

**Influence of Anatomic Depot on the Apoptotic Susceptibility of Adipose Progenitor
Cells**

Amanda Biernacka-Larocque

Thesis submitted to the Faculty of Graduate and Postdoctoral Studies
in partial fulfillment of the requirements for the MSc. degree in Biochemistry

Department of Biochemistry, Microbiology and Immunology

Faculty of Medicine

University of Ottawa

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Abstract

Adipose tissue (AT) expands through hypertrophy and hyperplasia. Hyperplastic AT expansion requires an adequate number of adipose progenitor cells. This study investigates the influence of depot origin on the susceptibility of adipose progenitors to cell death, and measures the effect of macrophage-secreted factors on adipose progenitor survival. Using serum deprivation alone or in the presence of TNF α , omental (OM) versus subcutaneous (SC) adipose progenitors, obtained from human AT, displayed a 3- and 1.7-fold-increase in apoptosis, respectively, as assessed by Hoechst staining, ($p < 0.05$). Similar results were observed with cell enumeration. The ratio of OM/SC cell death from serum deprivation positively correlated with body mass index (BMI). The depot-specific difference in cell death was lost when TNF α and cycloheximide (CHX) were used. Monocyte-derived macrophages (MD-macrophages), isolated from human blood, did not have an effect on apoptosis. Depot-related differences in adipose progenitor apoptosis may influence AT remodeling and alter metabolic functionality in obesity.

Table of Contents

Abstract	ii
List of Abbreviations.....	v
1.0 General Introduction	1
Obesity	1
<i>Definition and Assessment</i>	1
<i>Causes of Obesity</i>	3
<i>Risks of Obesity</i>	4
Adipose Tissue	5
<i>Cellular Composition of Adipose Tissue</i>	5
<i>Adipose Progenitor Cells</i>	6
<i>Adipocytes</i>	7
<i>Forms and Function</i>	8
<i>Endocrine Function of Adipose Tissue</i>	9
<i>Adipose Tissue Depots</i>	9
Adipose Tissue Remodeling	11
<i>Adipose Tissue Expansion</i>	11
<i>Adipose Tissue Dysfunction</i>	12
<i>Endoplasmic Reticulum Stress</i>	13
<i>Hypoxia</i>	14
<i>Adipose Tissue Inflammation</i>	14
<i>Adipose Tissue Eosinophils</i>	15
<i>Adipose Tissue T Cells</i>	16
<i>Adipose Tissue B Cells</i>	16
<i>Adipose Tissue Macrophages</i>	16
Cell Death.....	17
Mechanism	20
<i>Extrinsic Pathway</i>	20
<i>Intrinsic Pathway</i>	21
Rationale	23
Hypothesis	23
Objectives.....	23
2.0 Materials and Methods	24
Cell Model used for Objectives.....	24
<i>Human Primary Adipose Progenitor Cells</i>	24

<i>Monocyte-Derived Macrophages</i>	24
<i>Inducers of Apoptosis</i>	25
Isolation and Culture of Human Adipose Progenitor Cells	25
Preparation of Macrophage Conditioned Medium.....	26
Cell Death Analysis.....	27
<i>Cell Enumeration</i>	27
<i>Hoechst Staining</i>	27
Statistical Analysis	28
3.0 Results.....	29
Depot Differences in Adipose Progenitor Cell Death.....	29
Results for Aim 1	29
<i>Effect of Serum Deprivation on the Cell Death of Adipose Progenitor Cells</i>	29
<i>Effect Serum Deprivation and TNFα on the Cell Death of Adipose Progenitor Cells</i> ...	35
<i>Effect of Serum Deprivation and TNFα/CHX on the Cell Death of Adipose Progenitor Cells</i>	35
Results for Aim 2	47
<i>MacCM on the Survival of Human Primary Adipose Progenitor Cells</i>	47
<i>Serum Deprivation on MacCM Survival Activity and Human Adipose Progenitor Cells</i>	47
<i>Serum Deprivation and TNFα on MacCM Survival Activity and Human Adipose Progenitor Cells</i>	49
<i>Serum Deprivation and TNFα with CHX on MacCM Survival Activity and Human Adipose Progenitor Cells</i>	51
4.0 Discussion	53
Conclusion and Proposed Model	61
5.0 References	63
6.0 Curriculum Vitae.....	78

List of Abbreviations

ANOVA	Analysis of variance
AT	Adipose tissue
ATM	Adipose tissue macrophage
ATP	Adenosine triphosphate
BAT	Brown adipose tissue
BMI	Body Mass Index
C/EBP	CCAAT-enhancer binding protein
CAD	Caspase-activated DNase
CD	Cluster of differentiation
CHX	Cycloheximide
cIAP	Cellular Inhibitor of Apoptosis
CLS	Crown-like structure
CT	Computed tomography
CVD	Cardiovascular disease
DEXA	Dual-energy X-ray absorptiometry
DISC	Death inducing signaling complex
DMEM	Dulbecco's modified eagle's medium
EDTA	Ethylenediaminetetraacetic acid
ER	Endoplasmic reticulum
FADD	Fas-Associated Protein with Death Domain
FBS	Fetal bovine serum
FFA	Free fatty acids
FLICE	Fas-associated protein with death domain-like interleukin-1 beta-converting enzyme
FLIP	FLICE-like inhibitory protein
FTO	Fat mass and obesity associated
GLUT4	Glucose transporter type 4
GM-CSF	Granulocyte-macrophage colony-stimulating factor
GWAS	Genome-wide association studies
HIF-1 α	Hypoxia-inducible factor-1 alpha
IAP	Inhibitor of apoptosis
ICAD	Inhibitor of caspase-activated DNase
IGF	Insulin growth factor
IKK β	Inhibitor of nuclear factor kappa B kinase subunit beta
IL	Interleukin
IRS-1	Insulin receptor substrate-1
JNK	c-Jun N-terminal kinase
LD	Lipid droplet
LPS	Lipopolysaccharide
MacCM	Macrophage-conditioned medium
MCP-1	Monocyte chemotactic protein-1
MD-macrophages	Monocyte-derived macrophages
MHO	Metabolically healthy obese
MRI	Magnetic resonance imaging
NAFLD	Non-alcoholic fatty liver disease

NAIP	NLR apoptosis inhibitory protein
NEFA	Non-esterified fatty acids
NFκB	Nuclear factor kappa B
OAT	Omental adipose tissue
OM	Omental
PBMC	Peripheral blood mononuclear cell
PBS	Phosphate buffered saline
PDGF	Platelet-derived growth factor
PPARγ	Peroxisome proliferator-activated receptor gamma
RIPK3	Receptor-interacting protein kinase 3
ROS	Reactive oxygen species
RPMI	Roswell Park Memorial Institute
SAT	Subcutaneous adipose tissue
SC	Subcutaneous
SGBS	Simpson-Golabi-Behmel syndrome
SVF	Stromal vascular fraction
T2D	Type 2 diabetes
TG	Triacylglycerol
T _H 1	Type 1 helper T cells
T _H 2	Type 2 helper T cells
TNFα	Tumor necrosis factor alpha
TNFR	Tumor necrosis factor receptor
TRAIL	TNF-related apoptosis-inducing ligand
Tregs	T regulatory cells
UPR	Unfolded protein response
VAT	Visceral adipose tissue
WAT	White adipose tissue
WC	Waist circumference
WT	Wild type
zVAD-FMK	Carbobenzoxy-valyl-alanyl-aspartyl-(β-O-methyl)-fluoromethyl ketone

List of Figures

- Fig. 1** Primary human adipose progenitor cell apoptosis induced by serum deprivation.
- Fig. 2** Apoptosis induced by serum deprivation correlates with BMI.
- Fig. 3** Primary human adipose progenitor cell death induced by serum deprivation.
- Fig. 4** Cell death induced by serum deprivation correlates with BMI.
- Fig. 5** Primary human adipose progenitor cell apoptosis induced by serum deprivation with TNF α .
- Fig. 6** Apoptosis induced by serum deprivation with TNF α correlates negatively with BMI.
- Fig. 7** Primary human adipose progenitor cell death induced by serum deprivation with TNF α .
- Fig. 8** Cell death induced by serum deprivation with TNF α does not correlate with BMI.
- Fig. 9** Primary human adipose progenitor cell apoptosis induced by serum deprivation with TNF α and CHX.
- Fig. 10** Apoptosis induced by serum deprivation with TNF α and CHX does not correlate with BMI.
- Fig. 11** Primary human adipose progenitor cell death induced by serum deprivation with TNF α and CHX.
- Fig. 12** Cell Death induced by serum deprivation with TNF α and CHX does not correlate with BMI.
- Fig. 13** Serum deprivation with TNF α for 6 h is sufficient to induce primary human adipose progenitor cell apoptosis.
- Fig. 14** Serum deprivation with TNF α for 24 h is sufficient to induce primary human adipose progenitor cell death.

Fig. 15 MacCM survival activity on primary human adipose progenitor cells in the presence of serum deprivation.

Fig. 16 MacCM survival activity on primary human adipose progenitor cells in the presence of serum deprivation with TNF α .

Fig. 17 MacCM survival activity on primary human adipose progenitor cells in the presence of serum deprivation with TNF α and CHX.

Fig. 18 Model of how apoptotic inducers, either intrinsic (serum withdrawal) or extrinsic (TNF α), influence the apoptotic susceptibility of adipose progenitor cells.

1.0 General Introduction

Obesity

Definition and Assessment

Obesity is defined as an excess accumulation of fat mass (adipose tissue; AT). Since the 1970's, the prevalence of obesity has increased significantly worldwide. Estimates from 2009 indicate that ~24% of Canadians are obese, representing a large increase from ~14% in 1989 (McGuire et al., 2011). Increases in the prevalence of obesity have been substantial, widespread, and have arisen over a short time. However, there is some evidence of a plateau in adult and childhood obesity rates that provides some hope that the epidemic might have peaked in some developed countries (Ng et al., 2014).

There are numerous methods to measure obesity, with advantages and disadvantages to each. Measurements of body weight and height are used most frequently as they provide a rapid and economical way to determine adiposity. Body mass index (BMI) is calculated as weight in kilograms (kg) divided by height in meters squared (m^2). Individuals with a BMI ≥ 25 kg/ m^2 are considered overweight and those with a BMI ≥ 30 kg/ m^2 are classified as obese. Because the risk of adverse health effects increases at higher levels of BMI, obesity is divided into three categories. For male and female adults aged 20 and over, obesity class I is defined as a BMI of 30.0 to 34.9 kg/ m^2 obesity class II is defined as a BMI of 35.0 to 39.9 kg/ m^2 and obesity class III is defined as a BMI of 40.0 kg/ m^2 or higher. BMI has some limitations in the analysis of fat mass. The calculation is solely dependent on the net weight and height of the individual and does not consider the distribution of muscle and bone mass.

There is a potential risk of overestimating adiposity in individuals with high muscle mass and underestimating the fat deposit in those with less lean body mass.

In contrast to BMI, waist circumference (WC) is a better indicator of central adiposity (Knowles et al., 2011). It is an indicator of health risk associated with excess fat around the waist (also described as an 'apple' body shape). A WC of 102 cm (40 inches) or more in men, or 88 cm (35 inches) or more in women, is associated with health problems such as type 2 diabetes (T2D), cardiovascular disease (CVD) and hypertension. Even if the BMI of an individual is in the normal weight range, a high WC demonstrates some health risk.

Historically in the research setting, total body fat was measured by densitometry based on the principles of water displacement, assuming just two body compartments: fat (density about 0.7 g/ml) and fat-free tissue (about 1.0 g/ml) (Han et al., 2006). According to this principle, if two individuals of the same weight on land have different proportions of body fat and lean tissue, the one with more body fat and less lean tissue would weigh less under water. Today, densitometry is not frequently used as it is labour-intensive, expensive and fails to indicate body fat distribution.

Imaging techniques such as computed tomography (CT), magnetic resonance imaging (MRI) and dual-energy X-ray absorptiometry (DEXA) allow whole body or regional assessments of body fat. CT and MRI are considered to be the most accurate methods for measuring tissue, organ and whole-body fat mass. Specific abdominal AT depots can be measured, including the subcutaneous (SC) and visceral depots. DEXA quantifies bone mineral density and lean soft tissue, from which AT mass is indirectly estimated (Manninen, 2006). DEXA cannot accurately distinguish between different types of fat. Imaging is very

expensive and some techniques (CT and DEXA) can expose patients to radiation, so its use is limited, especially with repeated measurements (Han et al., 2006).

Causes of Obesity

AT mass depends on the relative intake versus expenditure of calories. In a state of chronic positive energy imbalance, AT expands and obesity ensues. Hypernutrition and a sedentary lifestyle are the main factors contributing to obesity; however, genetic predisposition also has a profound effect on energy balance. Genetic influences on obesity have been estimated to contribute 40-70% to the variation in body weight within a population, by affecting energy intake and expenditure (Tung and Yeo, 2011). Although obesity is generally considered a multifactorial disease, monogenic forms of obesity exist. Monogenic forms of obesity usually result in an early-onset severe form of weight gain. Melanocortin 4 receptor loss-of-function mutations represent the most common monogenic form of obesity, accounting for ~5% of severe early onset obesity (Calton et al., 2009; Hainerova et al., 2007; Hinney et al., 2006; Krakoff et al., 2008; Lubrano-Berthelier et al., 2006; Stutzmann et al., 2008). This hypothalamic receptor recognizes α -melanocyte stimulating hormone and signals to decrease food intake. Loss-of-function mutations in the leptin gene or the leptin receptor account for ~3% of severe cases of obesity (Farooqi et al., 2002). Leptin was the first weight-regulating adipocyte secreted factor (adipokine) to be identified (Zhang et al., 1994; Halaas et al., 1994). Leptin exerts pleiotropic effects on metabolism and energy homeostasis by acting on both central and peripheral tissues (Bjorbaek and Kahn, 2004; Lago et al., 2007) and reduces appetite by acting on its hypothalamic receptor (Montague et al., 1997).

It is believed that the remaining heritability lies within a large number of genetic variants affecting multiple genes (Ramachandrapa and Farooqi, 2011). In order to identify genetic mutations that associate with obesity, many genome-wide association studies (GWAS) have been conducted. GWAS have currently identified ~30 genetic loci affecting the risk of developing obesity (McCarthy, 2010). Currently, loci identified by GWAS account for ~10% of the heritability of obesity (Ramachandrapa and Farooqi, 2011). The first and strongest identified association between body weight and multiple variants in genetic loci was the fat mass and obesity associated *FTO* gene. Mutations in the *FTO* loci are associated with a 3 kg increase in body weight and a 1.7-fold increased risk of obesity (Frayling et al., 2007). A recent study (Smemo et al., 2014) revealed that the obesity-associated noncoding sequences within *FTO* are connected with the homeobox gene *IRX3*. The obesity-associated *FTO* region directly interacts with the promoters of *IRX3* as well as *FTO* in human, mouse and zebrafish. Furthermore, obesity-associated single nucleotide polymorphisms are associated with expression of *IRX3*, but not *FTO*, in human brains. A reduction in body weight of 25 to 30% was observed in *Irx3*-deficient mice, through the loss of fat mass and increase in basal metabolic rate. *IRX3* is a target of obesity-associated variants within *FTO* and may provide a new determinant of body mass and composition.

Risks of Obesity

Obesity is a growing public health concern throughout the world because it is associated with many diseases. As previously mentioned, it is caused by a combination of environmental and genetic factors. Obesity is associated with cardiac and metabolic risk factors which lead to increased morbidity and mortality. Cardiometabolic complications are related to a broad spectrum of pathological conditions, including insulin resistance, T2D,

non-alcoholic fatty liver disease (NAFLD), dyslipidemia, hypertension, CVD and some types of cancer (Conway and Rene, 2004; Khandekar et al., 2011).

It is widely believed that insulin resistance is the main etiological factor that contributes to the development of obesity-related complications. Even though obesity is commonly linked to the onset of cardiometabolic abnormalities, not all obese individuals suffer from metabolic dysfunction and insulin resistance. This subset of apparently healthy obese subjects is referred to as metabolically healthy obese (MHO). Several studies have confirmed the existence of MHO individuals, accounting for as much as 25% of the obese population (Karelis, 2008; Karelis et al., 2004; Messier et al., 2010; Primeau et al., 2011). MHO individuals are characterized by normal insulin sensitivity, a low prevalence of hypertension, and a favourable lipid and inflammation profile (Hinnouho et al., 2013).

Nutrient excess causes AT to undergo rapid and dynamic changes through adipocyte hypertrophy (increase in adipocyte size) and hyperplasia (increase in adipocyte number). In an obese state, AT remodeling is often associated with pathological changes. However the idea of a MHO state suggests that some individuals avoid the pathological consequences associated with obesity on the basis of healthy AT expansion primarily by hyperplasia. For this reason it is crucial to consider mechanisms of AT expansion.

Adipose Tissue

Cellular Composition of Adipose Tissue

Adipocytes constitute the main cellular component of white AT (WAT) and comprise between 50-70% of the cellular mass of AT (Hauner, 2005). In addition to adipocytes, WAT contains non-adipocyte cellular components which are collectively referred to as the stromal vascular fraction (SVF). These cells include adipose progenitor cells (preadipocytes) (20-

40%), fibroblasts, smooth vascular endothelial cells (1-10%) and a variety of immune cells (10-50%), including AT macrophages (ATMs).

Adipose Progenitor Cells

AT is derived from the mesenchyme and contains stromal progenitors at various stages of adipogenic commitment. Less committed progenitors (mesenchymal stem cells) can differentiate into several cell types, including osteoblasts, chondrocytes, myoblasts and adipocytes when provided with the appropriate signals. Adipose progenitors are defined as either adherent stromal cells possessing adipogenic potential, or as stromal cells expressing a limited number of cell surface proteins (Rodeheffer et al., 2008; Tchoukalova et al., 2007; Zuk et al., 2002; Tran et al., 2012; Cawthorn et al., 2012). Methods for human adipose progenitor cell identification vary due to a lack of consistent cell surface markers capable of distinguishing multipotent cells from committed adipose progenitor cells, in contrast to more defined protocols for murine cells.

Committed adipose progenitor cells undergo growth arrest and subsequent terminal differentiation into adipocytes (Tang and Lane, 2012). Exposure of growth-arrested adipose progenitors to differentiation inducers (IGF1/insulin, glucocorticoid and cAMP-elevating agents) triggers DNA replication, re-entry into the cell cycle (a process known as mitotic clonal expansion) and an adipogenic transcription factor cascade. These events lead to expression of adipocyte genes. Peroxisome proliferator-activated receptor gamma (PPAR γ) is the master regulator of adipogenesis. PPAR γ is a member of the nuclear-receptor superfamily, and is both necessary and sufficient for adipogenesis. Several CCAAT-enhancer binding proteins (C/EBPs) participate in adipogenesis. Early induction of C/EBP β and C/EBP δ during adipogenesis leads to the up regulation of C/EBP α during the terminal

stages. As a result, the transcription of lipogenic genes is activated, including those that support fatty acid synthesis, desaturation, and uptake, as well as triacylglycerol (TG) synthesis.

Adipocytes

The adipocyte serves as the energy reservoir within AT. Adipocytes contain a single lipid droplet (LD), consisting of a phospholipid monolayer encapsulating a neutral lipid core. The lipid core is composed primarily of TG (Frayn et al., 2003). TG is synthesized when energy is in excess. Lipolysis within the adipocyte LD occurs to meet energy demand and is defined as the breakdown of TG into glycerol and individual non-esterified fatty acids (NEFA). Furthermore, adipocytes are unique in that they do not form a lot of cholesterol ester.

Cellular dating analysis has shed new light on the turnover of adipocytes. A comparison of ^{14}C levels in adipocyte genomic DNA with declining atmospheric ^{14}C levels estimated that ~10% of adipocytes within human SC tissue turn over each year (Spalding et al., 2008). The number of fat cells stays constant in adulthood in lean and obese individuals, even after marked weight loss, indicating that the number of adipocytes is set during childhood and adolescence (Spalding et al., 2008). The notion that the total number of fat cells remains constant in adults has been challenged (Tchoukalova et al., 2010). Since adipocytes are post-mitotic in nature, generation of new adipocytes occurs via the recruitment and differentiation of adipogenic progenitor cells.

Forms and Function

AT exists in two forms, WAT and brown AT (BAT), each possessing unique functions. WAT stores excess energy as triglycerides and BAT is specialized in the dissipation of energy through the production of heat.

BAT is a thermogenic organ producing heat by uncoupling mitochondrial electron transport from adenosine triphosphate (ATP) production. This is made possible by the expression of uncoupling protein-1 (UCP-1) in the mitochondria of brown adipocytes (Cannon et al., 1982). Although human BAT was long thought to disappear after birth, recent positron emission tomography imaging studies have revealed functional BAT in adults, located primarily in the neck region (Cypess et al., 2009; van Marken Lichtenbelt et al., 2009; Virtanen et al., 2009). Uncoupled oxidation of NEFA within brown adipocytes significantly contributes to whole body energy expenditure during cold exposure (Ouellet et al., 2012).

WAT is a highly active endocrine organ that is critical for the regulation of energy storage within the body during periods of fasting and feeding. In the fed state, insulin increases energy uptake and storage in AT (glucose uptake and lipogenesis) and decreases energy breakdown and release from AT (lipolysis) (Frayn et al., 2003). In the fasting state, and during periods of exercise, sympathetic innervation releases norepinephrine within AT to stimulate lipolysis (Frayn et al., 2003).

The major white and brown adipose depots are located in anatomically different regions in both rodents and humans. Beige AT is a recently identified AT composed of UCP-1 positive adipocytes and is present in scattered deposits in adult human WAT (Harms and Seale, 2013). Beige cells can activate a thermogenic mechanism that burns stored fat to

produce heat. Even though beige and brown fat share similar characteristics, they arise from different cellular lineages.

In the interest of our laboratory, my studies focus on WAT.

Endocrine Function of Adipose Tissue

AT is an endocrine organ that secretes numerous molecules that affect the function of other tissues (Lago et al., 2007). Signaling molecules released from AT are referred to as adipokines. Adipokines influence food intake, systemic insulin sensitivity, nutrient balance and play a role in muscle insulin sensitivity and glucose uptake, liver metabolism, and the vasculature (Lau et al., 2005; Mora and Pessin, 2002). Additionally, adipokines are important immune regulatory molecules, acting as either anti-inflammatory (adiponectin, Interleukin (IL)-10), or pro-inflammatory (IL-6, IL-1 β , tumor necrosis factor alpha; TNF α) autocrine/paracrine signals (Bradley et al., 2008; Hotamisligil et al., 1995; Ouchi et al., 2010; Turer and Scherer, 2012). These molecules are produced from a variety of cell types within the AT, including adipocytes, adipose progenitor cells, and immune cells (Hotamisligil et al., 1993; Shoelson et al., 2006; Romeo et al., 2012; Hotamisligil and Erbay, 2008).

Adipose Tissue Depots

AT is a multi-depot organ composed of SC fat (beneath the skin), and visceral fat (intra-abdominal fat), found around internal abdominal organs. AT depots differ with respect to location, structure and function. Lineage tracing experiments have suggested distinct progenitor subpopulations may give rise to adipocytes in different depots (Chau et al., 2014; Seale et al., 2011). Distinct adipocyte origins and local microenvironment may contribute to the differences in metabolic activity of each depot.

The majority of SC fat is deposited in the femoral-gluteal regions, back and anterior abdominal wall. About 80% of all body fat is SC (Ibrahim, 2010). Abdominal fat is present in two main depots: SC and intra-abdominal. Visceral AT (VAT) is present around abdominal viscera in the mesentery and in the omentum. The greater omentum is the largest peritoneal fold within the abdomen and is known for its immunologic function. The omentum aids in isolating peritoneal infection and absorbing contaminants through the mesothelial stomata (Collins et al., 2009). Visceral fat accounts for up to 10-20% of total fat in men and 5-8% in women and tends to increase with age in both genders (Wajchenberg, 2000).

As compared to VAT, SC fat is more cellular, that is, it has a higher proportion of smaller cells because of the higher differentiation potential of subcutaneous adipocytes (Walker et al., 2007). SC fat is more densely vascularized than visceral fat, and it retains higher angiogenic potential (Gealekman et al., 2011).

Adipocyte progenitor cells isolated from VAT and SC AT (SAT) differ with respect to their ability to proliferate and differentiate into adipocytes (Macotela et al., 2012; Tchkonina et al., 2007). PPAR γ -agonist-stimulated adipose progenitor cell differentiation is higher in SAT versus VAT (Walker et al., 2008).

Human visceral adipocytes have higher basal and catecholamine-induced lipolytic activity as compared to SAT (Ahmadian et al., 2010). Accordingly, the majority of circulating free fatty acids (FFA) is derived from the SC fat. GLUT4 and IRS-1 mRNA levels are lower in omental AT (OAT) than in SAT (Veilleux et al., 2009). As compared to SC fat cells, visceral adipocytes express less adiponectin (Yang et al., 2008) and adiponectin receptor (AdipoR1) (Rasmussen et al., 2006). Similarly, leptin mRNA expression and protein

secretion is lower in OAT (Van Harmelen et al., 1998). Generally, VAT secretes more pro-inflammatory cytokines, such as IL-6, than the SC fat depot (Fontana et al., 2007). Such an expression profile contributes to systemic inflammation associated with visceral obesity and obesity-associated metabolic disorders like insulin resistance and CVD (Torres-Leal et al., 2010; Fontana et al., 2007).

Adipose Tissue Remodeling

Adipose Tissue Expansion

Accumulation of AT occurs through hyperplasia and hypertrophy (Gesta et al., 2007). Differentiation of adipose progenitor cells into mature adipocytes is crucial to maintain normal function of AT and to meet energy storage demands.

Hyperplastic AT expansion involves the recruitment and differentiation of adipose progenitor cells into adipocytes. Expansion predominantly through hyperplasia distributes the excess energy among many newly generated adipocytes, which serves to maintain the metabolic function of each adipocyte. Hyperplastic AT expansion is associated with preserved insulin sensitivity in humans and animal models. An increase in adipocyte number depends on a sufficient number of functional adipose progenitor cells to form new adipocytes (Heilbronn et al., 2004).

Hypertrophic AT expansion occurs when excess energy is stored as triglycerides in existing adipocytes, resulting in hypertrophy (Heilbronn et al., 2004). During a state of positive caloric imbalance, a deficit in the number of adipocyte progenitor cells and/or their ability to differentiate or proliferate would impair hyperplastic AT growth (Strissel et al., 2007). As a result, AT expansion predominantly through hypertrophy will occur (Danforth,

2000; Heilbronn, et al., 2004). Several studies suggest an adipogenic deficit may exist in obese humans. The total number of adipose progenitor cells is reduced in obese individuals compared to lean individuals (Onate et al., 2012; Tchoukalova et al., 2007). Adipocyte hypertrophy is observed in AT sampled from obese patients, which correlates with an impaired adipogenic capacity of isolated adipose progenitor cells (Kloting et al., 2010; van Harmelen et al., 2003). Expression analysis has shown that adipogenic-related genes from AT sampled from insulin-resistant, obese individuals are downregulated relative to AT collected from MHO individuals (Kloting et al., 2010). Obese patients with hypertrophic AT and insulin resistance generate 70% fewer adipocytes per year compared to MHO patients with hyperplastic AT (Arner et al., 2010; Arner and Spalding, 2010). The number of adipose progenitor cells and their adipogenic capacity appears to influence AT function.

Weight gain through AT hyperplasia is commonly seen in MHO individuals, which represent up to 25% of obese humans (Bluher, 2010; Kloting et al., 2010). Therefore hypertrophic AT can be thought of as dysfunctional fat, whereas hyperplastic AT represents a functional form of fat.

Adipose Tissue Dysfunction

The molecular mechanism by which adipocyte hypertrophy results in dysfunctional AT is complex. An excess of lipid within the adipocyte leads to endoplasmic reticulum (ER) stress and hypoxia, which consequently results in the production and secretion of pro-inflammatory cytokines.

Endoplasmic Reticulum Stress

Excess lipid storage appears to cause functional abnormalities of the ER and mitochondria that are central to the pathophysiologic effects of obesity. The storage and handling of intracellular lipids requires the synthesis of many proteins necessary for fatty acid transport, modification, esterification, and packaging within lipid droplets (de Ferranti and Mozaffarian, 2008). The ER is an organelle that serves many functions, one of which includes the synthesis of nascent proteins by translating messenger RNA into a polypeptide sequence. When there is a continuous need to store TG, adipocytes must expand in size while continuously being stressed to synthesize more proteins for LD formation (Boden, 2009; Zha and Zhou, 2012). When the demand for protein synthesis exceeds the capacity of the ER, an unfolded protein response (UPR) is initiated. Under normal conditions, the UPR involves the activation of double-stranded RNA-dependent protein kinase-like ER kinase, inositol-requiring protein-1, and activating transcription factor 6, which act to restore ER function by upregulating protein chaperones, stimulating ER biogenesis, and inhibiting protein translation (Boden, 2009). Stress to the ER occurs when the increased demand for protein synthesis continues. Lipid accumulation in adipocytes causes the activation of JNK and IKK β . These inflammatory signaling pathways regulate protein phosphorylation and transcriptional events leading to pro-inflammatory cytokine production (TNF α , IL-6, adiponectin, leptin, monocyte chemoattractant protein-1; MCP-1) (Jiao et al., 2011; Hirosumi et al., 2002). ER stress is observed in adipose tissue of insulin-resistant obese mice and humans, and inhibition of this stress in mice improves insulin sensitivity (Boden, 2009; Ozcan et al., 2004; Ozcan et al., 2006).

Hypoxia

Healthy expansion of AT depends on uniform vascularization of the growing tissue (Wronska and Kmiec, 2012). Inadequate vascularization results in an insufficient supply of O₂. In an obese state, as AT mass expands, clusters of adipocytes become hypoxic due to their distance from the tissue microvasculature. Hypoxia in AT has been linked to insulin resistance and the metabolic dysfunction (Trayhurn et al., 2008).

Under hypoxic conditions, hypertrophied adipocytes increase expression of the hypoxia-dependent protein known as hypoxia-inducible factor-1 alpha (HIF-1 α) (Rausch et al., 2008). The primary function of HIF-1 α is to promote vascularization through the upregulation of pro-angiogenic factors. Nevertheless, HIF-1 α also signals through the pro-inflammatory transcription factor, nuclear factor kappa B (NF κ B), turning on the expression of numerous insulin desensitizing pro-inflammatory genes, including TNF α , IL-1 β , IL-6 and MCP-1. Adipocyte-specific deletion of HIF-1 α appears to provide protection from obesity-associated insulin resistance (Jiang et al., 2011).

Adipose Tissue Inflammation

Obesity-associated chronic AT inflammation is a key contributing factor to metabolic and cardiovascular dysfunction (Van Gaal et al., 2006). Numerous studies have shown that the immune system and metabolism are highly integrated (McNelis and Olefsky, 2014). A variety of immune cells reside in AT. The composition of AT immune cells includes myeloid cells from the innate immune system, such as macrophages and eosinophils, and lymphoid cells from the adaptive immune system, such as T and B lymphocytes (Makki et al., 2013). The immune cell population of AT is predominantly classified into two groups: pro-

inflammatory or anti-inflammatory (Makki et al., 2013). The balance between these populations seems to influence AT function and homeostasis.

In a non-obese state, AT T_H2 T cells, T_{reg} cells, eosinophils and M2-like resident macrophages predominate. T_{reg} cells and eosinophils and M2-like macrophages secrete cytokines that contribute to the anti-inflammatory, insulin-sensitive phenotype. In obesity-induced inflammation, immune cells are recruited from the circulation and contribute to AT inflammation. Monocytes respond to chemotactic signals and transmigrate into the AT and become polarized to the highly proinflammatory M1-like state (Osborn and Olefsky, 2012). Once recruited, these M1-like macrophages secrete proinflammatory cytokines that work in a paracrine fashion. Obesity causes the eosinophil content to decline and induces a shift in AT T cell populations with a decrease in T_{reg} content and an increase in CD4⁺ T_H1 and CD8⁺ effector T cells, which secrete proinflammatory cytokines. B cell numbers also increase and activate T cells, which potentiate M1-like macrophage polarization, inflammation and insulin resistance. Cytokines and chemokines from the AT can also be released into the circulation and work in an endocrine manner to promote inflammation in other tissues (Osborn and Olefsky, 2012).

Adipose Tissue Eosinophils

Eosinophils are associated with parasitic infections, allergies and asthma. In a lean state, AT eosinophils secrete IL-4 and IL-13 which contributes to the anti-inflammatory, insulin-sensitive phenotype. AT M2-like macrophages maintain glucose homeostasis and are induced by IL-4. One study demonstrated that eosinophils are the major IL-4-expressing cells in WAT of mice, and, in their absence, M2-like macrophages are greatly attenuated. Eosinophils migrate into AT by an integrin-dependent process and reconstitute M2-like

macrophages through an IL-4- or IL-13-dependent process. In an obese state, eosinophils appear to decrease in number.

Adipose Tissue T Cells

AT contains innate immune cells which work in conjunction with adaptive immune cells. The adaptive immune system includes T and B cells, which respond to specific peptide antigens. T cells were first discovered to reside within AT in 2007 (Wu et al., 2007). T cells exist as both resident and recruited populations in AT. In a non-obese state, T regulatory cells (Tregs), which represent a subpopulation of T cells, diminish innate and adaptive immune reactions. They secrete IL-10 and stimulate IL-10 secretion from M2-like macrophages. Tregs represent ~ 3% of all white blood cells present in AT (Feuerer et al., 2009; Sun et al., 2012). The AT Treg population seems to decrease with the enlargement of adipose mass, and is associated with more AT inflammation (Feuerer et al., 2009; Nishimura et al., 2009).

Adipose Tissue B Cells

B cells, defined by expression of CD19, are present in AT and increase in number as obesity develops (Duffaut et al., 2009). The increase in B cell population appears to activate T cells which sustain an M1-like population, and thus contributes to obesity-associated insulin resistance and AT inflammation (McDonnell et al., 2012; Osborn and Olefsky, 2012).

Adipose Tissue Macrophages

ATMs may be associated with inflammation, or alternatively, tissue remodeling and resolution of inflammation, depending on the extent of adiposity and activation state of the macrophage. Macrophage-secreted paracrine factors may play a role in AT homeostasis,

including progenitor cell survival, proliferation and differentiation into adipocytes (Molgat et al., 2011; Molgat et al., 2012; Calder et al., 2011; Dalmás et al., 2011). Pro-inflammatory ATMs may promote hypertrophic AT expansion by inhibiting adipose progenitor cell proliferation and differentiation, whereas anti-inflammatory ATMs may promote hyperplastic and metabolically functional AT expansion through the maintenance of an adequate number of responsive progenitors (Molgat et al., 2012; Sorisky et al., 2013). Our laboratory has previously shown that macrophage-conditioned medium (MacCM) promotes 3T3-L1 adipose progenitor cell survival in a platelet-derived growth factor (PDGF) receptor-dependent manner. Furthermore, we showed that the MacCM pro-survival effect observed with the 3T3-L1 cell line model extends to interactions between human MD-macrophages and human subcutaneous adipose progenitor cells (Molgat et al., 2012). However, the survival response to macrophage-secreted factors between different depots has not been investigated. Depot differences in apoptotic susceptibility between the two progenitor pools may provide insight into the pathogenesis of obesity and metabolic dysfunction.

Cell Death

There are two types of cell death: programmed and non-programmed. Programmed cell death is mediated by an intracellular process and is carried out in a controlled manner. Apoptosis and pyroptosis are forms of programmed cell death. Furthermore, necrosis is an example of a non-programmed process that occurs as a result of infection or injury. Recently, necroptosis has been recognized as an alternate form of programmed necrosis.

Apoptosis is the most characterized type of programmed cell death because of its importance in development, aging, homeostasis and in the pathogenesis of different diseases such as cancer. Apoptotic cells die in a controlled manner in response to a variety of extrinsic

(activation of TNF receptors) or intrinsic signals (DNA damage, mitochondrial disruption) (Igney and Krammer, 2002; Elmore, 2007). The hallmarks of apoptotic cell death include exposure of phosphatidylserine on the extracellular face of the plasma membrane, activation of caspases, disruption of mitochondrial membrane potential, cell shrinkage, DNA fragmentation and DNA condensation (Hacker, 2000; Kerr et al., 1972).

Pyroptosis is a cell death pathway that is caspase 1-dependent and inherently inflammatory (Fink and Cookson, 2005; Bergsbaken et al., 2009). Caspase-1 is not involved in apoptotic cell death and caspase-1-deficient cells respond normally to most apoptotic signals. Pyroptosis is triggered by pathological stimuli, such as stroke, heart attack or cancer, and is also crucial for controlling microbial infections (Fink and Cookson, 2005; Bergsbaken et al., 2009).

Necrosis is an uncontrolled cell death characterized by cell swelling, as well as destruction of the plasma membrane and subcellular organelles, without nuclear fragmentation and condensation (Linkermann and Green, 2014). Necrotic cell death is considered a heterogeneous phenomenon including both programmed and accidental cell death. Necrosis is often defined in a negative manner, as a type of cell death that involves rupture of the plasma membrane without the controlled mechanisms of apoptosis. Necrosis is considered to be a toxic process where the cell is a passive victim and follows an energy-independent mode of death.

Necroptosis, programmed necrosis, is a caspase-independent form of cell death that can be induced with TNF α only in the presence of a caspase inhibitor, such as zVAD-FMK (Linkermann and Green, 2014). It is dependent on receptor-interacting protein kinase 3 (RIPK3) and formation of the necrosome. Several upstream signaling elements of apoptosis and necroptosis overlap, and sensitivity to each death pathway is regulated (sometimes in

opposing ways) by shared regulatory molecules, such as FLICE-like inhibitory protein (FLIP) and the cellular inhibitors of apoptosis proteins cIAP1 and cIAP2.

The protein synthesis blocker cycloheximide (CHX) sensitizes human adipocytes for CD95-induced apoptosis in a caspase-dependent manner (Fischer-Posovszky et al., 2011). Treatment with CHX changes the expression of pro- and anti-apoptotic proteins. FLIP expression decreases during CHX treatment. Reduction of FLIP levels results in undetectable amounts of FLIP at the CD95 death-inducing signaling complex (DISC) upon CD95 stimulation, thereby enhancing recruitment and activation at caspase-8. Down-regulation of FLIP by shRNA sensitizes adipose progenitor cells for CD95-induced apoptosis. In mice, AT mRNA levels of Flip are down-regulated upon fasting. Therefore, FLIP is an important regulator of apoptosis sensitivity in fat cells.

Apoptosis

Morphology

Distinct morphological changes occur during apoptosis (Hacker, 2000). During the early process of apoptosis, cell shrinkage and pyknosis are visible by light microscopy (Kerr et al., 1972). The cytoplasm is dense and the organelles are more tightly packed. Pyknosis, the result of chromatin condensation, is the most characteristic feature of apoptosis. On histologic examination with hematoxylin and eosin stain, apoptosis involves single cells or small clusters of cells. The apoptotic cell appears as a round or oval mass with dark eosinophilic cytoplasm and dense purple nuclear chromatin fragments.

Electron microscopy is the best way to characterize the subcellular changes. Early during the chromatin condensation phase, the electron-dense nuclear material aggregates peripherally under the nuclear membrane although there can also be uniformly dense nuclei. Extensive plasma membrane blebbing occurs followed by karyorrhexis and separation of cell

fragments into apoptotic bodies during a process called budding. Apoptotic bodies consist of cytoplasm with tightly packed organelles with or without a nuclear fragment. The organelle integrity is still maintained and all of this is enclosed within an intact plasma membrane. These bodies are subsequently phagocytosed by macrophages, parenchymal cells, or neoplastic cells and degraded within phagolysosomes. There is essentially no inflammatory reaction associated with the process of apoptosis nor with the removal of apoptotic cells because apoptotic cells do not release their cellular constituents into the surrounding interstitial tissue. Instead, they are quickly phagocytosed by surrounding cells thus likely preventing secondary necrosis; and the engulfing cells do not produce anti-inflammatory cytokines (Savill and Fadok, 2000; Kurosaka et al., 2003).

Mechanism

The mechanisms of apoptosis are highly complex and involve an energy-dependent cascade of molecular events. There are two main apoptotic pathways: the extrinsic or death receptor pathway and the intrinsic or mitochondrial pathway. However, these pathways can be linked and each can influence the other (Igney and Krammer, 2002; Elmore, 2007).

Extrinsic Pathway

The extrinsic signaling pathway that initiates apoptosis involves transmembrane receptor-mediated interactions. These involve death receptors that are members of the TNF receptor gene superfamily (Locksley et al., 2001). The most well-known ligands and corresponding death receptors include FasL/FasR, TNF α /TNFR1, Apo3L/DR3, Apo2L/DR4 and Apo2L/DR5 (Chicheportiche et al., 1997; Ashkenazi and Dixit, 1998; Peter and Krammer, 1998; Suliman et al., 2001; Rubio-Moscardo et al., 2005). The binding of Fas ligand to Fas receptor results in the binding of the adapter protein Fas-Associated Protein

with Death Domain (FADD) and the binding of TNF ligand to TNF receptor results in the binding of the adapter protein Tumor necrosis factor receptor type 1-associated DEATH domain protein (TRADD) with recruitment of FADD and RIP (Hsu et al., 1995; Grimm et al., 1996; Wajant et al., 2002). FADD then associates with procaspase-8 via dimerization of the death effector domain. At this point, DISC is formed, resulting in the autocatalytic activation of procaspase-8 (Kischkel et al., 1995). Once caspase-8 is activated, the execution phase of apoptosis is triggered. Death receptor-mediated apoptosis can be inhibited by a protein called c-FLIP which will bind to FADD and caspase-8, rendering them ineffective (Kataoka et al., 1998; Scaffidi et al., 1999).

Intrinsic Pathway

The intrinsic signaling pathway involves non-receptor mediated stimuli that produce intracellular signals that act directly on targets within the cell and are mitochondrial initiated events. Examples include radiation, toxins, hypoxia, hyperthermia, viral infections and free radicals.

All of these stimuli cause changes in the inner mitochondrial membrane that result in loss of the mitochondrial transmembrane potential and release of normally sequestered pro-apoptotic proteins from the intermembrane space into the cytosol (Saelens et al., 2004). Cytochrome *c*, Smac/DIABLO, and the serine protease HtrA2/Omi (Cai et al., 1998, Du et al., 2000, van Loo et al., 2002) activate the caspase-dependent mitochondrial pathway. Cytochrome *c* binds and activates Apaf-1 as well as procaspase-9, forming an apoptosome (Hill et al., 2004; Chinnaiyan, 1999). The clustering of procaspase-9 in this manner leads to caspase-9 activation. Smac/DIABLO and HtrA2/Omi are reported to promote apoptosis by

inhibiting inhibitors of apoptosis (IAP) protein activity (van Loo et al., 2002; Schimmer, 2004).

The control of these apoptotic mitochondrial events occurs through members of the Bcl-2 family of proteins (Cory and Adams, 2002). They control mitochondrial membrane permeability and can be either pro-apoptotic or anti-apoptotic. Twenty-five genes have been identified in the Bcl-2 family. Some of the anti-apoptotic proteins include Bcl-2, Bcl-x, Bcl-XL, Bcl-XS, Bcl-w, BAG, and some of the pro-apoptotic proteins include Bcl-10, Bax, Bak, Bid, Bad, Bim, Bik, and Blk. It is thought that the main mechanism of action of the Bcl-2 family of proteins is the regulation of cytochrome *c* release from the mitochondria via alteration of mitochondrial membrane permeability.

The Executioner Pathway

The extrinsic and intrinsic pathways both converge at the point of the execution phase, considered the final pathway of apoptosis. Execution caspases activate cytoplasmic endonuclease, which degrades nuclear material, and proteases that degrade the nuclear and cytoskeletal proteins. Caspase-3, caspase-6, and caspase-7 function as effector or executioner caspases, cleaving various substrates that ultimately cause the morphological and biochemical changes seen in apoptotic cells (Slee et al., 2001).

Caspase-3 is considered to be the most important of the executioner caspases and is activated by any of the initiator caspases (caspase-8, caspase-9, or caspase-10). Caspase-3 specifically activates the endonuclease Caspase-activated DNase (CAD). In proliferating cells CAD is complexed with its inhibitor, ICAD. In apoptotic cells, activated caspase-3 cleaves ICAD to release CAD (Sakahira et al., 1998). CAD then degrades chromosomal DNA within the nuclei and causes chromatin condensation. Caspase-3 also induces cytoskeletal reorganization and disintegration of the cell into apoptotic bodies.

Phagocytic uptake of apoptotic cells is the last component of apoptosis. Phospholipid asymmetry and externalization of phosphatidylserine on the surface of apoptotic cells and their fragments is the hallmark of this phase. Although the mechanism of phosphatidylserine translocation to the outer leaflet of the cell during apoptosis is not well understood, it has been associated with loss of aminophospholipid translocase activity and nonspecific flip-flop of phospholipids of various classes (Bratton et al., 1997).

Rationale

The survival of differentiation-competent adipose progenitor cells may influence the mechanism by which AT expands, in a depot-specific manner. The implication of macrophage-secreted factors in the regulation of adipose progenitor cell differentiation and proliferation suggests that adipose progenitor cell survival may also be affected. Adipose progenitor cell survival through the inhibition of apoptosis would maintain a population of progenitors capable of expanding the adipocyte pool through adipogenesis. In contrast, loss of adipose progenitors through apoptosis would contribute to an adipogenic deficit, predisposing to excess adipocyte hypertrophy and dysfunctional AT.

Hypothesis

Depot origin influences susceptibility of adipose progenitor cells to apoptosis.

Objectives

***Objective 1:** To compare cell death between SC and OM progenitor cells in response to various apoptotic stimuli.*

***Objective 2:** To evaluate the effect of macrophage-secreted factors on the cell death of SC versus OM progenitor cells.*

2.0 Materials and Methods

Cell Model used for Objectives

Human Primary Adipose Progenitor Cells

Human primary adipose progenitor cells were isolated by size fractionation and centrifugation from the SVF of digested SC and OM AT matched from the same individual (Skurt and Hauner, 2012). They possess a fibroblast-like morphology and are not completely defined with respect to cell surface protein expression (Decaunes et al., 2011; Zimmerlin et al., 2010). The human adipose progenitor cell is a relevant cell model; however variability exists between cell responses due to donor heterogeneity. Human primary adipose progenitor cells that undergo excessive proliferation through excessive passaging eventually lose the ability to differentiate.

Monocyte-Derived Macrophages

MD-macrophages are isolated from the peripheral blood mononuclear cell (PBMC) layer after Ficoll-gradient centrifugation of whole blood (Johnson et al., 1977). Following seeding into culture dishes, adherent monocytes differentiate into macrophage phenotype. MD-macrophages can be activated towards pro- or anti-inflammatory phenotypes with different cytokine treatments; basally, MD-macrophages are mildly skewed towards an anti-inflammatory activation state (Daigneault et al., 2010; Martinez et al., 2006). MD-macrophages are a useful primary human macrophage cell model; however donor-related experimental variability may be a factor.

Inducers of Apoptosis

We stimulated apoptosis in our human adipose progenitor cells by serum deprivation, serum deprivation with 438 ng/mL recombinant human TNF α (Niesler et al., 1998), or with a combination of 10 ng/mL TNF α and 10 mg/mL CHX (Molgat et al., 2012).

Isolation and Culture of Human Adipose Progenitor Cells

SC and OM AT samples were obtained or matched from the same patients undergoing elective abdominal surgery (approved by the Ottawa Health Science Network Research Ethics Board, OHSN-REB). Subsets of patients (3-5), from the pool of twenty (12 female and 8 male), were used for each individual study. Mean age (\pm SD) was 49.7 ± 2.2 years, and mean BMI was 28.6 ± 0.7 kg/m². The inclusion criteria were as follows: all patients were between 18 and 70 years of age, no patients had diabetes, no patients were on glucocorticoids and none underwent dramatic changes in weight within six months prior to surgery. Adipose progenitor cells were isolated as described (Artemenko et al., 2005). AT samples (2-15 g) were received in a disposable sterile plastic specimen bottle with cold DMEM/F12 media with 2X antibiotics. Samples were rinsed with PBS to remove blood. Fibrous material, such as connective tissue and capillaries, were removed from AT by dissection and discarded. The remaining tissue was cut into small pieces, weighed and digested with collagenase CLS type I to isolate individual cells from matrix proteins without damaging the cells and influencing their growth potential. The first digestion was carried out for 30-45 minutes at 37°C in a shaking incubator. The digested tissue was subjected to progressive size filtration through a nylon mesh (250 μ M). The remaining tissue was digested (30 minutes) and filtered once again. The cell suspension was centrifuged for 10 minutes at 200 g, and then incubated in an erythrocyte lysis buffer for 10 minutes at room

temperature. After several washing and centrifugation steps, the floating mature adipocytes were aspirated. The SVF was re-suspended in DMEM supplemented with 10% FBS, 100 U/ml penicillin, 0.1 mg/ml streptomycin, and the cells were counted using the Neubauer hemocytometer. Adipose progenitor cells were seeded at 2.5×10^5 - 5.0×10^5 in 100 mm tissue culture dishes. Adipose progenitor cells were cultured in DMEM supplemented with 10% FBS, 100 U/ml penicillin, 0.1 mg/ml streptomycin, and 50 U/ml nystatin (Calbiochem, Merck KGaA; Darmstadt, Germany), and grown until confluent.

Preparation of Macrophage Conditioned Medium

To prepare MacCM from human MD-macrophages, PBMCs were isolated from blood donated by healthy volunteers (two female and two male; mean age (\pm SD) was 23 ± 0.4 years; approved by the OHSN-REB). Collected blood (120 mL) was pooled into a 500 ml bottle and diluted 2:1 with PBS + 2 mM EDTA (two part 1x PBS, one part whole blood). Centrifuge tubes were filled with 15 ml Ficoll-Hypaque (GE Healthcare; Uppsala, Sweden), and layered with 30 ml diluted blood. Blood was centrifuged ($520 \times g$) for 30 minutes. The top serum (yellow) layer was discarded and the interphase containing the PBMCs (white layer) was collected and placed in a new centrifuge tube. The tube was filled with PBS + 2 mM EDTA and centrifuged at $520 \times g$ for five minutes. The PBS was discarded and the wash and centrifugation step was repeated. The PBS was discarded and the pellet was resuspended in 3 mL of RPMI supplemented with 100 U/ml penicillin and 0.1 mg/ml streptomycin. Cells were counted using the Neubauer hemocytometer. PBMCs were seeded at a density of 1×10^6 cells/well in 12 well culture dishes. Monocytes were allowed to adhere for 1 h in serum-free RPMI, and they were subsequently differentiated into macrophages over 7 days in RPMI supplemented with 10% FBS, 100 U/ml penicillin, and 0.1 mg/ml streptomycin {{316

Daigneault, M. 2010; 320 Mayi, T.H. 2010} }. Differentiated human macrophages were exposed to RPMI supplemented with 100 U/ml penicillin, and 0.1 mg/ml streptomycin (1 mL/well) and collected 24 h later (Franco et al., 2006). MacCM and control media (RPMI with 100 U/ml penicillin, and 0.1 mg/ml streptomycin) were subjected to the same experimental conditions.

Cell Death Analysis

Cell Enumeration

Human adipose progenitor cells were grown on 35 mm dishes until confluent. The confluent human adipose progenitor cells (2.5×10^5 /35 mm dish) were placed in medium supplemented with 10% FBS, serum-free, serum-free with TNF α (438 ng/mL) alone, or with a combination of TNF α (10 ng/mL) and CHX (10 μ g/mL), for 24 h. After 24 h, floating cells were removed by aspiration, and adherent cells were trypsinized using 0.5 ml trypsin. Each dish was incubated at 37°C for 5 minutes. Once all the cells lifted, 0.5 ml of DMEM supplemented with 20% calf serum, 100 U/ml penicillin and 0.1 mg/ml streptomycin were added to each dish and the cells were transferred to a microfuge tube. Once in the microfuge tube, the cells were suspended by gently pipetting up and down three times, and a 10 μ l aliquot was placed on either side of the Neubauer hemocytometer. Viable cells were counted in duplicate using a using a light microscope. Each treatment was performed in duplicate.

Hoechst Staining

Primary human adipose progenitor cells were seeded at 2.5×10^5 /35 mm dish and grown on coverslips. Cells were placed in control medium (supplemented with 10% FBS), serum-free, serum-free with TNF α (438 ng/mL), or a combination of TNF α (10 ng/mL) with

CHX (10 µg/mL), for 6 h to induce apoptosis. In the macrophage studies, the apoptotic conditions for the adipose progenitor cells remained the same except cells were treated with MacCM or control media. The cells were washed three times with 1 ml PBS. Cells were fixed in 1 ml of 10% formalin (formaldehyde) for 1 h, and then washed twice with 1 ml PBS. The coverslips were removed and placed face up in the humid chamber. The cells were stained for 10 min with 50 µl of Hoechst staining solution (1 µg/ml). Individual coverslips were washed in three consecutive beakers containing PBS and one containing water. The coverslips were mounted face down onto glass slides using 15 µl of Moviol, and set to dry overnight in the dark. Cells were visualized and photographed (400 x mag) with a Zeiss Axio Imager.M1 microscope equipped with an AxioCam HRm digital camera (Carl Zeiss, Toronto, Canada). The number of cells counted was >400 cells per treatment. Percent apoptosis was calculated by dividing the total number of apoptotic nuclei by the total number of nuclei (counted by two independent observers, blinded to the conditions), multiplied by 100.

Statistical Analysis

Experiments were performed on cells isolated from at least 3 subjects. Comparison of means was performed by two-way ANOVA (with replication) and $P < 0.05$ was taken as significant. The Pearson Correlation was the statistical method used for all correlation analyses.

3.0 Results

Depot Differences in Adipose Progenitor Cell Death

Cell death was measured using Hoechst staining of condensed nuclei and cell enumeration. Adipose progenitor cells were treated for 6 and 24 h when assessed using Hoechst staining or cell counting, respectively.

Results for Aim 1

As expected (Fig. 1-14), no matter which of the three apoptotic conditions that were examined, apoptosis of adipose progenitor cells cultured in serum-containing medium was very low (<1%). No difference was found in this basal apoptotic index between SC and OM adipose progenitor cells.

Effect of Serum Deprivation on the Cell Death of Adipose Progenitor Cells

The effect of serum deprivation on the apoptosis of abdominal SC and OM adipose progenitor cells was assessed by Hoechst staining and expressed as the mean apoptotic index (% \pm SE). The SC depot showed minor apoptosis that was not significant (Fig. 1). The OM depot displayed significant apoptosis compared to the control (3.4 ± 0.7 vs 0.65 ± 0.17) ($P < 0.01$). Apoptosis was significantly greater in the OM depot than in the SC depot. OM adipose progenitor cells displayed a mean apoptotic index of 3.4 ± 0.7 , whereas SC adipose progenitor cells demonstrated a mean index of 1.2 ± 0.1 ($P < 0.05$).

There was a significant effect of donor BMI on the relative apoptotic susceptibility between the two types of adipose progenitors (Fig. 2). The same patient samples were used as in Fig. 1. The patient samples with the highest ratios of OM/SC % apoptosis also had the

highest BMIs ($R=0.9435$; $P=0.05$), with the apoptosis response of the OM versus SC adipose progenitor cells being BMI dependent.

As assessed by cell enumeration, each depot had minor percent cell death that was not significant, and there was no depot difference (Fig. 3). Serum withdrawal resulted in a trend of greater percent cell death in the OM depot (30.0 ± 4.0) compared to the SC depot (19.0 ± 4.0), but did not reach significance ($P=0.12$).

We did not observe a significant depot difference; however there was a significant effect of BMI of the donors on the relative death susceptibility between the two types of adipose progenitors (Fig. 4). As previously observed with Hoechst staining, OM/SC % cell death positively correlated to the patient BMIs ($R=0.9590$; $P=0.0099$). The same patient samples were used as in Fig. 3.

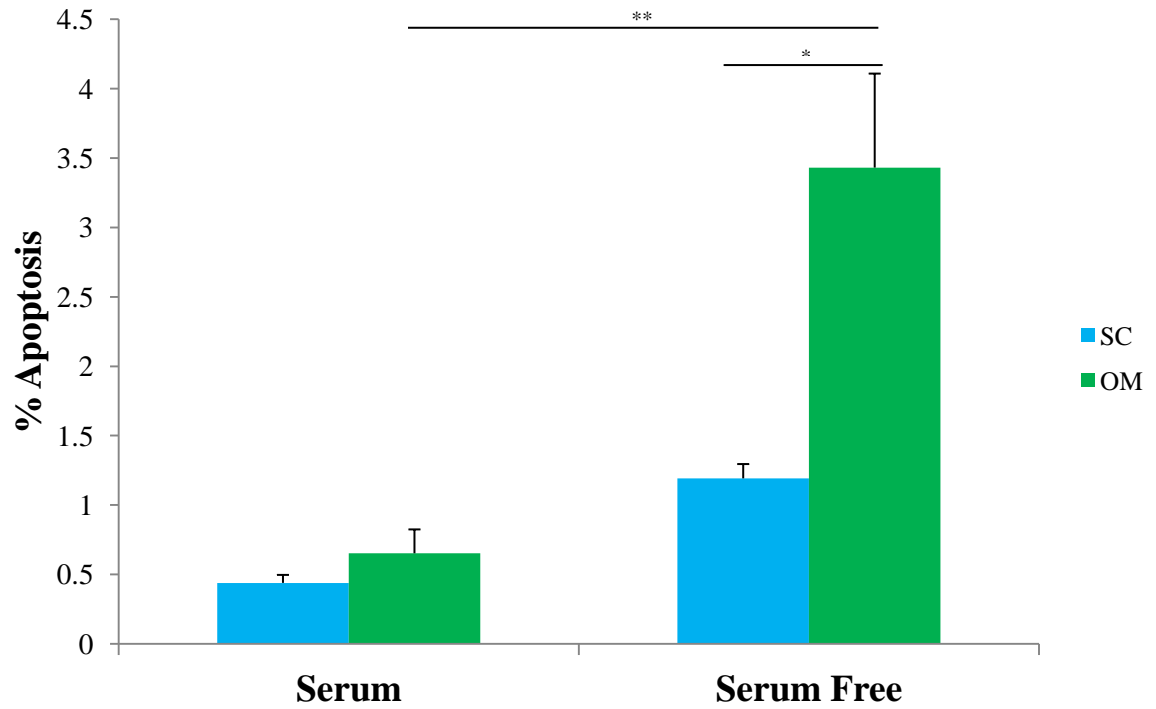


Fig. 1 Primary human adipose progenitor cell apoptosis induced by serum deprivation. Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free media for 6 h. Cells were fixed then stained with Hoechst dye. Staining was visualized by fluorescence. Hoechst staining was performed on duplicate dishes. Results are the mean \pm SE of 4 separate matched patient samples. *P<0.05, **P<0.01.

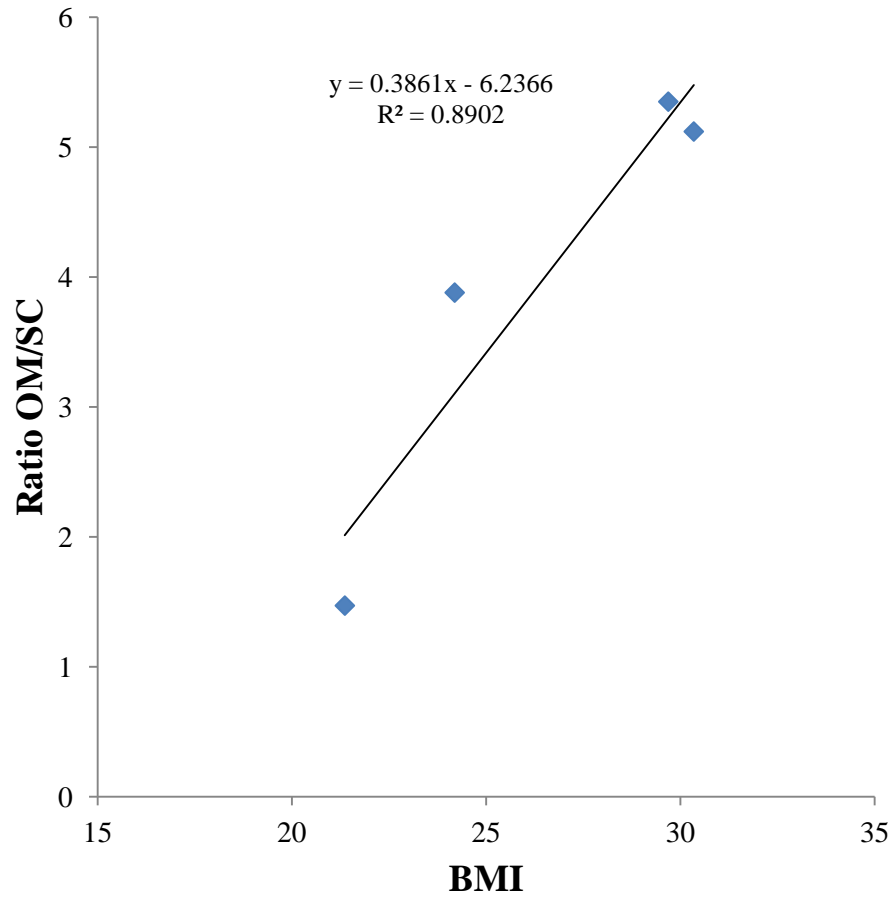


Fig. 2 Apoptosis induced by serum deprivation correlates with BMI. Scatter plot shows the BMI correlation of the 4 donors on the relative apoptotic susceptibility between the two types of adipose progenitors. $P = 0.0546$. Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium for 6 h. Cells were fixed then stained with Hoechst dye. Staining was visualized by fluorescence. Hoechst staining was performed on duplicate dishes. Results are the mean \pm SE of 4 separate matched patient samples.

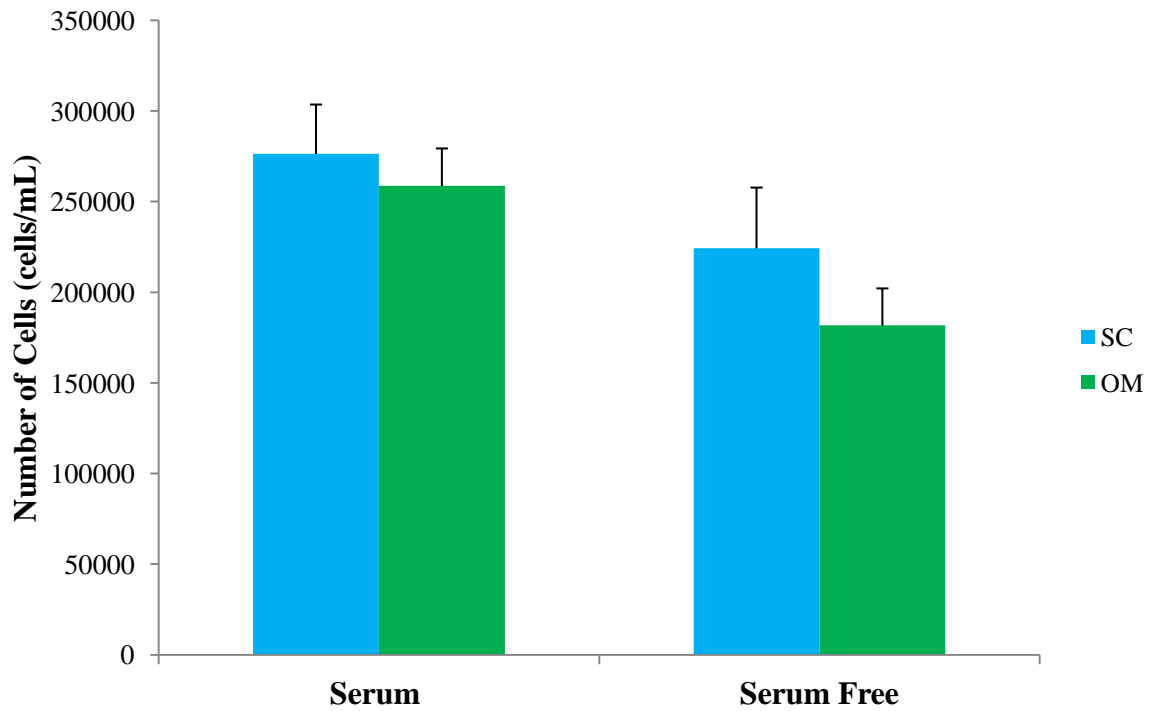


Fig. 3 Primary human adipose progenitor cell death induced by serum deprivation. Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium for 24 h. Cell enumeration was performed on duplicate or triplicate dishes. Results are the mean \pm SE of 5 separate matched patient samples and are not significant.

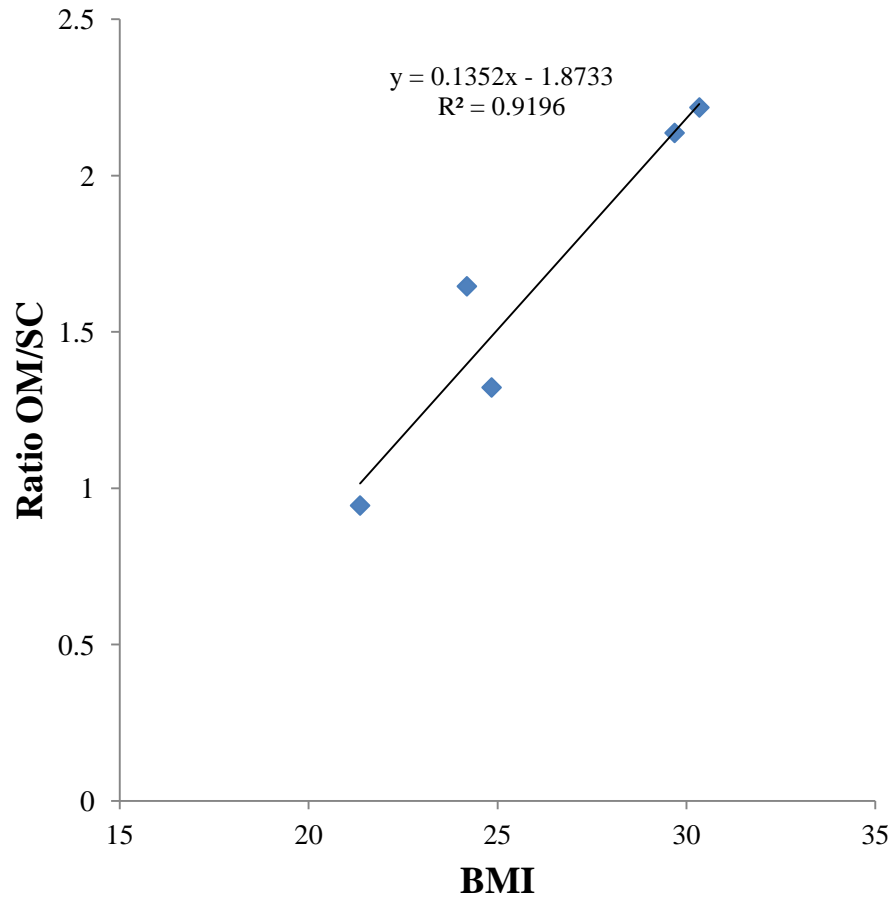


Fig. 4 Cell death induced by serum deprivation correlates with BMI. Scatter plot shows the BMI correlation of the 5 donors on the relative death susceptibility between the two types of adipose progenitors. $P = 0.0099$. Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium for 24 h. Cell enumeration was performed on duplicate or triplicate dishes. Results are the mean \pm SE of 5 separate matched patient samples.

Effect Serum Deprivation and TNF α on the Cell Death of Adipose Progenitor Cells

The effect of serum deprivation and TNF α on the apoptosis of abdominal SC and OM adipose progenitor cells was assessed by Hoechst staining and represented as the mean apoptotic index (% \pm SE). The SC depot showed significant apoptosis compared to the control (3.1 ± 0.5 vs 0.5 ± 0.1) ($P < 0.01$) (Fig. 5). The OM depot also displayed significant apoptosis compared to the control (0.6 ± 0.1 vs 5.1 ± 0.2) ($P < 0.01$). Apoptosis was significantly greater in the OM depot than in the SC depot. OM adipose progenitor cells displayed a mean apoptotic index of 5.1 ± 0.2 , whereas SC adipose progenitor cells demonstrated a mean index of 3.1 ± 0.5 ($P < 0.01$). TNF α increased the level of apoptosis beyond that observed in serum-free medium alone.

In contrast to serum deprivation alone, there was a negative effect of BMI of the donors on the relative apoptotic susceptibility between the two types of adipose progenitors (Fig. 6). The same patient samples were used as in Fig. 5. The patient sample ratios of OM/SC % apoptosis negatively correlated with their BMIs ($R=0.9997$; $P=0.0099$).

Cell enumeration revealed that each depot had significant percent cell death compared to its respective control ($P < 0.01$) (Fig. 7). OM adipose progenitor cells underwent significantly more percent cell death (40.0 ± 2.0) versus cells from the SC depot (28.0 ± 0.2) ($P < 0.01$). Cell death induced by serum deprivation with TNF α did not correlate with BMI (Fig. 8). The same patient samples were used as in Fig. 7.

Effect of Serum Deprivation and TNF α /CHX on the Cell Death of Adipose Progenitor Cells

When TNF α in combination with CHX was added to the serum-free medium, Hoechst staining revealed that both SC and OM depots underwent significant apoptosis (14.8

± 4.3 versus 11.9 ± 2.8 , $P < 0.01$) (Fig. 9). However, no depot difference was observed under these conditions. Apoptosis induced by serum deprivation with TNF α and CHX did not correlate with BMI (Fig. 10). The same patient samples were used as in Fig. 9.

Cell enumeration also showed that each depot had significant percent cell death compared to its respective control ($P < 0.01$) (Fig. 11). However, there was no depot difference in percent cell death (44.0 ± 4.0 versus 43.0 ± 3.0) ($P = 0.878$). Similarly, cell death induced by serum deprivation with TNF α and CHX did not correlate with BMI (Fig. 12). The same patient samples were used as in Fig. 11.

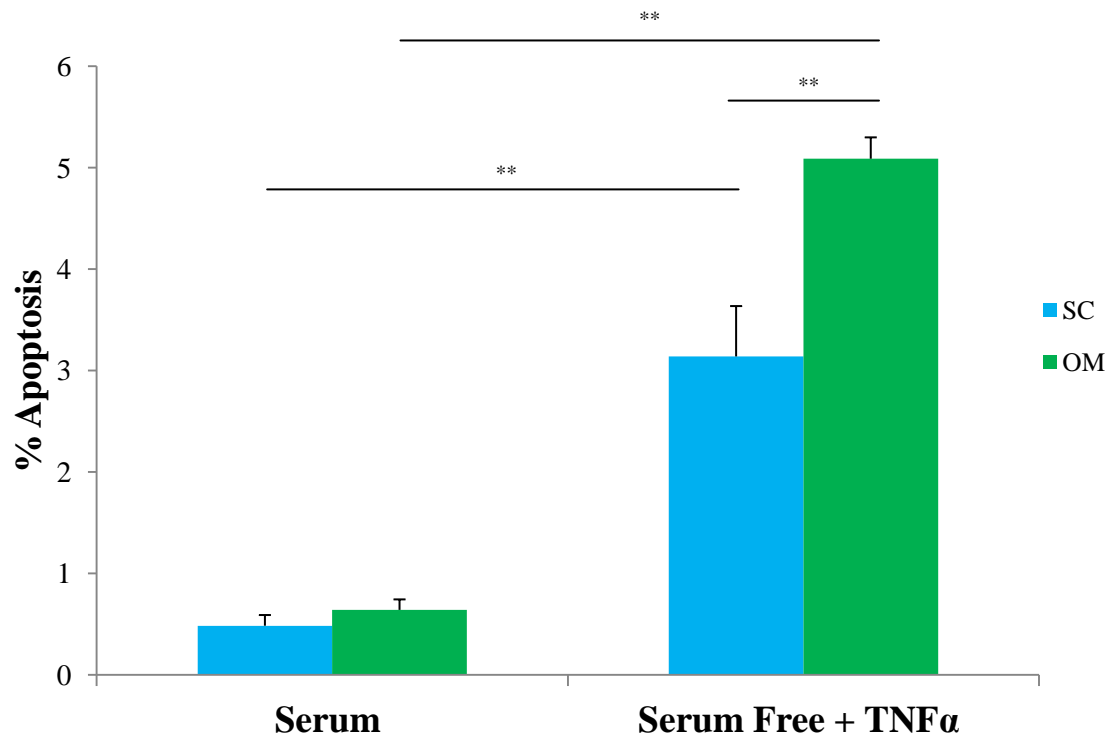


Fig. 5 Primary human adipose progenitor cell apoptosis induced by serum deprivation with TNF α . Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium with 438 ng/mL of TNF α for 6 h. Cells were fixed then stained with Hoechst dye. Staining was visualized by fluorescence. Hoechst staining was performed on duplicate dishes. Results are the mean \pm SE of 3 separate matched patient samples. **P<0.01.

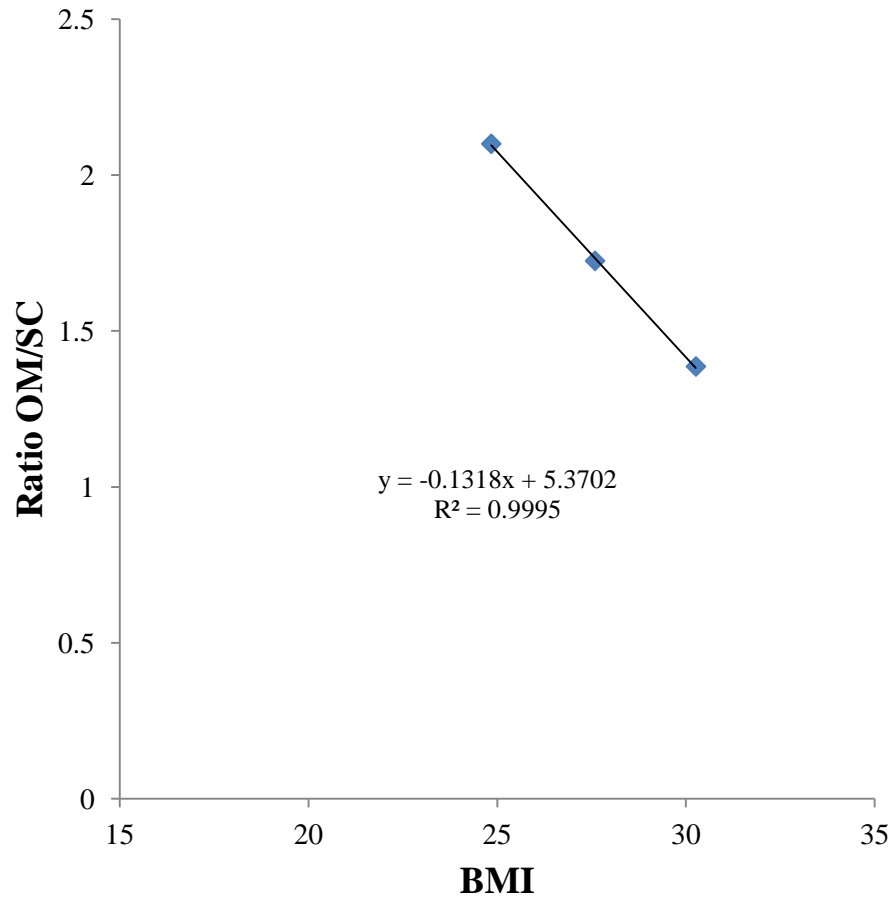


Fig. 6 Apoptosis induced by serum deprivation with TNF α correlates negatively with BMI. Scatter plot shows the correlation BMI of the 3 donors on the relative apoptotic susceptibility between the two types of adipose progenitors. P = 0.0099 Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium with 438 ng/mL of TNF α for 6 h. Cells were fixed then stained with Hoechst dye. Staining was visualized by fluorescence. Hoechst staining was performed on duplicate dishes. Results are the mean \pm SE of 3 separate matched patient samples.

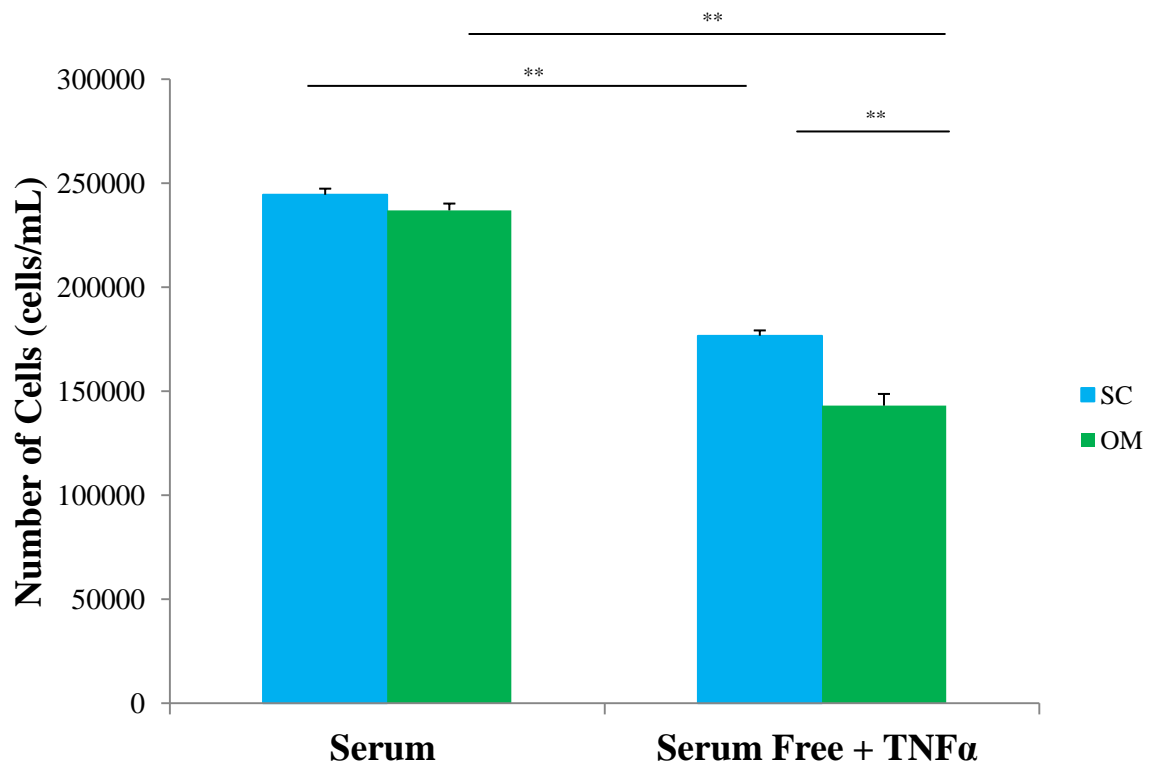


Fig. 7 Primary human adipose progenitor cell death induced by serum deprivation with TNF α . Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium with 438 ng/mL of TNF α for 24 h. Cell enumeration was performed on duplicate or triplicate dishes. Results are the mean \pm SE of 3 separate matched patient samples. **P<0.01.

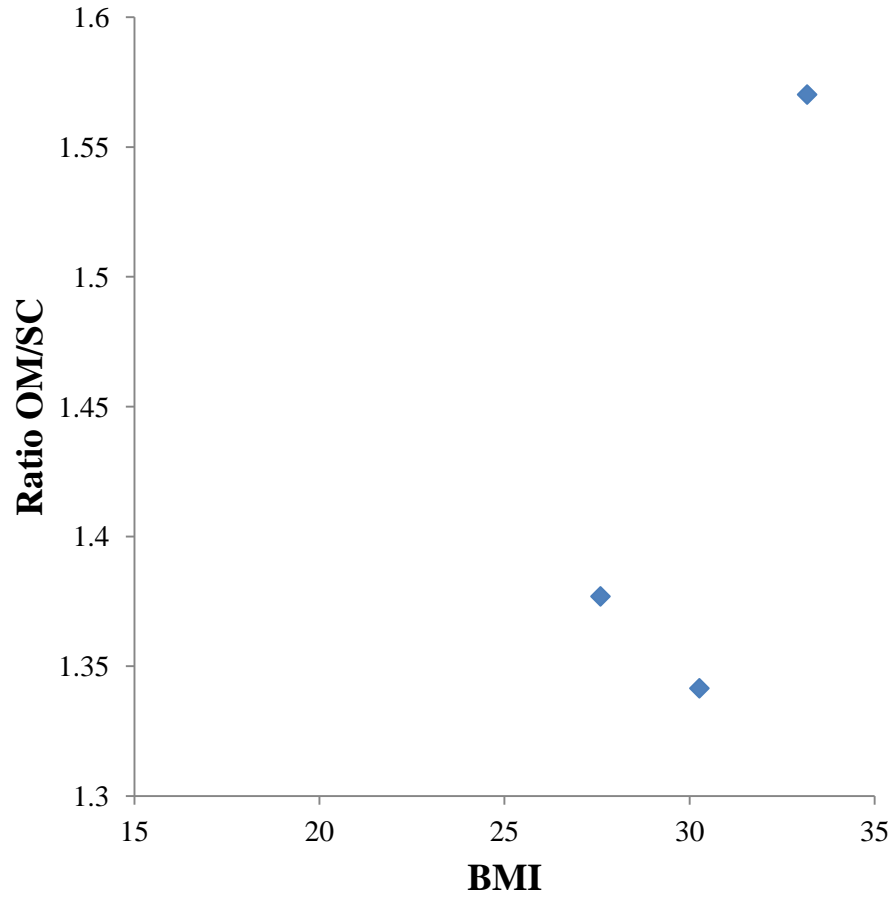


Fig. 8 Cell death induced by serum deprivation with TNF α does not correlate with BMI. Scatter plot shows the BMI correlation of the 3 donors on the relative death susceptibility between the two types of adipose progenitors. The data are not significant. Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium with 438 ng/mL of TNF α for 24 h. Cell enumeration was performed on duplicate or triplicate dishes. Results are the mean \pm -SE of 3 separate matched patient samples.

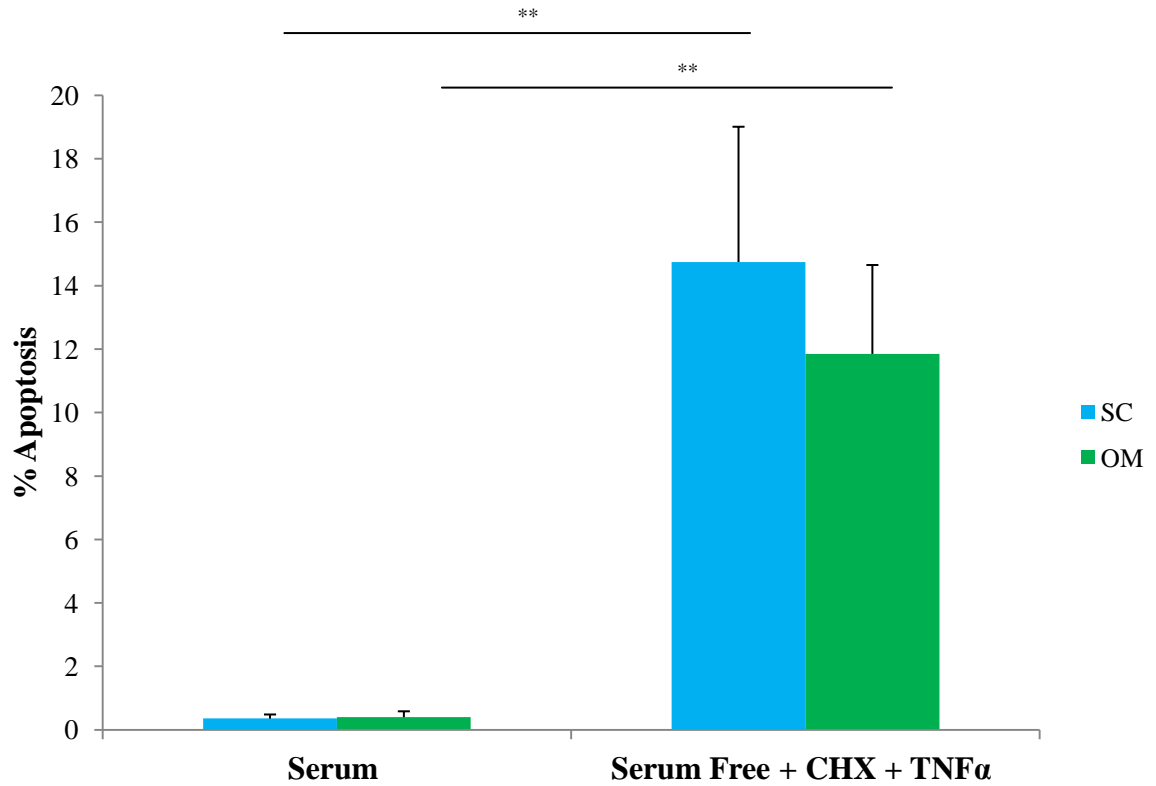


Fig. 9 Primary human adipose progenitor cell apoptosis induced by serum deprivation with TNF α and CHX. Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium with 10 ng/mL of TNF α and 10 μ g/mL CHX for 6 h. Cells were fixed then stained with Hoechst dye. Staining was visualized by fluorescence. Hoechst staining was performed on duplicate dishes. Results are the mean \pm SE of 3 separate matched patient samples. **P<0.01.

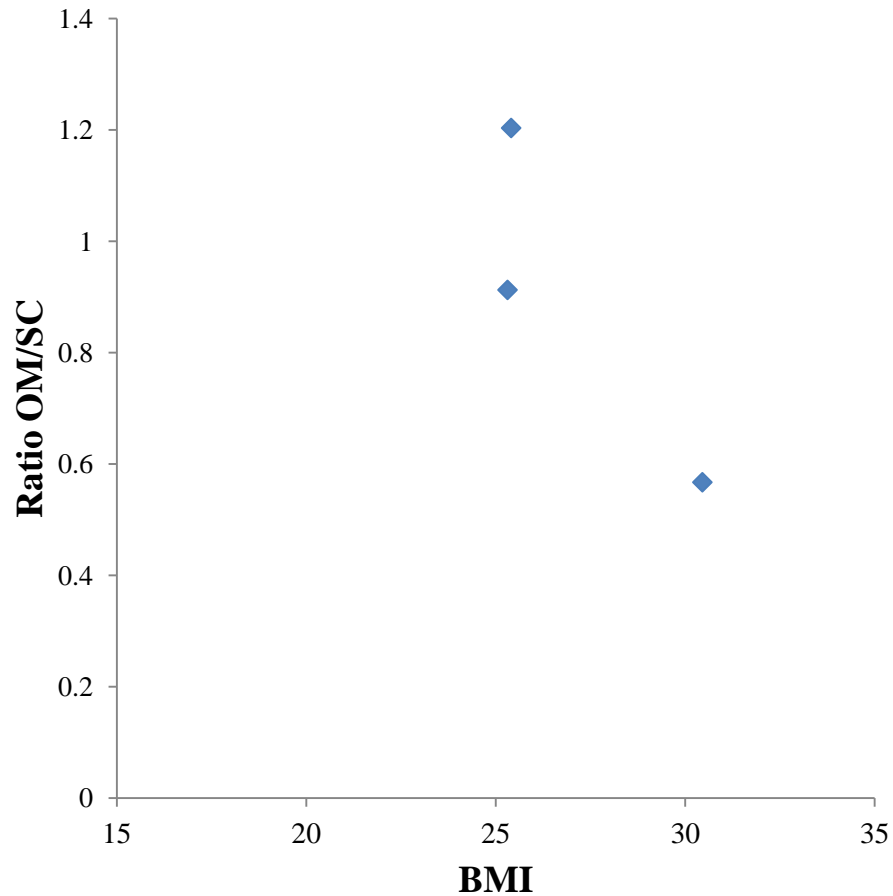


Fig. 10 Apoptosis induced by serum deprivation with TNF α and CHX does not correlate with BMI. Scatter plot shows the BMI correlation of the 3 donors on the relative apoptotic susceptibility between the two types of adipose progenitors. The data are not significant. Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium with 10 ng/mL of TNF α and 10 μ g/mL CHX for 6 h. Cells were fixed then stained with Hoechst dye. Staining was visualized by fluorescence. Hoechst staining was performed on duplicate dishes. Results are the mean \pm SE of 3 separate matched patient samples.

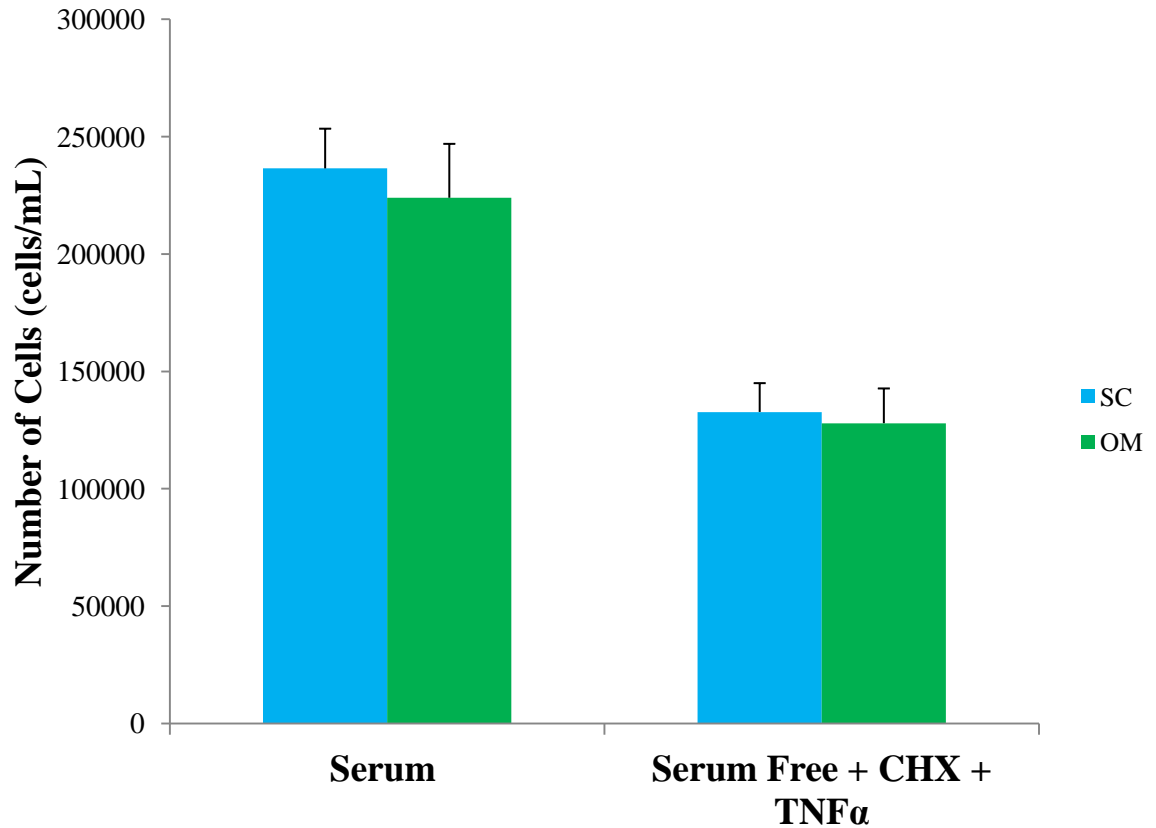


Fig. 11 Primary human adipose progenitor cell death induced by serum deprivation with TNF α and CHX. Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium with 10 ng/mL TNF α and 10 μ g/mL CHX for 24 h. Cell enumeration was performed on duplicate or triplicate dishes. Results are the mean \pm SE of 4 separate matched patient samples. **P<0.01.

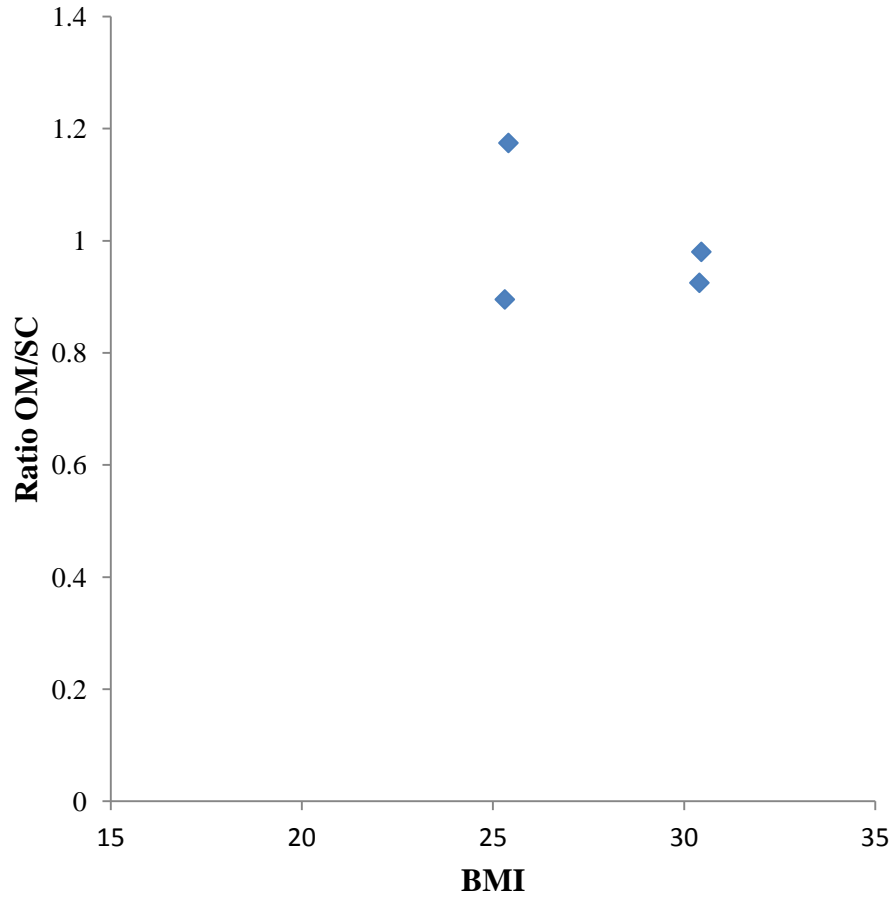


Fig. 12 Cell Death induced by serum deprivation with TNF α and CHX does not correlate with BMI. Scatter plot shows the BMI correlation of the 4 donors on the relative cell death susceptibility between the two types of adipose progenitors. The data are not significant. Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium with 10 ng/mL TNF α and 10 μ g/mL CHX for 24 h. Cell enumeration was performed on duplicate or triplicate dishes. Results are the mean \pm SE of 4 separate matched patient samples.

Optimal Detection of Cell Death Occurs at 6 and 24 h as Assessed by Hoechst Staining and Cell Enumeration under Conditions of Serum Deprivation and TNF α

Time course analyses were performed to assess whether 6 and 24 h treatment periods were optimal to detect cell death. Hoechst staining and cell enumeration were used to assess cell death under conditions of serum deprivation with TNF α . Additionally, I wanted to see if my current observations occurred at other time points.

Hoechst staining was conducted on cells treated with TNF α for 1 h, 4 h, 18 h, 24 h and 48 h (Fig. 13). A significant difference was found in the apoptotic index between treated SC (2.5 ± 0.6) and OM (8.9 ± 0.4) adipose progenitors ($P < 0.01$) at 4 h. The OM depot showed a trend of greater apoptosis compared to the SC depot at 18 h (SC, 1.7 ± 0.4 ; OM, 7.9 ± 1.5) and 24h (SC, 2.9 ± 1.0 ; OM, 6.9 ± 1.8), however this was not significant. After the 48 h treatment time, apoptosis appeared to decrease in the OM depot, eliminating any depot difference. I concluded that a treatment period of 4 to 6 h was optimal to assess apoptosis using the Hoechst staining.

Cell enumeration was used to assess cell death after serum deprivation and TNF α treatment for 24 and 48 h. Although both showed increased percent death rates, treatment for 24 h resulted in a trend of greater cell death in the OM depot (43.4 ± 3) compared to the SC depot (36.2 ± 3), but did not reach significance ($P = 0.12$) (Fig. 14). However, a significant depot difference was observed at 48 h (SC, $39.6 \pm 2\%$; OM, 55.9 ± 4 ($P < 0.05$)). I concluded that a treatment period of 24 to 48 h was optimal to cause cell death as assessed by cell enumeration.

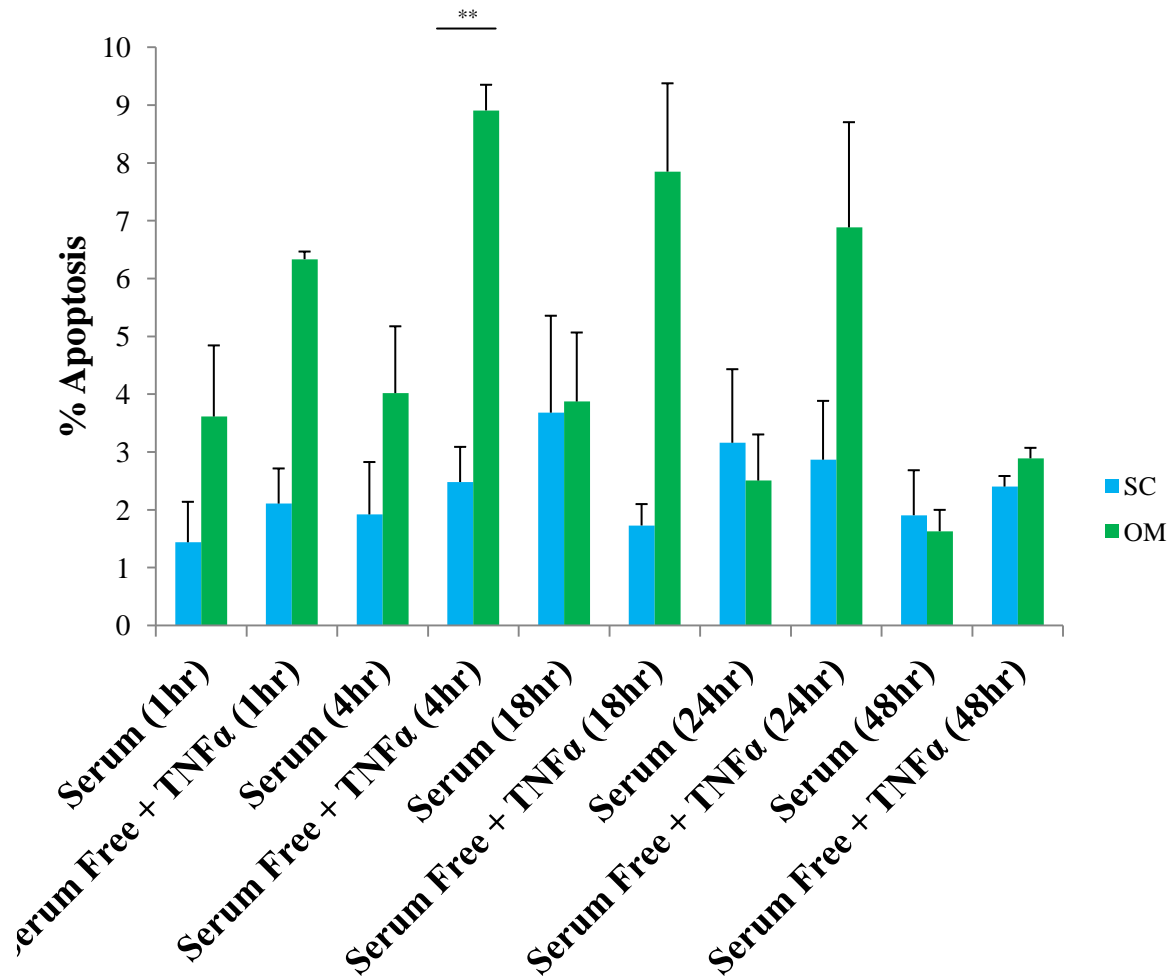


Fig. 13 Serum deprivation with TNF α for 6 h is sufficient to induce primary human adipose progenitor cell apoptosis. Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium with 438 ng/mL of TNF α for 1 h, 4 h, 18 h, 24 h and 48 h. Cells were fixed then stained with Hoechst dye. Staining was visualized by fluorescence. Hoechst staining was performed on duplicate dishes. Results are the mean \pm SE of 3 separate matched patient samples. **P<0.01.

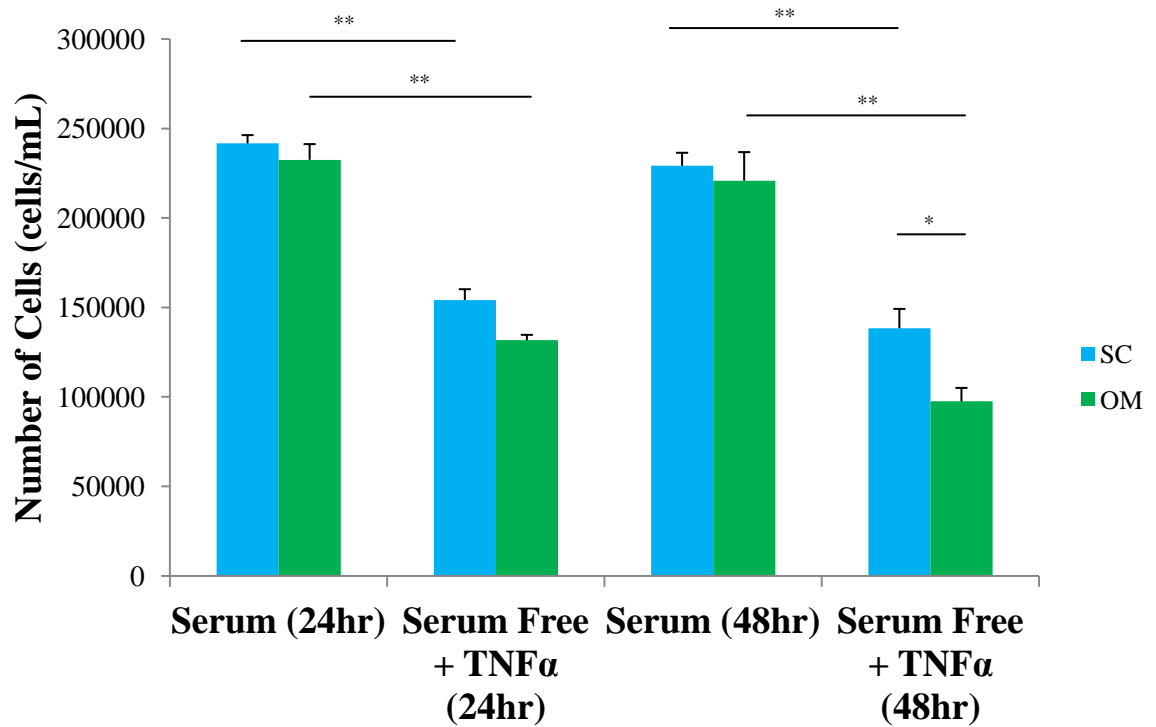


Fig. 14 Serum deprivation with TNF α for 24 h is sufficient to induce primary human adipose progenitor cell death. Human SC and OM adipose progenitor cells were grown to confluence. Cells were placed in serum-containing or serum free medium with 438 ng/mL of TNF α for 24 h or 48 h. Cell enumeration was performed on duplicate or triplicate dishes. Results are the mean \pm SE of 3 separate matched patient samples. *P<0.05, **P<0.01

Results for Aim 2

MacCM on the Survival of Human Primary Adipose Progenitor Cells

I determined whether there was a depot difference in the response to MacCM. Apoptosis was measured using Hoechst staining of condensed nuclei.

Serum Deprivation on MacCM Survival Activity and Human Adipose Progenitor Cells

MacCM did not suppress SC adipose progenitor cell apoptosis compared to the control media under conditions of serum withdrawal (Fig. 15). A similar 3.4 ± 0.2 % versus 3.5 ± 0.5 % apoptosis was observed with MacCM versus control media.

Under serum conditions, MacCM doubled the apoptosis of OM adipose progenitor cells versus the control media (3.1 ± 0.7 vs 1.7 ± 0.02) (Fig. 15), but the difference was not significant. MacCM suppressed OM adipose progenitor cell apoptosis compared to the control media under conditions of serum withdrawal. The mean apoptotic index was 6.6 ± 1.8 versus 7.8 ± 1.5 with MacCM versus control media, but the difference was not significant. Overall, there was significant OM adipose progenitor cell apoptosis in control media with serum deprivation ($P < 0.01$), and a trend with MacCM but was not significant.

Serum withdrawal in control media resulted in a significant depot difference (SC, 3.49 ± 0.51 %; OM, 7.82 ± 1.48 %) ($P < 0.05$) (Fig. 15). Serum deprivation in MacCM resulted in a depot difference but was not significant. This suggests that macrophages may have a pro-survival effect on OM adipose progenitor cells in the presence of serum withdrawal, resulting in an intrinsic depot difference. More studies will be needed to confirm this.

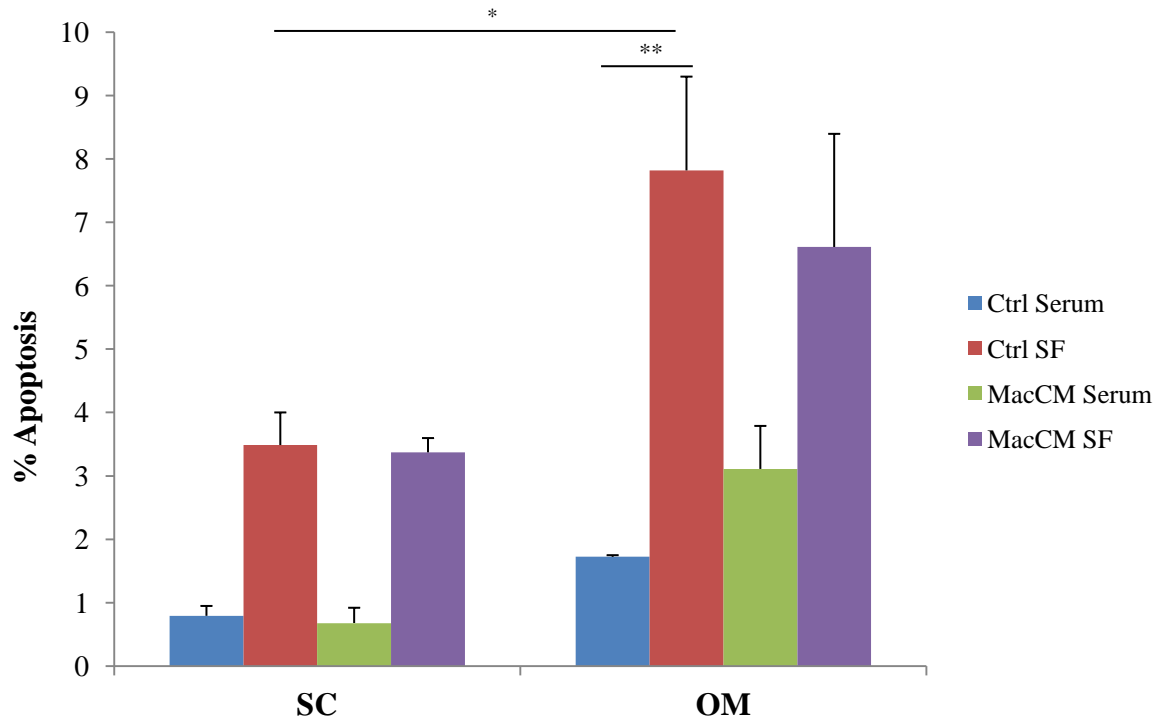


Fig. 15 MacCM survival activity on primary human adipose progenitor cells in the presence of serum deprivation. Human SC and OM progenitor cells were incubated for 6 h with serum-containing or serum-free medium in the presence of control medium or MacCM, as indicated. Apoptosis was assessed by quantification of Hoechst-stained apoptotic nuclei. N=3, *P<0.05, **P<0.001.

Serum Deprivation and TNF α on MacCM Survival Activity and Human Adipose Progenitor Cells

MacCM did not suppress SC adipose progenitor cell apoptosis compared to the control media under conditions of serum withdrawal and TNF α (Fig. 16). A similar 2.3 ± 0.2 % versus 2.1 ± 0.1 % apoptosis was observed with MacCM versus control media.

Under serum conditions, MacCM doubled the apoptosis of OM adipose progenitor cells versus the control media (2.9 ± 0.5 vs 1.4 ± 0.3) (Fig. 16), but the difference was not significant. MacCM suppressed OM adipose progenitor cell apoptosis compared to the control media under conditions of serum withdrawal and TNF α . The mean apoptotic index was 4.7 ± 1.6 versus 6.4 ± 1.0 with MacCM versus control media, but the difference was not significant. Overall, there was significant OM adipose progenitor cell apoptosis in control media with serum deprivation and TNF α ($P < 0.01$), and a trend with MacCM but was not significant.

Serum withdrawal and TNF α in control media resulted in a significant depot difference (SC, 2.1 ± 0.1 %; OM, 6.4 ± 1 %) ($P < 0.01$) (Fig. 16). Serum deprivation and TNF α in MacCM resulted in a depot difference but was not significant. Therefore, we have observed for the first time that macrophages may have a pro-survival effect on OM adipose progenitor cells in the presence of serum deprivation and TNF α , resulting in an intrinsic depot difference.

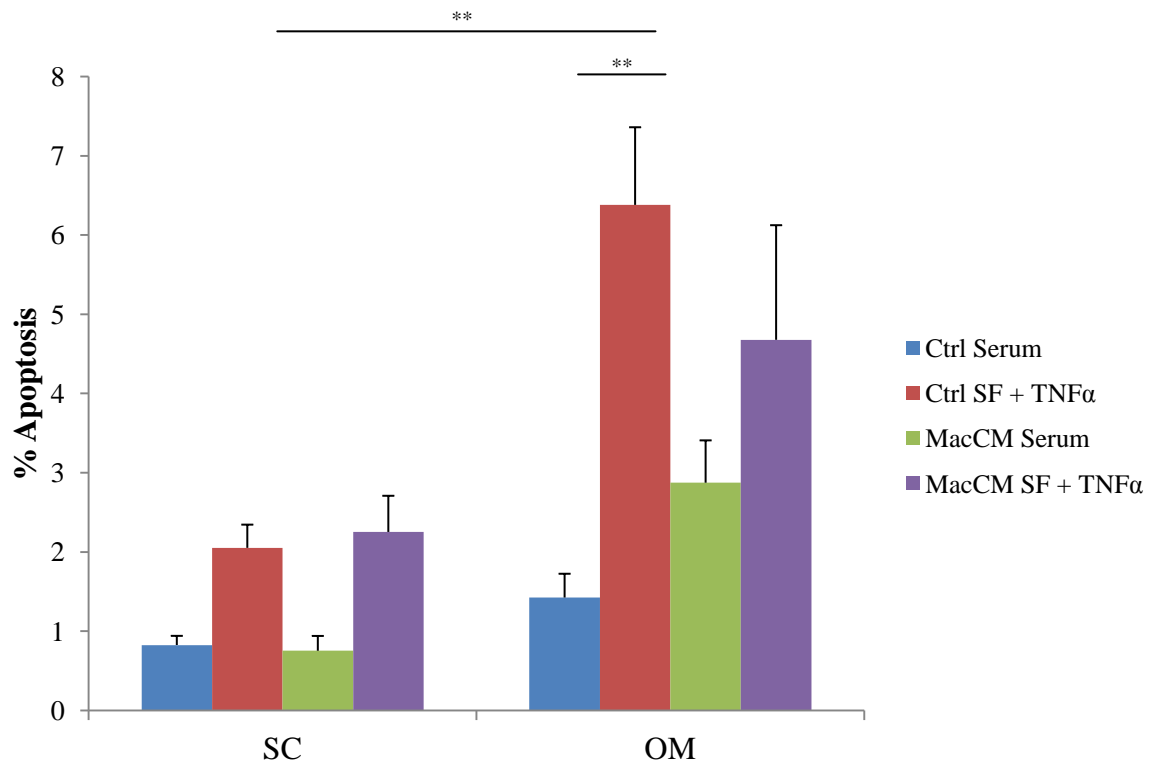


Fig. 16 MacCM survival activity on primary human adipose progenitor cells in the presence of serum deprivation with TNF α . Human SC and OM progenitor cells were incubated for 6 h with serum-containing or serum-free medium supplemented with 438 ng/ml TNF α in the presence of control medium or MacCM, as indicated. Apoptosis was assessed by quantification of Hoechst-stained apoptotic nuclei. N=4, **P<0.001.

Serum Deprivation and TNF α with CHX on MacCM Survival Activity and Human Adipose Progenitor Cells

Serum deprivation with TNF α and CHX in MacCM and control media caused significant apoptosis in the SC depot ($P < 0.01$). MacCM did not suppress SC adipose progenitor cell apoptosis compared to the control media under conditions of serum withdrawal and TNF α and CHX (Fig. 17). A similar 22.9 ± 5.8 % versus 24.6 ± 8.0 % apoptosis was observed with MacCM versus control medium.

Under serum conditions, MacCM doubled the apoptosis of OM adipose progenitor cells versus the control media (2.9 ± 0.5 vs 1.4 ± 0.3) (Fig. 17), but the difference was not significant. MacCM did not suppress OM adipose progenitor cell apoptosis compared to the control media under conditions of serum withdrawal and TNF α and CHX. The mean apoptotic index was 9.8 ± 0.6 versus 9.7 ± 1.2 with MacCM versus control media.

Serum withdrawal with TNF α and CHX in both MacCM and control media resulted in a trend of greater apoptosis in the SC depot compared to the OM depot but was not significant (Fig. 17). We have observed for the first time that that the SC depot showed more apoptosis than the OM depot. Macrophages did not appear to have a survival effect on either depot in the presence of serum deprivation with TNF α and CHX, eliminating any depot difference.

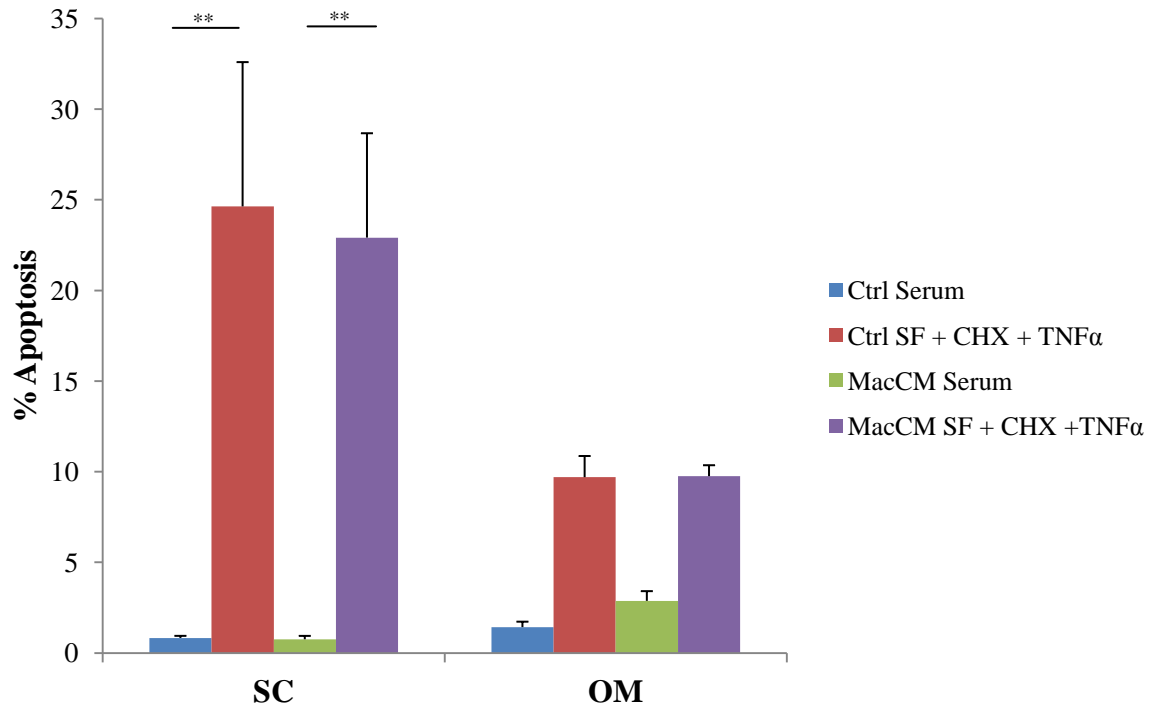


Fig. 11 MacCM survival activity on primary human adipose progenitor cells in the presence of serum deprivation with TNF α and CHX. Human subcutaneous and omental progenitor cells were incubated for 6h with serum-containing or serum-free medium supplemented with 10 mg/ml CHX and 10 ng/ml TNF α in the presence of control medium or MacCM, as indicated. Apoptosis was assessed by quantification of Hoechst-stained apoptotic nuclei. N=4, **P<0.001.

4.0 Discussion

Apoptosis is a cell death program that plays a crucial role in the regulation of tissue homeostasis (Elmore, 2007). Two main apoptotic pathways exist, the intrinsic (mitochondrial) pathway and the extrinsic (death receptor) pathway (Elmore, 2007; Fulda et al., 2010). The mitochondrial pathway is initiated by the release of apoptotic factors such as cytochrome c from the mitochondrial intermembrane space. The release of cytochrome c into the cytosol triggers caspase-3 activation through formation of the cytochrome c/Apaf-1/caspase-9-containing apoptosome complex. Stimulation of TNF death receptors, such as CD95 (APO-1/Fas), leads to the recruitment and activation of caspase-8 at the DISC, which in turn causes cleavage and activation of downstream effector caspases.

Few reports have been examined human adipose progenitor cell survival signaling. A recent report based on SGBS adipose progenitor cells implicates Akt2 in this response (Fischer-Posovszky et al., 2012). The reduced sensitivity of human adipose progenitor cells to apoptosis has been suggested to result from autocrine activation of pro-survival IGF-1 receptor signaling (Fischer-Posovszky et al., 2004).

My study included three pro-apoptotic conditions which involve distinct mechanisms for inducing apoptosis: serum withdrawal, serum withdrawal with TNF α and serum withdrawal with TNF α and CHX. We used two different cell death assays, Hoechst staining and cell enumeration, to examine depot-specific effects on adipose progenitor cell death.

Serum deprivation causes apoptosis by the removal of trophic factors essential for the survival of the cell (Kummer et al., 1997). Survival factor deprivation activates the intrinsic apoptotic pathway.

My study confirmed the greater predisposition of OM versus SC adipose progenitor cells to apoptosis when induced by serum deprivation. Hoechst staining revealed that serum deprivation led to significant apoptotic changes in 1.2% of SC versus 3.4% of OM adipose progenitor cells, respectively. Niesler et al was the first group to study apoptosis in human adipose progenitor cells from abdominal SC and OM depots (Niesler et al., 1998). They showed that serum deprivation led to apoptotic changes in 3% versus 7% of SC and OM adipose progenitor cells, respectively. They observed more overall apoptosis than me. Niesler et al. incubated their cells in serum-free media for 4 h and judged apoptosis by acridine orange staining of adherent cells. I deprived my cells of serum for 6 h and assessed apoptosis by Hoechst staining of adherent cells.

Cell enumeration data were consistent with Hoechst staining results, showing that OM versus SC adipose progenitor cells are more susceptible to cell death when induced by serum deprivation. Serum deprivation caused 19% versus 30% cell death in SC and OM adipose progenitor cells, respectively. Papineau et al. was the second group to publish a study that had examined depot-specific effects on adipose progenitor cell death, in which adipose progenitor cells derived from abdominal OM versus SC depots were found to be more susceptible to apoptosis (Papineau et al., 2003). They compared apoptosis of abdominal OM adipose progenitor cells with SC adipose progenitor cells subjected to serum deprivation. OM versus SC adipose progenitor cells exhibited a greater extent of percent cell death when placed in serum-free media (31% vs 16%). Papineau et al incubated their cells in serum-free media for 48 h, whereas my incubation time was a shorter 24 h. The depot difference could still be observed with a shorter duration of serum withdrawal.

I was able to demonstrate, with both of my cell death assays, that human primary adipose progenitor cells display a depot-specific susceptibility to cell death under conditions of serum withdrawal.

My study is the first to observe a positive correlation between BMI and cell death susceptibility between the two types of adipose progenitors (ratio OM/SC), when cell death is induced by serum deprivation. Further studies are needed to understand how BMI is linked to this difference in behavior.

Few reports have been published on depot-specific human adipose progenitor cell survival signaling. One study demonstrated that cIAP2 mRNA is expressed in a depot-specific manner (Niesler et al., 2001). cIAP2 is a potent inhibitor of apoptosis. In serum, cIAP2 mRNA was significantly over-expressed in OM versus SC adipose progenitor cells. Under conditions of serum withdrawal, cIAP2 mRNA expression was greater in SC versus OM adipose progenitor cells. This was due to a decrease in expression in the OM depot, whereas expression in the SC depot remained constant. In the presence of an apoptotic stimulus, lower cIAP2 expression in OM adipose progenitor cells may explain why they are more susceptible to death.

TNF α can induce cell death by activating caspase-8 or promote cell survival by activating NF κ B (Gupta, 2002). TNF α induces apoptosis by binding to cell surface receptors CD95, TNFR1 (TNF Receptor-1), TNFR2 (TNF Receptor-2), TRAIL-R1 and TRAIL-R2 (Fraser and Evan, 1996; Fischer-Posovszky et al., 2004). Growth factor withdrawal and death receptor stimulation by TNF α activate both the extrinsic and intrinsic apoptotic pathways.

My study confirmed the larger predisposition of OM versus SC adipose progenitor cells to apoptosis when induced by serum deprivation and TNF α . Hoechst staining revealed that serum deprivation with TNF α led to significant apoptotic changes in 3.1% and 5.1% of SC and OM adipose progenitor cells, respectively. Niesler et al were the first group to study apoptosis induced by TNF α in human adipose progenitor cells from abdominal SC and OM depots (Niesler et al., 1998). They showed that serum deprivation with TNF α led to apoptotic changes in 4% versus 8.5% of SC and OM adipose progenitor cells, respectively. My study showed similar overall apoptosis to their study. Niesler et al incubated their cells in serum-free media with TNF α for 4 h and judged apoptosis by acridine orange staining of adherent cells. I deprived my cells of serum for 6 h and assessed apoptosis by Hoechst staining of adherent cells. Similarly to Niesler et al, we supplemented the serum-free media with 438 ng/mL of TNF α .

My study is the only one that has used cell enumeration to assess cell death induced by serum withdrawal in combination with TNF α . Cell enumeration revealed 28% and 40% cell death in of SC and OM adipose progenitor cells, respectively.

Both of my cell death assays showed that human primary adipose progenitor cells display a depot-specific susceptibility to cell death under conditions of serum withdrawal with TNF α .

I observed a negative correlation between cell death susceptibility between the two types of adipose progenitors (ratio OM/SC) and BMI, when cell death is induced by serum deprivation with TNF α . This was an unexpected result based on what I observed when cell death was induced with serum deprivation alone. It is unclear why stimulating the extrinsic cell death pathway would reverse the correlation. It appears that the addition of TNF α

dominates over the removal of trophic factors in terms of activating the cell death pathways. Further studies are necessary to examine whether BMI can influence TNF α receptor expression, since this could be one possible way that TNF α would act differently based on BMI.

CHX reduces levels of cellular FLIP, a negative regulator of apoptosis that acts as an endogenous brake on caspase-8 activation (Fischer-Posovszky et al., 2011; Fischer-Posovszky et al., 2004; Tchoukalova et al., 2007). CHX sensitizes human adipocytes to TNF α -induced apoptosis (Buchmann et al., 2007).

My study is the first to describe the effect of serum deprivation in combination with TNF α and CHX on OM versus SC adipose progenitor cells to apoptosis. The difference in the apoptotic response observed between SC versus OM adipose progenitor cells that I observed was lost when cell death is induced with the more potent combination of TNF α and CHX. Hoechst staining revealed that both SC and OM depots underwent significant apoptosis (14.8% vs 11.9%). The loss of a depot effect when cell death is induced with TNF α and CHX suggests that FLIP may play an important role in the depot-specific apoptotic susceptibility of adipose progenitor cells.

These apoptotic inducers have been used together by others (Fischer-Posovszky et al., 2011; Fischer-Posovszky et al., 2004; Molgat et al. 2012). Molgat et al observed an approximate 20% induction of human SC adipose progenitor cell apoptosis with this combination. Their study did not look at OM adipose progenitor cells. In both studies, the cells were incubated for 6 h with serum-free media supplemented with 10 mg/mL CHX and 10 ng/mL TNF α . Apoptosis was assessed by quantification of Hoechst-stained apoptotic nuclei.

Consistent with Hoechst staining, cell enumeration revealed no depot difference in percent cell death. Serum withdrawal in combination with TNF α and CHX caused 44% and 43% cell death in of SC and OM adipose progenitor cells, respectively. My data add information on this topic, since there are no other studies in the literature using cell enumeration to evaluate cell death in the different depots in response to TNF α and CHX.

The difference in the apoptotic response observed between SC versus OM adipose progenitor cells is lost when cell death is induced with the more potent combination of TNF α and CHX. The loss of a depot effect when cell death is induced with TNF α and CHX suggests that FLIP may play an important role in the depot-specific apoptotic susceptibility of adipose progenitor cells. In the setting of a strong TNF α signal, we can no longer discriminate between OM and SC depot cell death. The introduction of CHX maximizes the death signal, perhaps overwhelming the subtleties that may differentiate the responsiveness of the two depots.

Obesity is accompanied by the infiltration of circulating blood monocytes into AT, producing an abundant population of inflamed M1-type macrophages. This process of macrophage infiltration is associated with adipocyte hypertrophy (Bluher, 2010). Therefore, macrophages might influence adipose progenitor cells by altering their survival response. Studies on apoptosis using human macrophage models and human adipose progenitor cell models have been reported (Molgat et al., 2012). One study by Molgat et al discovered that J774A.1 and RAW264.7 MacCM inhibit 3T3-L1 adipose progenitor cell apoptosis induced by serum deprivation, and identified platelet-derived PDGF as the principal anti-apoptotic macrophage-secreted factor (Molgat et al., 2009). The identity of the factors from human macrophages mediating human adipocyte cell survival is not yet known. Interactions

between immune cells and adipose progenitor cells are important to consider because they may influence the number of adipose progenitor cells and/or their differentiation capacity and induce adipose tissue dysfunction by inhibiting overall adipogenic capacity.

My study is the first study to describe the survival activity of MacCM on SC versus OM adipose progenitor cells under the three pro-apoptotic conditions described.

Under conditions of serum withdrawal, Hoechst staining was used to assess apoptosis. MacCM did not have a survival effect on the SC depot. Furthermore, the OM depot did not show any significant changes in overall apoptosis, but some trends were seen. The OM depot showed more apoptosis in serum-containing MacCM compared to the control media. The extent of apoptosis with serum removal in MacCM appeared to be less than in control medium.

Under conditions of serum withdrawal and TNF α , Hoechst staining was used to assess apoptosis. The results are similar to what we observed with serum withdrawal alone. MacCM did not have a significant survival effect on the SC or OM depots. However, the OM depot showed more apoptosis in serum-containing MacCM compared to the control media. MacCM suppressed apoptosis in the OM depot with the removal of serum and addition of TNF α .

I examined survival activity of MacCM on SC and OM adipose progenitor cells under conditions of serum withdrawal in combination with TNF α and CHX. One other study has described the survival activity of MacCM under these conditions but solely for the SC depot. Molgat et al observed that MacCM is capable of preventing TNF α and CHX and serum deprivation-dependent SC adipose progenitor cell apoptosis; suggesting that it impedes intrinsic and extrinsic apoptotic pathways (Molgat et al., 2012). Hoechst staining

was used to assess apoptosis. Our results did not show a pro-survival effect of MacCM as seen by Molgat et al. The difference could be due to patient heterogeneity from the different donors. In my study, MacCM did not have a significant effect on either the SC or OM depot; however more overall apoptosis was seen in the SC depot. OM adipose progenitor cells appear to resist apoptosis better than SC adipose progenitor cells under these conditions, although these were trends that did not reach significance.

My study is mostly limited by donor variation effects on human adipose progenitor cells and partially on MD-macrophages. It should be noted that macrophages are highly influenced by the local environment in vivo, with different classes of cytokines resulting in pro-inflammatory (classic) versus anti-inflammatory (alternate) states of macrophage activation. Indeed, some investigators describe AT macrophages in intermediate states between these two extremes. I did not rigorously characterize my MacCM as pro- or anti-inflammatory. There may have been some variation in the activation state of the macrophages. Molgat et al observed that MacCM inhibited apoptosis of primary human adipose progenitor cells (Molgat et al., 2012). MacCM from IL4-treated anti-inflammatory macrophages, but not LPS-treated pro-inflammatory macrophages, was able to protect human SC adipose progenitor cells from apoptosis.

Future studies are needed to examine cell death and cell survival mechanisms in SC and OM adipose progenitor cells. Specifically, it would be beneficial to characterize TNF α receptors in adipose progenitors from the SC and OM depots. The positive BMI correlations, (with only 4 or 5 patients), gives impetus to perform larger analyses in future studies. It would also be important to understand how the activation state of macrophages influences depot susceptibility to apoptosis. Lastly, it would be useful to examine cellular proteins

involved in the pro-survival and pro-apoptotic pathways in both SC and OM adipose progenitors, such as members of the Bcl-2 family, to provide insight on the differences in depot-related death.

Conclusion and Proposed Model

Chronic positive energy imbalance leads to obesity. The survival of differentiation-competent adipose progenitor cells may influence the mechanism by which AT expands. Intrinsic (serum deprivation) and extrinsic (TNF α) apoptotic inducers cause more death in the OM versus SC depot (Fig. 18). When a more potent apoptotic stimulus (TNF α and CHX) is used, the depot difference is lost. Since OM adipose progenitor cells have a greater predisposition to cell death, under mild apoptotic conditions, AT from the OM depot may expand via hypertrophy in patients with higher BMIs. The *in vitro* adipose progenitor cell survival function of macrophage-secreted factors raises the possibility that ATMs may function to promote adipose progenitor cell survival *in vivo*, which may be depot dependent. I looked at the effect of macrophages under the same three apoptotic conditions. I did not observe a macrophage effect in either depot. My study did not support previous work which suggested a pro-survival macrophage effect on the SC depot. Reasons for the observed differences are not clear, but donor heterogeneity may be a factor.

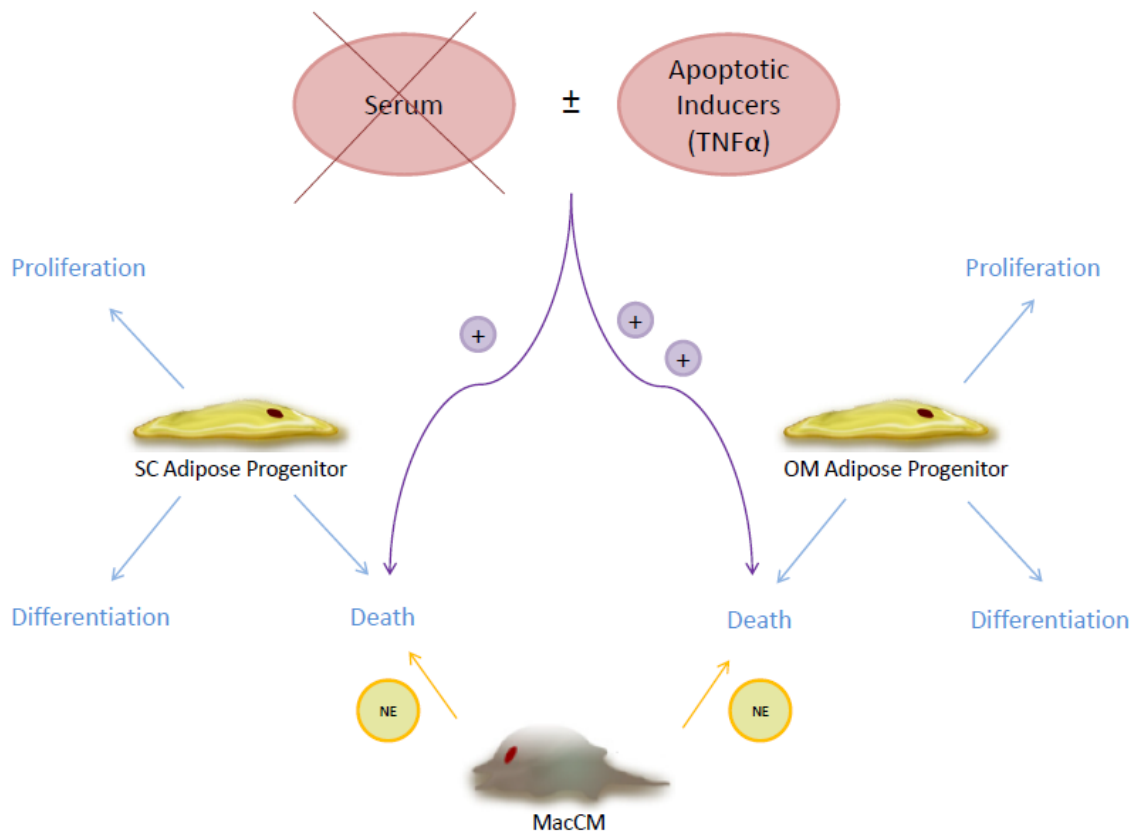


Fig. 18 Model of how apoptotic inducers, either intrinsic (serum withdrawal) or extrinsic (TNF α), influence the apoptotic susceptibility of adipose progenitor cells. A depot-dependent property was observed, with a higher degree of apoptotic sensitivity to serum withdrawal or serum withdrawal in combination with TNF α in OM versus SC abdominal human adipose progenitor cells. MacCM obtained from unactivated macrophages showed no effect on adipose progenitor cell survival in the presence of two apoptotic stimuli.

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6.0 Curriculum Vitae