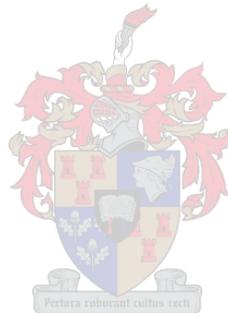


The anti-diabetic and insulin sensitizing potential of a watery extract of Agathosma tested in rat models of type 1 and type 2 diabetes.

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ABSTRACT

Introduction: Epidemiological data highlights that South Africa is currently facing a quadruple burden of disease of which non-communicable diseases (NCDs) are estimated to account for 29% of all deaths. These NCDs include, amongst others, cardiovascular disease, type 2 diabetes, hypertension, cancer, chronic lung disease and depression. Diabetes has become a major problem worldwide and in South Africa and is currently rated as the 5th largest cause of death by Statistics South Africa in 2011. This creates an enormous burden of disease on populations and the utilization of herbal remedies has escalated in popularity because of this. Buchu water is one of these herbal remedies advertised as having anti-diabetic properties. This water is a by-product of the extraction of the oil from the leaves of *Agathosma* and is already freely available to the public.

The **aim** of this study was therefore to use animal models of type 1 diabetes, and obesity and insulin resistance to scientifically verify or refute these claims.

Methods: We utilized male Wistar rats. Two different rat models were used: (i) a type 1 diabetic model; induced via a once-off intraperitoneal Streptozotocin (40mg/kg) injection ablating ~50% of pancreatic beta cells (T1D); (ii) A diet-induced obese model, rendering rats insulin resistant after receiving a high caloric diet for 16 weeks. Half of each experimental group was treated with diluted Buchu water for a period of 14 weeks and 16 weeks, respectively, while the rest consumed normal water. Water and food consumption were monitored, body weight and intraperitoneal fat measured, blood was collected to determine serum glucose and insulin levels, skeletal muscle was removed

to test insulin sensitivity using radiolabelled deoxyglucose, pancreas and skeletal muscle harvested and stored in liquid nitrogen for further biochemical analysis.

Results: One of the main findings of this study was that ingestion of Buchu water results in weight loss despite no decrease in food consumption. This occurred in both the pathological models and control animals. In the obese animals, this weight loss was due to a decrease in intra-peritoneal fat.

A second important finding was that the ingestion of Buchu water in all instances, whether given as treatment (treated with Buchu water 3 weeks after the start of the experiment) or as prophylactic (treated with Buchu water from the start of the start of the experiment), resulted in normalization of glucose levels in a type-1 diabetic model with residual beta-cell mass.

An insulin-sensitizing effect was not clearly established in skeletal muscle but this may be because of a large variation in values obtained, as well as the use of a slow-twitch muscle.

A definite effect on pancreatic insulin secretion has been demonstrated by raised C-peptide levels in the diet-induced obese model.

Conclusion: This study, with regard to the type 1 diabetic model, has confirmed the anti-diabetic effect of Buchu water by significantly lowering blood glucose levels of fasted and non-fasted blood and normalizing Intra-peritoneal glucose tolerance test (IPGTT) curves. This was however not so evident in the obese model utilized. Despite this, animals lost weight which was mainly intra-peritoneal fat.

ABSTRAK

Inleiding: Epidemiologiese data dui aan dat daar tans 'n viervoudige siektelading Suid Afrika in die gesig staar. Hiervan is nie-oordraagbare siektes (NCDs) vir ongeveer 29% van van sterftes verantwoordelik. Hierdie siektetoestande sluit kardiovaskulêre siektes, tipe 2 diabetes, hipertensie, kanker, kroniese longsiektes en depressie in. Diabetes is tans ook in Suid Afrika een van die groot gesondheidsprobleme en word deur die MNR 10de op die ranglys van oorsake van sterftes geplaas. Dit veroorsaak 'n groot siektelas op die populasie in geheel. As gevolg hiervan het die gebruik van natuurlike produkte om siektes te behandel, geweldig toegeneem. Buchuwater is een so 'n natuurlike produk wat geadverteer word om anti-diabetiese effekte te hê. Hierdie water is 'n afvalprodukt van die ekstraksie van Buchu-olie uit die blare van *Agathosma* en is alreeds vrylik aan die publiek beskikbaar.

Metodes: Manlike Wistarrotte is vir die studie gebruik. Twee verskillende modelle is gebruik naamlik (i) 'n tipe 1 diabetiese model daargestel deur 'n enkele intraperitoneale Streptozotocin (40mg/kg) inspuiting waarmee ~50% van die betaselle van die pankreas vernietig word en (ii) 'n dieet-geïnduseerde vetsugtige model waar rotte vir 16 weke op 'n hoë kalorie dieet geplaas word. Helfte van elke eksperimentele groep diere se drinkwater is deur verdunde Buchuwater vervang vir die volle 16 weke. Water- en kosiname is gemonitor, liggaamsgewig en intraperitoneale vetgewig bepaal. Bloedglukose is gemonitor en intraperitoneale glukosetoleransie kurwes opgestel. Bloed is gekollekteer om serum insulienvlakke te bepaal en skeletspier

insulienweerstandigheid is bepaal deur die opname van isotoopgemerkte deoksiglukose te meet. Pankreata is geoes en in vloeibare stikstof vir biochemiese analise gestoor.

Resultate: Een van die hoofbevindinge van hierdie studie was dat die inname van Buchuwater gewigsverlies in diere teweegbring het sonder dat hulle kosiname verminder het. Dit het in beide modelle, sowel in kontrol diere gebeur. In die vetsugtige diere was hierdie verlies as gevolg van verlies van intraperitoneale vet.

'N tweede belangrike bevinding was dat die inname van Buchuwater 'n normalisering van bloedglukosevlakke in die tipe 1 diabetiese diere met 'n betasel reserwe teweegbring het, beide wanneer dit as voorkomend of as behandeling gegee is.

Sensitisering teenoor die effekte van insulin in die skeletspiere van die vetsugtige model rotte kon nie waargeneem word met die inname van Buchuwater nie, deels as gevolg van 'n baie groot variasie in die resultate.

Effekte van die Buchuwaterinname op die betaselle van die pankreas en insuliensekresie is gevind.

Gevolgtrekking: Met betrekking tot die tipe 1 diabetiese model het die studie die antidiabetiese effekte van Buchuwater bevestig deur 'n beduidende verlaging van vastende sowel as nie-vastende bloedglukosevlakke en normalisering van IPGTT kurwes teweeg te bring. Hierdie effekte was nie so voor die hand liggend in die vetsugtige model nie maar hierdie diere het gewig, hoofsaaklik intraperitoneale vet, verloor.

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List of Abbreviations

Units

μl :	Microlitres
μM :	Micromolar
$^{\circ}\text{C}$:	degrees Celsius
mg/kg:	milligrams per kilogram
rpm:	revolutions per minute
V:	Volts
mm:	millimeters
pM:	Picomolar
nM:	Nanomolar
mM:	Millimolar
%:	Percentage
g:	Grams
ml:	Millilitres
mmol/L:	Millimole per litre
pmol/L:	Picomole per litre

Greek symbols

α :	Alpha
β :	Beta
δ :	Delta
ϵ :	Epsilon
γ :	Gamma

Other abbreviations

2DG:	2-Deoxy-D-3[H] glucose
^{125}I insulin:	Radiolabelled Iodinated insulin
ACD:	Acyl-CoA dehydrogenase
ADA:	American Diabetes Association
AdipoR1:	Adiponectin receptor1
AdipoR2:	Adiponectin receptor2
AMPK:	AMP-activated protein kinase
ANS:	Autonomic system
aPKC:	atypical protein kinase c
APS	Adapter containing pleckstrin homology domain and Src homology 2 domain
ATP:	Adenosine triphosphate

BMI:	Body mass index
BSA:	Bovine serum albumin
Bzip:	Basic leucine zipper
BW:	Body Weight
CAP:	cb1 associated protein
CCK:	Cholecystokinin
CK2:	Casein kinase 2
CPK:	Creatine phosphokinase
CNS:	Central nervous system
Cys:	Cysteine
DIO:	Diet induced obese
DHAP:	Dihydroxyacetone phosphate
DPP4:	Dipeptidyl peptidase 4
ECL:	Enhanced chemiluminescence
eIF4E:	elongation initiation factor 4E
ELISA:	Enzyme Linked Immunosorbent Assay
ER:	Endoplasmic reticulum
ETC:	Electron transport chain

FDA:	Food and Drug Administration
GAP:	Glyceraldehyde 3-phosphate
GCK:	Glucokinase
GLP-1:	Glucagon-like peptide-1
GLUTs:	Glucose transporters
Glut2:	Glucose transporter 2
GLUT 4:	Glucose transporter 4
GS:	Glycogen synthase
GSK-3:	Glycogen synthase kinase 3
H ₂ O:	Water molecule
HCl:	Hydrochloric acid
HOMA:	Homeostasis model assessment
IFN- γ R:	Interferon-gamma receptor
IKK:	I κ B kinase
IL-1 β R:	Interleukin-1 β receptor
IP:	Intraperitoneal
IPGTT:	Intraperitoneal glucose tolerance tests

IRS:	Insulin receptor substrate
JNK1:	c-Jun N-terminal kinase 1
LCAD:	Long-chain ACD
Maf A:	Musculoaponeurotic fibrosarcoma homolog A
MAREs:	Maf responsive elements
MCAD:	Medium-chain ACD
mTOR:	Mammalian target of rapamycin
Na ⁺ :	Sodium
Na ⁺ /K ⁺	Sodium-potassium
NAD ⁺ :	Nicotinamide adenine dinucleotide
NCDs:	Non-communicable diseases
NF-κB:	Nuclear factor-κB
NSB:	Non-specific binding
ob/ob:	Leptin deficient mice
p70s6k:	p70 ribosomal s6 kinase

PDK1:	Phosphoinositide dependent protein kinase 1
PDK2:	Phosphoinositide dependent protein kinase 2
PDZ:	a peptide sequence that is rich in Threonine, Lysine and Valine
Pdx-1:	Pancreatic duodenal homeobox 1
PEST:	a peptide sequence that is rich in proline (P), glutamic acid (E), serine (S), and threonine (T)
PH:	Pleckstrin homology
PI-3K:	Phosphatidylinositol 3-kinase
PIP2:	PtdIns 4, 5-bisphosphate
PIP3:	PtdIns 3, 4, 5-trisphosphate
PKB:	serine/threonine protein kinase B
PKC- θ :	Protein kinase C θ
PPAR- α :	Peroxisome proliferator-activated receptor- α
PTB:	Phosphotyrosine binding
PTEN:	Phosphate and tensin homolog deleted on chromosome 10
PtdIns:	Phosphatidylinositol
PVDF:	Polyvinylidene fluoride
QC:	Quality control
RIA:	Radioimmunoassay

ROS:	Reactive oxygen species
SAM:	Sterile alpha motif
SCAD:	Short chain ACD
SEM:	Standard error of the mean
Ser:	Serine
SGLT:	Sodium-glucose co-transporters
SGLT-1:	Sodium-glucose co-transporter 1
SH:	Src homology
SH2:	Src homology domain 2
SHIP:	Src homology 2 containing inositol-5-phosphatase
SHIP 1:	Src homology 2 containing inositol-5-phosphatase 1
SHIP 2:	Src homology 2 containing inositol-5-phosphatase 2
SOCS-3:	Suppressor of cytokine signalling 3
SREs:	Sterol-regulatory elements
SREBP-1:	Sterol regulating element binding protein 1
STAT-1:	Signal transducer and activator of transcription-1
STZ:	Streptozotocin
T:	Total counts
T1D:	Type 1 Diabetes
T2D:	Type 2 diabetes

TAD: Transactivation domain
TAG: Triacylglycerol
Thr : Threonine
TNFR: Tumor necrosis factor receptor
Tyr: Tyrosine

VLCAD: Very long chain ACD

WHO: World Health Organisation

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Motivation for research

South Africa is a country rich in floral biodiversity and cultural diversity [Light et al., 2005]. The Cape region of South Africa has veldt types with arguably the richest composition of indigenous aromatic plant species [Moolla et al., 2007]. Amongst these aromatic plants is the genus *Agathosma* [Moolla et al., 2007]. There are approximately 150 different species within the genus, which branches from a greater family called *Rutaceae* [Moolla et al., 2007]. These rutacious shrubs are typical of the fynbos (vegetation found in the Western Cape province of South Africa) and are particularly abundant in the mountainous areas of the Cape [Moolla et al., 2007]. The term “Buchu” primarily originated from the Khoisan (indigenous people of the western region of South Africa) and was given to any fragrant plant that could be dried and powdered [Moolla et al., 2007]. This name includes a wide variety of aromatic plant species, not singling out a specific genus [Moolla et al., 2007]. The Khoisan tribes relied on these plant materials for many centuries to maintain and/or promote good health. In this era, herbal remedies formed the backbone of healthcare and was the central source of medication [Light et al., 2005]. Today, the term “Buchu” refers to *Agathosma Betulina* (round-leaf buchu; ‘bergboegoe’; short buchu) and *Agathosma Crenulata* (oval-leaf buchu; ‘anysboegoe’; long-leaf buchu) [Moolla and Viljoen, 2008].

Europeans were first introduced to “Buchu” in the 1650’s, upon their arrival in the Cape [Moolla and Viljoen, 2008]. The use of these plants then spread to Europe and America

where it was extensively used for medicinal purposes [Moola and Viljoen, 2008]. Recently, more attention has been placed on the organoleptic properties of “Buchu” rather than on its impact on health, shifting interest towards oil extraction. Oils from these plants are obtained by means of hydro diffusion, a method called hydrodistillation. These oils are typically used in the perfume industry and as flavouring agents to enhance fruit flavours [Moola and Viljoen, 2008]. Currently, Buchu products are virtually found in every store, ranging from teabags, water, lotions, tonics, ointments and even brandy. These products have been approved by the American Food and Drug Administration (FDA), rendering Buchu safe for consumption.

The people of South Africa are faced with many challenges on a daily basis, especially where healthcare is concerned. Illnesses such as diabetes and cardiovascular diseases is a major source of morbidity and mortality in populations that cannot afford western medication [Light et al., 2005]. Such people are left with no other option but to consult traditional healers and make use of herbal remedies [Light et al., 2005]. There are many concerns associated with the use of indigenous plants in medicine. One of these issues stem from the fact that a large portion of knowledge based on herbal usage is anecdotal, posing great concern [Light et al., 2005]. The claims that Buchu exerts anti-microbial, anti-inflammatory, anti-oxidant and diuretic effects have been successfully validated by studies reviewed by Moola and Viljoen [Moola and Viljoen, 2008]. Claims that Buchu has anti-diabetic effects are anecdotal and needs to be validated scientifically. To date, only a few studies have been published on the pharmacological actions of buchu, underscoring the urgency for research in this regard.

Our aim was therefore, on request of the producing company, to determine the anti-diabetic and insulin sensitizing potential of a watery extract of *Agathosma* tested in rat models of type 1 and type 2 diabetes.

DISCLOSURE OF INTEREST

We hereby declare, as per contractual agreement between the University of Stellenbosch and Cape Kingdom Nutraceuticals (Pty) Ltd, (Contract number: S003211) the company licenced to distribute Buchu water, that there was no personal financial gain for the researchers in this work. The researchers only retained the right to publish these findings in peer reviewed scientific journals of their choice.

Signed on the1..... day ofDecember..... 2014

at.....Gordons Bay.....

.....

(Prof. B. Huisamen)

.....

(Me V Jansen)



CHAPTER 1

Literature review

1.1. The Digestive System

To maintain an optimal nutritional status, consumption of proteins, fats and carbohydrates are required.

Food entering the mouth is physically digested by the continuous grinding and chewing action of the teeth [*Raven and Johnson, 2001*]. In the oral cavity, salivary glands secrete mucus which aid in lubrication, provides protection against foreign invaders; bacteria, and moisten ingested food [*Fabian et al., 2012*]. Mucus is a liquid-like substance rich in amylase and immune cells [*Fabian et al., 2012*]. Amylase is an enzyme with a catalytic function to hydrolyse carbohydrates, converting starch to maltose [*Collins et al., 1993*]. After mastication, the digestive material in the mouth, known as the bolus, makes its way down the oesophagus towards the abdomen [*Matsuo and Palmer, 2008*]. This action is achieved via peristaltic wave-like movements of the oesophageal wall [*Matsuo and Palmer, 2008*]. Glands lining the abdominal wall secrete hydrochloric acid (HCl) and proteolytic enzymes, ensuring an acidic environment for proper protein denaturation. The material present in the abdomen after absorption is called chyme. Chyme makes its way to the intestine through the pyloric sphincter where it is further digested. The small intestine, specifically the duodenum, is the main site of

absorption. In the small intestine an enzyme called cholecystokinin (CCK) is secreted, preventing gastric emptying into the intestine and stimulating the release of digestive juices [*Powers and Pappas, 1989*]. This enzyme stimulates organs such as the liver and pancreas to assist with digestion by secreting bile and pancreatic juice, respectively. Bile travels from the liver to the duodenum via a common hepatic duct, where it emulsifies and degrades fat molecules. Pancreatic juice contains bicarbonate, in addition to other digestive enzymes which neutralizes the acidic chyme [*Fieker et al., 2011*]. Amylase secreted by the pancreas and intestine hydrolyzes the last traces of starch in chyme. Maltose gets broken down into glucose with the aid of the enzyme maltase. These glucose molecules are transported by the blood to the rest of the body, where they are used as energy. In the large intestine, no digestion takes place but water and ions are absorbed. Waste material exits the gastrointestinal tract via the rectum and is expelled by the anus. Figure 1 illustrates the digestion of starch only, as our main focus for this study is glucose metabolism.

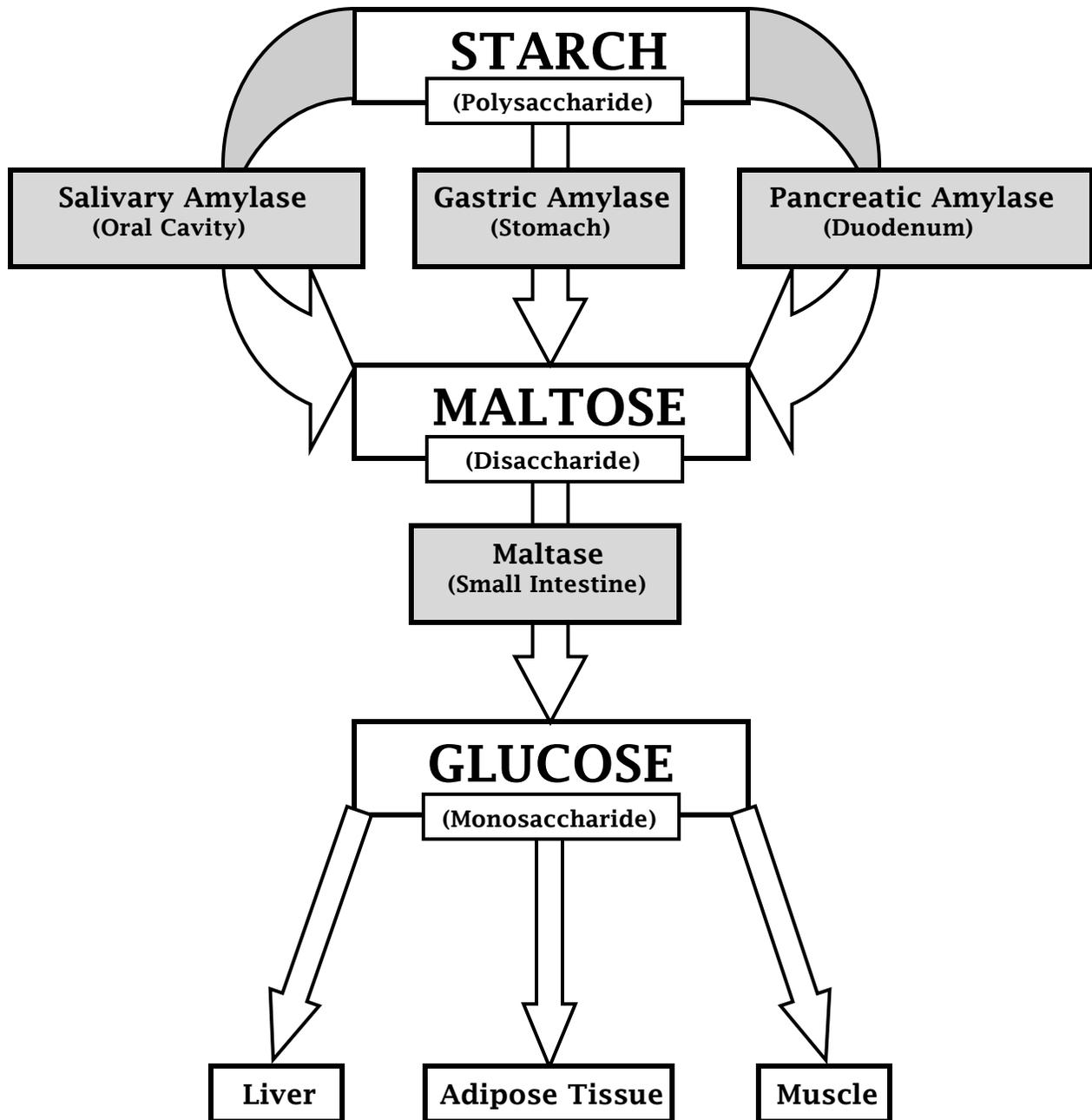


Figure 1: Breakdown of complex polysaccharides

Starch entering various compartments of the digestive system is broken down by specific enzymes, forming maltose. In the small intestine, maltase catalyzes the production of glucose from maltose. These glucose molecules are released into circulation and transported to a whole range of tissue to sustain life.

1.2. Glucose transport across the intestinal epithelium

Glucose is an important nutrient, playing a vital role in many biological processes within mammalian cells [Shah *et al.*, 2012]. These processes include cellular homeostasis and metabolism. In order for glucose to execute its function it has to make its way across the lipid bilayer of the cell. This mode of transportation is achieved with the help of carrier proteins, namely, glucose transporters (GLUTs) and sodium-glucose cotransporters (SGLT) [Bucci *et al.*, 2011]

After a meal, dietary glucose and sodium (Na^+) concentrations increase within the intestinal lumen. Epithelial cells lining the walls of the small intestine maintain homeostasis by transporting molecules and/or ions out of the cell. A low cytoplasmic Na^+ concentration is established in the enterocyte via active transport. The sodium-potassium (Na^+/K^+) ATPase pump, located on the basolateral membrane, lowers the cytoplasmic sodium concentration by actively transporting three sodium ions out of the enterocyte [Srichamroen, 2007]. This results in an ionic imbalance. To restore balance, two potassium ions found in blood vessels have to move against its concentration gradient into the cell with the help of adenosine triphosphate (ATP). The sodium-glucose co-transporter 1 (SGLT-1) allows Na^+ in the lumen to be transported into the enterocyte. Energy produced by sodium ions moving down their concentration gradient makes it possible for glucose to move against its concentration gradient [Steel and Hediger, 1998; Srichamroen, 2007]. This results in high levels of glucose accumulation within the cytosol. These glucose molecules move into circulation via facilitated diffusion to the necessary cells [Steel and Hediger, 1998, Srichamroen, 2007]. Below is a

diagrammatic figure depicting the movement of glucose from the intestine to its specific targets (figure 2).

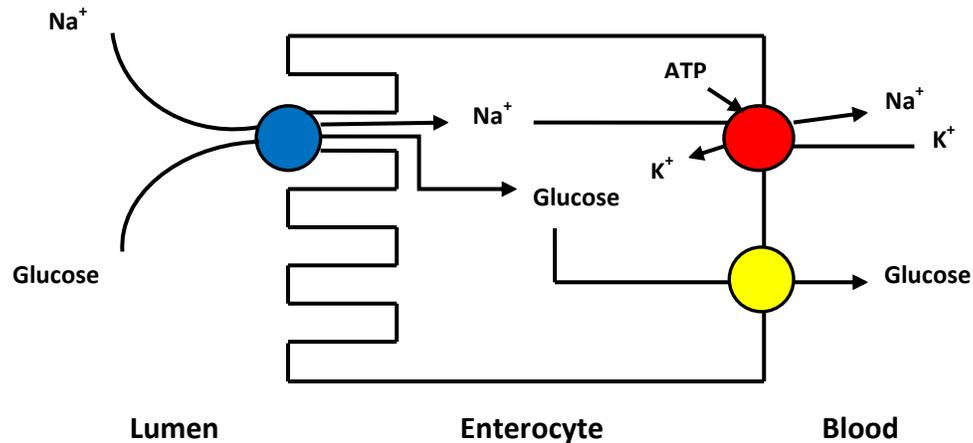


Figure 2: Glucose transport across the enterocyte [Wright, 1998].

- sodium-glucose co-transporter
- sodium-potassium (Na⁺/K⁺) ATPase pump
- glucose transporter 2

The diagram is a reconstruction of Wright, 1998. The sodium-glucose co-transporter and the Na⁺/K⁺ ATPase pump allow sodium ions to be transported from the lumen across the enterocyte into circulation. The movement of sodium ions provide enough energy enabling the transport of glucose into the enterocyte which enter circulation via facilitated diffusion.

1.3. The Pancreas

The pancreas is a gland situated in the abdominal cavity, partially connected to the duodenum [Torpy et al., 2012]. This gland functions both as an exocrine organ, secreting digestive juice into the small intestine, and an endocrine organ, producing hormones which regulate metabolism [Novak, 2008].

1.3.1. Exocrine pancreas

The exocrine portion of the pancreas is a major contributor to pancreatic mass. In these regions acinar cells are present [Jiang *et al.*, 2008]. Acinar cells form glands which secrete various enzymes necessary for digestion [Jiang *et al.*, 2008, Logsdon and Ji, 2013]. The journey of these enzymes to the duodenum is facilitated by pancreatic ducts [Logsdon and Ji, 2013]. Cells lining the duct secrete a watery, bicarbonate-rich fluid which flushes digestive enzymes into the small intestine [Afroze *et al.*, 2013]. Intestinal enzymes break down proteins, carbohydrates and fats into their respective monomers; allowing effortless absorption.

Table 1. Digestive juices secreted by exocrine cells

Digestive Enzyme	Function
Amylase	Digest starch
Chymotrypsin, Trypsin and Carboxypeptidase	Digest protein
Lipase	Digest Triglycerides
Cholesterol esterase	Digest cholesterol
Ribonuclease and deoxyribonuclease	Digest nucleic acid

1.3.2. Endocrine pancreas

Interacinar cells are irregularly shaped regions within the pancreas, known as the islets of Langerhans [Steiner *et al.*, 2010]. The presence of these islets were first documented in 1869 by a German physician, Paul Langerhans [Islam, 2009]. A healthy adult pancreas contains 1 million islets which accommodate approximately 2% of the pancreas [Leoni and Roman, 2010]. The islets of Langerhans are composed of many cells, playing a pivotal role in regulating glucose metabolism.

Table 2. Hormones secreted by the islets of Langerhans [Chen et al.,2012]

Endocrine cell	Hormone	Total islet cells (%)
Beta cell (β)	Insulin and Amylin	65-80
Alpha cell (α)	Glucagon	15-20
Delta cell (δ)	Somatostatin	3-10
Gamma cell (γ)	Pancreatic polypeptide	3-5
Epsilon cell (ϵ)	Ghrelin	<1

The α - and β - cells regulate blood glucose levels by secreting glucagon and insulin respectively [Soria et al., 2010]. These hormones have opposite effects, thus ensuring that fasting blood glucose levels remain within a normal range (4 to 8 mmol/L) [Andrews et al., 1998]. Glucagon, secreted by α -cells, increases the concentration of plasma glucose by stimulating glycogenolysis and gluconeogenesis by the liver. β -cells operate inversely, secreting insulin which stimulates glucose uptake by peripheral cells and enhances glycogenesis. Pancreatic β -cells will be discussed in more detail below.

1.4. Pancreatic response to hyperglycemia

Pancreatic β -cells respond to hyperglycemia by increasing glucose metabolism and ATP production [Layden et al., 2010]. This, in turn, increases the cytoplasmic ATP/ADP ratio, resulting in the closure of potassium channels [Layden et al., 2010]. These cells undergo depolarization causing voltage-gated calcium channels to open, allowing movement of extracellular calcium into the cell [Layden et al., 2010]. Calcium acts as an intracellular signal, stimulating exocytosis of insulin-containing vesicles and insulin

secretion into circulation [Li et al., 2007]. The secreted insulin is stored in mature vesicles that are readily available due to prior synthesis.

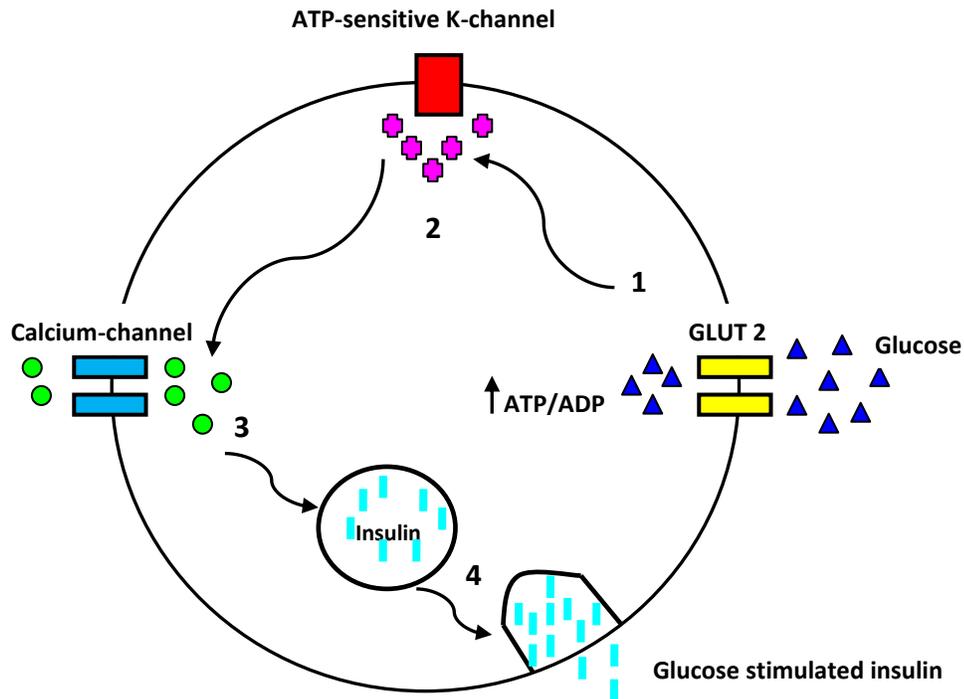


Figure 3: Insulin release by pancreatic β -cells [Layden et al., 2010]

The diagram is a reconstruction of Layden, 2010. Step 1, when β -cells are exposed to hyperglycemia they adapt by increasing metabolism. Step 2, an increase in metabolism causes ATP levels to rise, triggering the closure of potassium channels. Step 3, β -cells depolarize and initiate the opening of calcium channels. Step 4, calcium accumulates in the cell, stimulating insulin secretion.

1.5. The link between insulin action and diabetes mellitus

1.5.1. Insulin biosynthesis

When β -cells are exposed to hyperglycemia, certain pathways such as the IRS-2/PI-3 kinase/p70 s6k and CaM kinase pathway are activated. These kinases phosphorylate transcription factors involved in insulin transcription. Transcription factors interact with the promoter region of the insulin gene, transcribing mRNA. Insulin mRNA is translated to preproinsulin in the rough endoplasmic reticulum (ER) [Hartley et al., 2009]. A signalling peptide, attached to preproinsulin, directs movement into the lumen of the rough ER. Enzymes inside the lumen cleave the signalling peptide, converting preproinsulin to proinsulin. Three disulfide bonds hold proinsulin intact after folding [Yang et al, 2010]. Shuttle vesicles transport proinsulin from the ER to the golgi apparatus [Hartley et al., 2009]. In the golgi, proinsulin is packaged into immature secretory vesicles containing endoprotease and carboxypeptidase E [Robinson, 2013]. These enzymes cleave proinsulin, producing insulin and c peptides which are released during exocytosis [Halban and Irminger, 2003]. Insulin entering circulation binds to its target cell, activating an entire host of signalling cascades which stimulate glucose uptake, lipogenesis, protein synthesis and glycogenesis. All these processes will be discussed within the section “insulin signalling pathway in skeletal muscle” of this review.

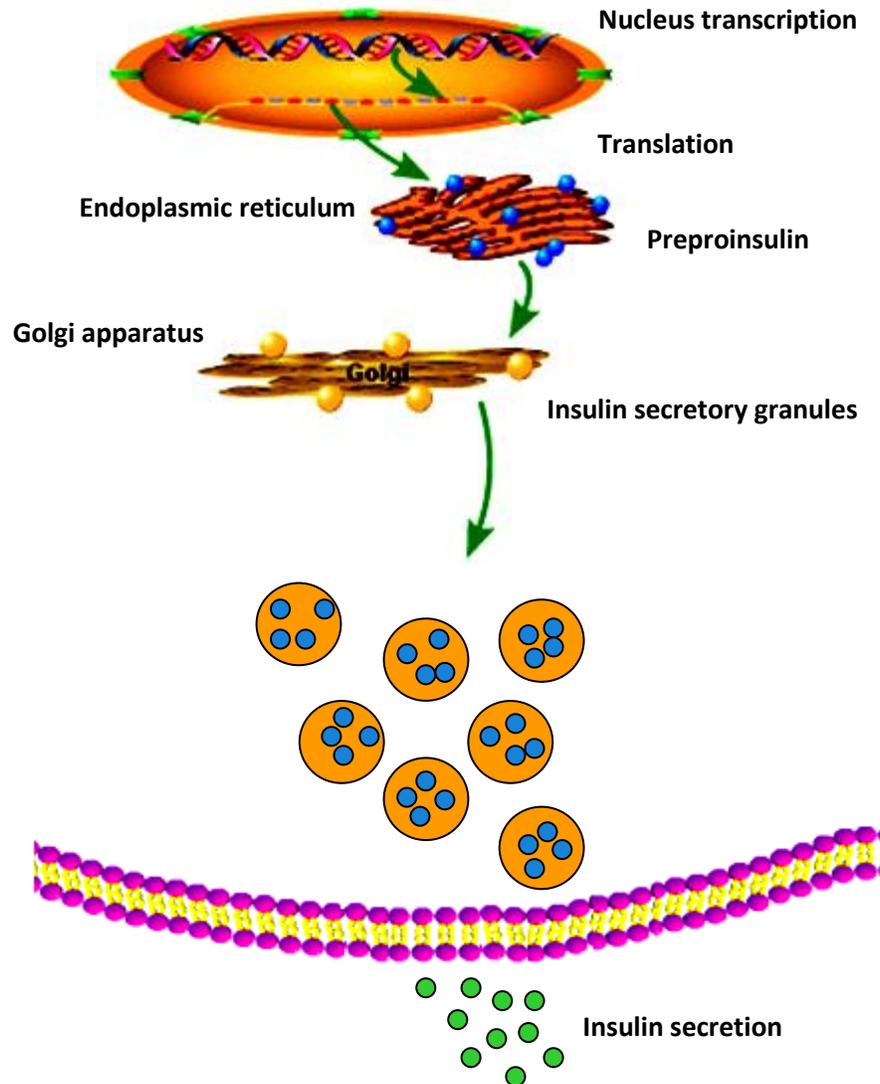


Figure 4: Insulin synthesis and secretion [Ren et al., 2007]

The diagram is a reconstruction of Ren, 2007. Hyperglycemia stimulates the transcription of insulin mRNA which is translated to preproinsulin on the endoplasmic reticulum. Preproinsulin undergoes various cleavage reactions ultimately producing and releasing insulin via exocytosis

1.5.2. Insulin action in regulating glucose homeostasis

Insulin is the most potent anabolic hormone, secreted primarily in response to hyperglycemia [Satiel and Pessin, 2002]. This hormone signals a cascade of events which promote glucose uptake, glycogenesis, lipogenesis, and protein synthesis; while inhibiting pathways and proteins involved in glucose production. Binding of insulin to the insulin receptor initiates a conformational change that elicits autophosphorylation and activates enzyme activity. The insulin receptor is a tetrameric protein which consists of two α subunits that protrude from the cell membrane and two transmembrane β subunits connected by disulphide bonds [Dominici et al., 2005]. Each β -subunit comprises a carboxyl terminus with three tyrosine residues located in the cytoplasmic region. Once phosphorylated, tyrosine motifs recruit src homology 2 (SH2) or phosphotyrosine binding (PTB) domain containing adapter proteins [Cipok et al., 2006; Kim and Sang, 2007].

Insulin receptor substrate (IRS), a PTB protein, binds to the insulin receptor and provides docking sites for downstream SH2 proteins. IRS plays a central role in all cells, linking receptor tyrosine kinases to, amongst others, the PI-3K/PKB pathway [Guo et al., 2006]. Tyrosine phosphorylated IRS recruits, binds and activates the regulatory subunit (p85) of the heterodimeric phosphatidylinositol 3-kinase (PI-3K) protein, relieving the inhibitory effect of the p110 catalytic subunit [Fröjdö et al., 2009; Das et al, 2013]. PI-3K can also bind directly to a phosphorylated tyrosine kinase receptor. PI-3K activation results in the migration of the protein to the cell membrane. At the cell membrane PI-3K interacts with phosphatidylinositol (PtdIns) 4, 5-bisphosphate (PIP2), catalyzing the

phosphorylation of PIP2 to PtdIns 3, 4, 5-trisphosphate (PIP3) [*Satiel and Pessin, 2002*]. PIP3 has a high affinity for intracellular proteins containing a pleckstrin homology (PH) domain [*Das et al, 2013*]. These phospholipids recruit phosphoinositide dependent protein kinase 1 (PDK1), PDK2 and serine/threonine protein kinase B (PKB) to the intracellular membrane where they interact and activate one another [*Fröjdö et al., 2009*]. PIP3 is able to prime PKB for phosphorylation by initiating a conformational change which allows easy accessibility to threonine 308 (Thr 308) residues. At the cytoplasmic membrane PDK2 phosphorylates PKB on its serine 473 (Ser 473) site subsequently increasing its affinity for PDK1, phosphorylating the Thr 308 residue of PKB. Full activation of PKB requires dual phosphorylation on both Thr 308 and Ser 473 sites. Once the PI3K/PKB pathway is activated, varied downstream kinases and genes that regulate glucose homeostasis are modified.

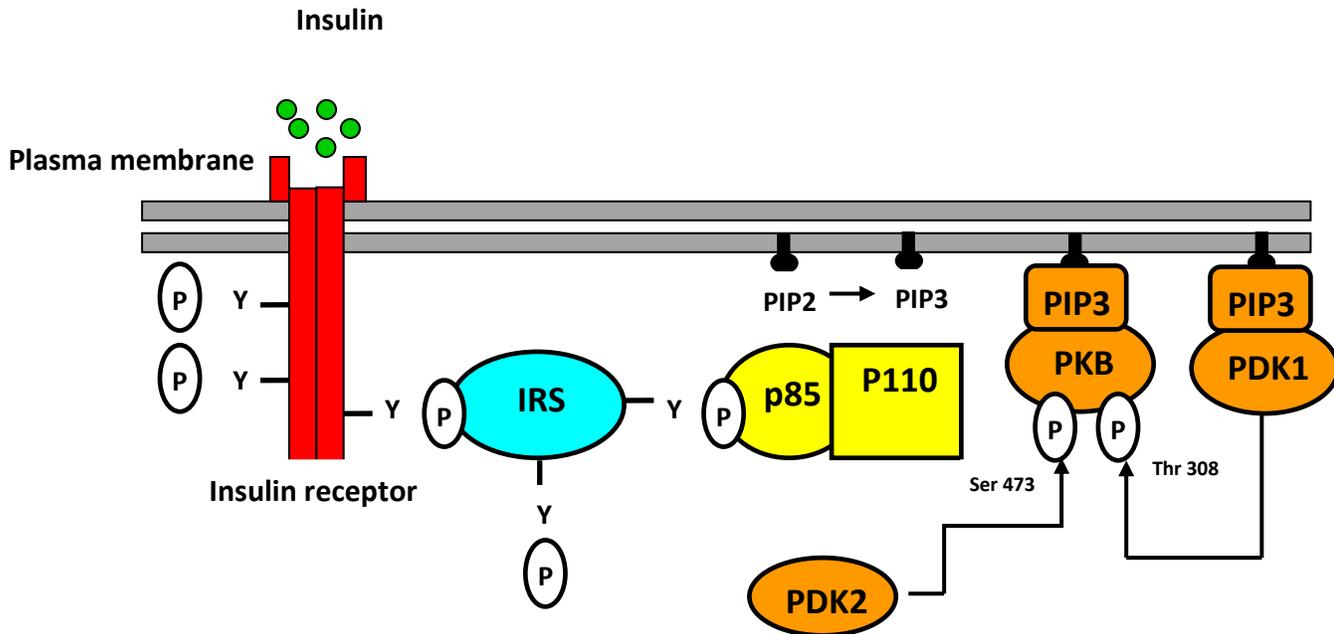


Figure 5: PKB/Akt activation pathway [Turban and Hajduch, 2011]

The diagram is a reconstruction of Turban and Hajduch, 2011. Binding of insulin to the insulin receptor triggers autophosphorylation, resulting in the phosphorylation and activation of an insulin receptor substrate protein, and phosphatidylinositol 3-kinase (PI-3K). The conversion of phosphatidylinositol (PtdIns) 4, 5-bisphosphate (PIP2) to PtdIns 3, 4, 5-trisphosphate (PIP3) is catalyzed by PI-3K. PIP3 recruits protein kinase B (PKB) to the plasma membrane where it is activated by phosphoinositide dependent protein kinase 1 (PDK1) and phosphoinositide dependent protein kinase 2 (PDK2).

1.5.3. Insulin signalling pathway in skeletal muscle

In skeletal muscle, activated PKB/Akt phosphorylates various proteins capable of lowering blood glucose levels by increasing glucose uptake, glucose oxidation and glucose storage. These cells combat hyperglycemia via the activation of numerous processes which will be discussed below.

1.5.3.1. Glycolysis and Glycogenesis

Active PKB/Akt promotes the translocation of glucose transporter 4 (GLUT 4) to the plasma membrane, stimulating glucose uptake. The mechanical procedure of GLUT 4 translocation will be discussed in the section “GLUT 4 translocation to the plasma membrane”. Glucose is a monosaccharide with many fates which are essential for sustaining life, e.g. it can either undergo glycolysis, for adenosine triphosphate (ATP) production, or be stored as a reserve fuel. The term glycolysis is derived from two Greek words, ‘Glykys’ meaning sweet and ‘lysis’ referring to the ability to split or break. Glycolysis is a series of metabolic processes which provides a quick burst of energy by degrading one molecule of glucose [*Pelicano et al., 2006*]. An in depth review on the glycolytic pathway, will be given in the section “Skeletal muscle metabolism”. Excess glucose in skeletal muscle is stored as glycogen. PKB/Akt phosphorylates glycogen synthase kinase 3 (GSK-3), alleviating its inhibitory effect on glycogen synthase (GS) thus promoting glycogen synthesis.

1.5.3.2 GLUT 4 translocation to the plasma membrane

In the presence of insulin, glucose enters the cell by facilitated diffusion, a passive process which requires no energy [*McCarthy and Elmendorf, 2007*]. The proteins responsible for glucose movement into the skeletal muscle and adipose tissue are glucose transporters, GLUT 1 and GLUT 4 [*McCarthy and Elmendorf, 2007*]. GLUT 1 is responsible for basal glucose uptake, and GLUT 4 for insulin-stimulated glucose uptake. These 12 membrane spanning transporters play a crucial role in maintaining blood glucose homeostasis [*McCarthy and Elmendorf, 2007*]. In the absence of insulin

stimulation, GLUT 4 continuously circulates between the plasma membrane and intracellular storage vesicles [McCarthy and Elmendorf, 2007]. More than 90% of GLUT 4 is localized within endosomal recycling compartments, while only a few are found at the cell surface [Thong et al., 2005]. Insulin shifts the movement of GLUT 4 containing vesicles towards the plasma membrane by increasing the rate of exocytosis [Thong et al., 2005]. The translocation of GLUT 4 is governed by two pathways, PI-3K dependent pathway and PI-3K independent pathway, which will be discussed in more detail.

1.5.3.2.1. PI-3K dependent pathway

Signalling events that set this pathway into motion are initiated by the binding of insulin to its receptor triggering a cascade of phosphorylation events [Chang et al., 2002; McCarthy and Elmendorf, 2007]. Tyrosine phosphorylated IRS catalyzes the activation of PI-3K, which in turn, leads to PIP3 generation [McCarthy and Elmendorf, 2007]. These phospholipids recruit pleckstrin homology (PH) domain containing proteins to the membrane where they are activated [Smith et al., 2011]. Both PKB/Akt and atypical protein kinase c (aPKC) are phosphorylated by PDK1 on Thr 308 and Thr 410 residues, respectively [Thong et al., 2005]. The precise mechanistic action of aPKC is not clear, however, it appears to have effects on both intracellular and surface target events of GLUT 4 trafficking [Thong et al., 2005]. There are many other proteins involved in GLUT 4 trafficking, docking and fusion such as Rab GTPase activity proteins, e.g. As160. Basally, As160 associates with the GLUT 4 vesicles, hydrolyzing Rab GTP to RabGDP [McCarthy and Elmendorf, 2007]. This inactive form of Rab prevents GLUT 4 translocation to the plasma membrane [McCarthy and Elmendorf, 2007]. Upon insulin

stimulation, PKB/Akt phosphorylates As160 on specific serine (Ser 588) and tyrosine (Tyr 642) residues, causing it to dissociate from the vesicle [Smith et al., 2011]. Phosphorylated As160 recruits and binds to an accessory protein, 14-3-3, which inhibits GAP activity towards Rab [McCarthy and Elmendorf, 2007]. The equilibrium shifts towards a more active GTP loaded Rab, promoting GLUT 4 trafficking [Smith et al., 2011]. Several studies have shown that PI-3K activation is necessary but not sufficient for insulin stimulated GLUT 4 translocation, thus shifting attention toward PI-3K independent pathways [Chiang et al., 2001].

1.5.3.2.2. PI-3K Independent pathway (CAP-Cbl-TC10 pathway)

Activation of one PI-3K independent pathway depends on tyrosine phosphorylation of a proto-oncogene. Upon insulin stimulation, insulin receptors are autophosphorylated recruiting adaptor proteins, APS (adapter containing pleckstrin homology domain and Src homology (SH) 2 domain) and CAP (Cbl associated protein), to the plasma membrane [Chang et al., 2002]. CAP phosphorylates tyrosine residues on Cbl by interacting with proline-rich domains [Chang et al., 2002]. This triggers the migration of the dimeric CAP-Cbl complex towards caveolin enriched lipid rafts [Liu et al., 2002]. The process of migration is facilitated through the association of an amino-terminal SH2 domain on CAP with the lipid raft protein, flotillin [Chang et al., 2002; Chiang et al., 2001]. Tyrosine phosphorylated Cbl recruits an adaptor protein, CrkII, along with C3G towards the lipid raft domain on the plasma membrane [McCarthy and Elmendorf, 2007]. This occurs in two stages; firstly Cbl binds to the SH2 domain of CrkII and secondly the SH3 domain of CrkII interacts with the proline domain of C3G, forming the

CrkII-C3G complex [Liu *et al.*, 2002; Chiang *et al.*, 2001]. Once translocated, the CrkII-C3G complex brings C3G into close proximity with the Rho family protein, TC10, residing in the raft domains of the membrane [Chang *et al.*, 2002; Chiang *et al.*, 2001]. This interaction catalyzes the hydrolysis of GTP to GDP, rendering TC10 active [Chiang *et al.*, 2001]. The activation of TC10 plays a critical role in the regulation of GLUT 4 translocation, docking and fusion with the plasma membrane [Chiang *et al.*, 2001]. Various studies have shown that TC10 interferes with actin dynamics and cytoskeletal arrangement, facilitating exocytosis of GLUT 4 [Thong *et al.*, 2005; Chiang *et al.*, 2001].

1.5.3.2.3 PI-3K Independent pathway (AMPK pathway)

For many years living organisms persevered by mechanistically adapting to nutritional and environmental stressors. In this section of the review, compensatory adjustments in response to contraction/exercise, will be discussed. When skeletal muscles are exposed to exercise, an intramuscular energy change occurs initiating numerous metabolic responses to restore energy balance [Winder, 2001]. One of the ways in which these cells counteract high-energy phosphate depletion as a result of exercise, is by alerting the AMP-activated protein kinase (AMPK) low fuel warning system [Winder, 2001; Nielsen *et al.*, 2003]. This system operates by switching off ATP utilizing processes, such as biosynthetic pathways while switching on ATP-generating pathways that include fatty acid oxidation and glucose uptake [Hardie, 2004; Russell *et al.*, 1999; Luiken *et al.*, 2003; Kudo *et al.*, 1995; Fryer *et al.*, 2000]. AMPK is a heterotrimer that is ubiquitously expressed in cells [Nielsen *et al.*, 2003]. These proteins consist of a catalytic alpha subunit containing the kinase domain and two regulatory subunits termed

beta and gamma [Sakamoto *et al.*, 2005]. All these subunits are necessary for the complete activation of AMPK [Winder, 2001]. The degree of activation depends on muscle glycogen concentration, pre-exercise diet, exercise duration, exercise intensity and training status [Nielsen *et al.*, 2003; Winder, 2001; Wojtaszewski *et al.*, 2003]. During muscle contraction, AMPK becomes allosterically activated by an increase in the AMP:ATP and creatine:phosphocreatine ratio [Wojtaszewski *et al.*, 2003; Hayashi *et al.*, 1998; Ponticos *et al.*, 1998; Hardie and Carling, 1997]. Once activated, AMPK stimulates GLUT 4 translocation to the plasma membrane by phosphorylating As160, similar to the pathway activated by PKB/Akt, thereby increasing glucose transport [Nielsen *et al.*, 2003]. An increase in the level of glucose molecules within the cell and the activation of catabolic processes result in ATP regeneration [Sakamoto *et al.*, 2005; Hayashi *et al.*, 1998; Fryer *et al.*, 2000; Hardie and Carling, 1997]. Figure 6 summaries the regulation and activation of AMPK.

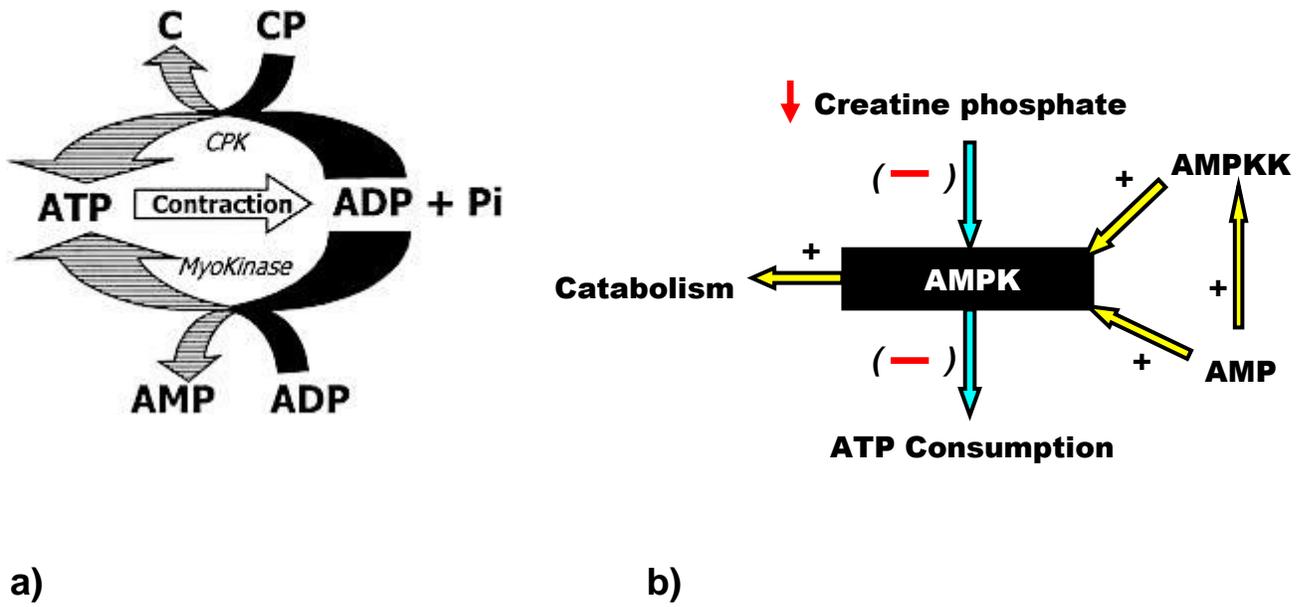


Figure 6: Regulation and activation of AMPK [Winder, 2001]

(—): Inhibit +: Stimulate ↓: Decrease

(a) Myokinase and creatine phosphokinase (CPK) are two enzymes that maintain physiologically normal ATP levels in skeletal muscle in response to contraction. During exercise, Myokinase increases the AMP concentration within the muscle by transferring a phosphate from one ADP to another ADP molecule. CPK stimulates the transfer of a phosphate from CP to ADP, forming ATP. (b)[a graphical modification of Winder, 2001] As a result, high levels of AMP can either stimulate AMPK activity directly or indirectly via AMPKK. A decrease in the concentration of creatine phosphate removes/relieves its inhibitory effects on AMPK activation.

1.5.4. Regulators of the insulin pathway

The P1-3K pathway plays a critical role in regulating a wide variety of biological processes through the generation of a potent second messenger, PIP3 [Sly *et al.*, 2003]. These processes include cell proliferation, growth, differentiation and survival [Kalesnikoff *et al.*, 2002]. PIP3 recruits and activates many PH domain containing

proteins, initiating a cascade of events necessary for cell survival [Conde *et al.*, 2011]. Cellular PIP3 levels need to be tightly regulated to prevent abnormal cell proliferation and impaired glucose metabolism [Conde *et al.*, 2011; Kennah *et al.*, 2009]. These levels are kept under control by lipid phosphatases, namely phosphatase and tensin homolog deleted on chromosome 10 (PTEN) and Src homology 2 containing inositol-5-phosphatase (SHIP) [Chow and Baker, 2006]. Both of these phosphatases modulate the PI-3K pathway by dephosphorylating PIP3, thus downregulating PKB/Akt activation.

1.5.4.1. PTEN

PTEN was first identified in 1997; and has a large region of homology to chicken tensin, bovine auxilin, and a protein tyrosine phosphatase domain [Waite and Eng, 2002]. This 54 KDa lipid phosphatase consists of three structural domains: a C2, amino-terminal and a tail domain [Parsons, 2004]. The amino-terminal domain contains a phosphatase catalytic region composed of β sheets surrounded by alpha helices [Waite and Eng, 2002]. This catalytic region has an enlarged active site that allows phosphoinositide substrates to enter the site with ease [Simpson and Parsons, 2001]. The width and depth of the active site is consistent with PTENs ability to dephosphorylate lipid substrates [He *et al.*, 2010]. The C2 domain is required for efficient binding of PTEN to the membrane [Parsons, 2004; Waite and Eng, 2002]. Studies have shown PTEN to have a higher affinity for membrane bound phospholipids, 'in vitro'. The tail domain contains a PDZ (Threonine, Lysine, Valine) -binding motif and a PEST (Proline, Glutamic acid, Serine, and Threonine) motif responsible for protein-protein interactions and PTEN stability, respectively [Waite and Eng, 2002]. PTEN appears to be

ubiquitously expressed within cells and its activity depends on PIP3 levels and/or post-translational modification [Gericke *et al.*, 2006; Chow and Baker, 2006]. The phosphatase activity of PTEN is down regulated by modifying it in two ways, either via phosphorylation of the tail domain or oxidation of the catalytic domain [Wang and Jiang, 2008]. Casein kinase 2 (CK2) is considered to be responsible for a large portion of PTEN phosphorylation [Gericke *et al.*, 2006]. Torres and Pulido (2001) demonstrated that CK2 phosphorylates PTEN on serine (Ser370, Ser380 and Ser 385) and threonine (Thr383) residues, 'in vivo' [Waite and Eng, 2002]. Phosphorylation of the tail domain causes a conformational change which masks the PDZ domain and enhances PTEN stability [Waite and Eng, 2002; Gericke *et al.*, 2006]. It is widely accepted that phosphorylation of PTEN is required for its inactivation to maintain PTEN cytosolic levels, prevent proteasomal degradation and slow PTENs interaction with phospholipids [Wang and Jiang, 2008; Waite and Eng, 2002]. GSK-3 has been reported to phosphorylate the tail domain of PTEN on Ser 362 and Thr 366 residues [Wang and Jiang, 2008].

PTEN can be inactivated through oxidation which is induced by reactive oxygen species (ROS). Insulin triggers a complex signalling cascade which enhances the production of ROS [Espinosa *et al.*, 2009]. Insulin stimulated ROS, catalyzed by NADPH oxidase, oxidizes cysteine (Cys 71 and Cys 124) residues in the catalytic domain of PTEN [Wang and Jiang, 2008; Espinosa *et al.*, 2009]. This oxidative process inhibits PTEN and allows PIP3 levels to rise, rendering PKB/Akt active. PTEN knockout mice are embryonically lethal whereas heterozygotes develop a variety of cancers [Sly *et al.*,

2003]. Overexpression of PTEN induces cell cycle arrest and results in a metabolic switch from aerobic glycolysis to anaerobic pathways. This protects cells from oncogenic transformation, thus promoting a healthier metabolism [Simpson and Parsons, 2001; Braccini et al., 2012].

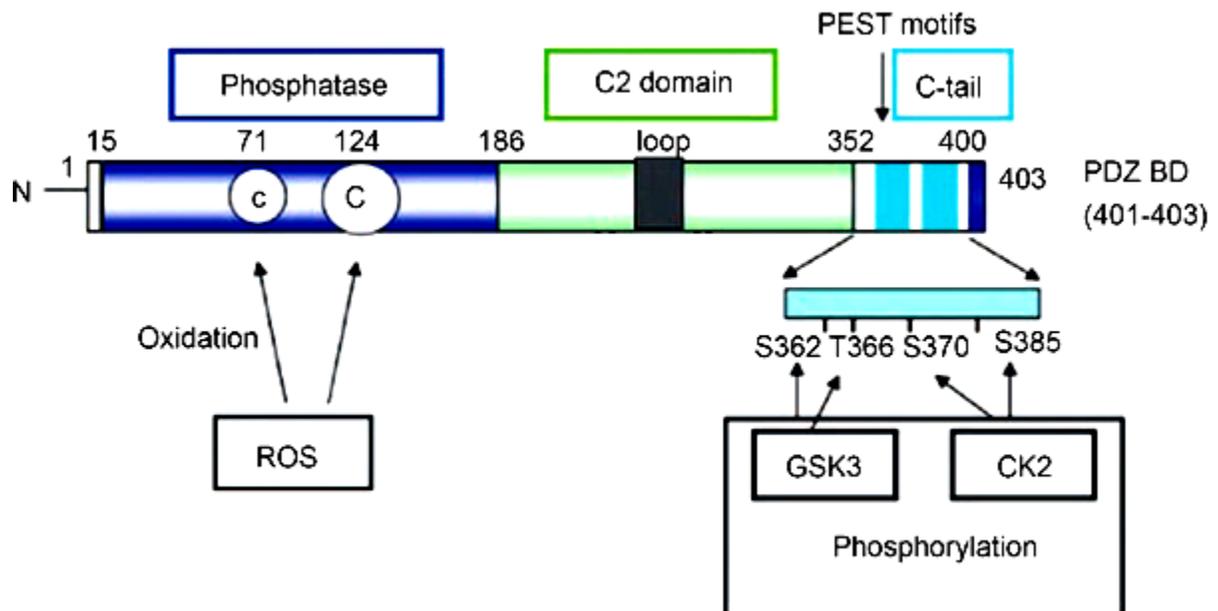


Figure 7: PTEN structure [Wang and Jiang, 2008]

Phosphate and tensin homolog deleted on chromosome 10 (PTEN) consists of three major structural domains: an amino-terminal (phosphatase domain), a C2 domain and a tail domain. PTEN is regulated by glycogen synthase kinase 3 (GSK3) and casein kinase 2 (CK2) via the phosphorylation of specific serine and threonine residues. Other factors such as reactive oxygen species can also regulate PTEN activity by oxidizing cysteine residues.

1.5.4.2. SHIP

The SHIP family of phosphatases includes two members, SHIP-1 and SHIP-2, which are isoforms of each other [Braccini *et al.*, 2012]. The expression of SHIP-1 phosphatase is restricted to hematopoietic cells while SHIP-2 is ubiquitously expressed in the brain and skeletal muscle [Braccini *et al.*, 2012; Kennah *et al.*, 2009; Conde *et al.*, 2011]. The SHIP-2 isoform contains an amino terminal, a central catalytic domain and a C-terminus [Conde *et al.*, 2011]. The amino-terminal SH2 domain and the catalytic domain is essential for binding proteins which consist of phosphorylated tyrosine residues and molecules exerting phosphatase activity on PIP3, respectively. The C-terminus is made up of a proline rich region and a SAM (sterile alpha motif) domain, which are important for SHIPs translocation to the plasma membrane [Sly *et al.*, 2003]. SHIP-2 is an important regulator of the PI-3K pathway especially in β -cells.

A study done by Laura and colleagues showed a complete lack of SHIP-2 in mice to be linked to prenatal death and hypoglycaemia [Sly *et al.*, 2003]. Various studies on SHIP-2 heterozygous mice have demonstrated enhanced insulin sensitivity, upon insulin stimulation [Conde *et al.*, 2011]. These mice exhibited higher levels of GLUT 4 translocation and glycogen synthesis when compared to normal control mice [Conde *et al.*, 2011].

A balance between the activation and inhibition of lipid phosphatases plays a critical role in glucose homeostasis and cancer development [Conde *et al.*, 2011]. It has been reported that phosphatases have a negative impact on insulin resistance associated with obesity [Gupta and Dey, 2009]. Insulin resistance appears to be linked to an

increase in phosphatase expression and/or activity in skeletal muscle and adipose tissue [Sly *et al.*, 2003]. Phosphatases are involved in many biological processes, thus phosphatase inhibition offers many challenges.

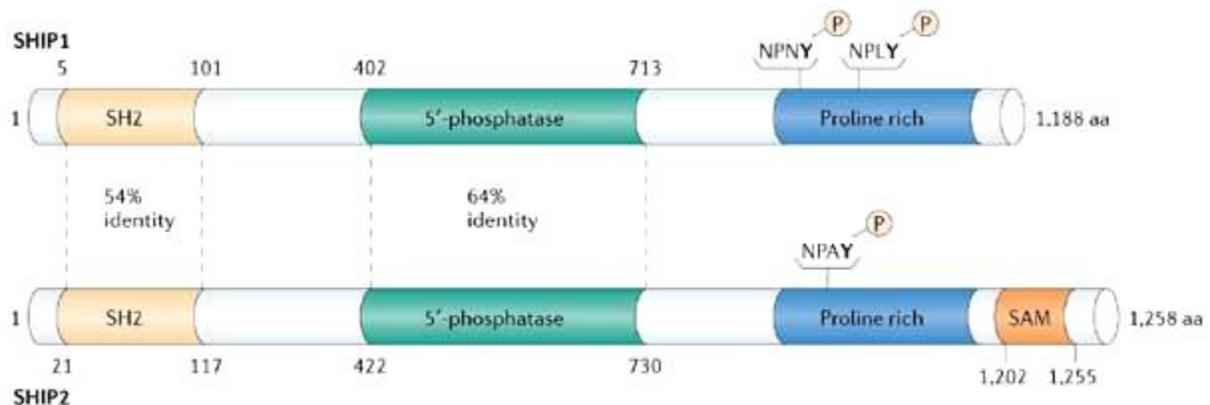


Figure 8: The difference between the SHIP structure [Lazar and Saltiel, 2006]

The Src homology 2 containing inositol-5-phosphatase 1 (SHIP 1) and Src homology 2 containing inositol-5-phosphatase 2 (SHIP 2) is the presence of a SAM domain. SHIP 2 consists of an amino-terminal SH2 domain, a central catalytic domain and a C-terminus. The C-terminus is made up of a proline rich region and a SAM domain, which are important for SHIPs translocation to the plasma membrane

1.5.5. Role of insulin in the development of diabetes

The presence of plasma insulin in response to a meal or high blood glucose levels is crucial in maintaining glucose homeostasis. A defect in insulin secretion or insulin action would have adverse effects on metabolism as well as on an individual's quality of life.

Diabetes mellitus is a disease which manifests as a result of an impairment in insulin response by peripheral tissue or an impairment of pancreatic insulin secretion.

1.6. *Diabetes Mellitus*

The World Health Organization estimated that 347 million people worldwide have diabetes mellitus, with approximately 80% of diabetic deaths occurring in low and middle income countries [*Mathers and Loncar, 2006; WHO, 2014*]. The earliest descriptive report of diabetes dates back to 1550 BC [*Moitra and Meiler, 2006*]. In this era, a physician, Mesy Ra, documented frequent urination (polyuria) on Egyptian papyrus, a characteristic symptom of the diabetic condition [*Moitra and Meiler, 2006*]. According to World Health Organisation (WHO), diabetes will be the 7th leading cause of death by the year 2030. Diabetes mellitus is a chronic disease associated with many complications and occur in individuals' of all ages. Diabetes is characterized by hyperglycemia which originates as a result of pancreatic β -cells not being able to produce sufficient insulin or the inability of target tissues to respond to insulin action. There are three main types of diabetes: Type 1, Type 2 and gestational diabetes. Diabetic individuals require lifelong management as there is as yet no cure for diabetes, only treatment options.

1.6.1 Type 1 Diabetes

Type 1 Diabetes (T1D) is an organ specific autoimmune disease caused by the immunological destruction of insulin producing pancreatic β -cells [Atkinson and Elsenbarth, 2001; Narendran et al., 2003; Atkinson and Elsenbarth, 2001]. T1D was formerly known as juvenile onset or insulin dependent diabetes mellitus, a term which is no longer used [Atkinson and Elsenbarth, 2001]. The American Diabetes Association (ADA) eliminated these terms based on the fact that not all T1D individuals are children or insulin dependent at onset [Atkinson and Elsenbarth, 2001]. T1D is a disorder of all ages with peak expression in children between the ages of 10-14 years [Atkinson and Elsenbarth, 2001]. It should be emphasized that patients with T1D are at an increased risk for developing other autoimmune diseases such as Graves' disease, Addison's disease and hypothyroidism [Atkinson and Elsenbarth, 2001]. An interplay between genetic susceptibility and environmental factors trigger the initial stages of pre-diabetes, followed by insulinitis [Barker, 2008]. The progression of pre-diabetes to overt diabetes is characterised by a loss of the first phase insulin response to intravenous glucose, glucose intolerance and loss of serum C-peptides [Thrower and Bingley, 2010]. Upon the development of overt diabetes the total mass of working β -cells is approximately 10-20%, corresponding with the reduced ability of the pancreas to produce sufficient insulin to maintain normoglycemia [Barker, 2008]. Once this point has been reached, insulin administration should be adhered to for life to reinforce a patient's survival [Thrower and Bingley, 2010]. Insulin treatment serves to be very beneficial by lowering blood glucose levels and stimulating residual β -cells, to regain functionality [Barker, 2008].

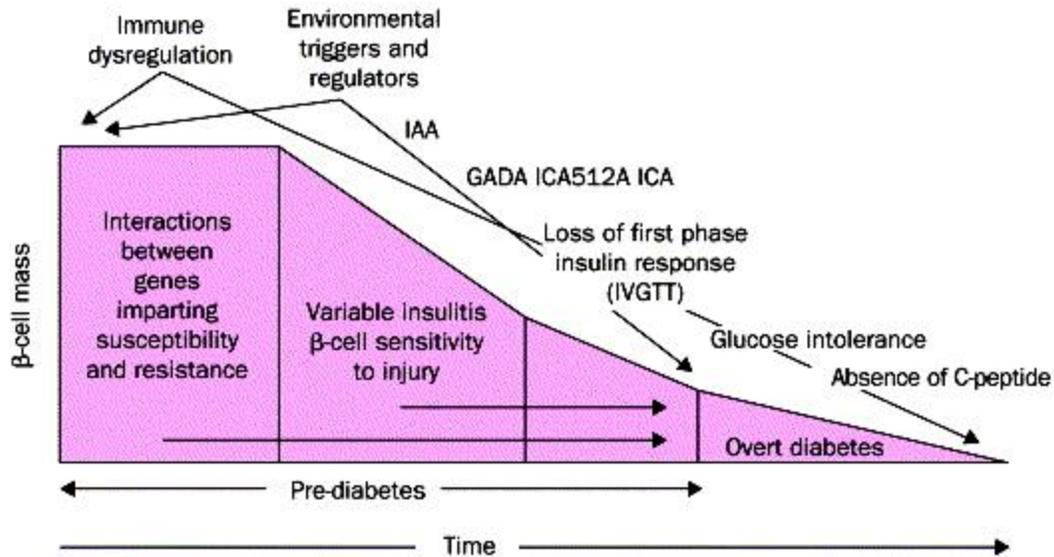


Figure 9: The pathogenesis progression of type 1 diabetes [Atkinson and Elsenbarth, 2001].

β-cell dysfunction is triggered by genetic and environmental factors, subsequently followed by insulinitis. Infiltration of inflammatory cells or proteins impairs β-cell function, ultimately leading to inflammation and β-cell death. The release of β-cell debris as a consequence of apoptotic death further exacerbates the autoimmune response, promoting overt diabetes. IAA, insulin autoantibodies; ICA, islet cell autoantibodies; GADA, autoantibodies to glutamic acid decarboxylase.

1.6.1.1 Pancreatic β-cell dysfunction

Inflammatory infiltration of β lymphocytes, macrophages, CD8 and CD4 T cells, initiates the destruction of β-cells via the activation of specific apoptotic pathways [Atkinson and Elsenbarth, 2001]. Potential mechanisms of β-cell destruction include pro-inflammatory cytokines, Fas/Fas ligand and reactive oxygen species [Atkinson and Elsenbarth, 2001]. These inflammatory destructive factors interact with β-cell cytokine receptors (tumor necrosis factor receptor (TNFR), interferon-gamma receptor (IFN-γR) and Interleukin-1β receptor (IL-1βR)), activating the MAP kinase pathway and a diverse group of

transcription factors, STAT-1 (signal transducer and activator of transcription-1) and NF- κ B. This ultimately results in functional impairment and apoptotic β -cell death [Atkinson and Elsenbarth, 2001]. Damaged β -cells release cell debris and auto-antigens which are recognized by auto-reactive effector T-cells, exacerbating the autoimmune response, thus promoting T1D [Thrower and Bingley, 2010].

The autoimmune destruction of β -cells varies widely between individuals and can occur over months and even years [Thrower and Bingley, 2010]. The rate at which destruction proceeds depends on an individual's tolerance to regulate the immune response [Ziegler and Nepom, 2010]. Therefore, prolonging complete eradication of β -cells would serve to be favourable in a clinical setup.

1.6.1.2 β -cell mass

As previously stated, β -cells secrete insulin which regulates glucose homeostasis by targeting various tissues. For this reason, β -cell mass is vital in the manifestation of diabetes mellitus and should be closely monitored. β -cell mass are dynamic components which readily adapt to changes in insulin demand or glucose concentrations. To maintain an optimal glucose level, an exquisite balance exists between insulin biosynthesis, stimulation and secretion.

The quantitative amount of β -cells present can be calculated based on the interplay between β -cell growth and loss. There are three mechanisms involved in β -cell expansion which include replication of existing differentiated β -cells, neogenesis of β -cells from undifferentiated precursors and hypertrophy [Masiello, 2006]. A reduction in

β -cell mass is associated with hypotrophy and β -cell death as a result of apoptosis, and/or necrosis. Altering any of these mechanisms would result in a change in β -cell mass.

Under normal conditions, β -cell growth and remodeling occurs prenatally, and continues for a short period of time after birth [Masiello, 2006]. During this time, β -cell replication is enhanced followed by a surge in β -cell neogenesis. This results in β -cell growth as a consequence of apoptotic activity being kept at a low level. The rate at which β -cell replication, neogenesis and apoptosis occur soon stabilizes as individuals enter childhood and adulthood, thus maintaining a relative constant β -cell mass [Masiello, 2006]. Various factors contribute to a reduction in β -cell mass, such as old age and the exposure of β -cells to cytotoxic factors, stimulating apoptosis.

1.6.1.3 β -cell neogenesis

As a result of β -cell dysfunction or death, research has shifted its focus to β -cell neogenesis. β -cell neogenesis is a mechanism that triggers the generation of new β -cells from precursor cells [Paris, 2004]. These precursor cells originate from (i) ductal cells (budding from duct epithelium), (ii) differentiated pancreatic cells through a process called transdifferentiation and (iii) intra islet precursors [Paris, 2004]. β -cell neogenesis is a well documented process that is involved in β -cell mass expansion and maintenance, when exposed to increased insulin demand. For this reason, β -cell neogenesis would serve to be beneficial in treating diabetes mellitus. There are various transcription factors promoting β -cell neogenesis which will be discussed in more depth.

1.6.1.4 Transcription factors promoting β -cell neogenesis

Transcription factors control several biological processes such as β -cell differentiation, proliferation, apoptosis, and pancreatic development [Rocques *et al.*, 2007]. The regulation of transcription factors is of utmost importance due to the link between β -cell dysfunction and diabetes. In this study we will be focusing on pancreatic duodenal homeobox 1 (Pdx-1) and musculoaponeurotic fibrosarcoma homolog A (Maf A).

1.6.1.4.1 Pdx-1

The pancreatic duodenal homeobox 1 protein is a homeodomain containing transcription factor that is essential for early pancreatic development and β -cell survival [Yang *et al.*, 2012]. During early prenatal development, Pdx-1 is mainly expressed in pancreatic progenitor cells, later giving rise to endocrine and exocrine cells [Yang *et al.*, 2012]. As the pancreas matures, Pdx-1 expression becomes restricted to β -cells. Pdx-1 maintains normal pancreatic function by regulating insulin, glucose transporter 2 (Glut2) and glucokinase (GCK) gene expression in the promoter region of β -cells. In the last decade, researchers have invested a lot of time in determining the importance of Pdx-1 expression. Genetic studies on homozygous and heterozygous Pdx-1 mutated mice have linked Pdx-1 to pancreatic agenesis and impaired glucose tolerance, respectively [Fujimoto *et al.*, 2010; Claiborn *et al.*, 2010]. There are many stimuli which stimulate Pdx-1 expression in β -cells such as glucose, oxidative stress and free fatty acids [Ardestani *et al.*, 2011]. Acute exposure of β -cells to glucose translocates Pdx-1 to the nucleus, inducing β -cell proliferation and insulin secretion [Ardestani *et al.*, 2011]. Prolonged exposure of β -cells to hyperglycemia exhibited increased DNA methylation

followed by a reduction in Pdx-1 expression [Yang *et al.*, 2012]. This impairs β -cell function and insulin secretion ultimately leading to β -cell death via apoptosis [Ardestani *et al.*, 2011; Yang *et al.*, 2012]. Pdx-1 expression is regulated by post-translational modification and cellular localization [Ardestani *et al.*, 2011].

Insulin resistance has detrimental effects on Pdx-1 expression and activity. During insulin resistance, the inhibitory effect of insulin on GSK-3 β and FoxO1 is lifted, reducing β -cell proliferation. GSK-3 β negatively regulates β -cell mass and function by phosphorylating Pdx-1 on specific serine (Ser61 and Ser66) residues, marking them for proteasomal degradation, thus, reducing its half life [Fujimoto and Polonsky, 2009]. FoxO1 blocks Pdx-1 expression via translocation, moving Pdx-1 from the nucleus to the cytosol [Fujimoto and Polonsky, 2009]. GSK-3 β and FoxO1 enhances β -cell death at a protein and transcriptional level, respectively [Fujimoto and Polonsky, 2009].

1.6.1.4.2 Maf A

Musculoaponeurotic fibrosarcoma homolog A is a transcription factor of the basic leucine zipper (bzip) family [Kannan *et al.*, 2012]. Members of the MAF family are divided up into two classes, “large” (Maf A, Maf B and c-Maf) and “small” (Maf F, Maf G and Maf K) MAF proteins, depending on their molecular size [Nishimura *et al.*, 2009]. Large Maf proteins consist of an additional amino-terminal transactivation domain (TAD) and binds to two palindromic sequences on the insulin promoter region called Maf responsive elements (MAREs), stimulating the transcription of target genes [Nishimura *et al.*, 2009; Rocques *et al.*, 2007]. Maf A is a unique transcription factor expressed

during late pancreatic development and restricted to pancreatic β -cells [Hunter et al., 2011]. The main role of Maf A is to maintain normal blood glucose levels in the body by regulating insulin gene expression [Jorgensen et al., 2007; Kataoka et al., 2002].

A study done by Nishimura and colleagues on Maf A deficient mice have shown a gradual reduction in the β to α cell ratio with age even though postnatal β -cell levels were normal [Nishimura et al., 2009]. These animals were glucose intolerant and developed diabetes; emphasizing the importance of Maf A as a regulator of β -cell maturation [Nishimura et al., 2009]. Zhao reported the transcriptional rate of insulin to be moderate when Maf A was expressed in the β -cell alone, but in accordance with Pdx-1, the synergistic action enhanced insulin promoter activity [Zhao et al., 2005].

1.6.1.5 Treatment: type 1 diabetes

T1D occurs as a result of autoimmunity against pancreatic β -cells, ultimately leading to β -cell destruction. Therefore, therapeutic strategies prolonging or preventing β -cell dysfunction would serve to be beneficial in treating T1D patients. Annihilation of β -cells by the immune system reduces the amount of endogenous insulin secreted into circulation. As a result of the body not producing sufficient insulin to sustain normal glucose homeostasis, these patients are required to take alternative sources of insulin for life. Patients are primarily treated with insulin injections taken on a regular basis. There are several other modes of administering insulin which include external insulin pumps, insulin inhalers and internal insulin pumps. These patients could also undergo more invasive treatments such as gene therapy, pancreatic islet transplantation and whole pancreas transplantation. Other treatment options available are β -cell replication,

reprogramming of mature β -cells and stem cell transplantation. These procedures are very expensive and is therefore not a common option in developing countries.

1.6.1.6 *The Streptozotocin-model of type 1 diabetes.*

Streptozotocin (STZ) is a glucosamine compound which contains a very reactive nitrosourea group [Wei et al., 2003; Arora et al., 2009]. This compound, derived from a soil microbe called *Streptomyces achromogenes*, was initially used as an antibiotic and later added to medication for the treatment of pancreatic cancer, specifically cancer of the islets of Langerhans [Motyl and McCabe, 2009]. Streptozotocin has a glucose moiety which is easily transported into pancreatic β -cells via glucose transporter 2, where it exerts its toxic effects by damaging DNA [Wei et al., 2003; Motyl and McCabe, 2009]. This leads to β -cell dysfunction, hypoinsulinemia and hyperglycemia; all characteristics associated with diabetes [Motyl and McCabe, 2009]. When inducing a T1D model, one should keep in mind that STZ performs at its best when stabilized [Motyl and McCabe, 2009]. STZ is stable at a pH of approximately 4 and it is for this reason that STZ is prepared in a citrate buffer with a pH of 4.5; thus enhancing stability and inducing diabetes [Motyl and McCabe, 2009]. The severity of type 1 diabetes depends on the species of the animal, age and the amount of STZ administered intravenously or intraperitoneally [Arora et al., 2009]. For example, a single dose of STZ is effective in inducing T1D in rat models while multiple low doses of STZ serves to be most effective in inducing T1D in mice models [Motyl and McCabe, 2009].

1.6.2 Type 2 Diabetes

Type 2 Diabetes, formerly accepted as adult onset diabetes, is a multi-factorial disorder that accounts for 90-95% of all diabetic cases worldwide, making it the most common type of diabetes known [Stumvoll *et al.*, 2005]. The pathological sequence for T2D is complex and entails many risk factors promoting its onset and development [Leahy, 2005]. T2D occurs as a result of insufficient insulin production by pancreatic β -cells or reduced insulin action at target tissues. Reports have shown insulin resistance to be present prior to β -cell dysfunction in type 2 diabetic individuals maintaining normal blood glucose levels [Leahy, 2005]. The progression from normoglycemia to glucose intolerance occurs as a result of reduced β -cell function rather than a spike in insulin resistance [Leahy, 2005]. Beta cell function varies and is dependent on the degree of insulin sensitivity [Leahy, 2005]. A reduction in insulin action stimulates the glucose homeostatic system to increase β -cell function by increasing β -cell mass [Stumvoll *et al.*, 2005]. This compensatory mechanism gradually loses its ability to produce the additional insulin needed to overcome insulin resistance, impairing the responsiveness of β -cells to glucose [Leahy, 2005]. As blood glucose levels rise, hyperglycemia promotes β -cell dysfunction by altering various metabolic pathways, enzymes and genes (impairing proinsulin transcription) important for proper functioning. Hyperglycemia deteriorates β -cells even further by stimulating the production of malonyl CoA (in skeletal muscle and the liver) that inhibits fatty acid oxidation, thus, favouring lipotoxicity [Leahy, 2005]. An excess of free fatty acids promote β -cell dysfunction and death by producing fatty acid metabolites such as ceramides and oxidative stress

precursors [Leahy, 2005]. In addition, the generation of amyloids contribute to defective β -cell function [Leahy, 2005].

1.6.2.1 The role of obesity in the development of insulin resistance

Obesity is a disease which affects individuals of all ages and both sexes, globally [Aballay et al., 2013]. This disease occurs as a result of excessive fat accumulation due to a chronic caloric imbalance, impairing an individual's health status [Pulgarón, 2013]. Obesity is assessed and defined by the body mass index (BMI) as being $\geq 30 \text{ kg/m}^2$ according to the World Health Organization [2013]. The BMI is calculated based on the weight in kilograms divided by the square of the height in meters [WHO, 2013].

Obesity has become a major public health problem prevailing in both developing and developed countries [Aballay, 2009]. This problem is further exacerbated by an increase in urbanization, changes in eating habits and a reduction in physical activity. According to WHO, more than 1,4 billion adults worldwide are overweight and of these individuals, over 200 million men and nearly 300 million women were obese [WHO, 2013]. This organization also predicted that these numbers would double by the year 2015 emphasizing the importance of treatment [Nguyen et al., 2010].

Obesity has a tremendous impact on society, drawing attention towards the economic and health sector. In terms of the economy, obesity exerts an enormous financial strain on the economic budget as more finances are pushed into treating obese related morbidities and secondary diseases [Dodd, 2008]. With regards to the health sector, obesity affects an individual's quality of life as it is associated with a variety of co-

morbidities such as type 2 diabetes (T2D), cardiovascular disease, sleep apnea and an array of cancers [*Stumbo et al., 2005; Sahani et al., 2010*]. These individuals exhibit a strong correlation between obesity and the development of the metabolic syndrome which encompasses dyslipidemia, hypertension, insulin resistance and proinflammation [*Chen and Morris, 2007*].

The section that follows will explain the link between obesity and insulin resistance as well as the manifestation of T2D. Current therapeutic strategies will also be discussed.

1.6.2.1.1 *The link between obesity and adipose dysfunction*

As previously stated, obesity stems from a caloric imbalance which arises when energy intake exceeds energy expenditure. The human body makes use of two main types of energy substrates to maintain survival, namely, glucose (carbohydrates) and free fatty acids (lipids). In this section, we will be focusing on triacylglycerol stores, circulating free fatty acids and the origin of insulin resistance.

Adipose tissues are the largest and main lipid storage depots in our body, playing a vitally important role in energy metabolism [*Goossens, 2008*]. These tissues are made up of many adipocytes which produce and secrete numerous adipokines, and cytokines in response to various stimuli. During the postprandial state, adipocytes regulate the influx of dietary fats via a buffering action which suppresses the release of free fatty acids into circulation and increases the activity of lipoprotein lipase, thus enhancing triacylglycerol clearance [*Goossens, 2008*]. Adipocytes of obese individuals are enlarged as a result of adipose tissue being overloaded with triacylglycerol (TAG)

[Goossens, 2008]. During the fed state these individuals are exposed to an additional amount of fatty acids that cannot be cleared effectively due to adipocytes reaching its optimum storage capacity [Goossens, 2008]. As a result, the number of fatty acids and triacylglycerol entering circulation increases. Non-adipose tissue such as the liver and muscle would try and mop up excess substrates in circulation by oxidizing fats, thus preventing any adverse metabolic effects [Goossens, 2008]. Over time these tissues lose the ability to oxidize fats efficiently leading to the accumulation of lipids which are associated with conditions (glucose intolerance, hyperlipidemia and hyperinsulinemia) related to insulin resistance. Insulin resistance is defined as a state of reduced responsiveness of target tissues to normal circulating levels of insulin [Sesti, 2006].

It should be noted that adipose tissue not only serve as the main TAG store in the human body but also secrete numerous adipokines and cytokines which affect insulin sensitivity [Kahn and Flier, 2000]. The role free fatty acids, adipokines and cytokines play in insulin resistance will be further discussed below.

1.6.2.1.2 Fatty acid induced insulin resistance

Free fatty acids play an extremely important role in insulin resistance of obese or overweight individuals by inducing hyperinsulinemia; impairing insulin action and impairing glucose metabolism [Golay and Ybarra, 2005]. Two mechanisms concerning the induction of insulin resistance, via the abundance of free fatty acids in circulation, has been postulated by Randle and Shulman [Randle et al., 1963; Shulman, 2000].

In the 1960's, Randle and colleagues proposed that elevated plasma FFA levels inhibit glucose oxidation by negatively influencing key enzymes in the glycolytic pathway of isolated rat heart muscles, and diaphragms [*Randle et al., 1963*]. The theory behind Randle's hypothesis states that an increase in lipid oxidation raises the mitochondrial acetyl-CoA/CoA and NADH/NAD⁺ ratios to a point where these factors are capable of inhibiting the enzyme pyruvate dehydrogenase [*Kovacs and Stumvoll, 2005*]. The cell would try and get rid of excess acetyl CoA by diverting it into the Krebs cycle, increasing the concentration of citrate. As citrate levels increase, phosphofructokinase activity is inhibited to prevent the accumulation of acetyl CoA by blocking the production of pyruvate [*Kovacs and Stumvoll, 2005*]. The inactivation of phosphofructokinase causes the level of glucose-6-phosphate to rise to an extent where it inhibits hexokinase II activity, thus reducing glucose uptake and ultimately impairing glucose homeostasis [*Kovacs and Stumvoll, 2005*]. There have been many conflicts with Randle's theory, which has been rectified by several authors investigating the link between lipid accumulation and the inhibition of insulin stimulated glucose uptake at a cellular level [*Golay and Ybarra, 2005*]. These studies have shown an influx of lipids to be associated with insulin resistance by inhibiting glucose transport and/or phosphorylation [*Kovacs and Stumvoll, 2005*]. This subsequently decreases the rate of glucose oxidation and storage by inhibiting glycogen synthase.

An investigation done by Shulman confirmed that high plasma fatty acid levels induce insulin resistance via the inhibition of glucose transport [*Shulman, 2000*]. Under normal physiological conditions, insulin mediates tyrosine phosphorylation of IRS which

stimulates PI-3K activation [Kovacs and Stumvoll, 2005; Shulman, 2000]. As discussed in section 1.5.2, active PI-3K triggers a cascade of events, promoting the translocation of GLUT to the membrane. Shulman hypothesized that the skeletal muscle of obese individuals are exposed to an abundance of lipid metabolites, such as fatty acyl CoA, ceramides and diacylglycerol, which negatively affect glucose uptake [Shulman, 2000]. A concentration hike in lipid metabolites sets off a range of adverse effects, triggering the serine/threonine kinase cascade by increasing the activity of protein kinase C θ (PKC- θ) [Kovacs and Stumvoll, 2005; Shulman, 2000]. Serine phosphorylation by PKC- θ sterically hinders IRS-1 tyrosine phosphorylation, reducing the activity of PI-3K by 50 % ultimately reducing the translocation of GLUT 4 to the membrane [Petersen and Shulman, 2006].

1.6.2.2 The link between adipocyte secretions and insulin resistance

Adipocytes secrete several bioactive compounds which play a crucial role in regulating blood pressure, lipid metabolism, inflammation and glucose metabolism [Rabe et al., 2008]. These secretory compounds include adipokines and cytokines. In this section, the influence of certain adipokines and cytokines on insulin resistance, will be discussed.

1.6.2.2.1 Adipokines

Leptin is a 16 kD hormone produced by the *ob* gene, playing an essential role in nutrient homeostasis [Fantuzzi, 2005; Elmquist, 2001]. Principally, leptin exerts its metabolic action in the hypothalamic region of the central nervous system (CNS) [Kahn and Flier, 2000]. Once leptin signals the CNS, the autonomic system (ANS) and the

neuroendocrine pathway are immediately alerted. In response, these pathways regulate food intake, energy storage, blood pressure and energy expenditure by modulating various metabolic processes in peripheral tissue, thus improving insulin sensitivity [Rabe *et al.*, 2008; Elmquist, 2001]. Aside from the ability of leptin to act via the CNS, it is capable of directly stimulating the liver, skeletal muscle and pancreatic β -cells [Kahn and Flier, 2000].

The adipo-insular axis is a feedback loop established between the adipose tissue and the pancreatic β -cell [Rabe *et al.*, 2008; Kieffer and Habener, 2000]. This axis is fully operational when body weight increases, which correlates positively with leptin levels. Leptin protects β -cells from detrimental effects associated with lipid accumulation by reducing lipid levels through fatty acid oxidation, thus improving β -cell function [Friedman, 2002]. In turn, viable β -cells secrete insulin which promotes both leptin biosynthesis and secretion by adipocytes. In summary, leptin promotes insulin sensitivity in all peripheral tissues. The theory behind this axis is that an accumulation of fatty acids in adipose tissue causes an increase in leptin levels, which protects β -cells from deleterious effects associated with lipid accumulation [Rabe *et al.*, 2008; Kieffer and Habener, 2000].

The link between leptin and insulin resistance was made evident in studies done on leptin deficient (*ob/ob*) mice [Friedman, 2002]. These *ob/ob* mice exhibited immune defects, decreased body temperature, infertility, hyperphagia, obesity, decreased energy expenditure, diabetes and hypercortisolemia which were associated with abnormalities in metabolic and/or endocrine pathways. Leptin treatment reversed all

adverse effects by decreasing the intracellular lipid content in all tissues [*Friedman, 2002*].

The concept of leptin resistance arose from obese individuals who portrayed high leptin levels without suppressing appetite or inducing weight loss [*Kahn and Flier, 2000*]. This occurs as a result of lipid accumulation within target tissues limiting insulin action, thus causing insulin resistance [*Friedman, 2002*]. As a result pancreatic β -cells would produce more insulin to compensate for the resistance leading to hyperinsulinemia. Hyperinsulinemia is thought to promote leptin synthesis and secretion via adipose tissue, further enhancing leptin resistance.

Adiponectin is an anti-inflammatory cytokine abundantly secreted by adipose tissue. As a result of adipocytes being the main source of adiponectin, one would expect serum adiponectin levels to rise with an increase in body weight but this is not the case [*Fantuzzi, 2005*]. Studies have shown adiponectin levels to be reduced in obese and insulin resistant subjects, while individuals suffering from anorexia expressed high levels of adiponectin [*Fantuzzi, 2005*]. In obese subjects, the administration of adiponectin improved whole body insulin sensitivity by targeting various tissues. In the skeletal muscle, adiponectin increases glucose uptake and fatty acid oxidation, while reducing hepatic glucose production [*Rabe et al., 2008*].

These insulin sensitizing effects are initiated when adiponectin binds to specific adiponectin receptors, adiponectin receptor1 (AdipoR1) and adiponectin receptor 2 (AdipoR2). The expression of AdipoR1 and AdipoR2 has been shown to be linked to the

activation of AMPK and peroxisome proliferator-activated receptor- α (PPAR- α), respectively [Rabe *et al.*, 2008]. Yamauchi *et al.* reported that a disruption in AdipoR1 and AdipoR2 correlated with an increase in insulin resistance as a result of a reduction in adiponectin binding and action [Yamauchi *et al.*, 2007]. Many human studies have shown adiponectin levels to be negatively related to type 2 diabetes, obesity and insulin resistance [Rabe *et al.*, 2008]. Therefore, boosting adiponectin levels or adiponectin receptor function would be beneficial in treating all negative components associated with the establishment of T2D.

1.6.2.2.2 Cytokines

Obesity is a chronic low-grade inflammatory state that is linked to the expression of various pro-inflammatory cytokines [Fantuzzi, 2005]. Numerous studies have reported a correlation between pro-inflammatory cytokines and clinical features associated with the metabolic syndrome such as BMI and insulin resistance [Sesti, 2006]. There are many other factors which promote the expression of pro-inflammatory cytokines involved in the manifestation of obesity-induced insulin resistance. These factors include oxidative stress that is generated as a result of lipid accumulation [Styskal *et al.*, 2012]. Oxidative stress can modulate insulin action either by targeting the insulin pathway directly or by stimulating the activation of proteins involved in inflammation. In this section we will be focusing on TNF- α and IL-6.

A study done by Hotamisligil and colleagues (1993) reported that TNF- α mediates insulin resistance in obese rodent models [Hotamisligil *et al.*, 1993]. This notion was

deduced when they observed high levels of TNF- α messenger RNA being expressed by adipose tissues which were further enhanced in adipose tissue of obese and diabetic rodent models. In addition, several other studies on TNF- α -null and TNF- α receptor-null mice support this hypothesis [Chen, 2006]. TNF- α signaling can directly alter insulin action by phosphorylating specific serine residues on the insulin receptor or insulin receptor substrate 1, thus inhibiting insulin signaling, giving rise to insulin resistance [Fantuzzi, 2005]. Other mechanisms by which TNF- α induces insulin resistance is by downregulating adiponectin expression, increasing IL-6 production, stimulating lipolysis and increasing the release of free fatty acids from adipocytes [Goossens, 2008]. Despite the correlation between TNF- α and insulin resistance, TNF- α neutralizing treatments have not shown improved insulin sensitivity in diabetic patients [Fantuzzi, 2005]. Instead, these patients were exposed to an increased risk of contracting opportunistic infections.

Interleukin 6 is a multifunctional cytokine which plays an important role in a wide range of processes [Simpson *et al.*, 1997]. For this review, we will only be focusing on the link which exists between IL-6 and insulin resistance. In the presence of obesity, an overload of nutrients in adipose tissue upregulates the release of free fatty acids and pro-inflammatory cytokines; activating resident macrophages [Chen, 2006]. Activated macrophages secrete TNF- α and IL-6 which recruit additional macrophages into adipocytes [Chen, 2006]. Increased levels of circulating TNF- α and IL-6 cause insulin resistance in adipocytes through several distinct mechanisms which include c-Jun N-terminal kinase 1 (JNK1) mediated serine phosphorylation and inactivation of IRS-1, I κ B

kinase (IKK)-mediated nuclear factor- κ B (NF- κ B) activation, and induction of suppressor of cytokine signaling 3 (SOCS-3) [Chen, 2006; Rabe et al., 2008]. Studies have shown IL-6 levels to be high in obese and insulin resistant subjects with an increase in hepatic glucose production [Rabe et al., 2008]. A reduction in weight has positive effects on insulin sensitivity amongst others, by lowering IL-6 expression.

1.6.2.3 Treatment: Type 2 diabetes

Type 2 diabetes is a disease which attracts a lot of attention and is constantly researched for the establishment of new anti-diabetic drugs which are safe and effective. Interest in the treatment of T2D patients arose as a result of these patients not being able to control glycaemia sufficiently in the presence of anti-diabetic drugs [Bailey, 1999]. Below is a flow chart indicating various treatment options available as well as a table containing a list of anti-diabetic drugs with their specific functions [Bailey, 1999; Shah et al., 2013; Doyle and Egan, 2007].

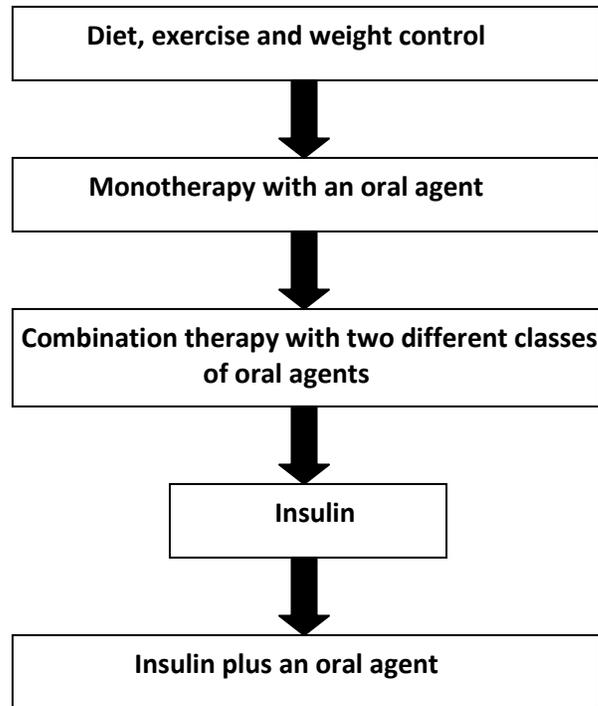


Figure 10: Type 2 diabetic treatment system [Bailey, 1999]

Initially, T2D patients undergo lifestyle changes (increased physical activity, healthier eating patterns and a reduction in weight). This option serves to be ineffective in approximately four-fifths of newly diagnosed patients causing them to move to the next treatment level [Bailey, 1999]. If a patient cannot maintain glycaemic control after being treated with an oral agent, be that in a combination of two oral agents or a single oral agent, insulin therapy would be required.

Table 3: List of anti-diabetic drugs [Bailey, 1999; Shah et al, 2013; Doyle and Egan, 2007].

Agent	Action
Sulfonylureas eg. Glipizide	Increase insulin secretion by stimulating β -cells
Biguanides eg. Metformin	Improve insulin sensitivity in peripheral tissue
Alpha-glucoside inhibitors eg. Acarbose	Slow carbohydrate digestion
Thiazolidinediones eg. Avandia	Improve insulin sensitivity in peripheral tissue
Glucagon-like peptide-1 (GLP-1) analogues	Increase insulin synthesis and secretion by stimulating β -cells
Dipeptidyl peptidase 4 (DPP4) inhibitors	Inhibit the breakdown of GLP-1
Insulin	Decrease hepatic glucose output and increase peripheral glucose utilization
Bariatric surgery (Weight loss surgery)	Alters the digestive system by restricting food intake. Mainly focusing on the stomach and/or intestine.

Thiazolidinedione is one of the anti-diabetic drugs removed from the market as a result of this drug promoting liver toxicity [Tolman and Chandramouli, 2003]

1.7 Skeletal muscle metabolism

Skeletal muscle is the most abundant tissue within the human body and is accountable for 40 percent of body weight [Andres et al., 1956]. This tissue demands energy in the form of adenosine triphosphate (ATP) for contractile purposes and to sustain proper cellular function. Skeletal muscle utilize numerous substrates depending on their exposure to specific stressors. At rest, skeletal muscle prefers using fatty acids as their main energy source which is followed by glucose [El-Bacha et al., 2010]. During hypoxia or intense physical activity for a long duration of time, skeletal muscle switches from fatty acid metabolism to glucose metabolism [Kessler and Friedman, 1998; El-Bacha et al., 2010]. A switch in metabolism stems from the fact that glucose oxidation results in a higher production of energy (in the form of high energy phosphate bonds) when oxygen

is scarce compared to fatty acid oxidation [Kessler and Friedman, 1998]. In this section of the review we will focus on fatty acid and glucose metabolism.

As stated above, fatty acids are the main source of energy in skeletal muscle during rest and mild-intensity exercise. As exercise intensity increases, glucose oxidation suppresses fatty acid oxidation [El-Bacha et al., 2010].

1.7.1 Fatty acid metabolism

The amount of fatty acids taken up by myocytes depends on the rate of lipolysis within adipose tissue. The lipolytic activity of adipocytes is enhanced when the body is exposed to metabolic stresses such as fasting or diabetes. These states ultimately lead to the accumulation of free fatty acids in blood, thus increasing fatty acid uptake and oxidation in peripheral tissue. Under normal conditions, insulin stimulates the clearance of circulating free fatty acids by inhibiting lipolysis and fatty acid β -oxidation.

Circulating free fatty acids enter the cell via fatty acid transporters or diffusion [Koonen et al., 2005]. Once inside the cell, fatty acids are surrounded by acyl-CoA synthetase, a cytosolic enzyme which adds an acyl-CoA group to fatty acids [Finn and Dice, 2006]. Long fatty acyl-CoA molecules are able to cross the outer mitochondrial membrane but not the inner membrane, therefore, requiring a transportation or shuttling mechanism [Jaswal et al., 2011]. Carnitine palmitoyl transferase I mediates the movement of fatty acids into the mitochondrial matrix by replacing the CoA group with carnitine. Inside the matrix, fatty acyl carnitine is converted back into fatty acyl CoA, with the help of carnitine palmitoyl transferase II, which is localized on the inner mitochondrial

membrane [Jaswal *et al.*, 2011]. Carnitine released from the fatty acyl molecule moves back to the outer mitochondrial membrane where it is reused.

In the mitochondrial matrix fatty acyl CoA undergoes β -oxidation. Mitochondrial β -oxidation is a step-wise reaction that repetitively breaks down long chain fatty acyl CoA to form acetyl CoA molecules. Acetyl CoA undergoes a whole range of reactions eventually producing ATP in the Krebs cycle. The number of acetyl-CoA molecules produced depends on the fatty acid carbon length being oxidized. The first step of fatty acid oxidation is the dehydrogenation of fatty acyl CoA [Kim and Battaile, 2002]. In this reaction, acyl-CoA dehydrogenase (ACD) catalyzes the conversion of fatty acyl CoA to trans 2 enoyl CoA and removes protons from fatty acyl CoA which are transferred to a FAD cofactor, yielding FADH₂ [Schultz, 2008]. There are four ACDs involved in fatty acid β -oxidation, namely, short chain (SCAD), medium-chain (MCAD), long-chain (LCAD) and very long chain (VLCAD) ACD [Kim and Battaile, 2002]. The acyl chain length of each ACD reflects their preferred substrate specificity, ensuring complete degradation of all fatty acids [Lea *et al.*, 2000; Schultz, 2008]. The second step in the β -oxidation cycle is a hydration reaction [Kim and Battaile, 2002]. The enzyme enoyl CoA hydratase together with a water molecule (H₂O) hydrates 2-trans-enoyl CoA to form L-3-hydroxy acyl COA [Schultz, 2008]. The third step is a dehydrogenation reaction catalyzed by L-3-hydroxy acyl COA dehydrogenase, with nicotinamide adenine dinucleotide (NAD⁺) as the cofactor [Kim and Battaile, 2002]. The hydroxyl group of L-3-hydroxy acyl CoA is oxidized to a keto group, producing 3- ketoacyl CoA and NADH [Kim and Battaile, 2002]. In the final step of β -oxidation, 3-ketoacyl CoA is cleaved by

thiolase to yield acetyl CoA and an acyl CoA molecule [Schultz, 2008]. Every cycle of β -oxidation sequentially shortens fatty acyl CoA molecules by two carbon atoms, producing one acetyl CoA as well as NADH and FADH₂ [Jaswal et al., 2011; Fillmore and Lopaschuk, 2013]. Acetyl CoA can either enter the Krebs cycle or be used in the production of ketone bodies [Frick et al., 2008].

1.7.2 Glucose metabolism

Insulin stimulated GLUT 4 translocation to the plasma membrane promotes glucose uptake, leading to the accumulation of glucose molecules within the cell [Huang et al., 2005]. Glucose transporter 4 is the insulin-responsive protein responsible for the transport of glucose across the plasma membrane into myocytes. Glucose uptake is triggered by insulin which is stimulated by high blood glucose levels. Insulin promotes GLUT 4 translocation to the membrane by activating PKB/Akt [Wang et al., 1999]. In diabetic patients, glucose uptake in skeletal muscle is drastically reduced as a result of insulin resistance or insufficient insulin secretion [Wilcox, 2005].

Glucose accumulation in skeletal muscle can either be stored as glycogen or enter glycolysis. The glycolytic pathway consists of three stages: the priming, splitting and energy producing stage (figure 11) [Berg et al., 2002; Pelicano et al., 2006]. During the priming stage, glucose is converted to fructose 1,6 bisphosphate via three reactions, catalyzed by various enzymes [Berg et al., 2002; Pelicano et al., 2006]. These reactions trap and destabilize glucose by the addition of two phosphoryl groups from ATP molecules [Berg et al., 2002]. In the splitting stage, fructose 1,6 bisphosphate is readily cleaved into two three-carbon fragments by aldolase, producing glyceraldehyde 3-

phosphate (GAP) and dihydroxyacetone phosphate (DHAP) [*Berg et al., 2002*]. GAP and DHAP are isomers, which are easily converted to the one or other with the help of triosephosphate isomerase [*Berg et al., 2002; Pelicano et al., 2006*]. In the presence of glycolysis, DHAP would be converted to GAP, rendering two molecules of GAP for every glucose molecule broken down [*Berg et al., 2002*]. The energy producing stage is a five step reaction converting two GAP molecules to pyruvate [*Berg et al., 2002; Pelicano et al., 2006*]. This stage produces four ATPs from a series of oxidative phosphorylation reactions [*Berg et al., 2002*]. The final glycolytic product, pyruvate, can either be converted to lactate or acetyl CoA via oxidative decarboxylation [*Berg et al., 2002*].

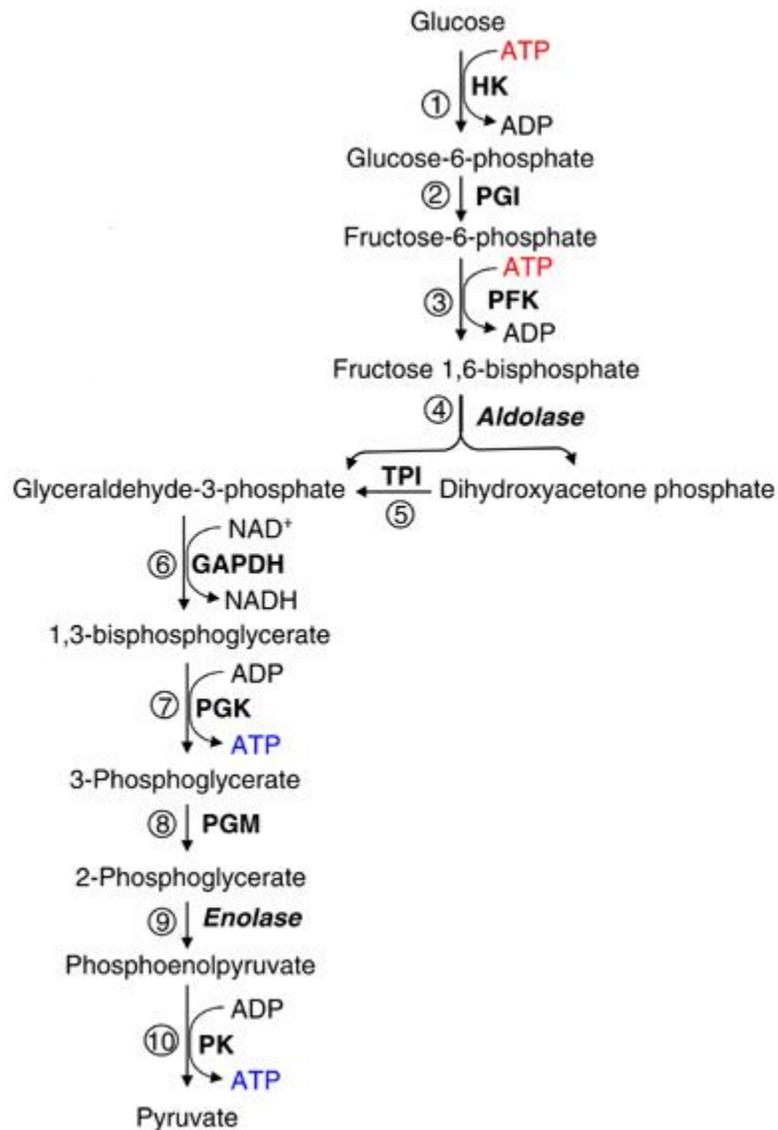


Figure 11: glycolytic pathway [Pelicano et al., 2006]

Each glucose molecule produces two pyruvate molecules via the stimulation of several enzymes. In step 1, glucose is phosphorylated to glucose-6-phosphate with the help of hexokinase. Glycogen can serve as a supplementary source of glucose-6-phosphate in the presence of metabolic stress, such as fasting. Every enzyme in the glycolytic pathway is tightly regulated. ATP, adenosine triphosphate; ADP, adenosine diphosphate; PK, Pyruvate kinase; PGM, phospho glycerate mutase; PGK, phospho glycerate kinase; GAPDH, glyceraldehyde phosphate dehydrogenase; TPI, triose phosphate; PFK, phosphofructokinase; PGI, phosphohexose isomerase; HK, hexokinase.

1.7.3 Oxidation of Acetyl CoA

The production of acetyl CoA from the oxidative cleavage of fatty acids or the decarboxylation of pyruvate, made available by glycolysis, is completely oxidized by the Krebs cycle and electron transport chain [Zubay, 2000].

1.7.3.1 Krebs cycle

The Krebs cycle, also known as the tricarboxylic acid or citric acid cycle, is the final catabolic pathway for the oxidation of fuel molecules and occupies a central position in metabolism [Koubaa et al, 2013; Hagopian et al., 2004]. The cycle is composed of a variety of enzymes and metabolites, which are important for the progression of many other pathways; therefore, its position is of utmost significance [Hagopian et al., 2004]. Acetyl CoA is the key substrate initiating the cyclic process. The Krebs cycle is an eight step reaction which generates carbon dioxide molecules and reducing equivalents, NADH and FADH₂ [Hagopian et al., 2004]. The cycle begins when a two carbon acetyl CoA molecule binds to oxaloacetate to form a six carbon molecule, citrate. The addition of a single water molecule is essential for the release of the CoA subunit from acetyl CoA. Citrate undergoes two consecutive decarboxylation events and several oxidative reactions, ultimately generating the four carbon compound, oxaloacetate [Zubay, 2000]. Each molecule of acetyl CoA produces two carbon dioxide molecules, one FADH₂ molecule and three molecules of NADH (+H⁺).

1.7.3.2 Electron transport chain

Reducing equivalents produced by β -oxidation and the Krebs cycle transport energy to the mitochondrial electron transport chain (ETC) [Rossignol and Frye, 2012]. The ETC is the final respiratory stage, consisting of a series of oxidative phosphorylation reactions for ATP generation [Rossignol and Frye, 2012]. This energy is produced by five multimeric complexes located on the inner mitochondrial membrane [Bayir and Kagan, 2008]. Once NADH and FADH₂ molecules release hydrogen atoms to complexes I and II, respectively, an electrochemical gradient is established. Electrons discharged by reducing equivalents moves down the chain of protein complexes with the help of two electron carriers, co-enzyme Q10 and cytochrome C [Rossignol and Frye, 2012]. In complexes I, III and IV, electrons give up some of their energy to extrude protons out of the mitochondrial matrix into the intermembrane space via active transport [Bayir and Kagan, 2008]. The movement of electrons generates an alkaline matrix and an acidic intermembrane space [Bayir and Kagan, 2008]. Electrons finally reach complex IV, where they bind to protons and an oxygen molecule to form water [Swerdlow, 2012]. Protons re-enter the matrix through complex V, a non-ETC enzyme, providing enough energy to synthesize ATP from ADP, which is utilized as energy by the rest of the body [Bayir and Kagan, 2008; Swerdlow, 2012].

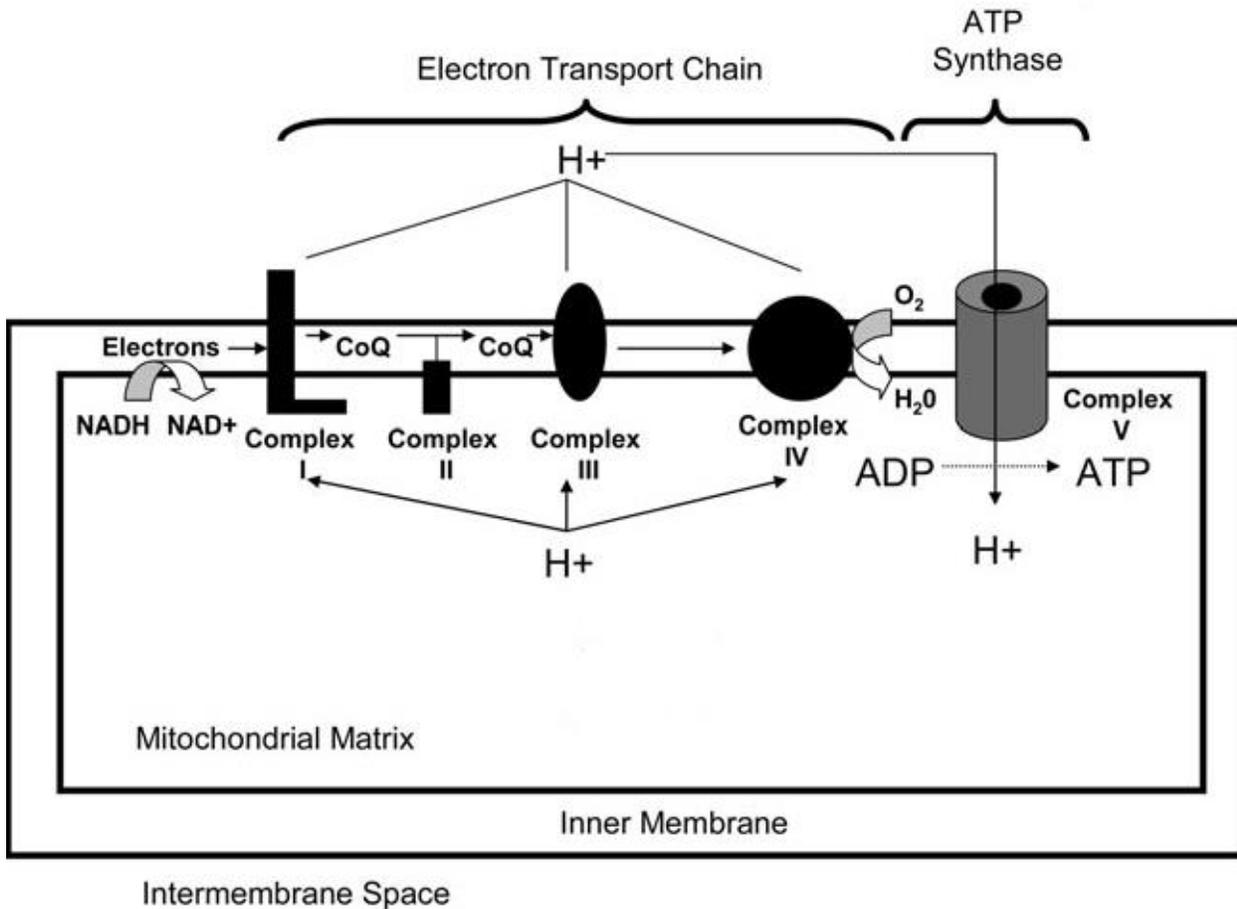


Figure 12: Electron transport chain [Swerdlow, 2012]

NADH and FADH₂ molecules donate electrons to the electron transport chain. The movement of electrons down the chain produces enough energy to transport protons across the mitochondrial membrane into the intermembrane space. Electrons bind to oxygen, the final electron receptor, and forms water. Protons move back into the mitochondrial matrix through ATP synthase, producing ATP. FADH₂, flavin adenine dinucleotide; NADH, nicotinamide adenine dinucleotide; CoQ, Coenzyme Q (ubiquinone); ADP, Adenosine diphosphate; ATP, Adenosine triphosphate; H⁺, proton.

CHAPTER 2

Materials and Methods

2.1. *Animal Care*

Male Wistar rats were used in this study. These rats were age and weight matched at the onset of the experiment. All animals were housed at the University of Stellenbosch Central Research Facility, which provided a simulated environment of the animals' natural habitat, exposing them to a temperature controlled room (22 °C - 24 °C) and a 12-hour light/dark cycle. Animals had free access to water and food for the duration of the experiment. All animals were fed normal rat chow, unless otherwise stated/specified, and specific groups in both diabetic models were treated with Buchu water. The project was approved by the Ethics committee of the University of Stellenbosch (Faculty of Health Sciences – protocol number SU-ACUM11-00003) and conforms to the principals revised in the South African National Standard for the Care and Use of Animals for Scientific Purposes (South African Bureau of Standards, SANS 10386, 2008).

2.2. *The administration procedure of Buchu (Agathosma)*

1.3L of the watery extract of Buchu, provided by the company Cape Kingdom, was mixed with tap water to make up a volume of 5000 ml. This mixture replaced water given to specific animal groups. The dosage of Buchu was calculated based on the

average weight of a 70 kg individual ingesting 350 ml of undiluted Buchu water/day. Equivalent surface area dose expressed as mg/kg was used for calculation of the dosage using the assumptions and constants of the paper by Freireich et al. 1996. For the initial estimations, it was assumed that a rat will drink 30ml of water per day.

2.3. Animal models

2.3.1. Streptozotocin-induced type 1 diabetes rat model

In this model, a total of 50 animals were used and the experiment lasted for a period of 14 weeks. Animals weighing approximately 250 g were randomly divided into two main groups: a control (n=20) and diabetic (n=30) group. All animals allocated to the diabetic group were subjected to a once off intra-peritoneal STZ injection of 40 mg/kg (dissolved in a citrate buffer; pH 4.5) and blood glucose levels were determined after 24 hours, and at 1 week. After 1 week, animals that have been injected with STZ whose blood glucose levels normalized spontaneously, were excluded from the experimental group. The main purpose for using STZ at this concentration was to induce a type 1 diabetic model, ensuring ablation of approximately 50% of pancreatic beta cells. This brings about high blood glucose levels ranging between 10 and 20 mmol/L but the animals still produce endogenous insulin. A commercial glucometer was used to monitor blood glucose levels by collecting blood from a single tail prick. For a diagrammatic interpretation of the divisional state of all animals involved in the STZ- induced type 1 diabetic model refer to figure 13. The food and water intake of the animals were monitored for a period of a week and 20 days, respectively, 3 weeks after the start of the experiment. The amount

of food consumed was measured by the following equation: Food consumed per day (g)
= food given (g) – food remaining in cage (g).

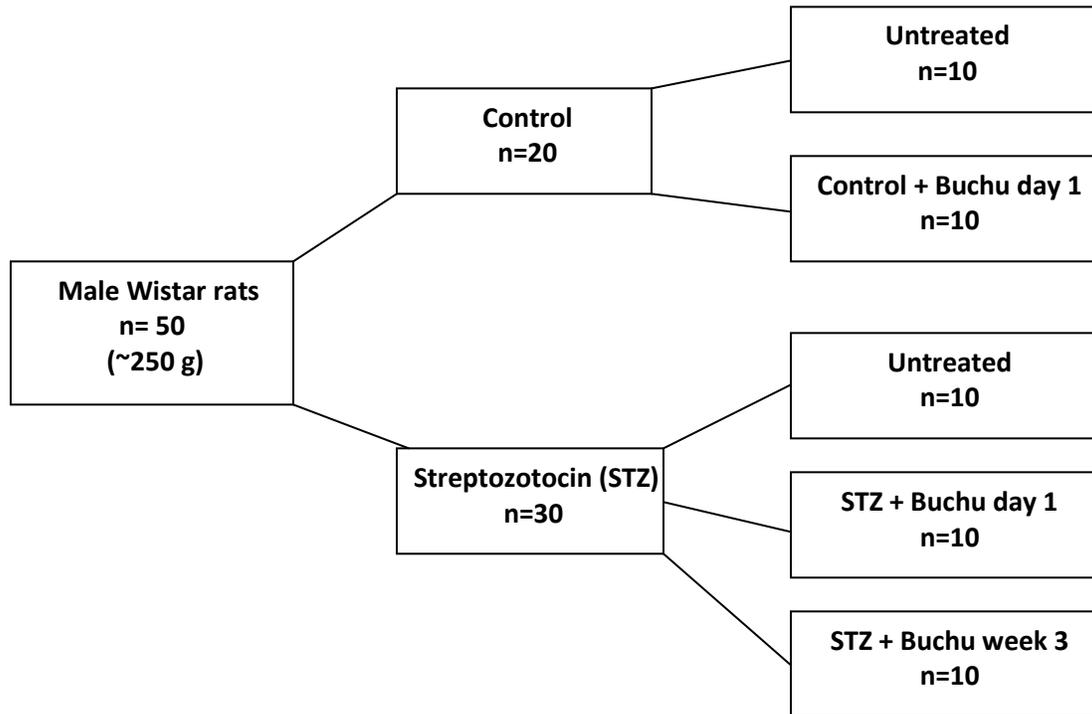


Figure 13: Schematic representation of the division of type 1 diabetic animals

Buchu day 1: The administration of Buchu water from the start of the experiment

Buchu week 3: The administration of Buchu water 3 weeks after the initiation of the experiment

Intraperitoneal glucose tolerance tests (IPGTT) were performed on all animals to determine the effect of Buchu water on whole-body insulin sensitivity. This was done by fasting animals overnight a week (week 13) prior to the time of sacrifice. Animals were anaesthetized (< 50 mg/kg pentobarbital) and fasting blood (1 ml) was collected from

the carotid artery for the determination of insulin levels (Coat-A-Count®) Radioimmunoassay (RIA) kit and baseline blood glucose levels determined. The animals were then injected intraperitoneally with a 50% sucrose solution, to give a final concentration 1 mg/kg. Blood glucose levels were monitored over a period of 120 minutes using a glucometer; blood was collected via a tail prick. At week 14, all the animals were anaesthetized with a 160 mg/kg overdose of a sodium pentobarbital intraperitoneal (IP) injection. When all sensation was absent, as indicated by no response on a foot pinch, the animals were sacrificed via exsanguination. Body weight was determined and IP fat dissected out and weighed. Blood samples were collected for biochemical determinations. Figure 14 illustrates on the experimental time frame and biochemical analysis.

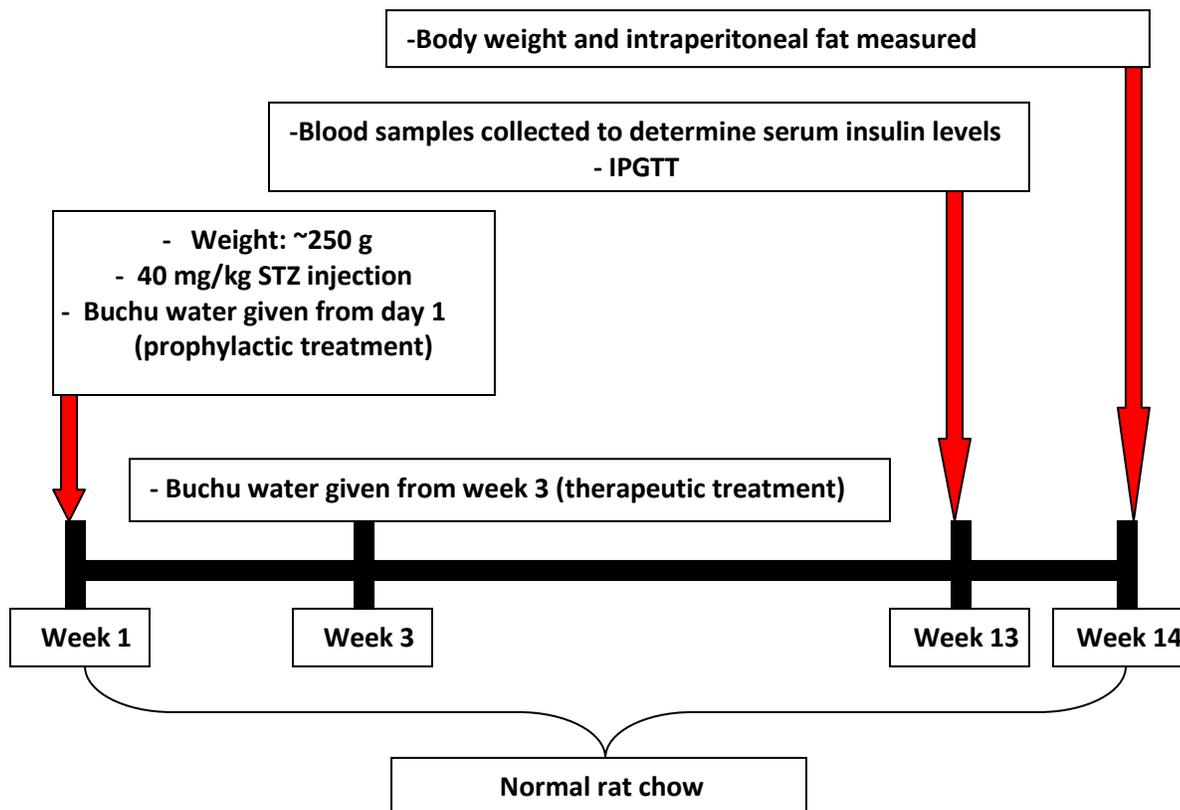
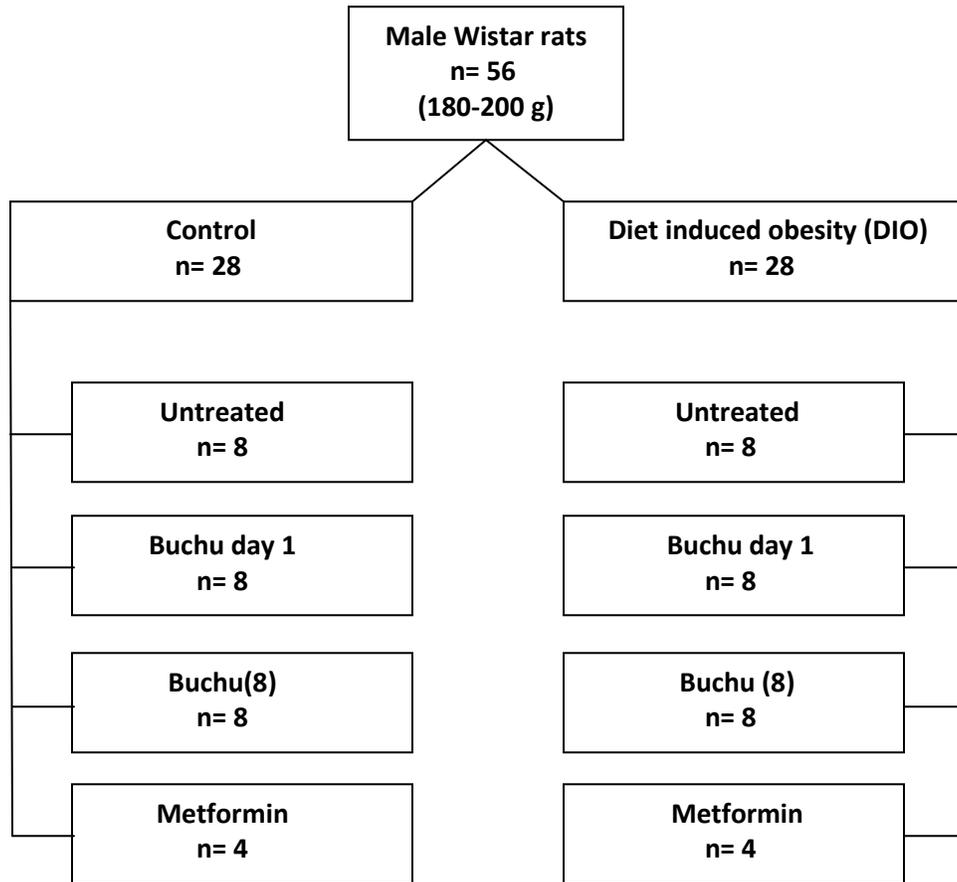


Figure 14: The time frame of the type 1 diabetic model

2.3.2. Diet-induced obese insulin resistant rat model

In this model a total of 56 animals were used and the experiment was conducted for a period of 16 weeks. Animals weighing between 180 and 200 g were divided into two groups: a control (n=28) and diabetic (n=28) group. The food and water intake of the animals were monitored on a daily basis. Animals were put on a high caloric diet containing normal rat chow supplemented with sucrose and condensed milk for a period of 16 weeks. Treatment with Buchu water commenced either at the onset of the change in diet or from week 8 after onset. A group of animals were treated with metformin as a positive control. Animals in this model were divided according to Figure 15.



Buchu(1) : Buchu treatment from day 1
Buchu (8) : Buchu treatment from 8 weeks
Metformin : Metformin treatment from 8 weeks

Figure 15: Schematic representation of the division of type 2 diabetic animals

Metformin treatment was given at a dose of 250 mg/kg/day by oral gavage. At week 15, IPGTTs' (procedure described above) were performed on all animals to test whole-body insulin sensitivity. A milliliter of fasting blood was collected for insulin determination. After recuperating for one week (week 16), animals were sacrificed via a 160 mg/kg sodium pentobarbital IP injection. Body weight and IP fat were measured and, blood samples were collected for biochemical analysis. Both soleus muscles were removed for determination of insulin sensitivity. The pancreas was removed and stored in liquid nitrogen for further biochemical analysis.

2.4. Western blot analysis

2.4.1. Sample preparation

Total proteins are extracted from pancreatic tissue of diet induced obese insulin resistant animals followed by Western blot analysis used to investigate the expression of certain proteins of interest. The extraction of proteins was made possible by means of a lysis buffer which consisted of a wide variety of reagents which inhibited phosphatases and enzymes involved in proteolysis. Table 4 summarizes the list of the reagents, their stock concentrations and purpose.

Table 4: List of reagents for the lysis buffer

Stock reagents	Content	Function
200 mM Tris-HCL	20 mM	Buffer with a pH of 7.5
10 mM EGTA	1 mM	A chelating agent that acts as a metallo-protease inhibitor
100 mM EDTA	1 mM	Metallo-protease inhibitor
1M NaCl	150 mM	Maintain ionic strength of medium
1 mM β -glycerophosphate	1 mM	Non-specific phosphatase inhibitor
2.5 mM tetrasodiumpyrophosphate	2.5 mM	Non-specific phosphatase inhibitor
100 mM sodium orthovanadate	1 mM	An inhibitor of protein tyrosine phosphatases, alkaline phosphatases and various ATPases
100% Triton-X100	1%	Non-ionic detergent for solubilizing membrane proteins
10 μ g/ml Leupeptin	10 μ g/ml	Protease inhibitor
10 μ g/ml Aprotinin	10 μ g/ml	Serine protease inhibitor
100 mM phenylmethyl sulfonyl fluoride	50 μ g/ml	Irreversible serine protease inhibitor

A Polytron PT10 homogenizer was used to homogenize tissue in 0.9 ml of ice cold lysis buffer. These samples were homogenized twice for 5 seconds on setting 4. The homogenized samples were placed on ice for 15 minutes, allowing the buffer to fully compromise cellular integrity. Once the samples have settled, the homogenates were transferred to specifically marked eppendorf tubes and centrifuged (14 000 rpm for 10 minutes), at 4°C. After centrifugation, the pellet was discarded and the supernatant transferred to a new eppendorf tube.

2.4.2. Bradford protein determination assay

Aliquots of the supernatant were used to determine protein concentrations of each sample, using the Bradford assay (Bradford, 1976). Tubes were arranged in a rack according to Figure 16.

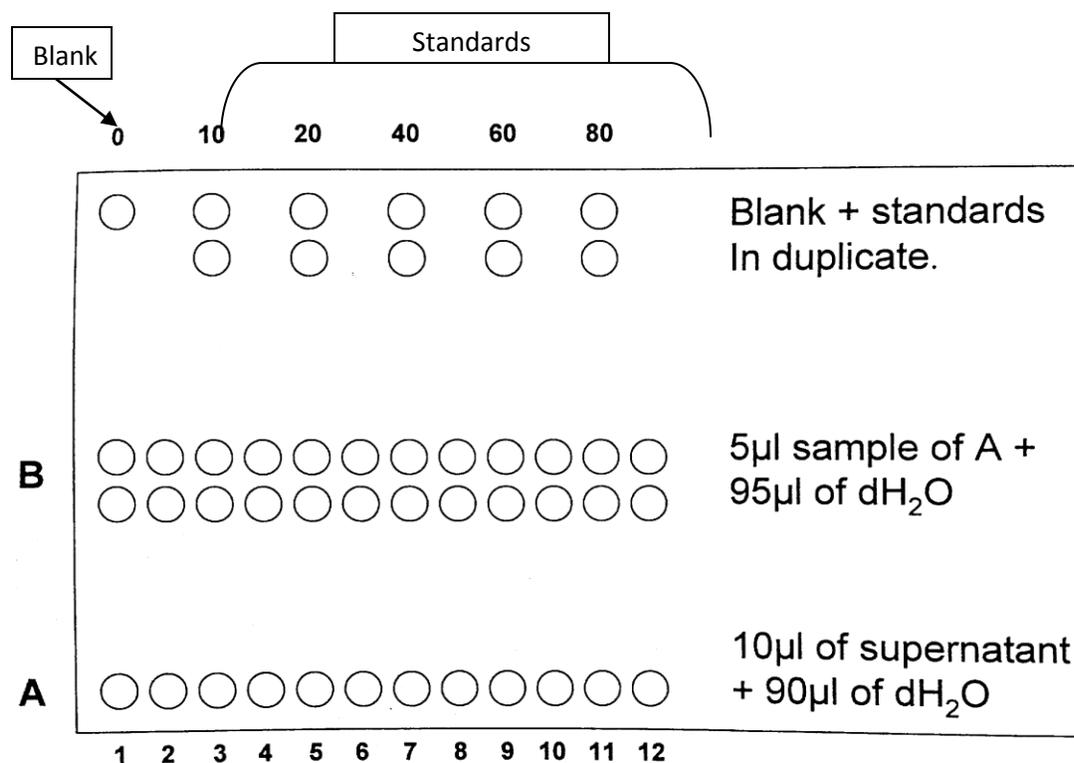


Figure 16: Tube arrangement for the Bradford protein assay

The supernatant obtained as described in section 2.4.1. was pipetted into tubes within line up **A**. A 1:10 dilution of the supernatant was made by the addition of dH₂O to dilute the detergent which would otherwise interfere with the assay. In line up **B** 5 µl of each diluted sample was pipetted accordingly, with the addition of 95 µl of H₂O. The blank tube contained 100 µl of H₂O. Diluted bovine serum albumin (BSA) of a known concentration, containing protein concentrations of 1-20 µg, were aliquoted into protein

determination tubes. The volume pipetted into each was (μl): 10, 20, 40, 60 and 80, followed by the addition of dH_2O , making a final volume of 100 μl . A 1:5 dilution of Bradford reagent (900 μl) was added to the blank, standards and tubes in line up **B**. Samples were left for 15 minutes to allow proper colour development then read spectrophotometrically at an absorbance wavelength of 595 nm. The protein content in each sample was calculated from the standard curve established by BSA. Samples were diluted with lysis buffer to render equal protein concentrations, and then diluted with Laemmli sample buffer. Aliquots were boiled for 5 minutes and stored at -80°C until required.

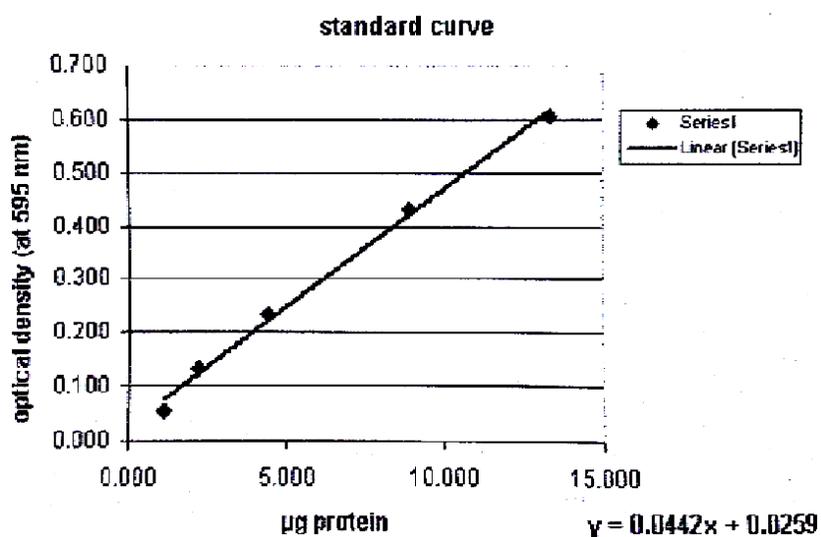


Figure 17: Standard curve generated from the optical density readings

2.4.3. Protein separation by gel electrophoresis

Stored aliquots were boiled for 5 minutes, then microfuged for 2 minutes at 15 000 rpm to remove particulate matter. The polyacrylamide gel was prepared and samples were loaded (Table 5 shows the proteins used, their concentrations and percentage polyacrylamide gel utilized). A protein ladder was included to serve as a marker to identify the molecular weight of a particular protein. These gels were then exposed to electrophoresis (SDS-PAGE) in running buffer containing 50 mM Tris, 384 mM glycine and 1% SDS, ensuring proper protein separation. A BioRad Mini Protean III system was utilized. Proteins were separated using two different settings: 1st run at 100 V, 200 mA for 10 minutes and 2nd run at 200 V, 200 mA for 50 minutes.

2.4.4. Transfer of proteins to a membrane

Running buffer was discarded and proteins were transferred to a polyvinylidene fluoride (PVDF) membrane (Immobilon™ P, Millipore). The transfer of proteins to the PVDF membrane was accomplished in transfer buffer (25 mM Tris, 192 mM glycine and 20% methanol) at an electrical current of 200V for 1 hour. At the end of the transfer period, the membrane was soaked in methanol for 30 seconds and allowed to air dry. Membranes were stained with Ponçeau Red reversible stain to visualize the transfer of proteins as well as equal loading.

2.4.5. Blocking non-specific sites with milk

Ponçeau Red was then rinsed off with TBS-tween (Tris-buffered saline containing 0.1% Tween-20) repeatedly followed by the membranes being blocked, non-specifically, with

5% TBS-tween fat-free milk (5% fat-free milk in Tris-buffered saline- 0.1% Tween 20) for 2 hours at room temperature. After the blocking period, membranes were rinsed with TBS-tween and then probed with primary antibodies directed against specific proteins (Table 5) overnight at 4°C.

2.4.6. Immunodetection of proteins

After being incubated overnight at 4°C, the membranes were washed with TBS-tween to remove any unbound primary antibody and incubated with secondary antibody (anti-rabbit immunoglobulin G, Horseradish-peroxidase conjugated secondary antibody) for one hour at room temperature. This enables the secondary antibody to bind to the already bound primary antibody. At the end of the incubation period, membranes were rinsed with TBS-tween and then covered with an enhanced chemiluminescence (ECL) detection reagent for 1 minute. The horseradish-peroxidase coupled to the secondary antibody in conjunction with the ECL chemiluminescent agent facilitates protein visualization by producing luminescence in proportion to the amount of protein present. Light emission was captured on radiography film and analyzed by laser scanning densitometry and suitable software (Silk Scientific Inc, USA).

In all instances, the mean of the total pixels of the bands generated by controls on a specific blot was set as 1 and used to normalize data as a ratio to controls.

Table 5: Western blot analysis

Protein	Molecular weight	Protein loaded	Polyacrylamide stacking gel	Separation gel	Blocking solution dilutions	Primary antibody dilutions	Secondary antibody dilutions
MafA	36 -47kDA	60µg	4%	10%	5% milk in TBS/Tween	20µl/5ml in TBS-Tween	3µl/20ml in 1% milk
Pdx-1	42kDA	60µg	4%	10%	5% milk in TBS/Tween	5µl/5ml in TBS-Tween	5µl/20ml in 2.5% milk

2.5. 2-Deoxy-D-3[H] glucose (2DG) uptake by soleus muscle

The soleus muscles were rapidly isolated and sliced into five thin longitudinal strips. Each strip was placed into a specific flat-bottomed incubation tube containing incubation medium and various other reagents (Table 6). The tubes were gassed with 5% carbon dioxide and 95% oxygen. The incubation medium consisted of: 6 mM KCl, 1 mM Na₂HPO₄, 0.2 mM NaH₂PO₄, 1.4 mM MgSO₄, 128 mM NaCl, 10 mM HEPES, 1.25 mM CaCl₂, 1 mM D-glucose, 2 mM pyruvate and 1% fatty acid free BSA (pH 7.4). The incubation tubes were placed in a shaking waterbath at a temperature of 37°C for 15 minutes. After 15 minutes, insulin was added from a 10 µM stock solution to specific tubes to render 1 nM, 10 nM and 100 nM insulin, and incubated for a further 30 minutes in the waterbath. Soleus muscle strips were incubated with 1.5 µCi/ml [³H]2DG, in a final concentration of 1.8 µM deoxyglucose, for an additional 30 minutes. To stop the glucose uptake reaction, phloretin from a stock solution (final concentration of 400 µM) was added to all tubes which were then removed from the waterbath. Phloretin is a compound which inhibits glucose uptake by inhibiting glucose transporters. Muscle

strips were washed 5 times with incubation medium, transferred to eppendorf tubes filled with 500 μl of 1M NaOH. The muscle was fully dissolved in the NaOH solution when placed into a 70°C waterbath for 1 hour. Finally, 500 μl of distilled water was added to each sample, resulting in a final NaOH concentration of 0.5 M. At this stage radioactivity within the tissue as well as the protein content could be determined. An aliquot of the homogeneous solution (200 μl) of each sample was mixed with 2 ml of scintillation fluid in counting vials which were stored overnight in the dark before being counted by a beta-scintillation counter.

The protein content of each sample was determined by the Lowry method [Lowry *et al.*, 1951] using a standard curve of known BSA concentrations and a 0.5 M NaOH blank. The protein assay was performed in duplicate with each tube containing 50 μl of a blank, standard or sample. Once the blank, standards and samples were loaded; 1 ml of reaction buffer was pipetted into each tube which was then vortexed, and allowed to react for 10 minutes at room temperature. The reaction buffer consisted of a 2% Na_2CO_3 , 1% $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ and 2% NaK-tartrate mixture. After 10 minutes, 100 μl Folin Ceioalceus reagent (Merck) (1:2 dilution with distilled water) was added, vortexed and left to stand for 30 minutes for full colour development. Absorbance was read at 750 nm against the blank. At the end of the assay a standard curve was drawn and unknown concentrations were determined.

Table 6: Composition of each tube in the glucose uptake protocol

	Basal (μl) (Tube 1)	Phloretin (μl) (Tube 2)	1nM Insulin (μl) (Tube 3)	10nM Insulin (μl) (Tube 4)	100nM Insulin (μl) (Tube 5)
Soleus muscle	Strip	Strip	Strip	Strip	Strip
Incubation medium	675	675	600	600	600
Phloretin	0	50	0	0	0
Insulin	0	0	75	75	75
2-deoxy-D-³H glucose	25	25	25	25	25
Phloretin (block)	50	0	50	50	50
Total (μl)	750	750	750	750	750

All samples were analysed in duplicate, a total of 10 tubes per assay.

2.6. Biochemical analysis

2.6.1. Blood sample collection

Blood samples were allowed to stand on ice for 30 - 60 minutes to permit clotting. Samples were then subjected to centrifugation for 10 minutes at 14 000 rpm at 4°C. The serum was then pipetted into eppendorf tubes and stored at -80°C for further biochemical analysis.

2.6.2. Serum insulin determination

The Coat-A-Count Insulin assay (Count-A-Count® Insulin Diagnostics Corporation; LA, USA) is a solid phase ¹²⁵I radioimmunoassay designed to quantitatively measure insulin in serum. In this assay ¹²⁵I-labeled insulin and insulin in the serum samples compete for sites on insulin-specific antibodies. These antibodies are immobilized to the wall of polypropylene tubes and competition can be terminated by simply decanting the supernatant. This step isolates the antibody bound fraction of radio-labelled insulin.

Components of the entire procedure were brought to room temperature (15-28°C), prior to the onset of the assay. All samples were analyzed in duplicate. Plain uncoated polypropylene tubes (12 x 75 mm) were labeled for total counts (T) and non-specific binding (NSB), respectively. Fourteen insulin-antibody coated tubes were labeled for standards and additional tubes were labeled for samples. The addition of insulin calibrators and iodinated insulin (¹²⁵I insulin) are depicted below.

Table 7: A representation of calibrators

Calibrator	Approximate $\mu\text{IU/mL}$ 1 st IRP [66/304]
A	0
B	5
C	15
D	50
E	100
F	200
G	350

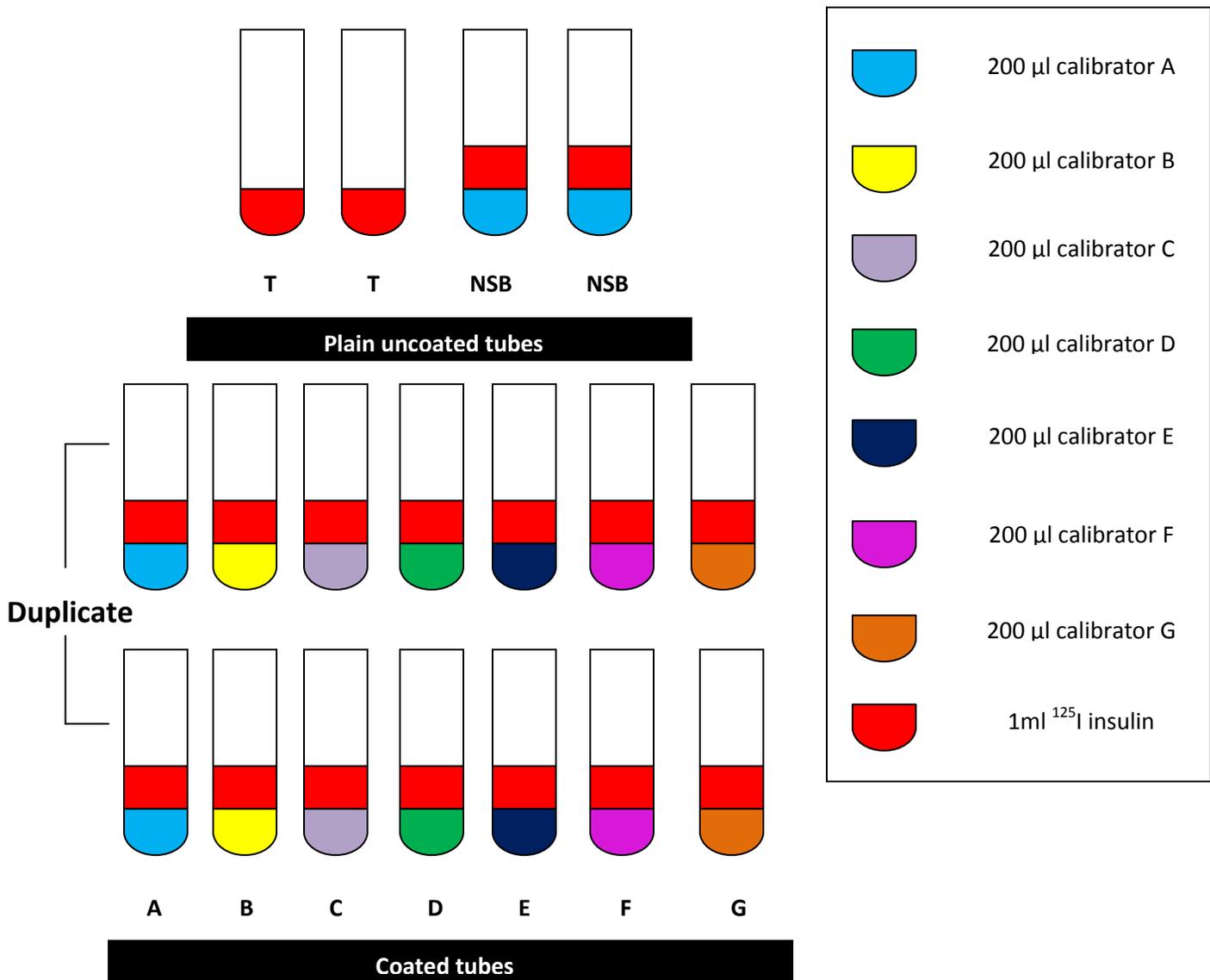


Figure 18: Diagrammatic layout of tube labelling and preparation

200 µl of standards or samples in duplicate, were pipetted into the bottom of the reaction tubes. Here after, the radio-labelled insulin was added, and the tubes were incubated for 18-24 hours at room temperature. After the elapsed time, samples were decanted thoroughly using a decanting rack, then struck repeatedly on absorbent paper to remove excess residue. Tubes were carefully dried to remove all traces of unbound radioactive material. Radioactivity of each tube was counted for 1 minute in a gamma counter. The standard curve (Figure 18: an example of a standard curve) formed a displacement curve of radio activity and the sample values were calculated from this.

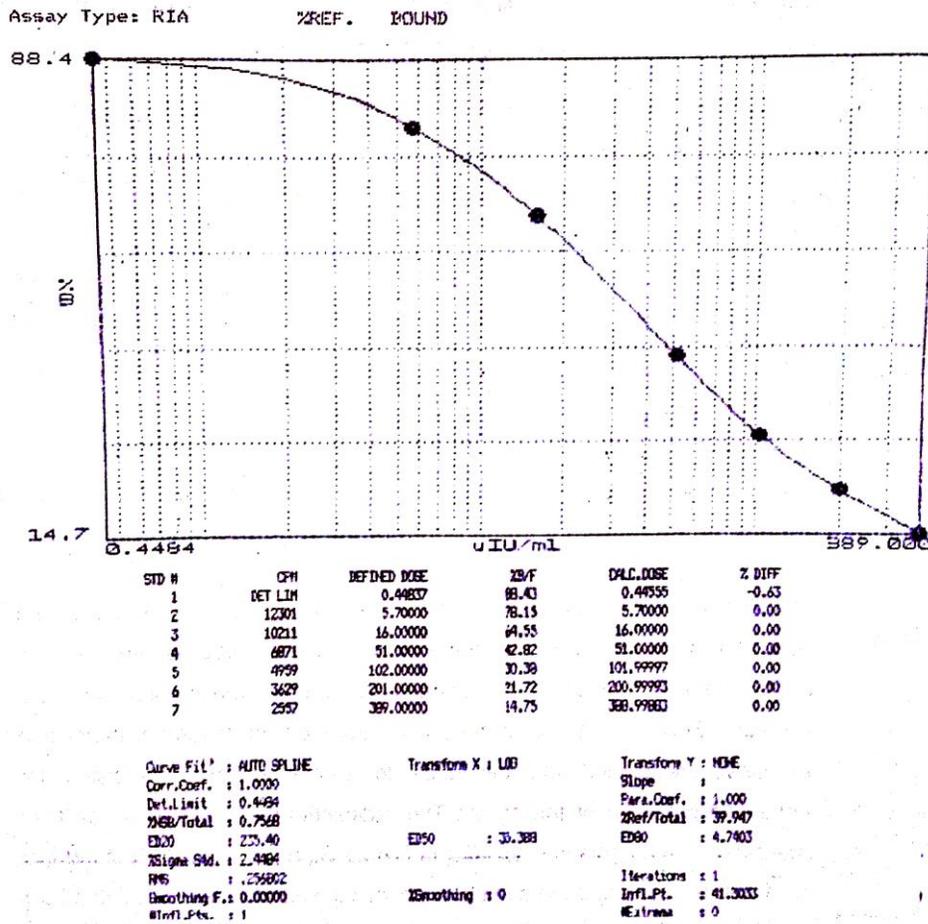


Figure 19: Standard curve generated by the gamma counter

2.6.3. Enzyme Linked Immunosorbent Assay (ELISA)

Previously stored serum was utilized to determine C-peptide levels of each sample using an Elisa kit (Abcam Ltd, Cambridge, UK). In this assay, C-peptide molecules in the sample bind to the wells of a microtiter plate, coated with a pre-titered amount of anchor antibodies. Binding of a second biotinylated antibody to insulin occur simultaneously. The microtiter plate consists of 96 wells which were divided into blanks, standards, quality control (QC) and samples as seen in Table 8.

Table 8: Microtiter plate arrangement

	1	2	3	4	5	6	7	8	9	10	11	12
A	Blank	200 pM	QC1	Etc.								
B	Blank	200 pM	QC1	Etc.								
C	25 pM	400 pM	QC2									
D	25 pM	400 pM	QC2									
E	50 pM	800 pM	Sample 1									
F	50 pM	800 pM	Sample 1									
G	100 pM	1,600 pM	Sample 2									
H	100 pM	1,600 pM	Sample 2									

This assay was done in duplicate

Washing procedure: Wells were washed three times with 300 µl of diluted (1x) wash buffer and then decanted. The remaining wash buffer was removed by inverting the plate and tapping it on absorbent towels several times.

Matrix solution (20 µl) was added to blank, standard and quality control wells. Followed by 30 µl of assay buffer to blank and sample wells. Standard and QC wells were filled with 10 µl of assay buffer. Rat insulin standards (20 µl) were added to specific wells in ascending order while 20 µl of QC1 and 20 µl of QC2 were added to wells labeled QC. The remaining wells were filled with 20 µl of the unknown sample. 50 µl of the antibody solution mixture (a mixture which consists of capture and detection antibody at a 1:1 ratio) were added to each well. The plate was then covered with a plate sealer and incubated for 2 hours at room temperature on an orbital microtiter plate shaker (400-500 rpm). After 2 hours, the plate sealer was removed and the solution decanted from the plate. Residual solution was removed using a tapping motion and wells were washed according to the washing procedure. Enzyme solution (100 µl) was added to each well, the plate covered and incubated on the shaker at room temperature for 30 minutes. Once the time has elapsed, the sealer was removed, the solution decanted and the wells washed according to the washing procedure. Substrate solution (100 µl) was added to each well, the plate sealed and placed on a shaker for approximately 20 minutes. In standard wells, a blue pigment was observed with intensities proportional to increases in insulin concentrations. Stop solution (100 µl) was added to each well, and then shaken by hand to ensure complete mixing of the solution. At this stage, the blue pigment turned into a yellow colour. The intensity of the yellow colour was read at an absorbance value of 450 nm and 590 nm in a plate reader and the two readings subtracted from each other. The standard curve (Figure 20: an example of a standard curve) obtained was used to quantitatively determine the concentration of C-peptides in experimental serum samples.

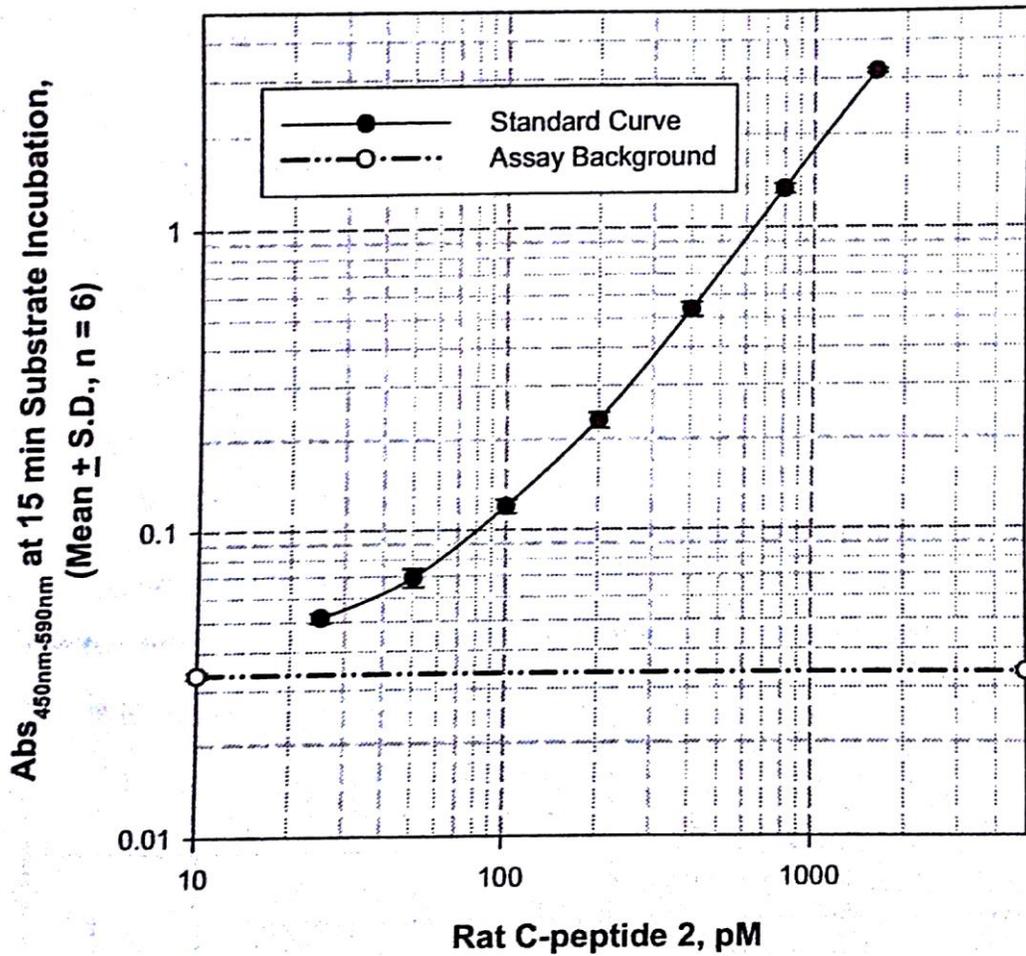


Figure 20: A graph of a typical standard curve

2.7. Statistical Analysis

Statistical analysis of data was performed using GraphPad Prism 5. All values are expressed as the mean \pm standard error of the mean (SEM). For multiple comparisons, the ANOVA (two-way when appropriate) followed by the Bonferroni post-hoc test was applied. A p-value of less than 0.05 ($p < 0.05$) was considered as statistically significant.

CHAPTER 3

Results

3.1. Type 1 Diabetes

The T1D model (STZ) was induced by using streptozotocin, a glucose moiety which is easily transported into pancreatic β -cells via GLUT 2 carrier proteins [Wei *et al.*, 2003; Motyl and McCabe, 2009]. Streptozotocin exerts its toxic effects by damaging DNA, eventually, leading to β -cell dysfunction, hypoinsulinemia and hyperglycemia; all characteristics associated with diabetes [Motyl and McCabe, 2009]. Refer back to Figure 14 for an illustration of the experimental procedure.

3.1.1. Biometric parameters

3.1.1.1. Food and water/Buchu consumption

On the first day of STZ administration; control and STZ animals were divided into their respective groups and treated with Buchu water at the start of the experiment (day 1) and three weeks after the initiation of the experiment (Buchu week 3). Each group contained 10 animals, 5 per cage. Animals that spontaneously normalized were excluded from the study. Food and water/Buchu water consumption were monitored for a period of 1 week and 20 days, respectively, 3 weeks after the start of the experiment. When comparing each cage, no significance was observed between any of the groups when inspecting food and water/Buchu water consumption (Figure 21 and Figure 22). However, a decrease in food consumption in STZ and control treated animals were

observed. This could be as a result of Buchu water having effects on the satiety centre thus reducing appetite. The bitter taste of Buchu water could have contributed to the reduced levels of Buchu water consumption seen in STZ and control animals.

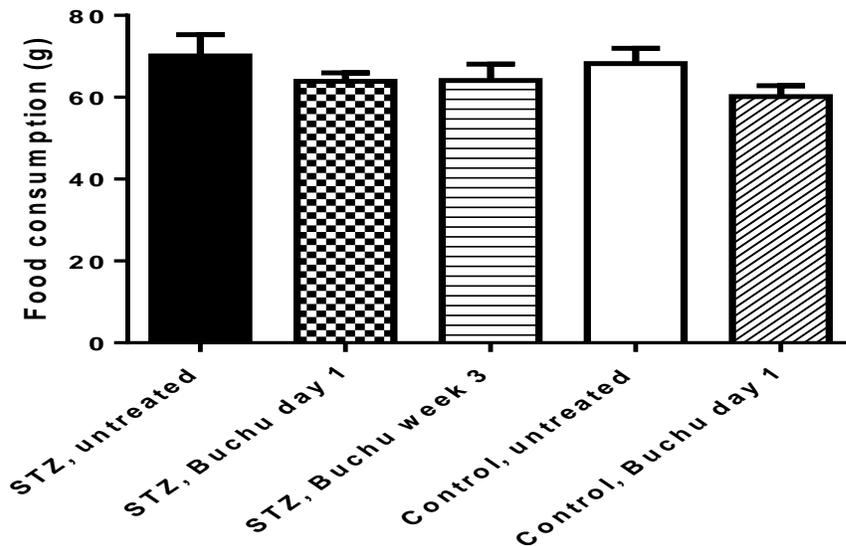


Figure 21: Food consumed by control and STZ animals, from week 3. Displayed is food consumption measured in grams (g) of streptozotocin (STZ) and control animals. The data is presented as a mean \pm SEM. (n=10/group)

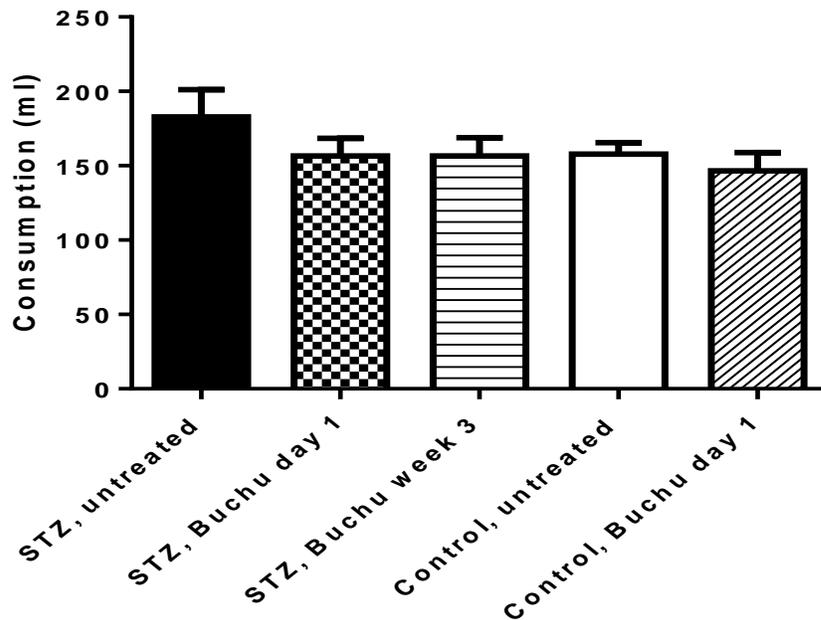


Figure 22: Water/Buchu water consumed by control and STZ animals, from week 3. Displayed is water/Buchu water consumption measured in millilitres (ml) of streptozotocin (STZ) and control animals. The data is presented as a mean \pm SEM. (n=10/group)

3.1.1.2. Body weight and intra-peritoneal fat mass

After 14 weeks of feeding, animals were anaesthetized and sacrificed. At this time point, their body weight and intra-peritoneal fat mass was determined. Measurements of each animal in their respective groups were recorded and plotted diagrammatically. When comparing each group, significantly lower body weight was observed in the STZ treated vs control animals (284.3 ± 9.9 vs 345.4 ± 7.6 g; $p < 0.0001$) (Figure 23). This lower weight was exacerbated by Buchu water ingestion in the STZ animals (284.3 ± 9.9 vs 242.4 ± 10.9 g (day 1; $p < 0.05$) and 240.3 ± 9.0 g (week 3; $p < 0.05$) respectively.

Similarly, control animals treated with Buchu water gained less weight than untreated animals (320.7 ± 6.2 vs 345.4 ± 7.6 g; $p < 0.05$) (Figure 23)

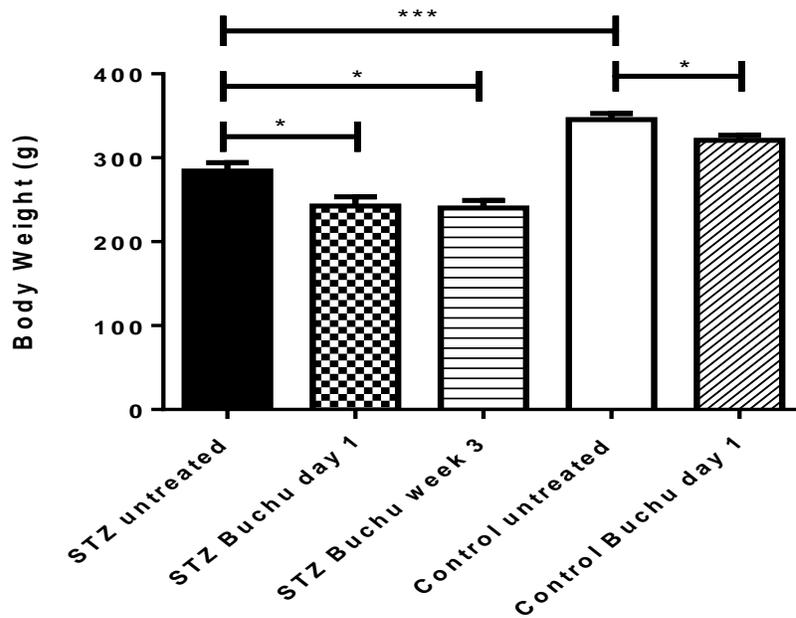


Figure 23: Body weight (BW) of control and STZ animals, with and without Buchu treatment, after 14 weeks. Displayed is body weight measured in grams (g) of streptozotocin (STZ) and control animals. The data is presented as a mean \pm SEM. (n=10/group). * $p < 0.05$, *** $p < 0.0001$

A difference in body weight was observed. However, STZ animals treated with Buchu presented with significantly more intra-peritoneal fat than the untreated animals (14.79 ± 2.5 g (day 1), 13.41 ± 1.6 g (week 3) vs 9.66 ± 0.7 g respectively).

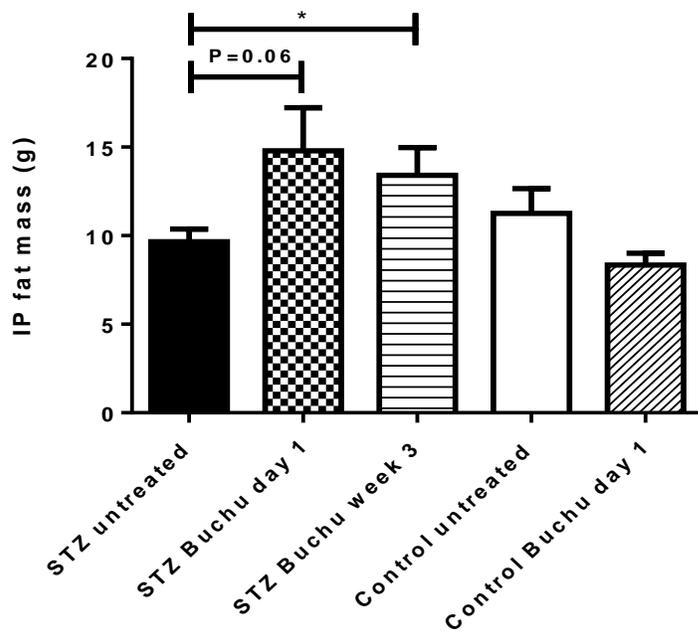


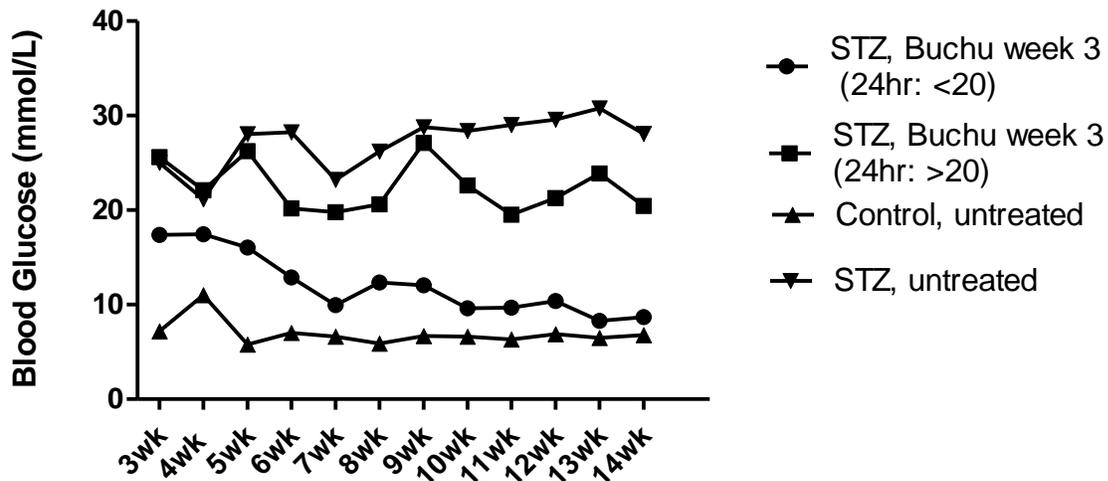
Figure 24: Intra-peritoneal (IP) fat of control and STZ animals, with and without Buchu treatment, after 14 weeks. Displayed is IP fat mass measured in grams (g) of streptozotocin (STZ) and control animals. The data is presented as a mean \pm SEM. (n=8/group). *p<0.05

3.1.2. Metabolic parameters

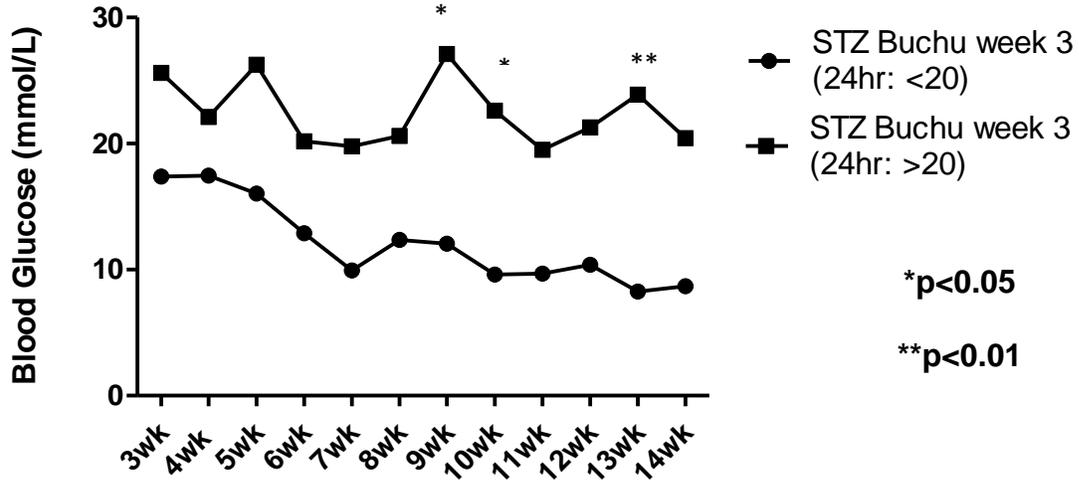
3.1.2.1. Blood Glucose Levels

On day 1, animals were divided into 4 groups containing 5 animals per cage. Respective animals were treated with STZ from day 1 and Buchu from week 3. Non-fasting blood glucose levels of all animals were determined weekly for 12 weeks, starting at week 3. A drop of blood from a tail prick was collected. After 14 weeks, blood glucose levels of STZ animals treated with Buchu were significantly lower than untreated STZ animals. A significant decline was also seen in STZ animals with blood glucose levels more than 20 mmol/L at the start of experimentation (Figure 25 (B) and (C)).

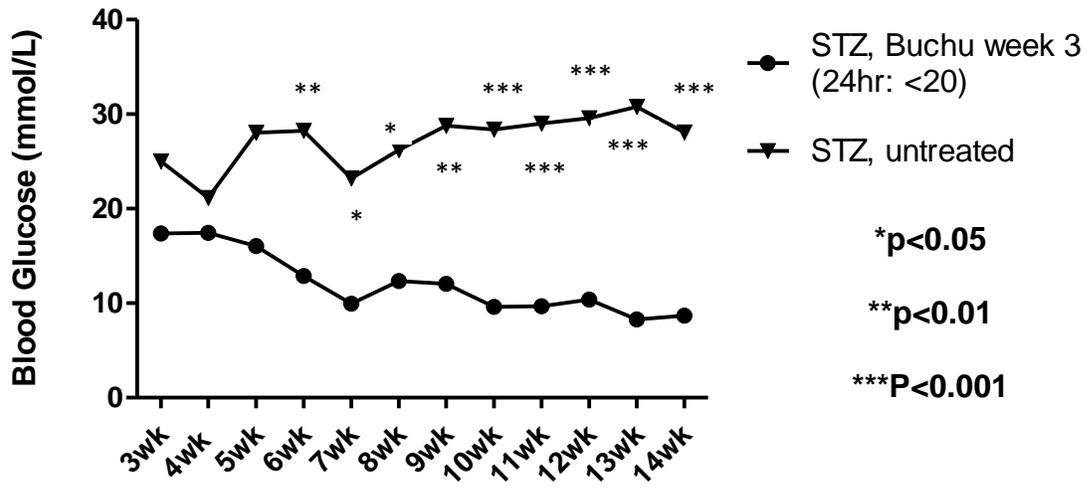
(A)



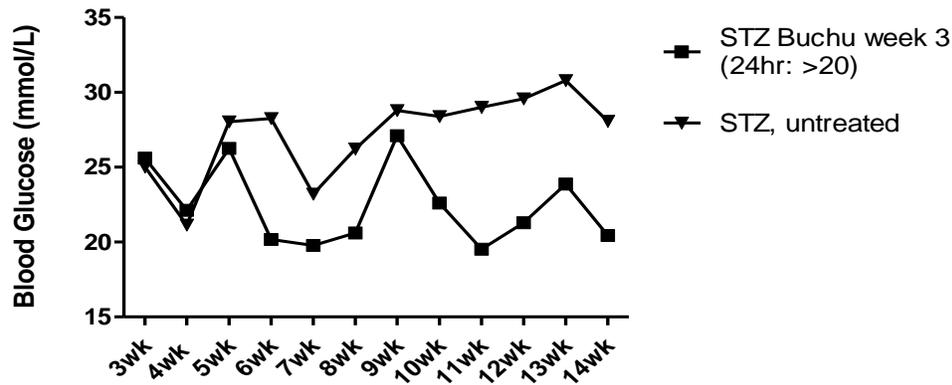
(B)



(C)



(D)



(E)

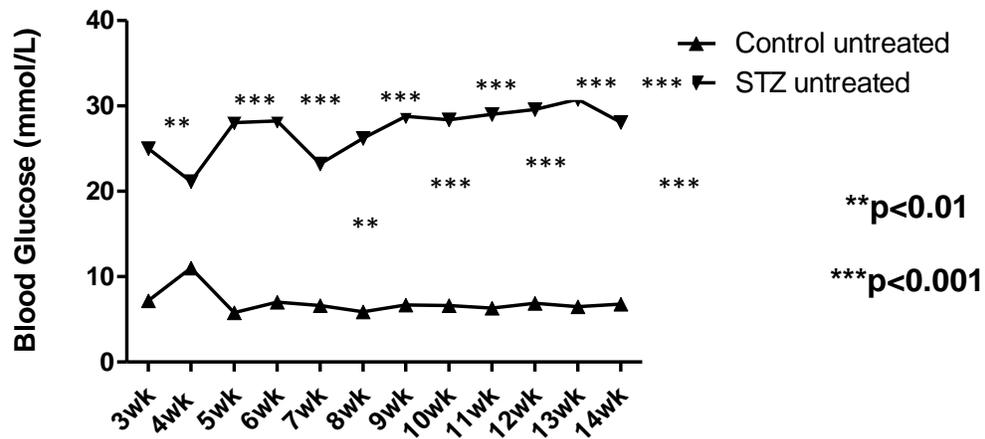
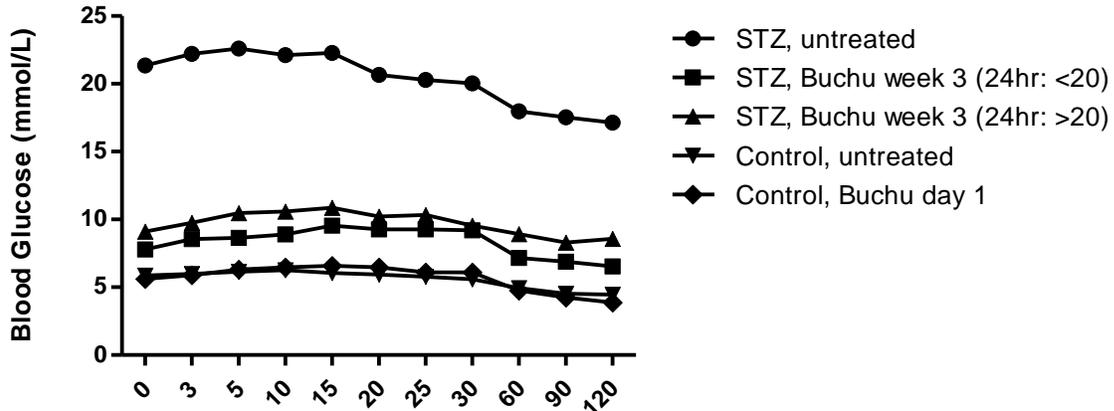


Figure 25: Weekly blood glucose levels of control and STZ animals, with and without Buchu treatment, for 12 weeks. (A) Representation of all groups, (B) Comparing treated streptozotocin animals with blood glucose levels at the onset of experimentation greater than (>20) and less than 20 mmol/L (<20), (C) Comparing treated streptozotocin animals (blood glucose levels < 20 mmol/L) with untreated streptozotocin animals, (D) Comparing untreated streptozotocin animals with treated streptozotocin animals (blood glucose levels > 20 mmol/L), and (E) Comparing untreated control and streptozotocin animals. Blood glucose levels were measured in a non-fasting state and expressed in mmol/L. The data is presented as a mean \pm SEM. (n= 5/group).

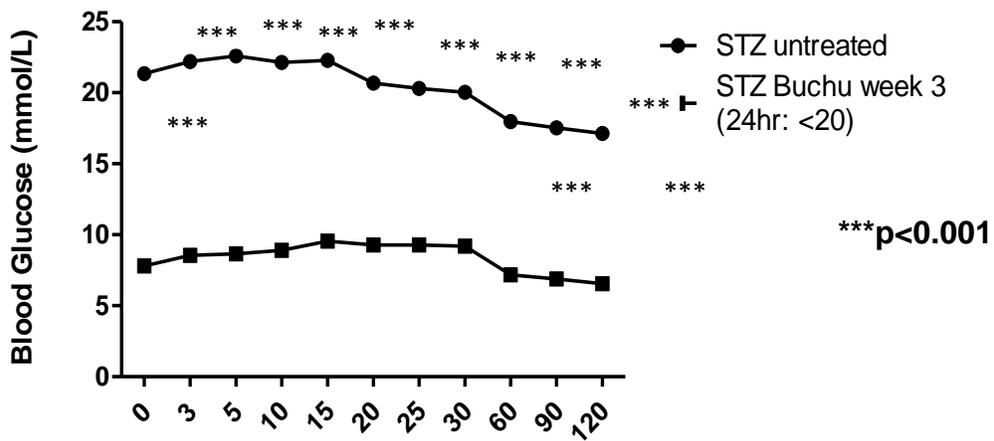
3.1.2.2. Intraperitoneal glucose tolerance test (IPGTT)

At 13 weeks, all animals following their respective treatment regimes, were fasted overnight. The next day, intraperitoneal glucose tolerance tests were performed on each animal for a period of 2 hours. When comparing treated and untreated controls, no significant difference was seen (Figure 26 (F)). However, a significant decrease (** $p < 0.001$) in blood glucose levels were observed when comparing treated and untreated streptozotocin animals (Figure 26 (B) and (C)). At the 2 hour mark, averages of each group were calculated and plotted using a bar graph (Figure 26 (G)). From this graph it is clear that the consumption of Buchu water resulted in an improved ability to handle a glucose load. (STZ= 17.1 ± 0.9 , STZ+Buchu= 7.6 ± 0.9 , control= 3.8 ± 0.1 and control+Buchu= 4.5 ± 0.1 mmol/L).

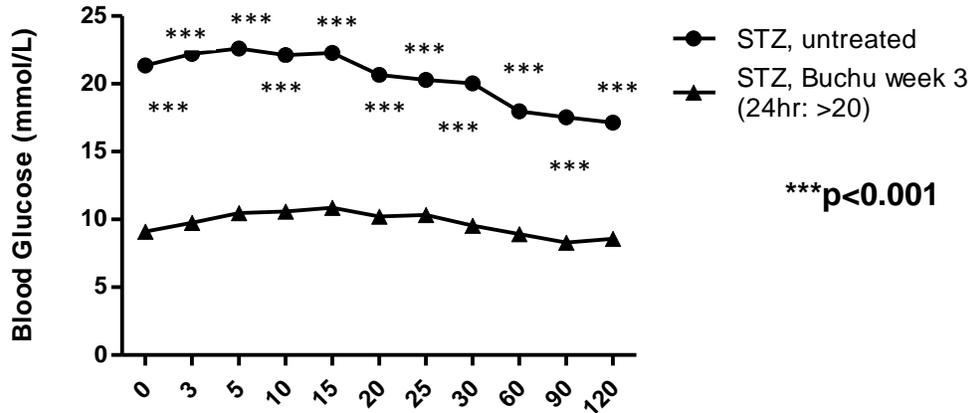
(A)



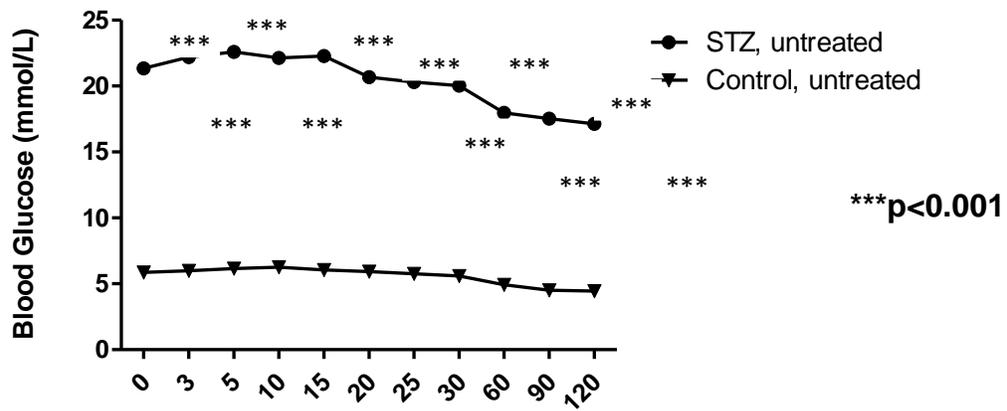
(B)



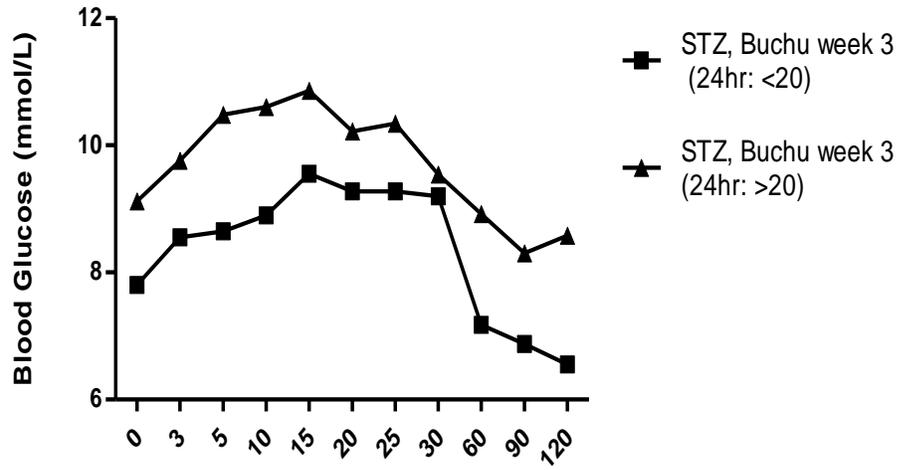
(C)



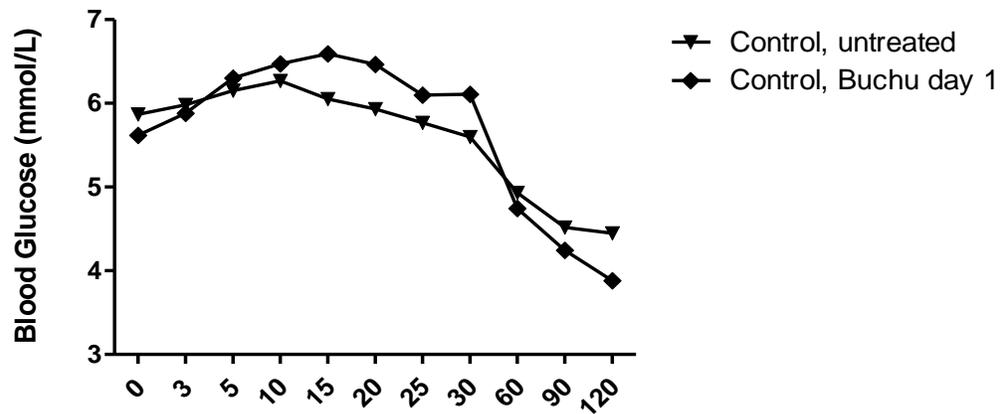
(D)



(E)



(F)



(G)

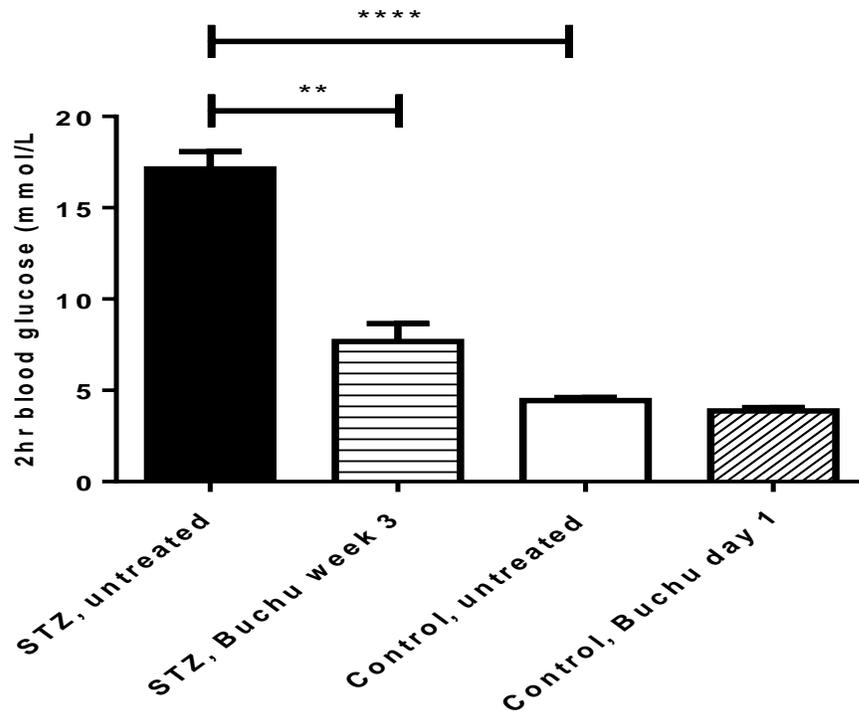


Figure 26: Intraperitoneal glucose tolerance test of control and STZ animals, with and without Buchu treatment, at 13 weeks. (A) Representation of all groups, **(B)** Comparing treated streptozotocin animals (blood glucose levels < 20 mmol/L) with untreated streptozotocin animals, **(C)** Comparing treated streptozotocin animals (blood glucose levels > 20 mmol/L) with untreated streptozotocin animals, **(D)** Comparing untreated streptozotocin and control animals, **(E)** Comparing treated streptozotocin animals with blood glucose levels greater than 20 mmol/L and less than 20 mmol/L, **(F)** Comparing treated and untreated control groups, and **(G)** IPGTT 2 hour values of control and streptozotocin groups. Blood glucose levels were measured in mmol/L. The data is presented as a mean \pm SEM. (n= 4-10/group). **P<0.01, ****P<0.0001.

3.1.2.3. Serum Insulin levels

Following 14 weeks on diet, no significant difference in fasting serum insulin levels were observed when treated and untreated STZ animals were compared, as well as between treated and untreated control animals (Figure 27).

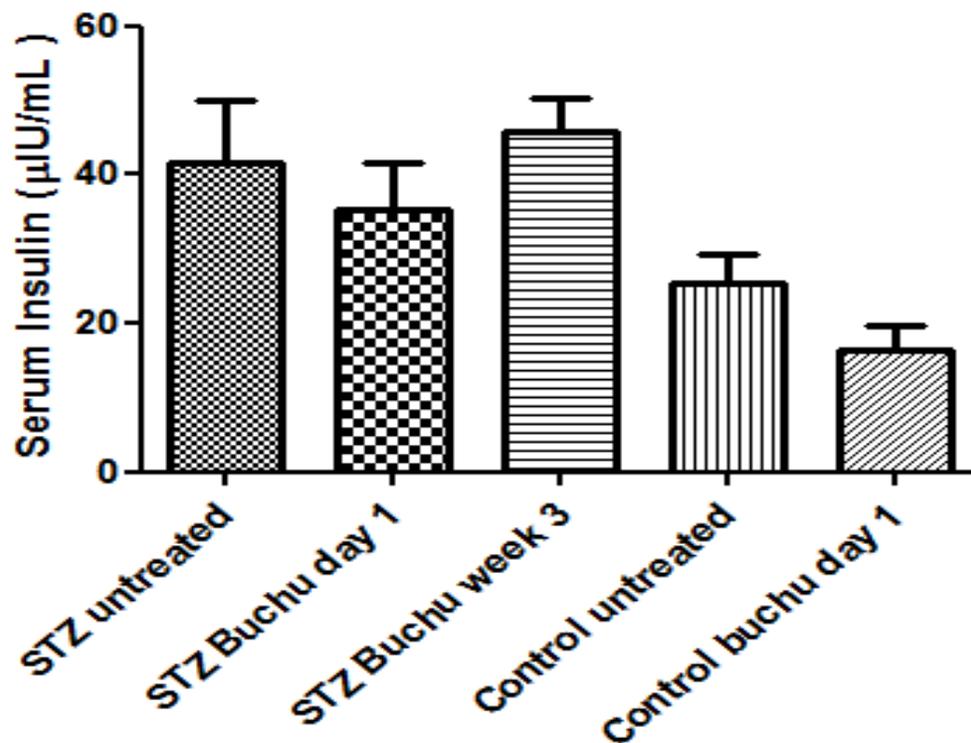


Figure 27: Fasting serum insulin levels in control and STZ animals, with and without Buchu treatment, after 14 weeks. Displayed, are fasting serum insulin levels of treated and untreated streptozotocin (STZ) and control animals. The data is presented as a mean \pm SEM. (n=5-7/group).

3.2. Type 2 Diabetes

The T2D model (DIO) was generated by feeding animals with a high caloric diet containing normal rat chow supplemented with sucrose and condensed milk for a period of 16 weeks. This diet correlates with changes seen in humans, changing from a rural to a more westernised diet. The diet induced obesity and insulin resistance. Below is a table (Table 9) indicating the macronutrient composition of diets consumed by control and DIO animals.

Table 9: Diet composition of controls versus DIO animals [Du Toit et al., 2008; Pickavance et al., 1999]

	Control	DIO
Carbohydrates	60%	65%
Protein	30%	19%
Fat	10%	16%
KJ/day	± 380KJ/day	± 575KJ/day

3.2.1. Biometric parameters

3.2.1.1. Food and water/Buchu consumption

On day 1, control and DIO animals were divided up into their respective groups, treated with Buchu at various time points. Each group contained 8 animals, 4 per cage. Food consumption was monitored for a period of 1 week while water/Buchu consumption was monitored daily for 10 days, both readings were recorded from week 8. There were no difference in the amount of food consumed (Figure 28). Furthermore, no significance was observed between any of the groups when inspecting water/Buchu water consumption (Figure 29).

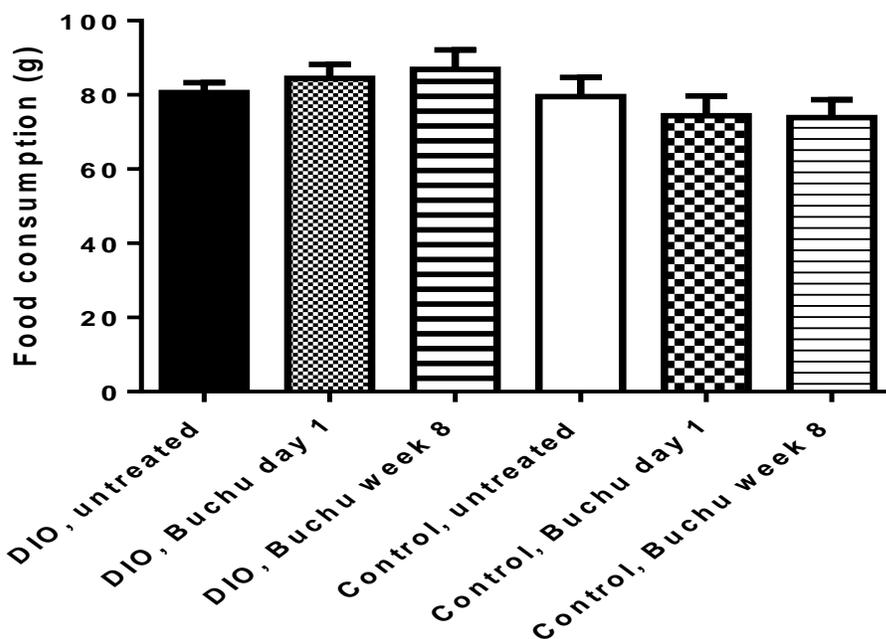


Figure 28: Food consumed by control and DIO animals, from week 8. Displayed is food consumption measured in grams (g) of diet induced obese (DIO) and control animals. The data is presented as a mean \pm SEM. (n=8/group).

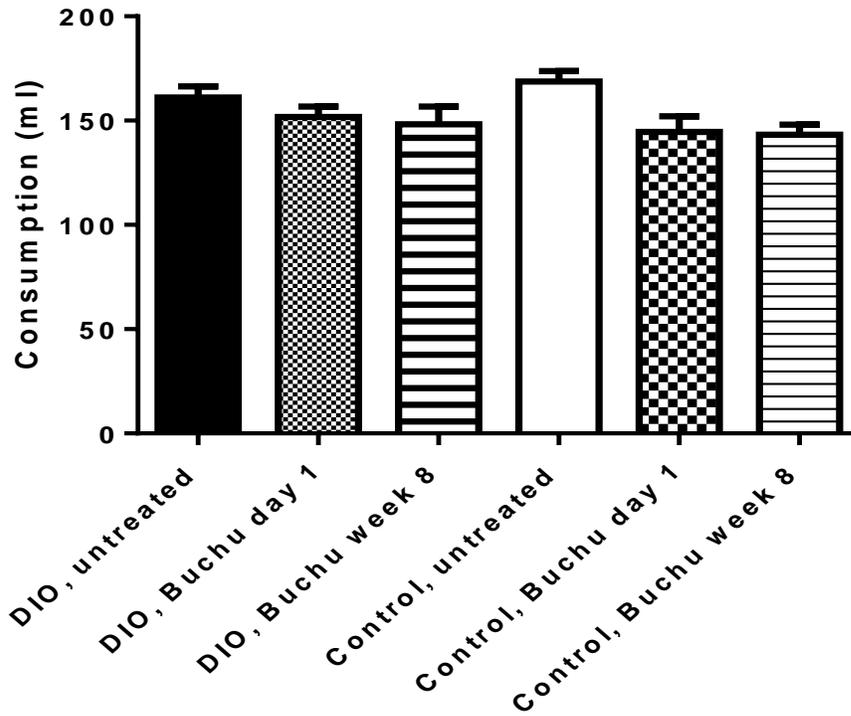


Figure 29: Water/Buchu water consumed by control and DIO animals, from week 8. Displayed is water/Buchu consumption measured in millilitres (ml) of diet induced obese (DIO) and control animals. The data is presented as a mean \pm SEM. (n=8/group)

3.2.1.2. Body weight and intra-peritoneal fat mass

After 16 weeks of feeding, animals were anaesthetized and sacrificed. Their body weight and intra-peritoneal fat mass were weighed. The DIO animals gained significantly more weight than their control counterparts (507.4 ± 12.3 vs 403.6 ± 20.1 g, $p < 0.0001$, $n=5$). When comparing each group, a significant difference in body weight was also observed between untreated and treated DIO animals (507.4 ± 12.3 vs 460.4 ± 8.4 (day 1) and 455 ± 9.7 g (wk8) $p < 0.05$, $n=5$ /group). Metformin treatment also resulted in significant less weight gain vs the untreated DIO animals (415.8 ± 14.9 vs 507.4 ± 12.3 g, $p < 0.0001$, $n=5$ /group) (Figure 30).

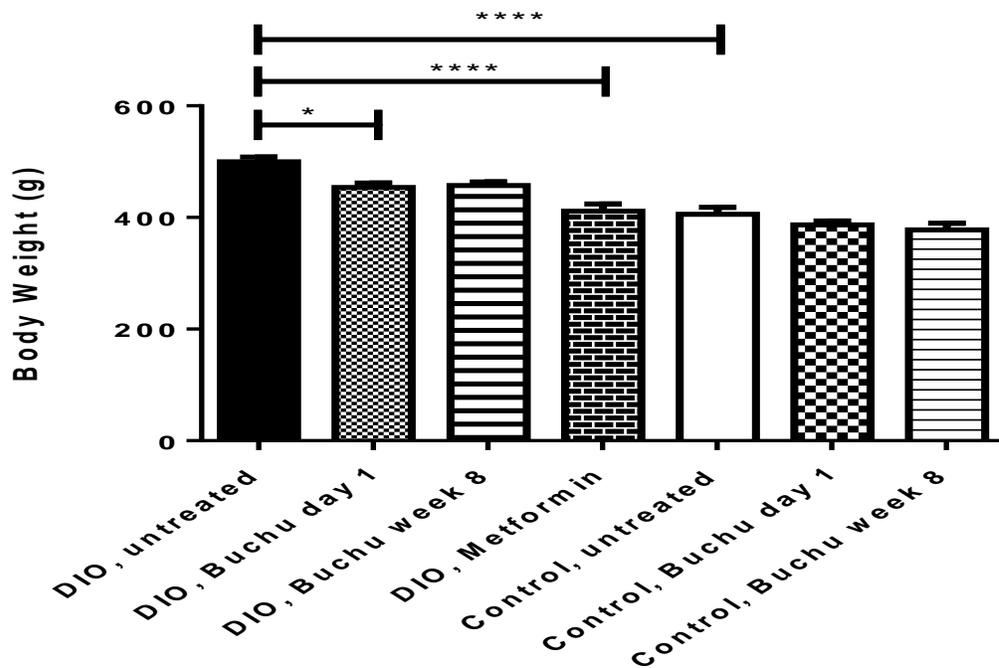


Figure 30: Body weight (BW) of control and DIO animals, with and without Buchu treatment, after 16 weeks. Displayed is body weight measured in grams (g) of diet induced obese (DIO) and control animals. The data is presented as a mean \pm SEM. ($n=5$ /group). * $p < 0.05$, **** $p < 0.0001$.

The DIO animals presented with significantly more intra-peritoneal fat mass than all the control groups (Figure 31). DIO=24.24±3.8g vs control=10.6±0.9g, control with Buchu from day 1 = 10.4±0.5g and control with Buchu from wk 8 = 9.3±0.5g, $p<0.001$, $n=5/\text{group}$. In addition, metformin resulted in significantly less intra-peritoneal fat mass gain with animals presenting with 12.1±1.3g vs DIO=24.24±3.8g, $p<0.05$ and $n=5/\text{group}$.

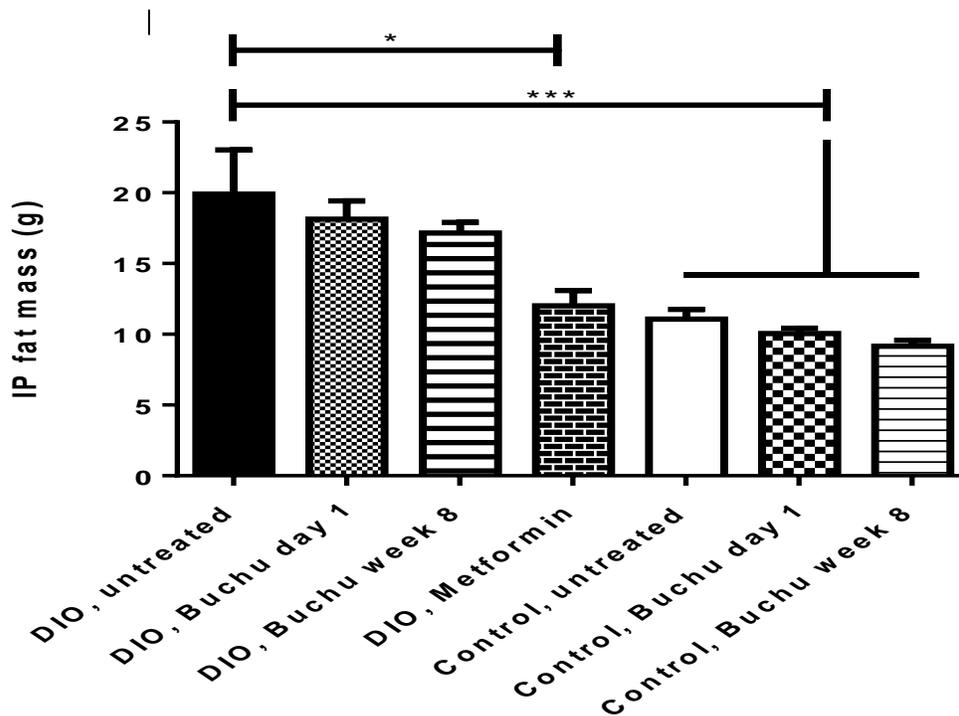


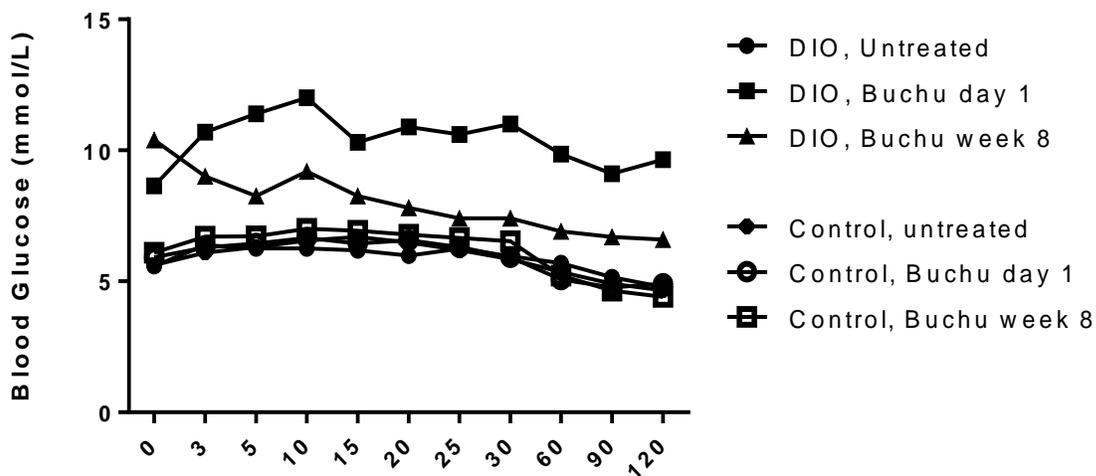
Figure 31: Intra-peritoneal (IP) fat of control and DIO animals, with and without Buchu treatment, after 16 weeks. Displayed is IP fat mass measured in grams (g) of diet induced obese (DIO) and control animals. The data is presented as a mean ± SEM. ($n=6-8/\text{group}$). * $p<0.05$, *** $p<0.001$.

3.2.2. Metabolic parameters

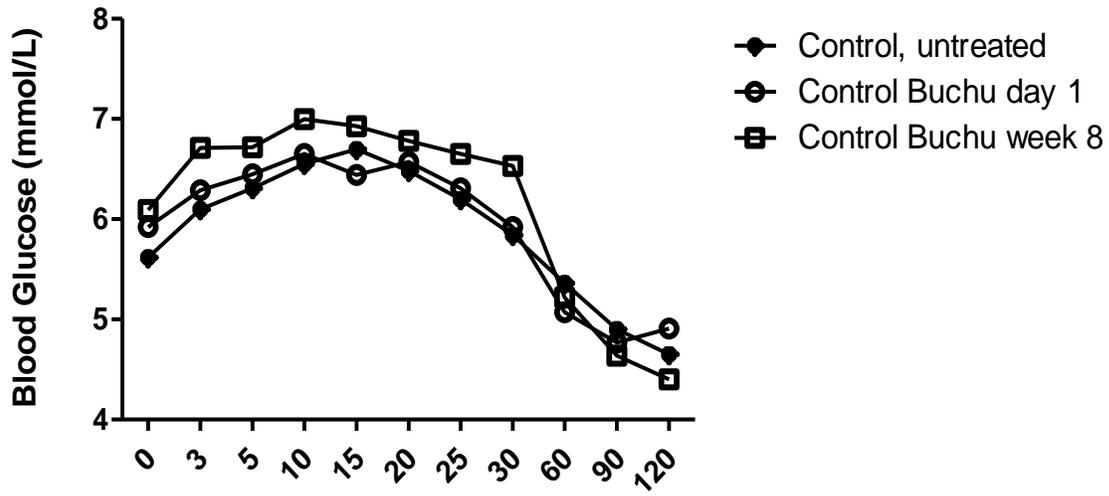
3.2.2.1. Intraperitoneal glucose tolerance test (IPGTT)

At 15 weeks, all animals following their respective treatment regimens were fasted overnight. The next day, intraperitoneal glucose tolerance tests were performed on each animal for a period of 2 hours. When comparing treated and untreated controls, no significant differences were seen (Figure 32 (B)). However, a significant difference in blood glucose levels were observed when comparing treated and untreated DIO animals (Figure 32 (D) and (E)).

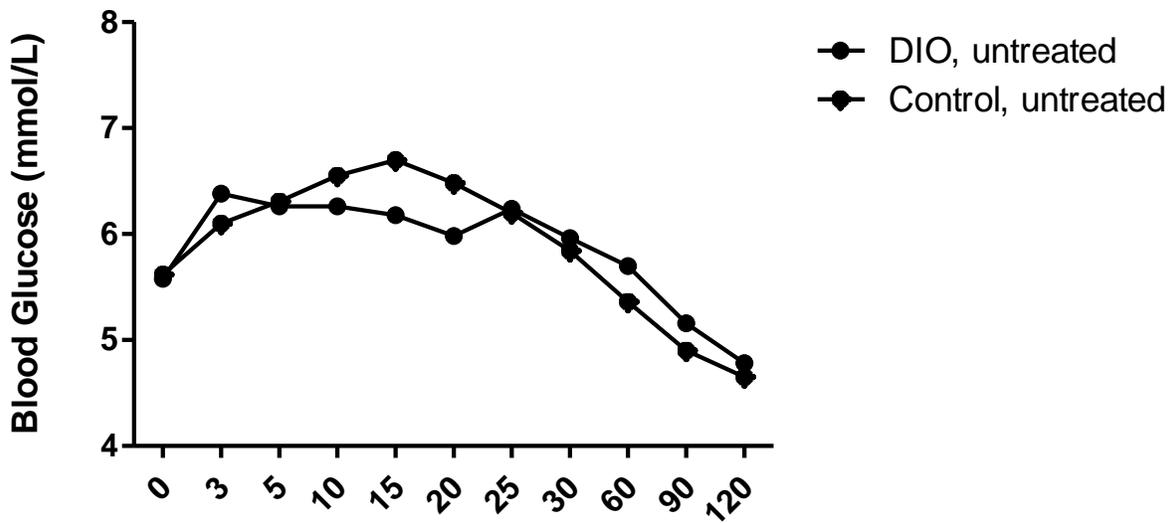
(A)



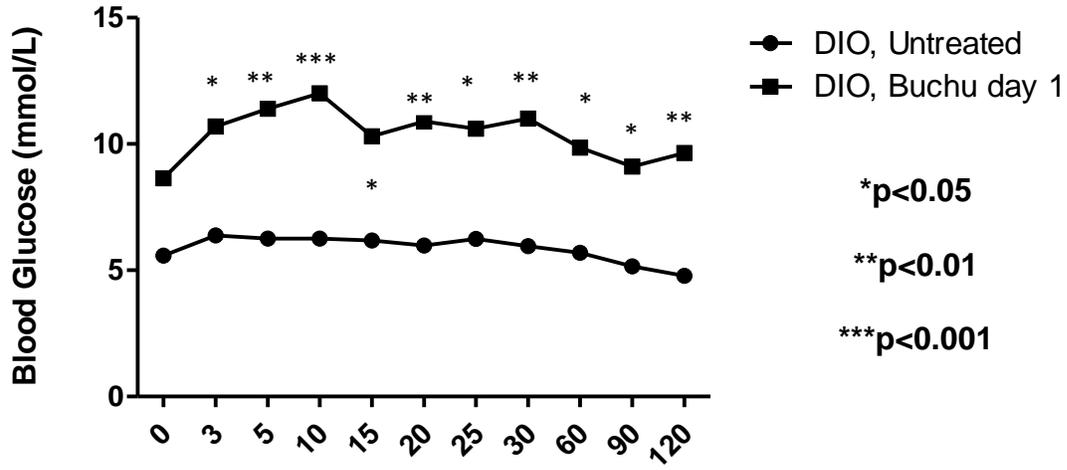
(B)



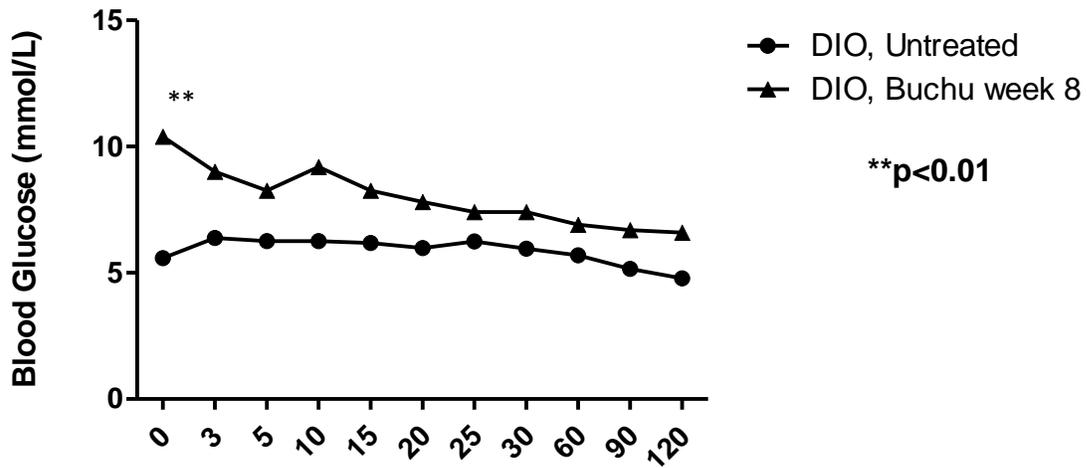
(C)



(D)



(E)



(F)

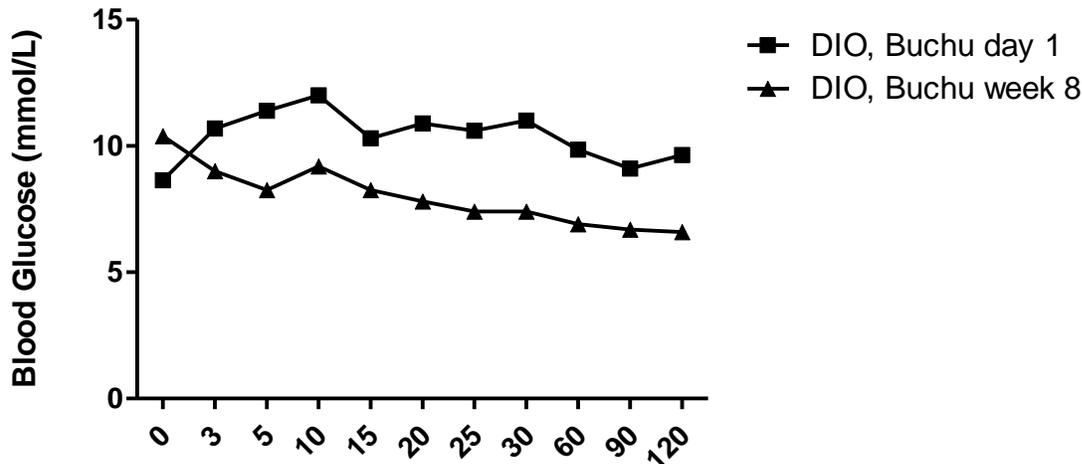


Figure 32: Intraperitoneal glucose tolerance test of control and DIO animals, with and without Buchu treatment, at 15 weeks. (A) Representation of all groups, **(B)** Comparing all control groups, **(C)** Comparing untreated DIO and control groups, **(D)** Comparing untreated DIO animals with treated DIO animals (buchu water from day 1), **(E)** Comparing untreated DIO animals with treated DIO animals (buchu water from week 8), **(F)** comparing DIO animals treated with Buchu water from day 1 and week 8. Blood glucose levels were measured in mmol/L. The data is presented as a mean \pm SEM. (n: 2-10/group)

3.2.2.2. 2-Deoxy-D-3[H] glucose (2DG) uptake by soleus muscle

At 16 weeks, 4 animals per group were anaesthetized, the soleus muscles were rapidly isolated and sliced into five thin longitudinal strips. Each strip was placed into a specific flat-bottomed incubation tube containing incubation medium and various other reagents (Table 6). The purpose of this procedure was to determine muscle sensitivity to insulin.

Neither basal glucose uptake levels nor insulin sensitivity differed in these muscles between the DIO and control animals or with ingestion of Buchu water by the animals.

(Figure 33)

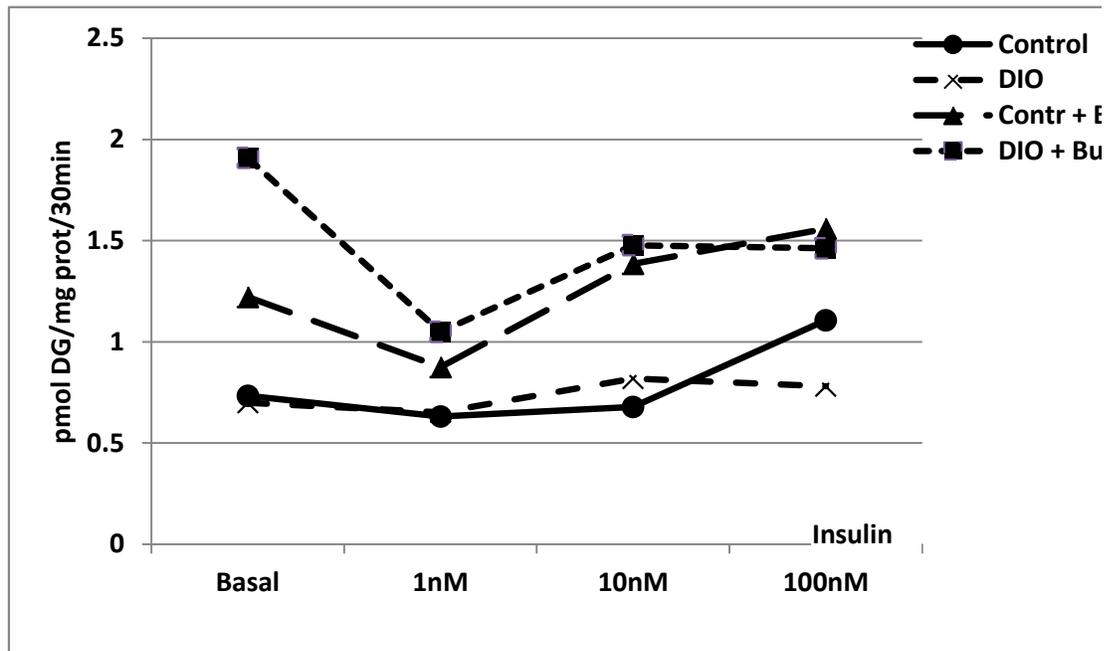


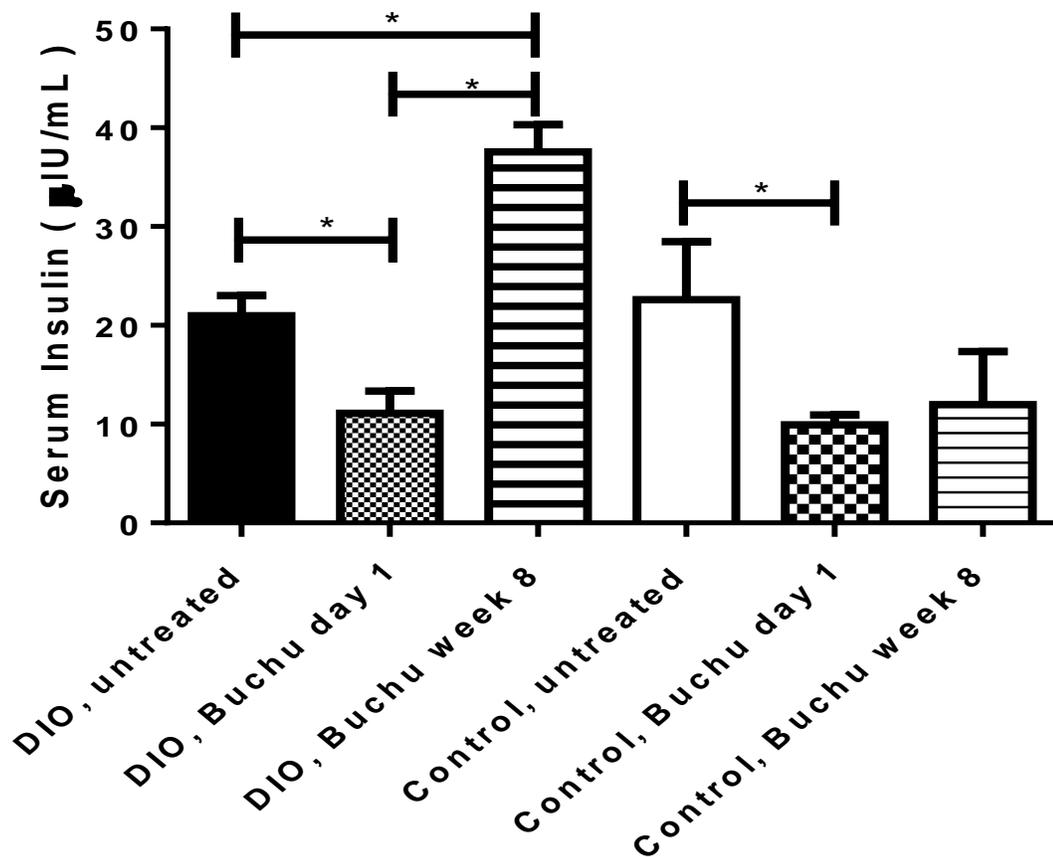
Figure 33: Glucose uptake by the soleus muscle of control and DIO animals, with and without Buchu treatment, after 16 weeks. Insulin sensitivity of the soleus muscle was determined by measuring the ability of the muscle to accumulate radio-labelled deoxy-glucose over a set time period. The data is presented as a mean \pm SEM. (n= 4/group)

3.2.2.3. Serum insulin levels

Following 16 weeks on diet, serum insulin levels were not significantly different between the control and DIO animals without Buchu treatment (22.58 ± 5.8 vs 20.99 ± 2). However, starting Buchu water treatment at the onset of the change in diet, resulted in lower insulin levels (DIO: 20.99 ± 2 vs 11.12 ± 2 ; Control: 22.58 ± 5.8 vs 9.95 ± 0.9).

Starting the Buchu water treatment on week 8 after onset of the obesity-inducing diet, could not lower insulin levels in the DIO animals. To the contrary, insulin levels were raised significantly (22.58 ± 5.8 vs 37.5 ± 2.7) (Figure 34A). Figure 34B depicts a 2-way ANOVA analysis of the effect of Buchu water on insulin levels in both control and DIO animals when used from day 1, therefore for the full duration of 16 weeks of the respective diets.

A)



B)

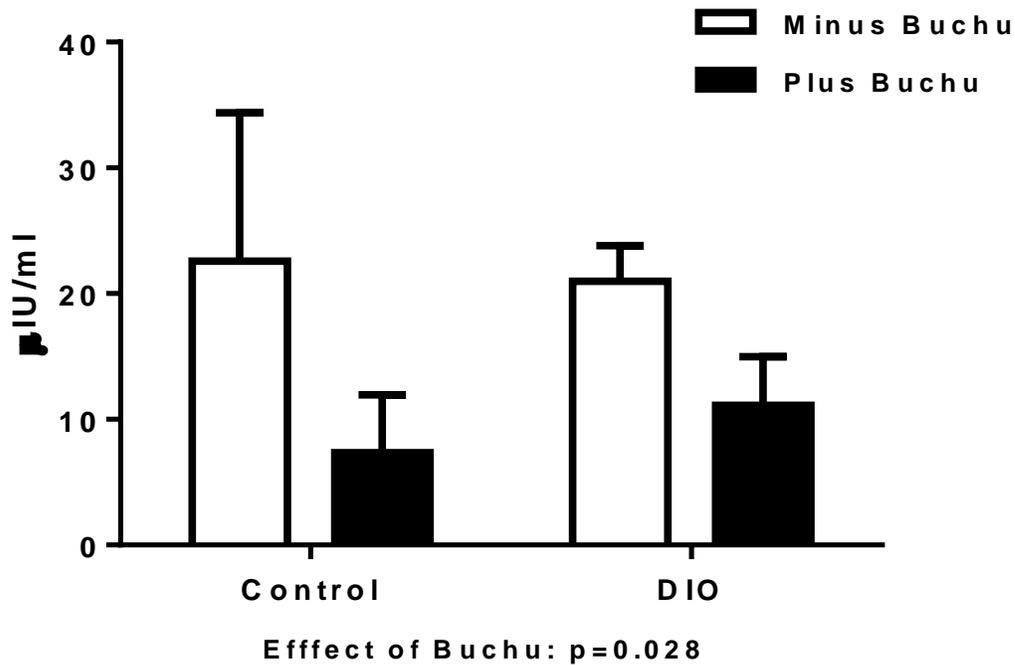


Figure 34: Fasting insulin levels in control and DIO animals after 16 weeks. Fasting blood was drawn under anaesthesia directly from the carotid artery and insulin levels determined using a RIA assay as described in Materials and Methods. The data is presented as a mean \pm SEM. (n=4/group) * $p<0.05$

3.2.2.4. C-peptide levels

C-peptide levels of blood collected from the animals treated with Buchu water from day 1

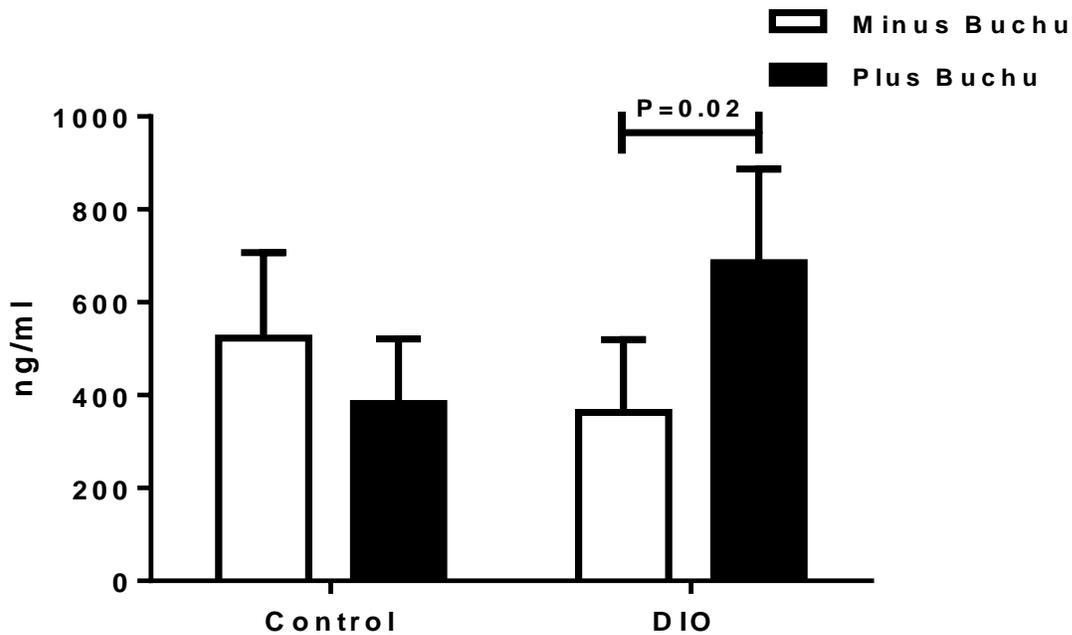


Figure 35: C-peptide levels in control and DIO animals after 16 weeks. A significant difference was found in C-peptide levels of treated vs untreated DIO animals. The data is presented as a mean \pm SEM. (n=4-6/group).

3.2.2.5 Pancreatic Transcription Factors

Following 16 weeks on their respective diets, animals were anaesthetized and pancreatic tissue isolated and stored at -80°C. These tissues were used to determine the effect of Buchu treatment on the expression of Pdx-1 and MafA in DIO and control animals. Ponceau staining was used as a loading control.

3.2.2.5.1. Pdx-1

Pdx-1 expression was downregulated in DIO pancreata compared to controls. A significance increase in Pdx-1 expression was observed when comparing treated and untreated DIO animals, while the total effect of Buchu treatment as indicated by a 2-way ANOVA, on Pdx-1 expression was significant (Figure 36).

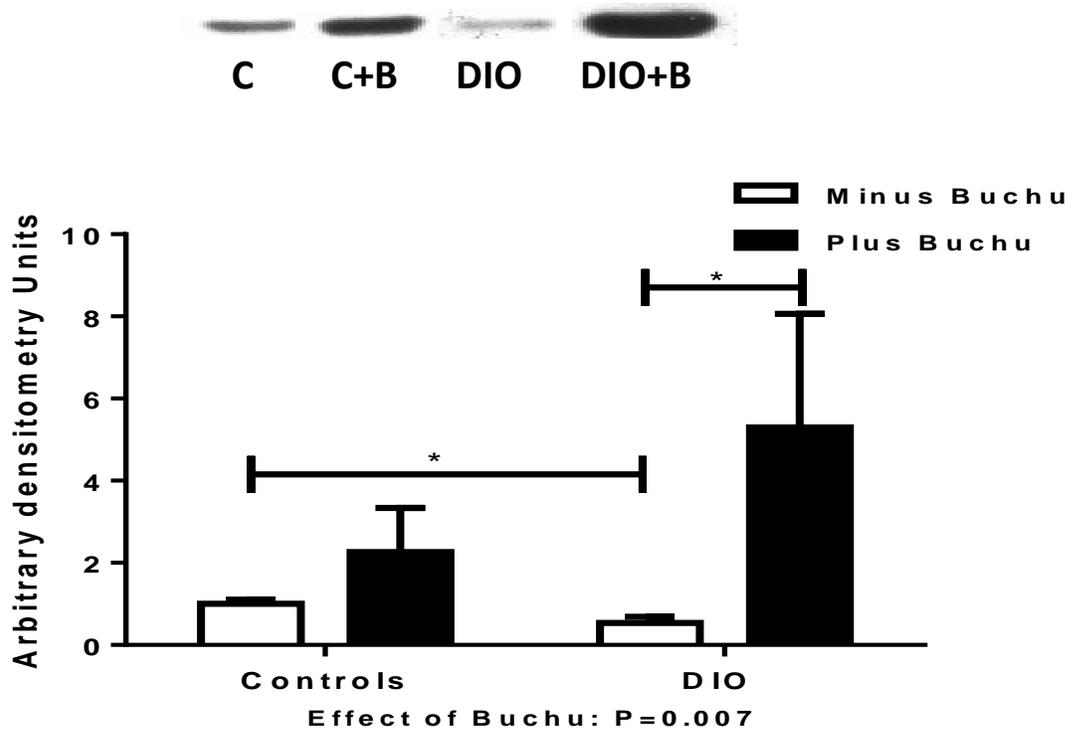


Figure 36: Total Pdx-1 expression in control and DIO groups after 16 weeks. Shown is an example of a western blot representing Pdx-1 expression as well as a graph depicting protein expression in arbitrary units. The data is presented as mean \pm SEM. The data is presented as a mean \pm SEM. (n = 4/group) *p<0.05

3.2.2.5.2. MafA

MafA expression was downregulated in DIO pancreata compared to controls. A significant increase in MafA expression was observed when comparing treated and untreated DIO animals. A 2-way ANOVA indicated a significant effect of Buchu water treatment on the expression of MafA (Figure 37).

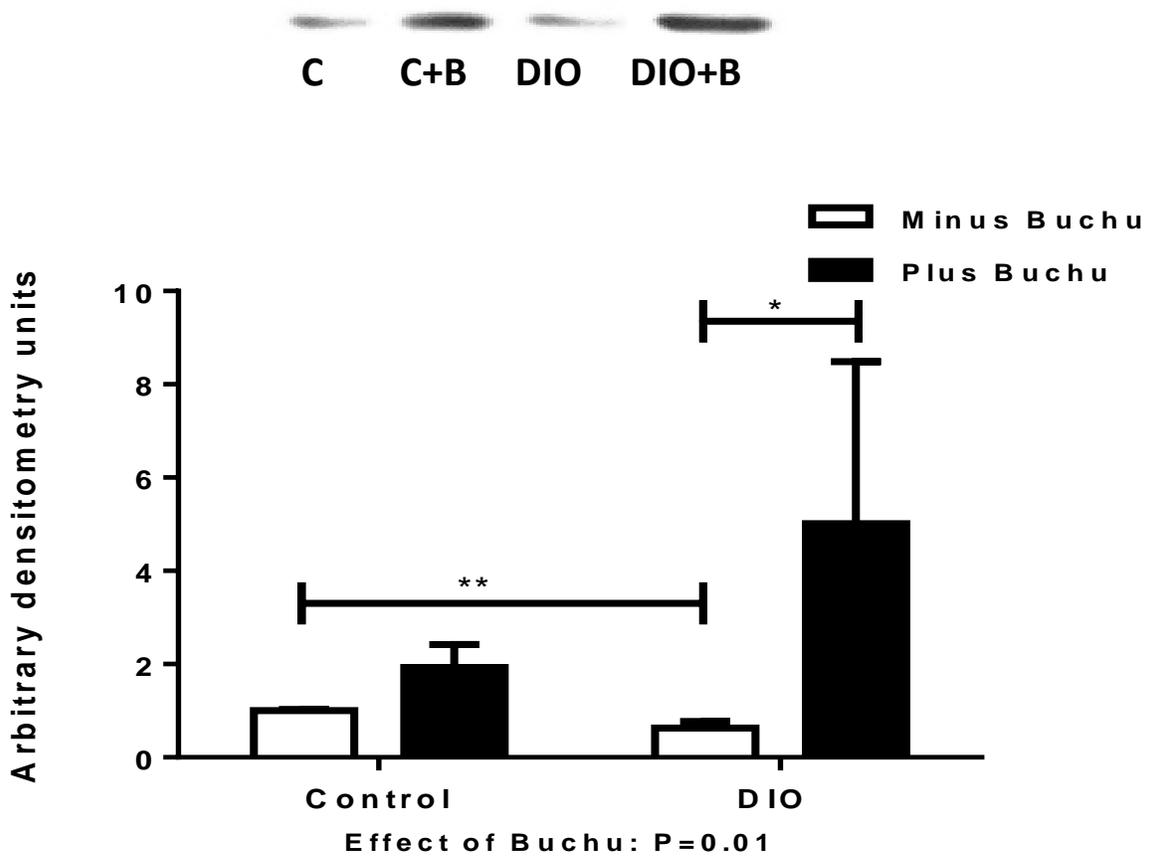


Figure 37: Total MafA expression in control and DIO groups after 16 weeks. Shown is an example of a western blot representing MafA expression as well as a graph depicting protein expression in arbitrary units. The data is presented as mean \pm SEM. The data is presented as a mean \pm SEM. (n = 4/group) *p<0.05, **p<0.01

CHAPTER 4

Discussion

It has been estimated that 347 million people worldwide have diabetes mellitus, with approximately 80% of diabetic deaths occurring in low and middle income countries [Mathers and Loncar, 2006; WHO, 2014]. Diabetes mellitus is a chronic disease associated with disastrous complications, wreaking havoc amongst individuals of all ages. According to the World Health Organisation (WHO), diabetes will be the 7th leading cause of death by the year 2030. As a result, much research has been conducted on the pathophysiology of diabetes mellitus as well as the establishment of safer, more convenient treatment options.

The people of South Africa are faced with many challenges on a daily basis, especially where healthcare is concerned. In developing countries, treating chronic diseases are either too expensive or inaccessible. South Africa is a country rich in floral biodiversity, shifting attention toward the medicinal use of indigenous plants [Light *et al.*, 2005]. There are many complex issues surrounding the use of indigenous plants in medicine. One of these issues stem from the fact that the use of medicinal plants were based on hearsay [Light *et al.*, 2005].

The indigenous plant of interest for this study belongs to the genus *Agathosma* and is collectively known as Buchu. It is claimed that Buchu exert various beneficial effects

which still need to be scientifically validated. A study reviewed by Moolla and Viljoen successfully validated that Buchu exerts anti-microbial, anti-inflammatory, anti-oxidant and diuretic effects [Moolla and Viljoen, 2008]. Whether buchu has any anti-diabetic properties, remains a question which demands scientific investigation.

The aim of our study was therefore to investigate the anecdotal claims of anti-diabetic effects experienced by individuals using Buchu water. Buchu water is the by-product of the extraction of Buchu oil. The latter is mainly isolated from the leaves of *Agathosma crenulata* and *Agathosma betulina*, both endemic to the mountains of the Western Cape in South Africa. The oil is used as a flavour enhancer in the perfume and food industries. The aqueous solution is currently marketed as a herbal remedy to treat various ailments e.g., urinary infections, rheumatism, arthritis and obesity. People ingesting the water started claiming insulin sensitizing potential necessitating scientific validation of these claims.

Moolla and Viljoen (2008) comprehensively reviewed the phytochemical composition of Buchu oil. In Buchu oil, there is only one family of substances that may be harmful – the pulegones. However, during fractionation, the pulegones are extracted in the oil fraction with less than 0.1% present in the water fraction. In addition to pulegone Buchu oil consists of limonene, menthone and diosphenol. Currently, little is known about the composition of Buchu water as well as the active substance present.

Main findings:

One of the main findings of this study is that ingestion of Buchu water results in weight loss despite unchanged food consumption. This occurred in both the models used as well as control animals. In the obese animals, this weight loss was due to the loss of intra-peritoneal fat.

A second important finding is that the ingestion of Buchu water in all instances, whether given as treatment or as prophylactic, resulted in normalization of glucose levels in a type-1 diabetic model with residual beta-cell mass.

An insulin-sensitizing effect has not been clearly established in the muscle of DIO animals but this may be because of a large variation in values obtained as well as the use of a slow-twitch muscle.

A definite effect on pancreatic insulin secretion has been demonstrated by raised C-peptide levels in DIO treated animals.

4. Diabetic models**4.1. Streptozotocin-induced type 1 diabetic model**

Type 1 Diabetes is an organ specific autoimmune disease caused by the immunological destruction of insulin producing pancreatic β -cells [Narendran *et al.*, 2003; Atkinson and Eisenbarth, 2001]. The destruction of β -cells minimizes β -cell mass, thus, exposing the body to hyperglycemia. High blood glucose levels are associated with a vast array of detrimental effects such as glucotoxicity and ketoacidosis.

Streptozotocin is a glucosamine compound, derived from a soil microbe called *Streptomyces achromogenes*, which is easily transported into pancreatic β -cells via glucose transporter 2, where it exerts its toxic effects by damaging DNA [Wei *et al.*, 2003; Motyl and McCabe, 2009; Arora *et al.*, 2009]. This leads to β -cell dysfunction, hypoinsulinemia and hyperglycemia; all characteristics associated with diabetes [Motyl and McCabe, 2009]. The severity of type 1 diabetes depends on the species of the animal, age and amount of STZ administered intravenously or intraperitoneally [Arora *et al.*, 2009]. In this study, we successfully developed a type 1 diabetic model by injecting rats with a single dose of STZ (40 mg/kg), intra-peritoneally. In these animals, approximately 50 % of the total pancreatic β -cell mass was ablated [George *et al.*, 2011] leading to blood glucose levels within the range of $>10<20$ mmol/L. Diabetic animals were further divided into a group with blood sugar values less than 20mmol/L and those with values exceeding 20mmol/L. This was clearly seen when weekly evaluating blood glucose levels of STZ animals after 11 weeks treatment (Figure 25). Additionally, fasting blood glucose levels of untreated STZ animals at week 13 were significantly higher compared to treated STZ animals (Figure 25 and Figure 26).

The streptozotocin-induced type 1 diabetic model was further used to determine the effect of Buchu water on certain biometric and metabolic parameters.

4.1.1. The effect of Buchu water on biometric parameters

In the current study, water/Buchu water and food consumption were monitored to determine whether all treated animals consumed equal amounts of Buchu water and

whether this consumption might influence their food intake. Daily measurements showed no significant differences within or between groups (Figure 21 and Figure 22).

After 14 weeks of feeding, all animals were anaesthetized with sodium pentobarbital and sacrificed. At this point, body weight and intra-peritoneal fat mass were measured. The data retrieved was plotted and clear differences in body weight between STZ treated and untreated animals were evident (Figure 23). As would be expected, the STZ animals gained less weight than their control counterparts but in both STZ animals, as well as in the control animals, ingestion of Buchu water resulted in significant lower weight gain over the treatment period [*Singh et al., 2006*]. The lower weight gain seen in STZ animals are not good and could result in ketoacidosis. However, when evaluating intra-peritoneal fat, the STZ animals ingesting Buchu water, accumulated more fat than untreated animals (Figure 24). In the setting of type 1 diabetes, intra-peritoneal fat accumulation but loss of body weight with equal food consumption, might point towards either muscle wasting or a higher thermogenic state. It is possible that Buchu water might act as a thermogenic supplement by increasing the metabolic rate of cells leading to weight loss [*Jitomir et al., 2008; Preuss et al., 2002*]. This is an aspect of the results that needs further investigation.

4.1.2. The effect of Buchu water on metabolic parameters

Non-fasting blood glucose levels of all animals were measured and recorded weekly for 13 weeks. From the data gathered, Buchu treatment resulted in a decrease in blood glucose levels over time with the most significant decrease observed in STZ animals

that had a lower blood glucose level (< 20 mmol/L) at the onset of experimentation (Figure 25).

At week 13, animals were fasted overnight then anaesthetized in order to perform intra-peritoneal glucose tolerance tests. All STZ animals that were treated with Buchu water, presented with normalized IPGTT curves (Figure 26). This was underscored by a 2hr value not significantly different from control animals (Figure 26G). It can therefore be concluded that, in this STZ model of type 1 diabetes, treatment with Buchu water normalized blood glucose values and served as an effective treatment in the absence of any other treatment.

Despite this normalization of the blood glucose values, we could not detect any significant differences in the insulin secretion of these animals (Figure 27). It is therefore possible that the Buchu water treatment may have lowered either the uptake of glucose from the intestinal mucosa by the SGLT-1 transporter [Steel and Hediger, 1998; Srichamroen, 2007] or it may have enhanced glucose excretion by inhibition of the SGLT-2 glucose transporters in the kidney [Review: Rosenwasser et al., 2013]. It has been shown that inhibitors of SGLT-2 improve glucose control to an extent comparable to other hypoglycemic agents while simultaneously reducing body weight. [Review: Rosenwasser et al., 2013]. These inhibitors, like canagliflozin or dapagliflozin, are of the most recent substances approved for treatment of diabetes. In addition, we have noticed that the insulin levels of STZ untreated animals were very high, this could have occurred as a result of inadequate insulin breakdown.

4.2. Diet-induced obese type 2 diabetic model

Type 2 Diabetes is a multi-factorial disorder that accounts for 90-95% of all diabetic cases worldwide, making it the most common type of diabetes known [Stumvoll *et al.*, 2005]. T2D occurs as a result of insufficient insulin production by pancreatic β -cells or reduced insulin action at target tissues. A strong correlation exists between T2D and obesity, while obese individuals undergo metabolic changes which encompass dyslipidemia, hypertension, insulin resistance and proinflammation [Chen and Morris, 2007; Stumbo *et al.*, 2005].

In our second model we set out to test treatment with Buchu using a type 2 diabetic model in which male Wistar rats were fed a high caloric diet for 16 weeks, while control animals were fed normal rat chow for the duration of the experiment. The high caloric diet consisted of normal rat chow supplemented with condensed milk and sucrose. In this respect, DIO animals consumed more energy than control animals per day. Several studies have validated that an energy imbalance, where energy intake exceeds energy expenditure, is linked to obesity and insulin resistance [Chen and Morris, 2007; Pulgarón, 2013]. Although this diet was sufficient in establishing hyperglycemia, it did not result in T2D as the fasting blood glucose values were still below 8 mmol/L.

4.2.1. The effect of Buchu water on biometric parameters

Food consumption was recorded over a period of 7 days with no differences in food consumption (Figure 28). In addition, water/ Buchu water consumption was monitored

for the duration of 20 days with no significant differences present within or between groups (Figure 29).

Body weight gain in untreated DIO animals was significantly higher than that of the untreated controls (Figure 30) despite similar food intake. This can be ascribed to the higher caloric density of the food that they ingested (Table 9). Additionally, when evaluating intra-peritoneal fat, a significant difference was seen when comparing the untreated DIO and control groups (Figure 31). It would therefore seem that the DIO animals became centrally obese.

Similar to what was observed in the STZ animals, the ingestion of Buchu water from day 1 of the change in diet by the DIO animals, resulted in significantly less weight gain, similar to the positive control, metformin. Metformin acts by lowering glucose production by the liver thereby curbing appetite, resulting in weight loss [*Hundal et al., 2000; Lee and Morley, 2012*]. However, treatment with Buchu water from week 8 of the diet, could not induce a significant reduction in weight gain. This effect was also not seen in the control animals treated with Buchu water. However, there is a clear trend for lower IP fat gain in both the DIO and the control animals ingesting Buchu water. This effect of lower weight gain induced by Buchu water despite equal food consumption, is not clearly understood but warrants an investigation of the fat depots of these animals and the accompanying adipokines that may affect this, e.g. leptin levels.

4.2.2. Anti-diabetic and insulin sensitizing effects of Buchu water

4.2.2.1. The effect of Buchu water on insulin secretion and glucose homeostasis

When pancreatic β -cells are exposed to hyperglycemia they adapt by increasing metabolism and ATP production [Layden *et al.*, 2010]. This adaptation causes a surge in the ATP/ADP ratio, resulting in the closure of the ATP-sensitive potassium channels leading to an influx of calcium. This results in increased insulin release via exocytosis [Layden *et al.*, 2010; Li *et al.*, 2007]. Insulin secreted by β -cells is readily available due to prior synthesis and storage in immature secretory vesicles containing endoprotease and carboxypeptidase E [Robinson, 2013]. Once β -cells are exposed to appropriate stimuli, proinsulin is cleaved releasing insulin and C-peptides into circulation [Halban and Irminger, 2003]. Insulin is a potent anabolic hormone, responsible for disposal of excess glucose in response to hyperglycemia [Satiel and Pessin, 2002]. Insulin lowers blood glucose levels by stimulating glucose uptake by peripheral tissue and lowering all processes involved in glucose production.

In the current study, IPGTTs done on various groups showed a significantly higher fasting blood glucose level in DIO treated animals compared to untreated DIOs, with no significant differences between untreated control and DIO animals (Figure 32). When monitoring glucose uptake in the soleus muscle under stimulated and basal conditions, no significant difference between groups was present (Figure 33). Interestingly, a significant increase in serum insulin levels of Buchu treated DIO animals at week 8 was observed when comparing this group to its untreated counterpart (Figure 34). However,

blood glucose levels were higher in DIO animals, even after treatment and although not significant the DIO muscle appears to be insulin resistant (Figure 33). This may account for increased insulin values.

4.2.3. Buchu water as an insulin sensitizing agent/ promoter

There are many factors capable of reducing insulin sensitivity at peripheral tissues such as insulin resistance and defects in insulin signalling. A strong relationship exists between insulin resistance and obesity which are associated with a variety of co-morbidities such as type 2 diabetes [*Stumbo et al., 2005; Sahani et al., 2010; Chen and Morris, 2007*]. In obese individuals energy intake exceeds energy expenditure, leading to an accumulation of free fatty acids. In these individuals, adipose tissue can no longer effectively clear circulating free fatty acids due to these tissues reaching their optimum storage capacity [*Goossens, 2008*]. Lipids would then accumulate in non-adipose tissue but with time they too will lose the ability to oxidize fat effectively [*Goossens, 2008*]. The accumulation of lipids in non-adipose tissue has detrimental effects on insulin sensitivity eventually causing insulin resistance within these tissues. For possible mechanisms in which free fatty acids causes insulin resistance refer back to section 1.6.2.1 of the literature review. In response to insulin resistance, β -cells would secrete more insulin to overcome resistance. This compensatory mechanism usually results in hyperinsulinemia, which is accompanied by glucose intolerance, hyperlipidemia and hyperglycemia. The manifestation of insulin resistance at insulin's target tissue usually occurs due to an impairment in insulin action. However, analyzing insulin sensitivity of soleus muscle did not show clear signs of peripheral insulin resistance in our DIO

model, nor did ingestion of Buchu water affect this, although there was a strong trend to enhanced insulin stimulated glucose uptake, the variation in data was quite large. A possible effect of the Buchu water on insulin sensitivity is underscored by the significant lowering of insulin levels with treatment for the full 16 weeks. An effect on insulin secretion induced by Buchu water treatment was clearly demonstrated by the fact that c-peptide levels were significantly raised in DIO treated animals. This effect was further investigated by analyzing pancreatic tissue for transcription factors known to be associated with enhanced insulin production.

4.2.4. Buchu water promotes β -cell neogenic activity

Adult β -cell mass are dynamic components which readily adapt to changes in insulin demand or glucose concentrations. To maintain an optimal glucose level, an exquisite balance exists between insulin biosynthesis, stimulation and secretion. β -cell mass is influenced by an interplay between β -cell growth and loss. For this study, we will only be focusing on β -cell growth, specifically, neogenesis.

β -cell neogenesis is a mechanism that triggers the generation of new β -cells from precursor cells [Paris, 2004]. These precursor cells originate from ductal cells (budding from duct epithelium), differentiated pancreatic cells through a process called transdifferentiation and intra islet precursors [Paris, 2004]. Under normal conditions, β -cell neogenesis is at its optimum working capacity prenatally and for a short period of time after birth [Masiello, 2006]. As individuals age, neogenesis stabilizes while apoptotic activity increases, leading to a reduction in β -cell mass [Masiello, 2006].

There are various transcription factors promoting β -cell neogenesis by targeting β -cell differentiation, proliferation, and/or pancreatic development [Rocques *et al.*, 2007].

In our study we determined the effect of Buchu treatment on the expression of transcriptional factors involved with β -cell neogenesis, namely, Pdx-1 and MafA. The levels of both of these transcription factors were significantly lower in pancreata from the DIO animals. This could therefore explain why the DIO model did not present with enhanced insulin secretion as would be expected. The overall effect of Buchu treatment was significant while increasing Pdx-1 and MafA expression (Figure 36 and Figure 37). This observation warrants further investigation as it is realized that stimulation of neogenesis in the adult pancreas may lead to pancreatic hyperplasia, β -cell maturation/survival and eventual pancreatic dysfunction.

4.3. Adverse effects of Buchu water

Buchu is an indigenous plant (herb) species from the Cape regions of South Africa which has been used commercially in tea, perfume, herbal tonics and lotions [Moolla *et al.*, 2007]. In recent years, the herb's medicinal uses were explored and research has accredited these plants with the possession of diuretic, anti-inflammatory and anti-septic properties [Moolla and Viljoen, 2008]. It should be noted that even though Buchu is a naturally occurring plant it does not necessarily classify it as safe. However, Buchu is approved by the American FDA for human consumption. Many studies have reported adverse effects of herbal remedies [Johnson W, 2007; Peters D, 2009].

CHAPTER 5

Conclusion

5.1 Conclusion

This study, with regard to the type 1 diabetic model, has confirmed the anti-diabetic effect of Buchu water by significantly lowering blood glucose levels of fasted and non-fasted blood and normalizing IPGTT curves. This was however not so evident in the DIO model utilized. Despite this, animals lost weight which was mainly intra-peritoneal fat in these animals.

5.2 Limitations of this study

The current study was done on male Wister rats only. Effects on female animals may be different. In respect to the DIO model, the effect of Buchu water on insulin resistance via adipose tissue secreted (adipokines and cytokines) was not investigated. Such an analysis could have shed more light on the metabolic effects observed. The effects on pancreatic tissue of the type 1 diabetic animals were also not studied. In view of the results obtained in the DIO animals, this is deemed important. Determination of the active compound present in Buchu water would help in explaining the results obtained.

5.3 Future perspectives

- The liver tissue of animals after ingestion of Buchu water should be studied to ascertain metabolic changes and possible toxicity.
- The kidneys should be studied especially with respect to the expression of the SGLT-2 glucose transporter. This should be accompanied by a study of the urine itself to determine kidney function.
- The studies on the soleus muscle which is a slow twitch muscle, should be extended to e.g. the gastrocnemius muscle. The latter may show more pronounced changes.
- The effect of Buchu water on weight loss should be studied in more detail.
- The effect of Buchu water on β -cell neogenesis in pancreata of STZ animals should be studied.

CHAPTER 6

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i. Journal articles

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