL as an anti-adipogenic agent to halt adipogenesis and eventually the progression to obese condition. In the present study, the cytotoxicity, anti-adipogenic and anti-obesity effect of SQEL were investigated in 3T3-L1 cells and diet-induced obese C57BL/6J mice.

Results from the present study revealed that the tested SQEL and eurycomanone concentrations are not cytotoxic to both differentiating pre-adipocytes and matured adipocytes. Concurrent treatment of SQEL and eurycomanone at non-cytotoxic concentrations to differentiating 3T3-L1 cells blocked adipogenesis. This finding was further strengthened by the observation of a concentration-dependent reduction in the number of cells with stained lipid droplets treated with SQEL and eurycomanone through microscopic inspection of the Oil Red O staining. A stronger adipogenic inhibitory effect showed by eurycomanone suggests that the anti-adipogenic property of SQEL could be mediated by the presence of eurycomanone which comprises 14% of quassinoid composition of SQEL. SQEL and eurycomanone also impaired lipogenesis as revealed by a dose-dependent reduction in the level of cytosolic triglyceride. Furthermore, SQEL and eurycomanone treatment also enhanced lipolysis that eventually reduced the

intracellular triglyceride content in mature adipocytes. These findings suggest that SQEL and eurycomanone block adipogenesis and regulate lipid metabolism in adipocytes.

The inhibitory effect of adipogenesis induced by SQEL and eurycomanone on the molecular regulation of transcription factors together with its downstream adipogenic-specific markers in differentiating 3T3-L1 cells was also studied. In the present study, the transcription factors PPAR γ and C/EBP α that expressed immediately upon the induction of pre-adipocyte differentiation were significantly downregulated by both SQEL and eurycomanone treatment. Subsequently, the expression of adipogenic markers such as FAS, LPL and KLF15 which are necessary for the phenotypical establishment of matured adipocyte were also impaired by the same treatment. On the other hand, Sirt1 and FoxO3a expression was enhanced by SQEL and eurycomanone during the early phase of adipogenesis in 3T3-L1 cells. These outcomes propose that the blockade of adipogenesis in differentiating 3T3-L1 cells following treatment with SQEL and eurycomanone is due to the repressive effect of the adipogenic-specific transcription factors and markers in which probably modulated by the Sirt1/FoxO3a/PPAR γ signalling.

As the involvement of adipogenesis is crucial in obesity progression, the anti-obesity effect of SQEL was assessed in the ND and HFD fed C57BL/6J mice. The administration of SQEL via intraperitoneal route for 12 consecutive weeks prevented both ND and HFD fed mice from significant body weight gain independent of their total calories consumed. Moreover, SQEL treatment has induced energy expenditure in adipose tissue of mice on HFD by elevating the expression of thermogenic genes, AMPK and PGC-1 α . Similarly, SQEL treatment also attenuated adipose tissue hypertrophy as evidenced by a significant reduction in the epididymal and perirenal fat pad mass in mice consumed HFD. Conclusively, these findings suggest SQEL consumption could prevent body weight gain by impairing the enlargement of adipose tissue that in turn reduces fatty tissue mass in

HFD-induced obese mice. Supplementation of SQEL improved glucose clearance, decreased serum triglycerides and cholesterol levels in both ND and HFD fed mice. Additionally, the development of hepatic steatosis was also significantly prevented in the obese mouse supplemented with SQEL. These findings suggest that SQEL treatment not only possesses anti-obesity property but also prevents the development of obesity-associated diseases in C57BL/6J mice.

Collectively, the outcomes of the present study are strongly suggestive of the novel effect of SQEL in inhibiting adipogenesis and has potential as a natural therapeutic agent in preventing the development of obesity.

6.2 Limitations of the study and future direction

Adipogenesis is a closely regulated process that involves the transition of cell proliferation to cell differentiation where both events leading to the commitment of the pre-adipocytes maturation into adipocyte (Fajas, 2003). The clonal expansion, a cell cycle re-entry is necessary to induce metabolic gene expression for the accumulation of cytosolic lipid droplets in adipocytes (Reichert & Eick, 1999). Therefore, *in vitro* adipogenic inhibitors could also act as the cell cycle blocking agents that impair the 3T3-L1 cell differentiation. Several bioactive compounds such as vitisin A and sulforaphane have been shown to induce cell cycle arrest at various stages of a clonal expansion that eventually blocked adipogenesis in 3T3-L1 cells (Choi *et al.*, 2012; Kim *et al.*, 2008). Hence, further study can be conducted to identify the possible modulation of the cell cycle by SQEL and eurycomanone-mediated adipogenesis inhibition in differentiating pre-adipocytes.

Lipolysis is the mobilization of triglycerides in adipose tissue that is hydrolyzed into free fatty acids and glycerol to provide energy to the body when needed. This catabolic process plays a crucial role in regulating triglycerides turnover and it is dysregulated in an obese individual thus contributing to several pathological conditions (Arner *et al.*, 2011). Previous studies have demonstrated that drugs that induce lipolysis prevent adipocyte hypertrophy, promote energy expenditure, reduced hyperlipidemia, hyperglycemia and attenuates obesity in mice (Chen *et al.*, 2017; Xiong *et al.*, 2015). Similarly, SQEL induced lipolysis as indicated by significant increase in glycerol production and a decrease in accumulated triglycerides in matured adipocytes. However, the mechanism of SQEL-induced lipolysis *in vitro* and its lipolytic effect in obese rodent has yet to be unveiled and warrants further studies. In the present study, the *in vivo* triglycerides and LDL lowering effects of SQEL was only moderately achieved. Hence, improvement to the current preparation of SQEL to yield greater efficacy is recommended. Furthermore, as EL is commonly taken orally, preparation given via oral route rather than intraperitoneal route can be tested.

Hypertension is one of the major contributory factors in the cardiovascular morbidity and mortality that strongly associated with obesity. Obesity is well known as a causative or a coexisting factor in the pathogenesis of blood pressure that leads to myocardial infraction, stroke and kidney failure (Susic & Varagic, 2017). In reality, dietary factors, metabolic, endothelial, vascular and inflammatory dysfunction are the potential mechanism linking obesity to hypertension (DeMarco *et al.*, 2014). A previous study found a purified fraction from *Eurycoma longifolia* plant has hypotensive properties and suggested it could be used as a conventional treatment for the control of hypertension (Tee *et al.*, 2016). However, the study was limited to the investigation of the purified fraction only in normal but not in the obese rodent. Since the results from current study strongly suggest the obesity preventive effects of SQEL in a diet-induced obese mouse model, the potential anti-hypertensive properties of SQEL in the obese animal model is worth exploring further.

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LIST OF PUBLICATIONS AND PAPERS PRESENTED

PUBLICATION

Original research article

Balan D, Chan K-L, Murugan D, AbuBakar S, Wong P-F. Antiadipogenic effects of a standardized quassinoids-enriched fraction and eurycomanone from *Eurycoma longifolia*. *Phytotherapy Research*. 2018;32:1332–1345. https://doi.org/10.1002/ptr.6065

CONFERENCE ATTENDED

Poster presentation

<u>Balan D</u>, Chan K-L, Murugan D, AbuBakar S, Wong P-F. Anti-adipogenic effect of a standardized quassinoids-enriched fraction of *Eurycoma longifolia*. 3rd Pan-Asian Biomedical Science Conference 2016, 7-8 December 2016, Premiera Hotel Kuala Lumpur, Malaysia.