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# $\alpha$ - AND $\gamma$ -MELANOCYTE STIMULATING HORMONES IN OBESITY

A study of the key central areas of metabolic regulation

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*"We know what we are, but know not what we may be"*  
William Shakespeare

## ABSTRACT

**Kim Eerola**

**$\alpha$ - and  $\gamma$ -melanocyte stimulating hormones in obesity: A study of the key central areas of metabolic regulation**

Institute of Biomedicine, Pharmacology, Drug Development and Therapeutics, and Drug Research Doctoral Program, University of Turku and Heart Center, Turku University Hospital and University of Turku, Finland

The melanocortin system is an important regulator of feeding, energy metabolism, and cardiovascular function and it consists of the pro-opiomelanocortin (POMC) derived melanocyte stimulating hormones ( $\alpha$ -,  $\beta$ - and  $\gamma$ -MSH) and their endogenous melanocortin receptors, MC1R to MC5R. In the hypothalamus,  $\alpha$ -MSH reduces food intake, and increases energy expenditure and sympathetic tone by binding to MC4R. Mutations affecting the MC4R gene lead to obesity in mammals. On the other hand, the metabolic effects of MC3R stimulation using agonists such as the endogenously expressed  $\gamma$ -MSH have been less extensively explored. The main objective of this study was to investigate the long-term effects of increased melanocortin tone in key areas of metabolic regulation in the central nervous system (CNS) in order to investigate the site-specific roles of both  $\alpha$ -MSH and  $\gamma$ -MSH.

The aim was to stereotaxically induce local overexpression of single melanocortin peptides using lentiviral vectors expressing  $\alpha$ -MSH (LVi- $\alpha$ -MSH-EGFP) and  $\gamma$ -MSH (LVi- $\gamma$ -MSH-EGFP). The lentiviral vectors were shown to produce a long-term overexpression and biologically active peptides in cell-based assays. The LVi- $\alpha$ -MSH-EGFP was targeted to the *arcuate nucleus* in the hypothalamus of diet induced obese mice where it reduced weight gain and adiposity independently of food intake. When the *nucleus tractus solitarius* in the brainstem was targeted, the LVi- $\alpha$ -MSH-EGFP treatment was shown to cause a small decrease in adiposity, which did not impact weight development. However, the  $\alpha$ -MSH treatment increased heart rate, which was attenuated by adrenergic receptor blockade indicative of increased sympathetic activity. The LVi- $\gamma$ -MSH-EGFP was targeted to the hypothalamus where it decreased fat mass in mice eating the standard diet, but the effect was abated if animals consumed a high-fat Western type diet. When the diet induced obese mice were subjected again to the standard diet, the LVi- $\gamma$ -MSH-EGFP treated animals displayed increased weight loss and reduced adiposity.

These results indicate that the long-term central anti-obesity effects of  $\alpha$ -MSH are independent of food intake. In addition, overexpression of  $\alpha$ -MSH in the brain stem efficiently blocked the development of adiposity, but increased sympathetic tone. The evidence presented in this thesis also indicates that selective MC3R agonists such as  $\gamma$ -MSH could be potential therapeutics in combination with low fat diets.

**Key words:** melanocortins, central nervous system, obesity, gene therapy, diet induced obesity

## TIIVISTELMÄ

**Kim Eerola**

### **$\alpha$ - ja $\gamma$ -melanosyyttejä stimuloivien hormonien sentraaliset vaikutukset lihavuudessa; aineenvaihdunnallisesti keskeiset aivoalueet hypotalamuksessa ja aivorungossa**

Biolääketieteen laitos, Farmakologia, Lääkekehitys ja Lääkehoito sekä Lääketutkimuksen tohtoriorjelma Turun Yliopisto, sekä Sydänkeskus, Turun yliopistollinen keskussairaala ja Turun yliopisto

Pro-opiomelanokortiini (POMC) on keskushermoston melanokortiinijärjestelmän keskeisin tekijä toimien esiasteena  $\alpha$ -,  $\beta$ -, ja  $\gamma$ -melanosyyttejä stimuloiville hormoneille (MSH), jotka säätelevät ruokahalua, energiatasapainoa sekä sydän- ja verenkiertojärjestelmää melanokortiinireseptorien (MC1-5R) välityksellä.  $\alpha$ -MSH:n sitoutuminen MC4-reseptoriin hypotalamuksessa vähentää syömistä, lisää energiankulutusta ja sympaattista tonusta akuutisti. MC4-reseptorin mutaatioiden tiedetään aiheuttavan lihavuutta sekä koe-eläimillä että ihmisillä, mutta keskushermostossa esiintyvän MC3-reseptorin ja tämän agonistin,  $\gamma$ -MSH:n roolista lihavuuden synnyssä ja aineenvaihdunnan säätelyssä tiedetään edelleen varsin vähän. Tämän väitöskirjan tavoitteena on ollut selvittää lentivirus-geeniterapian avulla  $\alpha$ -MSH:n ja  $\gamma$ -MSH:n pitkäkestoisia vaikutuksia keskushermoston metabolian säätelyn kannalta keskeisillä aivoalueilla.

Osana väitöskirjatutkimusta tuotimme  $\alpha$ -MSH (LV $\alpha$ -MSH-EGFP) ja  $\gamma$ -MSH (LV $\gamma$ -MSH-EGFP) lentivirukset, joiden funktionaalisuus varmistettiin solupohjaisilla menetelmillä. Virusten todettiin yli-ilmentävän pitkäkestoisesti kutakin MSH peptidiä ja tuottavan biologisesti aktiivista proteiinia.  $\alpha$ -MSH:n yli-ilmentäminen hypotalamuksen *arcuatus nucleus* (ARC)-tumakkeessa esti lihavuuden kehittymistä vähentäen hiirten painonkasvua vaikuttamatta ruuan kulutukseen. Vaikutus havaittiin myös aivorungon *nucleus tractus solitarii* (NTS)-tumakkeen alueella. Tällöin vaikutus näkyi lähinnä alentuneena rasvamassana. Tämän lisäksi  $\alpha$ -MSH-käsittelyn saaneilla hiirillä todettiin kohonnut sydämensyke, joka oli estettävissä adrenergisten reseptorien salpauksella viitaten kohonneeseen sympaattiseen tonukseen.  $\gamma$ -MSH yli-ilmennys ARC-tumakkeessa vähensi rasvamassan kehittymistä standardirehulla, mutta ruokittaessa koe-eläimiä runsasrasvaisella rehulla tämä ero rasvamassassa hävisi. Lihavuuden kehittyttyä runsasrasvaisen rehun vaihtaminen takaisin standardirehuun vähensi  $\gamma$ -MSH käsittelyn saaneiden hiirten rasvamassaa merkittävästi lisäämättä epäsuotuista sympaattista vaikutusta.

Väitöskirjatutkimus osoittaa, että  $\alpha$ -MSH aivojen ARC ja NTS tumakkeissa estää lihavuutta muilla kuin suoraan syömistä säätelevillä mekanismeilla ja että aivorungossa  $\alpha$ -MSH lisää sympaattista aktiivisuutta.  $\gamma$ -MSH:n myönteiset vaikutukset rasvamassaan olivat riippuvaisia dieetin koostumuksesta. Tämän väitöskirjan löydökset laajentavat ymmärrystä MSH-peptidien sentraalisista vaikutuksista ja näiden peptidien soveltamisesta lihavuuden hoidossa.

**Avainsanat:** melanokortiinit, keskushermosto, lihavuus, sympaattinen hermosto, ravitsemus

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**ABBREVIATIONS**

5-HT	serotonin
aa	amino acid
ACTH	adrenocorticotrophic hormone
AgRP	agouti related peptide
ANOVA	analysis of variance
ARC	arcuate nucleus of the hypothalamus
BAT	brown adipose tissue
BMI	body mass index
BDNF	brain derived neurotrophic factor
CMV	cytomegalo virus
CNS	central nervous system
DIO	diet induced obesity
DMEM	Dubelcco's modified Eagles medium
EGFP	enhanced green fluorescent protein
eNOS	endothelial nitric oxide synthase
FACS	fluorescent activated cell sorting
FCS	fetal calf serum
FFA	free fatty acid
FITC	fluorescein isothiocyanate
GABA	$\gamma$ -aminobutyric acid
GPCR	G protein-coupled receptor
HDL	high density lipoprotein
HEK293T	human embryonic kidney cells 293T
HR	heart rate
i.p.	intraperitoneal
IGTT	intraperitoneal glucose tolerance test
iNOS	inducible nitric oxide synthase
IRES	internal ribosomal entry site
LDL	low density lipoprotein
LPL	lipoprotein lipase
LVi	lentiviral vectors with IRES
mRNA	messenger ribonucleic acid
NA	noradrenaline
NO	nitric oxide

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NOS	nitric oxide synthase
NPY	neuropeptide Y
NTS	nucleus tractus solitarius
RER	respiratory exchange ratio
PBS	phosphate-buffered saline
PFA	paraformaldehyde
POMC	pro-opiomelanocortin
PRCP	prolylcarboxypeptidase
PVN	paraventricular nucleus
SEM	standard error of mean
SNS	sympathetic nervous system
sBP	systolic blood pressure
T2D	type 2 diabetes
TEE	total energy expenditure
TRH	thyrotropin releasing hormone
UPC1	uncoupling protein 1
VLDL	very-low density lipoprotein
VSMC	vascular smooth muscle cell
WAT	white adipose tissue
WHO	World Health Organization
$\alpha$ -MSH	$\alpha$ -melanocyte stimulating hormone
$\beta$ -MSH	$\beta$ -melanocyte stimulating hormone
$\gamma$ -MSH	$\gamma$ -melanocyte stimulating hormone
QUICKI	quantitative insulin sensitivity check index

## LIST OF ORIGINAL PUBLICATIONS

The thesis is based on the following original publications, which are referred to in the text by Roman numerals I-III:

- I** Eerola K, Nordlund W, Virtanen S, Dickens AM, Mattila M, Ruohonen ST, Chua SC Jr, Wardlaw SL, Savontaus M, Savontaus E (2013). Lentivirus-Mediated  $\alpha$ -Melanocyte-Stimulating Hormone Overexpression in the Hypothalamus Decreases Diet Induced Obesity in Mice. *Journal of Neuroendocrinology* **25**(12):1298-307
- II** Eerola K, Rinne P, Penttinen AM, Vähätalo L, Savontaus M, Savontaus E (2014).  $\alpha$ -MSH Overexpression in the Nucleus Tractus Solitarius Decreases Fat Mass and Elevates Heart Rate. *Journal of Endocrinology*. In press
- III** Eerola K, Virtanen S, Vähätalo L, Ailanen L, Cai M, Hraby V, Savontaus M, Savontaus E.  $\gamma$ -melanocyte stimulating hormone overexpression in the hypothalamus augments anti-obesity effects in diet induced obese mice. *Manuscript in preparation*

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In addition, the thesis also presents some unpublished data.

## 1. INTRODUCTION

Obesity is a major threat to human health; according to the WHO in 2008, affecting nearly 500 million men and women worldwide. The total costs of obesity to society approaches 6 % of the gross domestic product (GDP) in Western countries (Williams & Frubeck. 2009). The prevalence of obesity has more than doubled since 1980 and there is now growing concern that in 2011 nearly 43 million children under the age of five were obese (WHO). Obesity predisposes to the development of the metabolic syndrome, which is characterized by impaired glucose metabolism accompanied with at least two of the following parameters; elevated blood pressure, dyslipidemia, central obesity and microalbuminuria (WHO).

Environmental factors are undoubtedly a major contributor to the prevalence of obesity in the Western world, however, it fails to explain why people living in the same environment have varying susceptibilities to develop a high body mass index (BMI). WHO defines obesity by the BMI that is a person's weight in kilograms divided by the square of his/her height in meters ( $\text{kg}/\text{m}^2$ ). BMI over or equal to 25 is overweight, whereas BMI over 30 defines obesity. The heritability of obesity has been proposed to account for 40-77% of the variation in BMI (Allison, *et al.* 1996, Haworth, *et al.* 2008). In view of the major heritability factor, the study of obesity genetics has been advantageous in clarifying the regulation of energy metabolism and in explaining the development of human obesity (Ramachandrappa & Farooqi. 2011). Moreover, transgenic animal models have nonetheless proven to be useful in understanding the molecular and physiological basis of obesity and human disease. The considerable number and complex regulation of the genes involved in obesity has naturally raised more questions than solutions about metabolic regulation.

The pro-opiomelanocortin system (POMC) is part of a complex network of neurons governing the physiological and behavioral responses involved in obesity (Garfield, *et al.* 2009). POMC derived melanocortin peptides are downstream mediators of leptin, a hormone that closely correlates with body adiposity and the long-term regulation of food intake and energy expenditure. The POMC derived peptides, particularly the melanocortins have been shown to exert multiple physiological effects both centrally and in the periphery.

In order to investigate the central role of neuropeptides in obesity, lentiviral gene delivery vectors expressing biologically active melanocortin peptides were produced and their site-specific role investigated in key central areas of metabolic regulation in mice in this thesis work.

## 2. REVIEW OF LITERATURE

### 2.1 GENERAL BACKGROUND

#### 2.1.1 *Regulation of energy balance*

The central nervous system is a key regulator of energy homeostasis by responding to anorexigenic (factors that reduce hunger) and orexigenic (factors that increase hunger) signals both centrally and peripherally. It is essential that there is a balance between energy intake and energy expenditure in order to maintain normal body weight. The regulatory pathways governing body energy homeostasis are complex and despite the prevalence of obesity today, many individuals do seem to be able to adapt to the energy rich environment.

The prevailing knowledge about basic physiology has laid the foundation for the theories about the regulation of energy homeostasis. One of the first of these was the “glucostatic theory” formally proposed by John Mayer, which postulated that the rise and fall in blood glucose levels were regulating feeding (Mayer. 1953). As the glucostatic theory focused on short-term regulation, the concept adipostat theory introduced long-term regulation of energy balance (Mayer. 1955). The theory of regulation of body homeostasis by negative-feedback loops proposed by Cannon in 1932 introduced the concept where an organism employed a reference signal or a “set-point” to a homeostatic signal, which was defended by compensatory mechanisms (Cannon. 1932). Richter introduced the aspect of instinctive behavior as ways to defend these homeostatic “set-points” (Richter. 1942). Early on, the CNS was seen as the target of these signals and obesity was contributed to anatomical abnormalities associated with this organ. Although damage inflicted on the basomedial hypothalamus was known to induce obesity in humans as early as in 1840 (Mohr. 1993), it was abnormalities in the pituitary gland that were initially thought to be the cause of the endocrine imbalance (Babinski. 1900, Frohlich. 1902). Indeed, the neuronal populations of POMC and AGRP/NPY in the basomedial hypothalamus that were later found to govern the regulation of feeding and body energy homeostasis.

##### 2.1.1.1 *LONG TERM SIGNALS OF ENERGY STATE*

In mammals, adipose tissue serves the primary site for long-term store of energy. Adipocytes secrete leptin, a hormone that correlates with total fat mass and mediate information about energy storages to the central nervous system (CNS). The optimal function of adipose tissue as an endocrine tissue is fundamental for health and deficiency in leptin or leptin receptor signaling causes severe obesity (Campfield, *et al.* 1995, Halaas, *et al.* 1995, Stephens, *et al.* 1995, Zhang, *et al.* 1994). Several areas of the CNS essential for the regulation of body metabolism harbor leptin receptors, and the activation of these impact energy metabolism in addition to the gonadal, thyroid and adrenal axes (Ahima, *et al.* 1996). Starvation and the subsequent decreases in fat reserves decrease the level of

circulating leptin and activate orexigenic pathways (Frederich, *et al.* 1995). In obesity, prolonged exposure to elevated levels of leptin has been associated with the increase in sympathetic nervous system activity; these nerves are also involved in the mobilization of lipids (Bartness & Song, 2007). The elevation of sympathetic tone also affects many other organs such as blood vessels, kidney, and heart since these are all innervated by postganglionic sympathetic nerves.

### 2.1.1.2 *GLUCOSE HOMEOSTASIS*

The supply of nutrients is essential to all living creatures. Despite an adaptation to varying environments and food sources, the brain and muscle cells of higher mammals prefer carbohydrates as their source of energy. Carbohydrates are stored as glycogen throughout the body, especially in muscle cells and the liver. Moreover, the level of glucose in the bloodstream is tightly regulated in order to maintain a steady supply of energy to maintain a conscious state without it reaching toxic concentrations. Glucagon and insulin secreted by the pancreatic islets of  $\alpha$ - and  $\beta$ -cells respectively, share the main responsibility for regulating blood glucose levels (Unger & Cherrington, 2012). Insulin decreases blood glucose levels by increasing the uptake of glucose by cells by inducing recruitment of glucose transporters to the cell membrane in the liver and other peripheral tissues and by decreasing gluconeogenesis in the liver. On the other hand, glucagon increases gluconeogenesis and in the liver and the release of stored glycogen as glucose primarily from the liver. Glycogen can be synthesized by the liver in active process called glycogenesis, converting metabolites from both protein and fat into glycogen. In obesity, the excess supply of nutrients increases the amounts of fatty acids and glucose to be removed from the bloodstream and this requires the synthesis of increased amounts of insulin. Elevated and prolonged exposures to circulating insulin levels lead to the desensitization of the insulin response, which further increases the synthesis of insulin and causes more stress on the pancreas. Ultimately, prolonged inflammation and stress leads to the fibrosis and destruction of the insulin producing cells of the pancreas, resulting in the development of diabetes.

### 2.1.1.3 *ENERGY INTAKE*

Energy intake is regulated by a plethora of factors governing meal initiation, termination, and frequency and in humans, also social factors. Moreover, the energy requirements modulate the balance between orexigenic and anorexigenic signals and this impacts on both energy expenditure and meal frequency.

There are both hormonal and neural factors governing meal initiation. Positive associations to a particular food source are mediated through cues from both visual and olfactory sensory neurons that help to alert that it is mealtime. In the CNS, the secretion of orexigenic peptides increase hunger and food intake, whereas the effects of anorexigenic peptides are inhibitory. Ghrelin, a gut-derived hormone stimulates feeding and is secreted during meal intervals and peak its levels before meal initiation. The effects of ghrelin are mediated via afferent neurons to the CNS. The gut plays a role also in meal termination through the secretion of cholecystokinin (CCK), which is a gut-

derived hormone secreted during mealtime. Together with the stimulation of mechanical stretch receptors in the gut wall, the effects of CCK on satiety are mediated by receptors on vagal afferent neurons projecting to the brain stem. In humans, social factors can greatly influence meal size. The term “social facilitation of eating behavior”, describes how the number in the company during a mealtime increases the amount of calories ingested (De Castro. 1995).

#### 2.1.1.4 ENERGY EXPENDITURE

Under normal circumstances, total energy requirements exist in a balance with total energy expenditure. However, changes in energy intake can influence energy expenditure to some extent. The total expenditure of energy (TEE) is composed of resting energy expenditure (REE), active thermogenesis, the thermic effect of food and physical activity, which all show significant individual variances. REE accounts for almost two thirds of the daily energy requirement. Many different aspects of normal body function require energy. For instance, the brain and smooth muscle cells of the heart, thorax, gut and intestines require a constant supply of energy in the form of glucose. Furthermore, energy intake requires a large input of energy from the smooth muscle cells surrounding the gut walls, in order to mechanically process food. Thermogenesis is essentially a byproduct of cellular work, however, many mammals are able to produce heat in metabolically active fat tissues, named brown adipose tissue (BAT). In rodents, BAT is activated foremost by cold exposure, generating heat in the vicinity of vital organs such as kidneys, heart as well as around major blood vessels. Food ingestion of high fat diets has also been shown to activate BAT and in recent human studies active BAT has been detected in healthy adults after cold exposure (Virtanen, *et al.* 2009). Thermogenesis by BAT is actively regulated in the CNS by several factors such as insulin, leptin, CRF and serotonin and inhibited by at least two neuropeptide Y (NPY) and galanin (Morrison SF 2014). In rodents, sympathetic outflow neurons from the hypothalamus release noreadrenaline that activates  $\beta$ 3-adrenoceptors in BAT. The stimulation of  $\beta$ 3- adrenoceptors activates intracellular signaling pathways that promote the expression of uncoupling protein 1 (UCP-1), which drives thermogenesis.

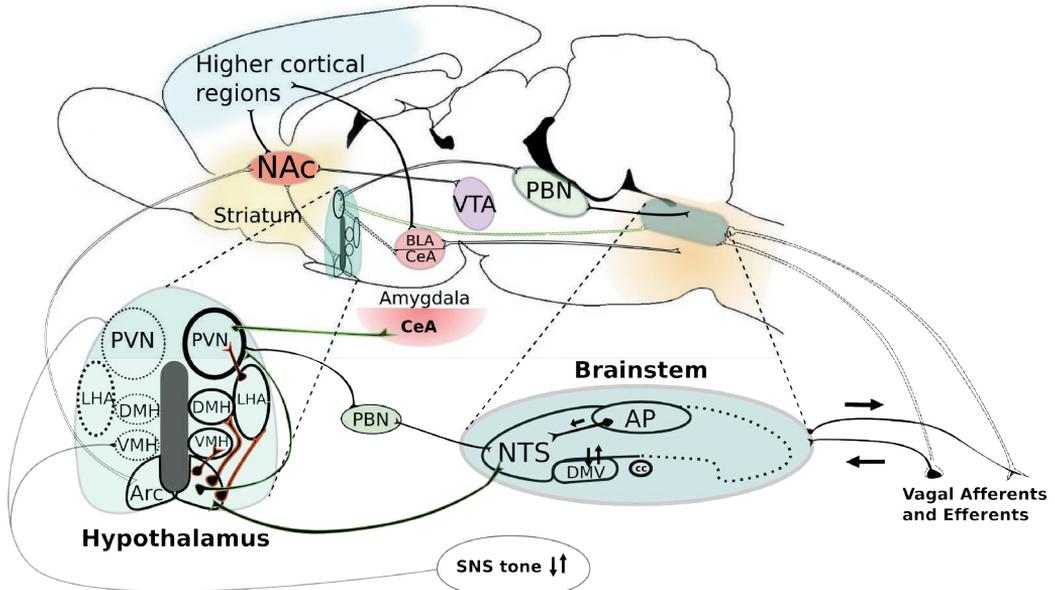
#### 2.1.1.5 CENTRAL REGULATION OF ENERGY BALANCE

The CNS receives its metabolic input both through humoral factors and direct signals from vagal afferent neurons. The hypothalamus is considered as the main central origin of energy control, being affected mainly by humoral effector molecules such as leptin, and insulin. The brain stem additionally receives humoral signals from glucose, ghrelin and neuronal signals from vagal afferent neurons. The vagal afferent signals to the brain stem originate from the mouth, esophagus, stomach, intestine and liver. Moreover, the forebrain also has a role in the control of eating through the reward pathway. Energy expenditure through thermogenesis is a centrally controlled process where the stimulation of SNS outflow neurons activates BAT to produce heat. The forebrain, caudal brain stem and the hypothalamus are linked together through several different and complex neural pathways. Furthermore, most of these neuronal pathways are regulated through negative feedback and there are several overlapping functions.

The most extensively studied feeding center, the hypothalamus is a prime example of the complexity of neuronal pathways. The arcuate nucleus (ARC) of the hypothalamus is composed of the orexigenic NPY/AGRP- and anorexigenic POMC-neurons. Both of these neuronal populations express receptors for serotonin, leptin and insulin and stimulation of POMC neurons release alpha-MSH ( $\alpha$ -MSH) and gamma-MSH ( $\gamma$ -MSH) while NPY/AGRP neurons release neuropeptide Y (NPY), AGRP and GABA. Some of these targets of these products are second-order neurons of the paraventricular nucleus (PVN). The ARC AGRP/NPY neurons project to the orexigenic centers of the lateral hypothalamic area (LHA) and the ventromedial nucleus (VMH). Moreover, the AGRP/NPY neurons of the dorsomedial nucleus of the hypothalamus (DMH) also innervate to the PVN to inhibit food intake. The hypothalamus also harbors other neuronal networks involved in energy metabolism. For instance, the lateral hypothalamic area receives orexigenic signals from the nucleus accumbens (NAc) in the forebrain and in response it releases orexin and melanin-concentrating hormone (MCH). The hypothalamus is also a key regulator SNS activity *i.e.* both the VMH and the PVN stimulate whereas the LHA outflow inhibits SNS neurons in the spinal cord. The SNS innervates many important organs and tissues such as heart, blood vessels, kidney and adrenal glands that are responsible for hemodynamics. Moreover, SNS innervates also important metabolic tissues such as the pancreas, WAT and BAT where increased SNS activity induces thermogenesis. (Williams & Frubeck. 2009)

The caudal hindbrain is also an important regulator of metabolism. The area postrema (AP), a target of circulating humoral factors, mediates information through its connections to the nucleus tractus solitarius (NTS). Moreover, the NTS collates a large input of information related to feeding from the periphery through neuronal signals from the afferent neurons. The dorsal motor nucleus of the vagus (DMV) communicates with the NTS and affects peripheral organs via the efferent neurons. Moreover, the NTS is also connected to the oral motor system to affect meal initiation and termination. The hypothalamus and the brain stem are interconnected through several distinct neural projections. For instance, orexinergic neuronal projections from the NTS to the hypothalamus are linked via the parabrachial nucleus (PBN) and the POMC projections from the PVN and the ARC are directly connected with the NTS. The brain stem also largely influences basolateral amygdala (BLA) and the nucleus accumbens (NAc) of the forebrain, which are key regulators of reward. (Williams & Frubeck. 2009)

In obesity, the forebrain is mostly recognized for its involvement in the reward pathway, mediating orosensory pleasure and regulating food intake. It is significant that the reward pathways are able to impact normal body homeostasis by regulating the hedonic energy intake. The neurotransmitters dopamine, GABA, acetylcholine and the endocannabinoids are central mediators of the effects in the forebrain. The endocannabinoids control food preference through endocannabinoid receptors in NAc and in the hypothalamus. The NAc together with the central nucleus of the amygdala (CeA) are involved in opioid mediated eating behavior, while the BLA and higher cortical regions controls food palatability (Balleine, *et al.* 2003). The neural pathways involved in the regulation of body metabolism in the rodent brain are visualized in Figure 1.



**Figure 1.** Neural pathways in body metabolism in rodents. Orexigenic (red) and anorexigenic (green) projections. Hypothalamic regions; Arcuate nucleus (ARC), Ventromedial hypothalamus (VMH), Dorsomedial hypothalamus (DMH), Lateral Hypothalamus (LHA), Paraventricular nucleus (PVN). Structures of the Brain stem; Area postrema (AP), Nucleus tractus solitarius (NTS), Dorsomotor nucleus of vagus (DMV), Striatum; Nucleus accumbens (NAc). Mesencephalon; Ventral tegmental area (VTA), Parabrachial Nucleus. Amygdala; Basolateral complex (BLA) and Central nucleus (CeA), Sympathetic nervous system (SNS). Background information for the generation of figure 1 was obtained from (Williams & Frubeck. 2009).

### 2.1.2 Genetics of obesity

Genes, environmental and social factors contribute to the prevalence of obesity today. It has been proposed that obesity is largely genetically determined, and that changes in the expression of genes and genetic mutations are responsible for as much as 77% of the prevalence of obesity (Haworth, *et al.* 2008). The environmental factor is major contributor to the prevalence of obesity, but it fails to explain why people living in the same environment have varying susceptibilities to develop severe obesity. The progress of finding susceptibility genes and factors that contribute to the development of obesity has been slow and has mostly been determined in monogenic diseases and in genetic syndromes. There are many mutations that have been identified in obesity affecting the CNS and the function of adipose tissue. Animal models of obesity have been useful for investigating metabolic disease and many of the diseases affecting these have proved to be translational to humans. Environmental factors, such as exposure to energy rich diets are often required for the development of obesity. Moreover, it has been demonstrated that in certain populations, there will always be subjects of low- and high-gainers complicating the interpretation of the true effects of genes (Bouchard. 1991). The existence of high and low-gainers may be due to epigenetic factors since mice of

the same genetic strain show significant alterations in the expression of genes related to adipose tissue function (Koza, *et al.* 2006). Secondly, social and environmental stressors have an important impact on feeding behavior and also affect the regulation of energy balance (De Castro, 1995). A variety of stress-evaluation tests have been developed for animals in order to understand the impact of behavior and social factors on genes and diets or obesity treatments, however, many of these have proved inadequate since they cannot be translational to the human disease. The reward pathways in the CNS are especially important in human obesity and recently there have been advances in measuring palatability and food preference also in animals. The genes that cause obesity in humans mostly involve mutations in adipose tissue function and regulatory pathways in the CNS. The genes of modern humans seem to be maladapted to cope with today's energy rich environment. Mutations which affect a combination of genes are part of a larger set of metabolic diseases known as polygenic or common disorders, whereas the most severe cases of obesity involve monogenic mutations.

The monogenic forms of human obesity are severe cases of early onset obesity and involve mutations in single genes such as leptin. In humans, a leptin mutation can cause severe obesity from a young age although this kind of obesity is treatable by daily injections with a recombinant protein. Up to 3 % of patients with severe obesity have been identified as carriers of a dysfunctional leptin gene (Farooqi, 2007). There is evidence that the downstream signaling pathways of leptin are equally important. For instance POMC and its derivatives are also important for normal body homeostasis *i.e.* some subjects with null mutations in the POMC gene are hyperphagic and obese from an early childhood. Characteristic features of individuals with a dysfunctional POMC gene is that they are ACTH deficient and show hypopigmentation of the hair and skin (Krude, *et al.* 1998). There are also well-described point mutations in the POMC gene leading to the loss of parts of the pro-peptide encoding for  $\beta$ - and  $\alpha$ -MSH (described in detail in later chapters) (Biebermann *et al.*, 2006; Y. S. Lee *et al.*, 2006). Therefore, mutations in the enzymes involved in the processing of POMC, the prohormone convertase 1 (PCSK1) and carboxypeptidase E (CPE) genes can cause obesity in humans. Mutations in the receptors of the melanocortin peptides such as the MC4R are thought to be responsible for 5-6 % of all early onset obese patients (Farooqi, *et al.* 2003). There are also several identified mutations in the molecules downstream of MC4R such as in the brain-derived neurotrophic factor (BDNF), which is a part of a larger set of growth factors that activate tropomyosin-related kinase B (TrkB) (Xu, *et al.* 2003). Mutations and changes in the BDNF loci are also associated with early-onset obesity (Han, *et al.* 2008). Mutations and translocations in the hypothalamic transcription factors such as the single minded 1 (SIM1) thought to be located downstream of MC4R, evoke severe obesity in a manner similar to MC4R mutations (Hung, *et al.* 2007). The FTO gene mutation has been identified in genome wide association studies (GWAS) and is associated in homozygotes with a 1,67-fold increase in obesity probability and a 3-4kg increase in body weight (Frayling, *et al.* 2007). FTO is expressed in the hypothalamus and is linked to energy intake rather than energy expenditure (Cecil, *et al.* 2008). In experimental animals, the overexpression of the FTO gene in mice causes obesity while mice with a non-functional gene are small and exhibits increases in energy expenditure (Church, *et al.* 2010).

## 2.2 MELANOCORTIN SYSTEM

The melanocortin system consists of the pro-peptide POMC and several downstream cleavage products, which mediate their actions through melanocortin receptors in key neuronal populations in the CNS. Two different 1<sup>st</sup> order neuronal populations, the POMC expressing neurons and AGRP/NPY expressing neurons receive information about nutritional status from the periphery and affect behavior and metabolism depending on which population dominates. Circulating humoral and nutritional factors such as leptin, insulin and glucose affect the plasticity of POMC neurons. The central melanocortin system regulates peripheral lipid and glucose metabolism independently from energy intake and energy expenditure (Nogueiras, *et al.* 2007) and a significant involvement in hemodynamic processes and in inflammation (Humphreys, *et al.* 2011).

### 2.2.1 POMC

Pro-opiomelanocortin (POMC) is a 31 kDa pro-peptide which is expressed in the pituitary, medulla and in distinct areas of the CNS and in the periphery. All POMC-derived peptides present in the bloodstream are synthesized from the anterior pituitary with the only exception being the placenta. The distribution, synthesis and composition of these peptide fragments are tissue specific and the processing mechanisms of POMC permit the synthesis of a variety of different regulatory peptides such as ACTH,  $\beta$ -endorphin and the three melanin stimulating hormones alpha, beta and gamma ( $\alpha$ -,  $\beta$ -,  $\gamma$ -MSH). Other less prominent peptides derived from POMC are the Corticotrophin-Like Intermediate Protein (CLIP) and beta-lipotropin ( $\beta$ -LPH) (Figure 2).

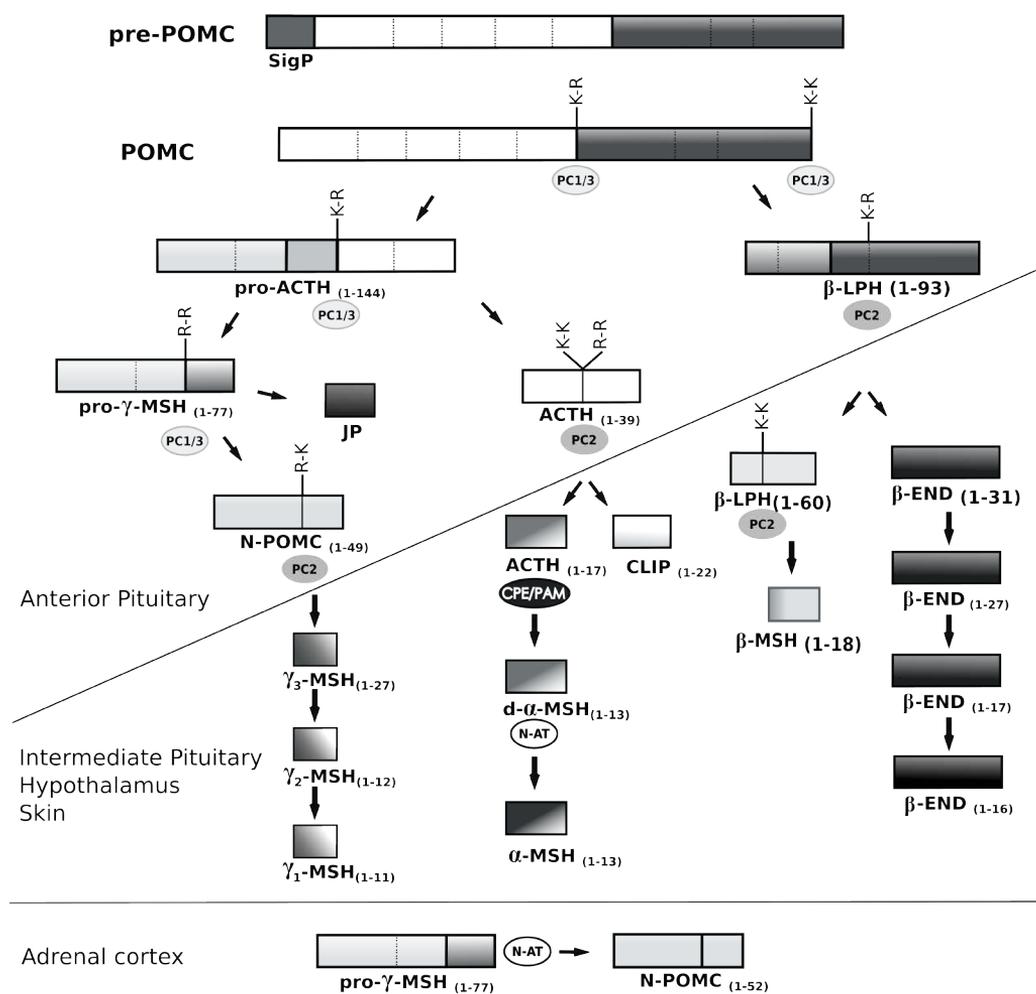
In the CNS, POMC derived melanocortin peptides regulate energy balance mainly through the activation of MC4R (Butler, *et al.* 2000, Elmquist, *et al.* 1999, Huszar, *et al.* 1997). The natural antagonist of melanocortin receptors, the agouti related peptide (AGRP), exerts an orexigenic effect on energy metabolism. The melanocortins, particularly  $\alpha$ -MSH, have also been shown to harbor anti-inflammatory properties and to modulate hemodynamics and sympathetic tone (Baltatzi, *et al.* 2008, Catania, *et al.* 2010, Humphreys, *et al.* 2011). The POMC derived endogenous opioid  $\beta$ -endorphin has also been shown to influence energy balance and  $\beta$ -lipotropin ( $\beta$ -LPH), the precursor of both  $\beta$ -endorphin and  $\gamma$ -LPH is known to be a strong inducer of lipolysis (Bodnar & Klein. 2005, Eichhorn, *et al.* 1995, Richter, *et al.* 1990). Both  $\beta$ -endorphin and its precursor  $\beta$ -LPH are jointly released in physiologically stressful situations such as in pain and during physiological exercise (Petraglia, *et al.* 1990, Salar, *et al.* 1991).

The expression of the POMC gene in the anterior pituitary is increased by corticotropin-releasing hormone (CRH) and vasopressin and inhibited by glucocorticoids. The stress induced increase in POMC gene-expression in the pituitary also increases ACTH secretion. ACTH, a known ligand of MC2R, increases the production of corticosteroids from adrenal membranes. The CLIP peptide has been shown to trigger and prolong the duration of paradoxical sleep in the dorsal raphe nucleus (Cespuglio, *et al.* 1995, Wetzell, *et al.* 1994).

### 2.2.1.1 POMC PROCESSING

The processing mechanisms of the precursor POMC allow for tissue specific synthesis of different peptides and peptide compositions. The molecular basis for the processing of POMC occurs by the recognition of eight different basic amino acid pairs and one quadruplet in the pro-peptide sequence, which is cleaved by prohormone convertases (PC) PC1/3 and PC2 (Figure 2). PCs belong to the subtilisin family of  $\text{Ca}^{2+}$ -dependent serine proteinases (Seidah, *et al.* 1990, Seidah, *et al.* 1991) and the cleavage of POMC can be regulated by the availability of PC enzymes. The activity of PC1/3 is inhibited by the neuroendocrine-specific-inhibitor proSAAS and PC2 by 7B2 (Fricker, *et al.* 2000, Lindberg, *et al.* 1995).

Processing of POMC in the pituitary is a classical example of the differences in the pro-hormone modification since in this organ, POMC is more extensively cleaved in the intermediate than in the anterior lobe (Figure 2). The corticotropic cells are responsible for the synthesis of POMC in the anterior lobe and processing by PC1/3 results in the generation of pro- $\gamma$ -MSH, pro-ACTH and  $\beta$ -LPH (Eipper & Mains. 1980). Pro-ACTH can be further cleaved by PC1/3 to form N-terminal pro-opioid corticotropin (N-POC), joining peptide and ACTH (Figure 2). In the melanotropes of the intermediate lobe of the pituitary gland, in the skin and in hypothalamus, ACTH<sub>1-39</sub> is cleaved by PC2 to form CLIP, ACTH<sub>1-17</sub> and  $\beta$ -LPH.  $\beta$ -LPH is further cleaved by PC2 to form  $\beta$ -endorphin<sub>1-31</sub> and  $\gamma$ -LPH (Mains & Eipper. 1981). A small portion of  $\beta$ -LPH is metabolized to  $\beta$ -endorphin in the anterior pituitary.  $\beta$ -endorphin<sub>1-31</sub> can be further targeted in the C-terminus to yield  $\beta$ -endorphin<sub>1-26</sub>,  $\beta$ -endorphin<sub>1-27</sub> and a dipeptide glycylglutamine (Boileau, *et al.* 1982, Mains & Eipper. 1981, Smyth & Zakarian. 1980, Smyth, *et al.* 1988). The N-terminal fragment of pro- $\gamma$ -MSH is partially cleaved at an arginine-lysine site to produce both N-POMC<sub>1-49</sub> and Lys- $\gamma$ <sub>3</sub>-MSH (Bennett. 1986). In humans, N-POMC is processed to  $\gamma$ -LPH and  $\beta$ -MSH. Moreover, in the adrenal cortex, the adrenal secretory protease (AsP) can act upon pro- $\gamma$ -MSH two residues downstream from the dibasic site to produce a mitogen, N-POMC<sub>1-52</sub>. In addition, the synthesis of  $\alpha$ -MSH requires the activity of both carboxypeptidase (CPE) and peptidyl  $\alpha$ -amidating monooxygenase (PAM) which first produce desacetyl- $\alpha$ -MSH (da- $\alpha$ -MSH) and further by N-acetyltransferase (N-AT) to form the mature  $\alpha$ -MSH. N-AT also diminishes the opiate activity of  $\beta$ -endorphin (Figure 2). The availability of  $\alpha$ -MSH in active sites is regulated by a degrading enzyme called propylcarboxypeptidase (PRCP) (Wallingford, *et al.* 2009), which targets the active  $\alpha$ -MSH<sub>1-13</sub> in the C-terminus producing the inactive  $\alpha$ -MSH<sub>1-12</sub>-form. Excess pro-POMC is produced in order to ensure the availability of the precursor for the rapid synthesis of ligands to ensure receptor activation (Pritchard & White. 2007).



**Figure 2.** The processing of POMC by PC1/3 and PC2 enzymes, which are expressed in a tissue dependent manner. Figure modified from (Mountjoy. 2010)

### 2.2.2 Melanocortins

The melanocortins are a well-studied group of neuropeptides. In 1919 Atwell and coworkers isolated a hormone that later would be called melanocyte stimulating hormone due to the way it stimulated pigment cells of both mammalian and amphibian origin to produce melanin (Fitzpatrick & Lerner. 1953, Gordon. 1953). The POMC derived peptides, particularly ACTH and the melanocortins are structurally similar and share a conserved core region (Met-Glu-His-Phe-Arg-Trp) where Glu is substituted for a Gly in the  $\gamma$ -MSH peptides (Table 1). The MSH peptides and their receptors are all part of the melanocortin system, which is centrally part of a larger neuronal network regulating and sensing the energy state.

**Table 1.** Comparison of POMC derived ACTH, melanocortins and their analogues. Modified from (Tatro, 1996).

D-Trp- $\gamma$ -MSH	Tyr-Val- <b>Met-Gly-His-Phe-Arg-D-Trp</b> - Asp-Arg-Phe-Gly
ACTH	Ser-Tyr-Ser - <b>Met-Glu-His-Phe-Arg-Trp</b> - Gly-Lys-Pro-Val- + 26 Amino acids
$\alpha$ -MSH	Ac-Ser-Tyr-Ser - <b>Met-Glu-His-Phe-Arg-Trp</b> - Gly-Lys-Pro-Val
$\gamma$ 2-MSH	Tyr-Val - <b>Met-Gly-His-Phe-Arg-Trp</b> - Asp-Arg-Phe-Gly
(Lys)- $\gamma$ 1-MSH	(Lys)-Tyr-Val - <b>Met-Gly-His-Phe-Arg-Trp</b> - Asp-Arg-Phe-NH <sub>2</sub>
(Lys)- $\gamma$ 3-MSH	(Lys)-Tyr-Val - <b>Met-Gly-His-Phe-Arg-Trp</b> - Asp-Arg-Phe-Gly- + 14 Amino acids
$\beta$ -MSH *	Asp-Ser-Gly-Pro-Tyr-Ly: <b>Met-Glu-His-Phe-Arg-Trp</b> - Gly-Ser-Pro-Lys-Asp
NDP-MSH	Ac-Ser-Tyr-Ser - Nle- <b>Glu-His-D-Phe-Arg-Trp</b> - Gly-Lys-Pro-Val-NH <sub>2</sub>
Melanotan	Nle-Asp- <b>His-D-Phe-Arg-Trp</b> - Lys
SHU9119	Nle-Asp- <b>His-D-Nal-Arg-Trp</b> - Lys

Conserved amino acids shown in **bold** (Lys) = may or may not be present

Ac = N-acyl

\* = Bovine

NDP-MSH and melanotan are synthetic analogues of  $\alpha$ -MSH

SHU9119 is an antagonist of both MC4R and MC3R

### 2.2.2.1 $\alpha$ -MSH

The most widely studied and best known POMC derived melanocortin,  $\alpha$ -MSH, has been shown to possess several different functions both peripherally and centrally. Among the central properties of  $\alpha$ -MSH is to mediate the anorexigenic effects of leptin, which is produced by the fat storing cells or adipocytes in the periphery. POMC neurons play a key role in mediating the effects of leptin are in hypothalamus (Cowley, *et al.* 1999, Elmquist, *et al.* 1999). Here,  $\alpha$ -MSH is released by POMC neurons and it acts on downstream neurons in the paraventricular nucleus known to express melanocortin receptors, MC4R, and also to a smaller degree MC3R (Adan, *et al.* 1997, Chen, *et al.* 2000). POMC neuronal projections are also able to affect other brain regions such as the NTS of the brain stem where  $\alpha$ -MSH can influence meal size after binding to local melanocortin receptors (Zheng, *et al.* 2010). Short-term intracerebroventricular administration of  $\alpha$ -MSH or synthetic analogues have been shown to decrease feeding, reduce adiposity and improve glucose metabolism (McMinn, *et al.* 2000, Murphy, *et al.* 1998, Nogueiras, *et al.* 2007).

There is significant overlap in the central effects of  $\alpha$ -MSH. Skibicka and Grill compared the effects of a melanocortin agonist in different brain regions which were known to be linked to sympathetic outflow with respect to feeding, locomotor activity and core body temperature.  $\alpha$ -MSH exerted an anorexic response in the PVN and the retrochiasmatic area (RCh) of the hypothalamus and the NTS and pontine parabrachial nucleus (PBN) of the brain stem, whereas core body temperature was increased by its ability to stimulate the rostral ventrolateral medulla (RVLM) of the brain stem. Interestingly, only the administrations of  $\alpha$ -MSH to the PVN and the PBN were able to stimulate spontaneous locomotor activity (Skibicka & Grill, 2009). In addition,  $\alpha$ -MSH has been able to correct hyperphagia in leptin and POMC deficient animals when the peptide was administered peripherally (Cettour-Rose & Rohner-Jeanraud, 2002, Yaswen, *et al.* 1999).

There is emerging evidence demonstrating the link between the melanocortins and the HPA axis. For instance, neurons expressing  $\alpha$ -MSH and AGRP located in the ARC innervate the PVN and the medial amygdala, which are brain regions known to regulate the HPA-axis. In line with this hypothesis, stress induced anorexia in rodents can be reversed following intracerebroventricular (ICV) injections of melanocortin antagonists (Liu, *et al.* 2007, Vergoni, *et al.* 1999). Moreover, the melanocortin system is associated with adrenal function, as the expression levels of MC4R are not elevated in adrenalectomized rats during re-feeding (Germano *et al.* 2008). Centrally,  $\alpha$ -MSH also affects blood pressure through the sympathetic system due to the activation of the MC4R (Butler & Cone. 2002, Hill & Dunbar. 2002, Humphreys, *et al.* 2011, Matsumura, *et al.* 2002, Ni, *et al.* 2006).

The effects of  $\alpha$ -MSH as an anti-inflammatory mediator have been well studied both *in vitro* and *in vivo*. A central mechanism for these effects is the capability of  $\alpha$ -MSH to inhibit the activation of the nuclear transcription factor NF- $\kappa$ B, which controls the expression of many of the factors involved in inflammation *e.g.* cytokines and their receptors, growth factors, chemokines and adhesion molecules (Catania, *et al.* 2010). Moreover,  $\alpha$ -MSH has been shown to induce the expression of a known anti-inflammatory mediator, IL-10 (Bhardwaj *et al.*, 1996). In addition,  $\alpha$ -MSH has protective effects on the vasculature by inhibiting the expression of vascular E-selectin and vascular cell adhesion molecule (VCAM)-1, two compounds capable of triggering deleterious vascular damage (Scholzen *et al.*, 2003). There is also recent data showing that  $\alpha$ -MSH is able to protect against vascular damage by regulating the availability of vascular nitric oxide (NO) (Rinne, *et al.* 2013).

PRCP governs the availability of active  $\alpha$ -MSH in some nerve terminals. In line with this proposal, PRCP null mice have elevated levels of  $\alpha$ -MSH and display a characteristic lean phenotype (Wallingford, *et al.* 2009). PRCP is widely distributed in the nervous system and the periphery. Centrally, PRCP is found abundantly expressed in the lateral hypothalamic perifornical region, an area known to trigger orexinergic signaling circuits and the paraventricular and in the ARC of the hypothalamus (Abbott, *et al.* 2000, Bittencourt, *et al.* 1992, de Lecea, *et al.* 1998, Horvath, *et al.* 1999, Sakurai, *et al.* 1998, Skofitsch, *et al.* 1985, Trivedi, *et al.* 1998, Wallingford, *et al.* 2009).

#### 2.2.2.2 $\beta$ -MSH

$\beta$ -MSH is the least studied melanocortin peptide because it is not supported by the mouse genome. This is because in mice there is the lack of the proximal di-basic site necessary for the proteolytic cleavage that produces the active peptide. Assumptions have therefore been made that  $\alpha$ -MSH, which is expressed in many organisms, is the main central agonist of MCR. Conversely,  $\beta$ -MSH has been implicated in human obesity and mutational studies have shown that the POMC gene displays heterozygous mutations close to the  $\beta$ -MSH peptide sequence (Challis, *et al.* 2002, Hinney, *et al.* 1998, Hinney, *et al.* 2006, Lee, *et al.* 2006). One of these mutations causes a fusion peptide to be formed with  $\beta$ -endorphin, which has been postulated to have a dominant-negative effect (Challis, *et al.* 2002). Loss of function mutations in the  $\beta$ -MSH gene could hypothetically produce an obese phenotype with normal cortisol levels

as compared to the loss of function mutations in the ACTH coding region (Harrold & Williams. 2006).  $\beta$ -MSH and the truncated form ( $\beta$ -MSH<sub>5-22</sub>) found in human hypothalamus are both capable of inhibiting feeding in a similar manner to  $\alpha$ -MSH (Abbott, *et al.* 2000, Bertagna, *et al.* 1986). Additionally in rats, a fragment of  $\beta$ -MSH ( $\beta$ -MSH<sub>4-7</sub>) has been shown to influence long-term satiety (Kotov, Martynov, Tolypgo, Kelesheva, & Sorochinskaia, 1984). A comparison of melanocortin peptides and their binding affinity for their receptors in transfected cell lines and in brain homogenates isolated from the rat hypothalamus has shown that  $\beta$ -MSH has higher affinity for the MC4R than  $\alpha$ -MSH (Harrold, *et al.* 2003, Schioth, *et al.* 1996). A histological analysis of the expression of ACTH,  $\alpha$ - and  $\beta$ -MSH in human post-mortem ARC samples revealed that  $\beta$ -MSH was expressed in human POMC neurons (Biebermann, *et al.* 2006). Food restriction is able to affect the level of  $\beta$ -MSH whereas the concentration of  $\alpha$ -MSH remains unchanged (Harrold, *et al.* 1999, Harrold & Williams. 2006). Furthermore, hypothalamic levels of  $\beta$ -MSH have been shown to negatively correlate with the plasma insulin concentration, whereas that of  $\beta$ -MSH is essentially unaffected by changes in levels of leptin (Cheung, *et al.* 1997). Similarly to other agonists of MCR,  $\beta$ -MSH has also been shown to inhibit NF- $\kappa$ B and is therefore a potent anti-inflammatory peptide (Muceniece, *et al.* 2005).

### 2.2.2.3 $\gamma$ -MSH

$\gamma$ -MSH exists in three different isoforms with varying affinities for the MC3R but its affinity for the MC4R is lower (Lindblom, *et al.* 1998, Roselli-Reh fuss, *et al.* 1993, Schioth, *et al.* 1996).  $\gamma$ -MSH is produced in the intermediate lobe of the pituitary where it potentiates ACTH-induced steroidogenesis (Farese, *et al.* 1983, Pedersen, *et al.* 1980, Seger & Bennett. 1986).  $\gamma$ -MSH is able to influence hemodynamics by controlling the sympathetic outflow and baroreflex function (Humphreys, *et al.* 2011). Furthermore,  $\gamma$ -MSH is natriuretic by directly affecting renal sodium excretion (Lymangrover, Buckalew, Harris, Klein, & Gruber, 1985). A few studies have also indicated that  $\gamma$ -MSH may be involved in the activation of the vasopressin pathway in the anteroventral region of the third ventricle (Callahan, *et al.* 1988, Gruber & Eskridge. 1986). Similarly to other melanocortins,  $\gamma$ -MSH has been shown to be anti-inflammatory and has been implicated in sexual behavior (Cragolini, *et al.* 2000, Getting, *et al.* 2001, Xia, *et al.* 2001).

The N-terminal fragment of POMC is cleaved by PC2 and produces a 25 amino acid long peptide,  $\gamma_3$ -MSH, which can be further N-glycosylated (Oki, *et al.* 1982, van Strien, *et al.* 1995). In pituitary cells,  $\gamma_3$ -MSH is able to elevate intracellular Ca<sup>+</sup> levels in growth hormone and prolactin secreting cell lines. Interestingly this activation can be blocked only to 50 % by the use of a melanocortin receptors antagonist (Denef, *et al.* 2003). In comparison to the shorter  $\gamma$ -MSH peptides,  $\gamma_3$ -MSH includes a long C-terminal fragment. The peptide sequence of both  $\gamma_2$ -MSH and  $\gamma_1$ -MSH are similar and have an 11 amino acid long core sequence with either a glycine or an amide group in the C-terminal end, respectively.  $\gamma_2$ -MSH is also selective for the MC3R in preference over both MC4R and MC5R, however,  $\gamma_2$ -MSH shows no selectivity between the MC3R and MC5R in mice (Joseph, *et al.* 2010). Moreover,  $\gamma_2$ -MSH has

about a 3-fold lower affinity for MC receptors compared with  $\gamma_1$ -MSH (Schioth, *et al.* 1996). In addition, both  $\gamma_1$  and  $\gamma_2$ -MSH have an additional lysine in the N-terminus, which appears to be essential for their full biological activity, at least in the adrenal gland (Pedersen & Brownie. 1983). In behavioral studies, intra-VTA administration of  $\gamma_2$ -MSH induced central analgesia and catalepsy, whereas  $\gamma_1$ -MSH administration stimulated grooming behavior and increased vertical activity (Klusa, *et al.* 1999). These behavioral responses have been speculated to involve the dopaminergic mesolimbic system where (similarly to  $\alpha$ -MSH)  $\gamma_1$ -MSH causes activation whereas  $\gamma_2$ -MSH inhibition of GABA<sub>A</sub> receptors (Jansone, *et al.* 2004). This conclusion was based on studies where  $\alpha$ -MSH mediated analgesia in the VTA could not be blocked by a melanocortin antagonist (Klusa, *et al.* 1998).

The cardiovascular effects of  $\gamma$ -MSH have been well characterized. For instance, intravenous or intracarotid injection of  $\gamma_2$ -MSH has pressor and cardioaccelerator effects which are mediated by the activation of sympathetic outflow (Gruber, *et al.* 1989). Interestingly the sympathetic effects of intravenous  $\gamma_2$ -MSH were independent of both MC3R and MC4R activation pointing to the activation of an entirely different receptor, the FMRFamide gated sodium channel (Humphreys, *et al.* 2011, Li, *et al.* 1996, Ni, *et al.* 2006, Wikberg, *et al.* 2000). The FMRFamide-gated sodium channel (FMRFamide) has important cardioexcitatory and sympathoexcitatory properties and it has been implicated in the development of salt-sensitive hypertension in rats (Huang & Leenen. 2002, Nishimura, *et al.* 2000). Although  $\gamma$ -MSH is able to increase sympathetic activity by activating the FMRFamide at high doses, low doses of  $\gamma$ -MSH have been shown to increase natriuresis and to decrease salt induced hypertension (Humphreys, *et al.* 2011, Lymanrover, *et al.* 1985). Furthermore, central microinjections directed to the NTS could reduce blood pressure due to a reduction in SNS activity (De Wildt, *et al.* 1994, Li, *et al.* 1996).  $\gamma$ -MSH has therefore been postulated to be involved in baroreflex function in the NTS while the natriuretic capacity is mediated by renal MC3R (Humphreys, *et al.* 2011). In line with this theory, elevated dietary sodium dramatically increases the expression of MC3R in the renal inner medullary duct and the level of  $\gamma$ -MSH in plasma and specifically in the neurointermediate lobe of the pituitary (Mayan, *et al.* 1996, Ni, *et al.* 2006). Furthermore, PC2 deficient mice that lack the correct processing of POMC to produce  $\gamma$ -MSH develop salt-sensitive hypertension, which is corrected by infusing  $\gamma$ -MSH peptide, not  $\alpha$ -MSH (Ni, *et al.* 2003, Ni, *et al.* 2006). In addition, infusion of  $\gamma$ -MSH in MC3R-deficient mice has no effect on arterial pressure indicating that  $\gamma$ -MSH mediated signaling of MC3R is required to excrete sodium when consuming a high sodium diet (Ni, *et al.* 2003).

MC3R deficient mice have also revealed a link between hypertension and glucose metabolism (Ni & Humphreys. 2008). Salt-sensitive hypertension can be corrected by infusion of  $\gamma_2$ -MSH or blockade of adrenergic receptors and both treatments also normalize fasting glucose levels (Mayan, *et al.* 2003). In this study, treating the salt-induced hypertension with the peripherally acting vasodilator compound, hydralazine, did not alter glucose homeostasis (Mayan, *et al.* 2003). In addition, the salt-induced hypertension elevated noradrenaline levels, but were corrected by infusion of  $\gamma_2$ -MSH. Bromocriptine blockade of pituitary activity in these mice increased plasma noradrenaline levels, but this could be restored by  $\gamma_2$ -MSH administration. In summary, these effects

indicate that it is the increased sympathetic activity that is responsible for the abnormal glucose metabolism. (Ni, *et al.* 2009)

### 2.2.3 Antagonists of melanocortin action

#### 2.2.3.1 AGOUTI SIGNALING PEPTIDE

The agouti gene encodes for a peripherally expressed 131-amino-acid protein, the agouti signaling peptide (ASIP), that controls the relative amounts of eumelanin (black-brown) and pheomelanin (red-yellow) produced by hair follicles (Lu, *et al.* 1994). The agouti protein inhibits melanocortin receptor-mediated production of eumelanin by directly blocking MC1R in melanocytes. Additionally, the agouti protein is an antagonist of the MC4R (Gantz, *et al.* 1993, Lu, *et al.* 1994) and it directly modulated feeding in lethal yellow  $A^Y$  mice (Dickerson & Gowen. 1947), which ubiquitously overexpress agouti and have an obese phenotype.

#### 2.2.3.2 AGRP

In 1997 Shutter and colleagues described a novel centrally expressed 132-amino acid protein named AGRP that showed 25% homology with agouti. AGRP is expressed only in the ARC of the hypothalamus (Ollmann, *et al.* 1997, Shutter, *et al.* 1997) and is 10-fold upregulated in genetically obese  $Lepr^{db}/Lepr^{db}$  and  $Lep^{ob}/Lep^{ob}$  mice with leptin signaling deficiency (Ebihara, *et al.* 1999, Ollmann, *et al.* 1997, Shutter, *et al.* 1997). AGRP is a competitive antagonist of both MC3R and MC4R and it co-localizes to neurons that express NPY (Buch, *et al.* 2009, Chen, *et al.* 1999). More recent data suggests that AGRP actually functions as a biased agonist on the MCRs, since it selectively couples to  $G_{i/o}$ , which decreases cAMP levels (Buch, *et al.* 2009). In addition, both AGRP and  $\alpha$ -MSH promote  $\beta$ -arrestin recruitment upon binding to MCRs (Breit, *et al.* 2006). The hypothalamus NPY/AGRP expressing neurons are distinct from neighboring POMC expressing neurons (Shutter, *et al.* 1997) and project to the adjacent hypothalamic areas in the PVN, DMN and LHA (Broberger, *et al.* 1998, Hahn, *et al.* 1998). The AGRP/ NPY neurons increase food intake both by antagonizing melanocortin signaling and by increasing the expression of the fast acting orexigenic peptide NPY and GABA (Krashes, *et al.* 2013, Morton & Schwartz. 2001). Both AGRP and NPY negatively correlate with leptin and the expression of both peptides is reduced following leptin treatment (Mizuno, *et al.* 1998). The increase in AGRP in response to fasting and in genetic leptin deficiency is considerably greater in comparison to that of NPY, which is indicative of a distinct mechanism for AGRP and NPY (Morton & Schwartz. 2001). Furthermore, the orexigenic effects of central AGRP administration have been shown to endure up to a week in contrast to the relatively acute feeding response following NPY delivery which lasts for only hours (Hagan, *et al.* 2000, Rossi, *et al.* 1998).

There is recent data suggesting that AGRP also promotes changes in nutrient partitioning and lipid metabolism in efferent tissues through the reduction of sympathetic activity, which increases adiposity (Dietrich, *et al.* 2010, Joly-Amado, *et al.* 2012). As a result, ablation of AGRP neurons at the neonatal stage leads to a phenotype with

increased adiposity and with an increased lipogenesis and triglyceride content in the liver on carbohydrate rich diets (Joly-Amado, *et al.* 2012). These AGRP deficient animals use lipids as their source of energy making them indistinguishable from WT-controls on a HFD (Joly-Amado, *et al.* 2012). AGRP ablation in adult mice is survivable when the animal has developed adequate fat reserves allowing time for compensatory routes to be activated (Wu, *et al.* 2012).

Although the general view of the orexigenic action of AGRP is that it is mediated by antagonism (or rather a kind of competitive/biased agonism) of the melanocortin receptors, there are studies demonstrating alternative routes for AGRP signaling. Administration of a GABA-agonist to the PBN rescues the phenotype in AGRP ablated mice (Wu, *et al.* 2009). Krashes *et al.* demonstrated that GABA and NPY were responsible for the acute feeding effect, whereas AGRP increased food intake in the long-term after fasting (Krashes, *et al.* 2013). These observations suggest that AGRP/NPY neurons also release GABA, as both are able to induce an orexigenic response in a complementary fashion (Krashes, *et al.* 2013).

## 2.2.4 NPY

NPY was one of the first peptides to be recognized as a potent orexigenic compound; it was initially isolated from porcine brain in 1982 (Tatemoto, *et al.* 1982). The 36-amino acid peptide NPY has been highly conserved in invertebrate and vertebrate species (Larhammar, 1996) and it shows homology with the other members of the NPY peptide family, peptide YY (PYY) and pancreatic peptide (PP) (Tatemoto, *et al.* 1982). Both NPY and PYY are able to activate the same receptors, Y<sub>1</sub>, Y<sub>2</sub>, Y<sub>4</sub>, Y<sub>5</sub> and Y<sub>6</sub>, all belonging to the same family of G<sub>i</sub>-coupled receptors (Larhammar, 1996). NPY is found in the nervous system both centrally and in the periphery and is able to interact with other classical stress mediators such as sympathetic neurotransmitters (*e.g.* catecholamines and purines) as well as hormones in the HPA-axis. The general view is that one of the main functions of NPY is to act as a mediator of stress since it is known to be involved in physiological processes linked to stress behavior including feeding (Tatemoto, *et al.* 1982), cardiovascular function (Jacques, *et al.* 1996), anxiety (Giesbrecht, *et al.* 2010), learning and memory (Flood & Morley, 1989), and circadian rhythm (Sindelar, *et al.* 2005).

### 2.2.4.1 NPY AND THE REGULATION OF FOOD INTAKE

Although NPY has many different effects in the central nervous system, the effect on feeding seems to be most prominent. ICV administration of NPY increases food intake in a dose dependent manner (Clark, *et al.* 1985, Levine & Morley, 1984) and chronic administration evokes a sustained hyperphagia and increased body weight resulting in obesity (Beck, *et al.* 1992, Zarjevski, *et al.* 1993). Increased NPY expression has been demonstrated in DIO animal models and in genetically obese rodent models such as MC4R-deficient mice (Kesterson, *et al.* 1997), agouti lethal yellow (*A/a*) mice (Kesterson, *et al.* 1997), leptin signaling deficient mice and rat (Kesterson, *et al.* 1997, Sanacora, *et al.* 1990, Wilding, *et al.* 1993) and in brown-adipose deficient mice (Tritos, *et al.* 1998). Investigations into

the action of NPY in specific locations in the hypothalamus have identified a feeding response in the PVN, LHA, VMN and the perifornical area (Stanley, *et al.* 1985). LHA is an important activator of the NPY system in the ARC and NPY in turn is able to suppress LHA neurons (Della-Zuana, *et al.* 2002, Fu, *et al.* 2004, Mercer, *et al.* 2011). There is a subpopulation of neurons in the DMN that transiently expresses NPY, whereas the primary input of NPY is from neuronal ARC projections (Bai, *et al.* 1985, Bouret, *et al.* 2004, Thompson & Swanson. 1998). AAV-mediated overexpression of NPY in the LHA and DMN causes hyperphagia and weight gain (Tiesjema, *et al.* 2007, Yang, *et al.* 2009) in lean rats whereas the knock-down of NPY results in a prolonged anorexigenic response in genetically obese OLETF rats (Yang, *et al.* 2009). NPY and AGRP expression co-localize to the same neurons in the hypothalamus and these inhibit POMC neurons by a dual mechanism. NPY binds to  $Y_1$  and  $Y_2$  receptors on downstream POMC neurons inhibiting their firing rate (Acuna-Goycolea, *et al.* 2005, Cowley, *et al.* 2001, Ghamari-Langroudi, *et al.* 2005, Roseberry, *et al.* 2004) and NPY has been implicated in the direct release of  $\alpha$ -MSH from POMC neurons by binding to  $Y_5$ -receptors (Galas, *et al.* 2002). Moreover, NPY regulation is mediated by an inhibitory mechanism of GABA release in parvocellular neurons of the PVN in post-synaptic fashion (Cowley, *et al.* 1999, Melnick, *et al.* 2007). This effect is most prominent in neuronal populations expressing MC4R (Ghamari-Langroudi, *et al.* 2011). Although NPY/AGRP and POMC neurons co-regulate each other through a similar mechanism, the NPY-mediated orexigenic action in the hypothalamic neurons is not dependent on melanocortin action, evidence for an independent regulatory mechanism for NPY (Aponte, *et al.* 2011).

With respect to the potency of NPY to act as an acute stimulator of feeding in the CNS, models with both germline genetic NPY ablation and overexpression have not produced any profound metabolic phenotype in either mouse or rat backgrounds. The reason is thought to be due to compensatory mechanisms and to the plasticity of the CNS. Thus, postnatal ablation of NPY/AGRP expressing neurons causes lethal starvation (Luquet, *et al.* 2005), whereas it is survivable in neonates neonates (Luquet, *et al.* 2005) and if the animal has attained sufficient fat reserves (Wu & Palmiter. 2011). The general effects of NPY are clear if deficient animals have been crossed with pre-existing obese genetic animal models. For instance, when NPY-deficient mice are crossed with leptin deficient  $Lep^{ob}/Lep^{ob}$  mice they produce a phenotype with a reduced food intake and increased energy expenditure (Erickson, *et al.* 1996). On the other hand, if transgenic animals overexpressing NPY (NPY-OE) are presented with a palatable diet where 50% of energy source originates from sucrose, the mice show a rapid development of obesity and increased food intake as compared to WT-control animals (Kaga, *et al.* 2001). Moreover, NPY-OE mice, which overexpress NPY in their noradrenergic neurons, develop increased adiposity and impaired glucose tolerance without affecting the total body weight (Ruohonen, *et al.* 2008).

### 2.3 MELANOCORTIN RECEPTORS

The POMC derived melanocortin peptides ( $\alpha$ -,  $\beta$ - and  $\gamma$ -MSH) and ACTH are endogenous agonists, whereas agouti signaling peptide (ASIP) and AGRP are endogenous antagonists of melanocortin receptors (MCR) (Table 2). There are five known MCR subtypes all

belonging to the family of seven-transmembrane guanine nucleotide-binding protein (G-protein)-coupled receptors (GPCR) (Cone. 2000). The MCR agonists bind with high affinity to their endogenous receptors and this causes a conformation change, which activates an intracellular cyclic adenosine monophosphate (cAMP) signaling pathway. The GPCRs all share high structural homology, although the MCRs are the smallest known type of GPCRs and show high subtype-specific sequence homologies. According to sequence alignment studies, the MC4R and MC5R showing 60% homology, the MC3R and MC1R and the MC2R and MC3R show both 45% and the MC2R and MC4R show 38% homology. In structural terms, the MCRs are composed of seven  $\alpha$ -helical transmembrane domains, an extracellular N-terminus and an intracellular C-terminus. In contrast to other GPCRs, the MCRs have short amino- and carboxy-terminal ends and an exceptionally short second extracellular loop (Yang. 2011). The MCRs possess an orthosteric binding-site for the endogenous agonist in the transmembrane region, whereas the endogenous antagonist may also bind to an allosteric site located on the extracellular loop (Oosterom, *et al.* 1999, Yang, *et al.* 1999, Yang & Harmon. 2003).

Translocation to the cell surface and ability of MCRs to induce cAMP activation are modified by Melanocortin 2 receptor accessory proteins 1 and 2 (MRAP1 and MRAP2). (Cooray & Clark. 2011, Hay, *et al.* 2006). MRAP2 is primarily expressed in the CNS, with distinct expression in the cerebellum, pons and parts of the hypothalamus (Asai, *et al.* 2013, Chan, *et al.* 2011). Interestingly, MRAP2 and MC4R mRNA co-localize in the paraventricular nucleus and MRAP2-deficient mice have been shown to display similar characteristics to that of MC4R-deficient mice (Asai, *et al.* 2013). In addition, *in vitro* data shows that MRAP2 enhances the effects of  $\alpha$ -MSH to induce cAMP release in MC4R and MC3R suggesting that MRAP2 is also able to regulate the other MCRs (Asai, *et al.* 2013).

There is increasing evidence indicating that some MCRs are also able to activate other signaling pathways such as calcium- and MAPK-mediated signaling (Chai, *et al.* 2007, Chai, *et al.* 2009). Furthermore, mutational studies have shown that specific amino acid residues in the MCRs are required to induce these different signaling pathways (Yang. 2011). In summary, the different binding potencies of the endogenous agonists, different signaling routes and the fact that MCRs have a distinctive tissue distributions result in a diverse set of different physiological functions.

**Table 2.** Agonist profile, tissue distribution and function of melancortin receptors. Adapted from (Getting. 2006)

Target	Binding capacity	Tissue distribution (mRNA)	Function
MC1-R	$\alpha$ -MSH > ACTH >> $\gamma$ -MSH	Melanocytes, Keratiocytes, Endothelial cells, Fibroblast, Immune cells, Astrocytes, Neurons	Pigmentary effects, Antipyretic/anti-inflammatory
MC2-R	ACTH	Adrenal cortex	Steroidogenesis
MC3-R	$\gamma$ -MSH = ACTH > $\alpha$ -MSH	Brain, Heart, Kidney	Autonomic functions, Regulation of energy energy homeostasis
MC4-R	$\alpha$ -MSH > ACTH >> $\gamma$ -MSH	Brain	Control of feeding and energy homeostasis, Erectile activity
MC5-R	$\alpha$ -MSH > ACTH > $\gamma$ -MSH	Lymphocytes, Exocrine glands	Regulaion of exocrine secretions, Immunoregulatory functions

### 2.3.1 MC1R

The MC1R is a 317-amino acid receptor protein and it was the first human MCR to be cloned (Chhajlani & Wikberg. 1992, Mountjoy, *et al.* 1992). The most prominent effect of MC1R activation is the stimulatory effect on the production of melanin, particularly eumelanin (brown-black pigment).  $\alpha$ -MSH is the main activator of melanogenesis as it has the highest binding affinity for the MC1R, this being closely followed by ACTH<sub>1-39</sub>. The relative binding affinity of  $\beta$ -MSH is lower than ACTH<sub>1-39</sub>, whereas the affinity of  $\gamma$ -MSH is considered weak and supposedly lacking in melanogenic activity (Table 2) (Abdel-Malek. 2001, Chhajlani & Wikberg. 1992, Suzuki, *et al.* 1996). Interestingly, the truncated peptides ACTH<sub>4-10</sub> and ACTH<sub>1-10</sub> do not activate the receptor, which highlights the requirement of the amino and carboxy-terminal ends of the biologically active  $\alpha$ -MSH (ACTH<sub>1-13</sub>) (Gantz, *et al.* 1993). Binding of  $\alpha$ -MSH to the MC1R in the melanocytes of the skin activates an intracellular signaling cascade, which in turn elevates intracellular cAMP levels further activating the rate limiting enzyme in the process of melanogenesis, tyrosinase (Abdel-Malek, *et al.* 1995, Hunt, *et al.* 1994). The mRNA expression of MC1R is upregulated by melanocortins, endothelin-1 and the microphthalmia-associated transcription factor (MITF) (Abdel-Malek. 2001, Aoki & Moro. 2002).

In addition to its crucial role in the protection of the skin from UV rays, MC1R activation is essential in other physiological functions. MC1R have been described to be involved in the regulation of the immune system where it has been shown to reduce the activation and translocation of the pro-inflammatory cytokine NF- $\kappa$ B (Manna & Aggarwal. 1998). Furthermore, activation of MC1R in inflammatory cells has been shown to increase the levels of the anti-inflammatory cytokine IL-10 (Bhardwaj, *et al.* 1996). To date, mRNA expression of the MC1R has been described in various immune cells; macrophages (Star, *et al.* 1995), antigen presenting and cytotoxic lymphocytes (Neumann Andersen, *et al.* 2001), astrocytes (Wong, *et al.* 1997), (Bohm, *et al.* 1999) dendritic cells in the circulation (Becher, *et al.* 1999, Salazar-Onfray, *et al.* 2002) and in fibroblasts (Bohm, *et al.* 1999). MC1R is also expressed in endothelial cells (Hartmeyer, *et al.* 1997) and in certain specific neurons of the periaqueductal gray substance in both humans and rats (Xia, *et al.* 1995).

Interestingly, ligand affinity to the MC1R on immunological and endothelial cells appears to be greater than on melanocytes and the effects of MC1R activation in the former cell types produce a physiological response at a picomolar concentration level rather than at the nanomolar level in the latter (Suzuki, *et al.* 1996). Furthermore, the mRNA expression of MC1R is considerably lower in endothelial and immunological cells as compared to that in melanocytes (Catania, *et al.* 2004).

### 2.3.2 MC2R

The MC2R is known as the ACTH receptor and it is structurally different from the other MCR *e.g.* it shares only 38% sequence identity with the MC4R. The MC2R receptor sequence encodes for a 297-amino acid G-protein coupled receptor (GPCR), which is expressed in the adrenal gland. Here, ACTH<sub>1-39</sub> is the only known ligand to display affinity

for the MC2R and it influences the production and release of steroids via PKA activation from the adrenal cortex in accordance with the circadian rhythm and in reaction to stress (Buckley & Ramachandran. 1981, Lefkowitz, *et al.* 1970, Mountjoy, *et al.* 1992). ACTH<sub>1-39</sub> is known to increase the expression of its endogenous receptor in the adrenal gland (Mountjoy, *et al.* 1994). MC2R mRNA has been found in the *zona glomerulosa*, where MC2R is responsible for the production of mineralocorticoids and in the *zona fasciculata*, where it controls the production of glucocorticoids (Mountjoy, *et al.* 1992). MC2R is less prominently present in the *zona reticularis* and only in scattered areas of the adrenal medulla (Xia & Wikberg. 1996). Although some studies have indicated the presence of MC2R on murine adipocytes (Boston & Cone. 1996), the human adipocytes have been consistently shown to lack such expression and therefore ACTH does not appear to regulate lipolysis in humans (Chhajlani. 1996). Moreover, only the adrenal cells and cell lines with endogenous expression of MCRs are able to express the MC2R since it requires the presence of a small membrane protein, the MCR accessory protein (MRAP) (Metherell, *et al.* 2005, Noon, *et al.* 2002). The MC2R has specialized MRAP domains, which are involved in the transport of the receptor (Sebag & Hinkle. 2007, Webb, *et al.* 2009).

### 2.3.3 MC3R

The MC3R is a 361 amino acid receptor protein which has been considered as the main receptor of  $\gamma$ -MSH, although it shows similar potency to that of ACTH<sub>1-39</sub> and  $\alpha$ -MSH (Table 2). The MC3R is fully activated by the truncated peptides ACTH<sub>4-10</sub> and ACTH<sub>1-10</sub>, which suggests that the HFRW-core region is required for this activation (Gantz, *et al.* 1993). The MC3R belongs to the GPCR-family, but is coupled to both cAMP- and inositol phospholipid-Ca<sup>2+</sup> signaling systems (Kim, *et al.* 2002). The MC3R was the third MCR to be cloned and it is expressed in several peripheral tissues such as placenta, gut, kidney, heart, in human monocytes and in mouse peritoneal macrophages (Gantz, *et al.* 1993, Getting, *et al.* 1999, Taherzadeh, *et al.* 1999). In contrast to the MC4R, the central distribution of MC3R is more distinct with abundant expression in the hypothalamic ARC, VMH and in the DMH and in the limbic system (Jegou, *et al.* 2000). The MC3R has also been detected in the hippocampus, septum, thalamus and the midbrain (Roselli-Reh fuss, *et al.* 1993).

The MC3R is involved in the regulation of energy metabolism, inflammatory, autonomic and hemodynamic functions (Butler, *et al.* 2000, Catania, *et al.* 2004, Catania, *et al.* 2004, Chen, *et al.* 2000, Humphreys, *et al.* 2011, Humphreys, *et al.* 2011). The MC3R possesses an auto-inhibitory function on POMC neurons, however MC3Rs are expressed on both the orexigenic AGRP/NPY and on POMC neurons (Berthoud, *et al.* 2006, Li, *et al.* 1996, Skibicka & Grill. 2009). In addition, the MC3R has been linked to the regulation of lipolysis in WAT, which is directly innervated by corticotrophin-releasing hormone (CRH) neurons from the PVN (Bowers, *et al.* 2004, Renquist, *et al.* 2012, Shi & Bartness. 2001). The MC3R has been postulated to increase renal natriuresis in salt-induced hypertension (Humphreys, *et al.* 2011). There are clear indications that the MC3R has anti-inflammatory potential (Getting, *et al.* 1999, Getting & Perretti. 2000, Getting, *et al.* 2002, Getting, *et al.* 2003) and the receptor has been shown to

exert protective effects in situations of myocardial ischemia or in subsequent reperfusion induced injuries in rats (Guarini, *et al.* 2002). More details about the function of MC3R are reviewed in chapter 2.4.2.3, which describes the MC3R-KO mouse.

### 2.3.4 MC4R

The MC4R gene encodes for a 332-amino acid protein that covers a single exon and it was the second neural MCR to be cloned. It shows high homology with the MC1R and it also shows similar activation potency with respect to its agonists;  $\alpha$ -MSH and ACTH<sub>1-39</sub> have the highest affinity followed by  $\beta$ -MSH, whereas  $\gamma$ -MSH and the truncated peptide, ACTH<sub>4-10</sub> activate the receptor to a lesser extent (Roselli-Reh fuss, *et al.* 1993). The presence of PRO<sup>12</sup> in ACTH<sub>1-39</sub> is required for the activation of the receptor (Gantz, Konda, *et al.*, 1993). The MC4R is highly conserved and shows a remarkable 93% homology between the human and the rat genomes (Alvaro *et al.*, 1996). The MC4R is only found centrally where it exhibits a widespread expression profile in comparison to that of the MC3R, *i.e.* MC4R is expressed in the cortex, hypothalamus, thalamus, brain stem and the spinal cord (Mountjoy, *et al.* 1994)

Evidence gathered from genetic screening studies have revealed that mutations affecting the MC4R gene are involved in the development of obesity in approximately 5 % of all obese subjects. The human data is supported by evidence from animal studies where MC4R-deficient mice develop hyperphagia, hyperinsulinemia and hyperglycemia (Huszar *et al.*, 1997). These animals show enhanced caloric efficiency similar to MC3R-deficient and agouti lethal yellow mice (Ste Marie, *et al.* 2000). Since a double knockout of both MC3R and MC4R leads to increased obesity as compared to MC4R knockout alone, both of these receptors appear to have major roles in the development of obesity (Chen, *et al.* 2000). The MC4R is also believed to be involved in the activation of SNS. Indeed, there is recent evidence from MC4R-deficient mice with selective rescue of the receptor on cholinergic neurons in the brain stem and in the spinal cord clearly demonstrating that the MC4R is responsible for both a decrease in parasympathetic tone and an increase in SNS activity (Sohn, *et al.* 2013). Furthermore, the cholinergic MC4Rs are also responsible for the regulation of insulin release since rescue of the receptor in these neuronal populations in MC4R-deficient mice were able to restore hyperinsulinemia (Scott, *et al.* 2011). The MC4R increases SNS driven activity to both BAT and WAT although these actions involve differential routes (Brito, *et al.* 2007, Song, *et al.* 2005, Song, *et al.* 2008). In addition to the metabolic effects, the MC4R was also reported to modulate erectile function and sexual behavior (Van der Ploeg, *et al.* 2002, Wessells, *et al.* 1998).

### 2.3.5 MC5R

The MC5R gene was the last MCR to be cloned and identified in humans (Gantz, *et al.* 1994) and in mouse (Labbe, *et al.* 1994); it encodes for a 325-amino acid protein. The MC5R and MC4R show the highest homology among the MCRs and resemble each other with respect to their capability to bind the different agonists. The highest potency

is exhibited by  $\alpha$ -MSH followed by ACTH<sub>1-10</sub> and ACTH<sub>4-13</sub>, whereas the activity of ACTH<sub>4-10</sub> is substantially weaker as compared to that found for MC3R (Labbe, *et al.* 1994). The MC5R is only expressed in the peripheral tissues *e.g.* liver, lung adipose tissue, skin, skeletal muscle, thymus, immune cells, testis, ovary, mammary gland, stomach and in the duodenum (Catania, *et al.* 2004). The MC5R are expressed on both T-lymphocytes (Taylor & Namba. 2001) and in B lymphocytes (Buggy. 1998) and these findings point to a role for the MC5R in immune regulation. Indeed,  $\alpha$ -MSH has been shown to activate the JAK/STAT phosphorylation pathway by binding to the MC5R (Buggy. 1998). Furthermore, the CD25<sup>+</sup> CD4<sup>+</sup> regulatory T-cells are induced by  $\alpha$ -MSH via the MC5R (Taylor & Namba. 2001). MC5R-deficient mice show decreased production of sebaceous lipids in the hair follicles of the skin, which leads to a severe defect in water repulsion and subsequently to defective thermoregulation (Chen, *et al.* 1997). This receptor is required for the production of porphyrins in the Harderian gland as well as for both tear and protein secretion from the lacrimal gland (Chen, *et al.* 1997, Entwistle, *et al.* 1990).

## 2.4 GENE MODIFIED ANIMAL MODELS IN OBESITY RESEARCH

The purpose of describing the animal models in the following chapter is to highlight the differences and similarities of the models used in metabolic research. The variability between dominant changes and loss-of-function mutations will be explained although many show overlapping or opposing characteristics. The spontaneous mutations in the early laboratory animals lay the foundation for the development of the ever-growing number of animal models of present time. The involvement of genetic mapping has later revealed that many of the metabolic phenotypes of the early genetic models are the consequences of mutations related genes and their signaling cascades. A comparison of the characteristics of these animal models is compiled in Table 3.

### 2.4.1 *Leptin signaling deficiency*

Leptin signaling deficiency involves either a loss-of-function mutation in the gene encoding leptin (*Lep<sup>ob</sup>/Lep<sup>ob</sup>*) or in the leptin receptor gene (*Lepr<sup>db</sup>/Lepr<sup>db</sup>*) in mice and *Lepr<sup>fa</sup>/Lepr<sup>fa</sup>* in rat). Both mutation types cause a similar phenotype characterized by severe obesity with insulin resistance.

#### 2.4.1.1 *THE OBESE (Lep<sup>ob</sup>/Lep<sup>ob</sup>) MOUSE*

The *Lep<sup>ob</sup>/Lep<sup>ob</sup>* mouse was discovered in an outbred colony in 1949 at the Roscoe B. Jackson Memorial Laboratory, Bar Harbor, Maine. The phenotype is inherited via an autosomal recessive mutation positioned on chromosome 6 (Coleman & Hummel. 1973) and it was transferred to the well-characterized C57Bl background (Ingalls, *et al.* 1950). The mice were severely obese, hyperinsulinemic and hyperglycemic (Garthwaite, *et al.* 1980, Mayer. 1953). The pancreatic islets of these mice are up to ten-fold larger than in wild-type animals and have therefore been used in many studies involving  $\beta$ -cell function (Bray & York. 1979). The development of diabetes in *Lep<sup>ob</sup>/Lep<sup>ob</sup>* mice has helped in

**Table 3.** Comparison of the specific metabolic characteristics of obese Lep<sup>ob</sup>/Lep<sup>ob</sup>, Lep<sup>ob</sup>/Lep<sup>ob</sup>, Lep<sup>ob</sup>/Lepr<sup>ob</sup>, A/a, MC3R-KO, MC4R-KO, CPE-KO and POMC-KO mice and the genetically lean PRCP-KO and MSH-OE. + = increase, - = decrease, N = normal, ND = not defined, (M) = only in male. Table modified from (Butler & Cone, 2002)

Characteristics	Leptin and MC-signaling deficiency										Increased MC-tone		
	Lep <sup>ob</sup> /Lep <sup>ob</sup>	Lepr <sup>ob</sup> /Lepr <sup>ob</sup>	A/a	MC3R-KO	MC4R-KO	CPE-KO	POMC-KO	PRCP-KO	MSH-OE				
<i>Food intake</i>	++	++	+	N	+	++	+	-	N				
<i>Weight gain</i>	++	++	++	+N	++	+++	++	-	-				
<i>NAL</i>	-	-	+	-	+	+	+	-	-				
<i>Fat mass</i>	++	++	+	+	++	+++	++	-	- (M)				
<i>Lean mass</i>	-	-	+	-	+	+	ND	+	N				
<i>Glucose</i>	++	+	+(M)	+	+++	+++	N	N	N				
<i>Insulin</i>	+++	+++	+	+	++	N	N	-	-				
<i>Leptin</i>	---	+++	+++	+	++	++	++	ND	N				
<i>HPA-axis</i>	+	+	+	+	N	N	--	ND	-				
<i>SNS-activity</i>	-	-	-	N	-	N	-	ND	+				
<i>Thyroid function</i>	-	-	N	N	N	-	ND	-	Increased				
<i>Metabolic rate</i>	Decreased	Decreased	Decreased	N	Decreased	Decreased	Decreased	Increased	Increased				
<i>Locomotor activity</i>	Decreased	Decreased	Decreased	Decreased	Decreased (M)	N	ND	Increased	Decreased				
<i>Thermogenesis</i>	Impaired	Impaired	N	N	Impaired	Impaired	ND	Increased	N				
<i>Reproduction</i>	Infertile	Infertile	Functional	Functional	Functional	Infertile	ND	ND	Decreased				
<i>Immune function</i>	Impaired	Impaired	Impaired	N	N	Impaired	Impaired	N	Decreased				

the study of diabetes related illnesses such as in cardiomyopathy and in abnormal left ventricular function (Giacomelli & Wiener. 1979). An additional characteristic of these animals is that they are infertile and have impaired immune functions. Over 40 years after the discovery of the Lep<sup>ob</sup>/Lep<sup>ob</sup> mouse, extensive work using positional cloning was undertaken to identify the cause of the phenotype and in 1994, Friedman and co-workers identified leptin as a circulating factor produced by adipose tissue (Friedman, *et al.* 1991, Zhang, *et al.* 1994). The phenotype could be almost completely reversed by exogenous leptin therapy or by transfection of the leptin gene (Halaas, *et al.* 1995, Larcher, *et al.* 2001, Pelleymounter, *et al.* 1995).

The mice gain weight rapidly regardless of the initial hypophagia showing both hyperplastic and hypertrophic growth of both subcutaneous and intra-abdominal fat (Alonso & Maren. 1955). The Lep<sup>ob</sup>/Lep<sup>ob</sup> mice have impaired longitudinal growth and thus have a shorter anus to nose length as compared to wild-type littermates (Dubuc. 1976). Not only is the fat mass increased, but it is also redistributed to non-adipose tissue such as liver and muscle and the protein deposition is reduced due to the decreases in glucose uptake and glycogen synthesis (Le Marchand-Brustel & Jeanrenaud. 1978). During the progression of obesity, the animals also develop glucose intolerance, fasting hyperglycemia and resistance to exogenous insulin (Bergen, *et al.* 1975, Liu & Yin. 1974, Thurlby & Trayhurn. 1978). At 6 months of age, the weight accumulation attenuates and even starting to decline. There are small variations in the phenotype depending on the background.

#### 2.4.1.2 THE DIABETIC (*Lepr<sup>db</sup>/Lepr<sup>db</sup>*) MOUSE

The mutation causing the phenotype in diabetic *Lepr<sup>db</sup>* - mice originates in chromosome 4 (Coleman & Hummel. 1973) and encodes for the leptin receptor gene (Chehab, *et al.* 2004). A number of different alleles have been identified and the mutation has been bred into several different backgrounds. The phenotype of these mice is almost identical to that of the Lep<sup>ob</sup>/Lep<sup>ob</sup> mice if the mutation is on the same background and includes the db<sup>3J</sup>-allele (Hummel, *et al.* 1972).

The initial development of the phenotype in *Lepr<sup>db</sup>/Lepr<sup>db</sup>* mice is similar in all backgrounds. In comparison to the phenotype of Lep<sup>ob</sup>/Lep<sup>ob</sup> mice, a small increase in insulin levels is observed by day 10-12 (Coleman & Hummel. 1973) accompanied by increased adiposity (Le Marchand-Brustel & Jeanrenaud. 1978). Insulin levels continue to rise modestly until the time of weaning when levels increase rapidly by as much as 10-fold in comparison to wild-type littermates at two to three months of age. On the C57BL/KS background, the hyperinsulinemia is transient and after three months of age the insulin levels suddenly drop due to atrophy of the  $\beta$ -islets and the animals start to lose weight before dying at six to eight months of age (Like & Chick. 1970). Conversely, on the C57BL/6J background, the state of hyperinsulinemia is retained and as a result the mice show a mild hyperglycemia, but display severe obesity similarly to that of Lep<sup>ob</sup>/Lep<sup>ob</sup> mice (Coleman & Hummel. 1973, Hummel, *et al.* 1972). The weight of the kidneys is increased with glomerular infiltration approximately at the age of five months (Like, *et al.* 1972). Similarly to the situation in Lep<sup>ob</sup>/Lep<sup>ob</sup> mice, fat is deposited in both subcutaneous and intra-abdominal areas with hypertrophic growth on the

C57BL/Ks background, whereas the C57BL/6J show both adipose tissue hypertrophy and hyperplasia (Meade, *et al.* 1979). Hyperphagia is observed after weaning (Le Marchand-Brustel & Jeanrenaud. 1978), however, the obesity is not caused attributable solely to hyperphagia and the reduced locomotor activity (Cox & Powley. 1977, Yen & Acton. 1972).

#### 2.4.1.3 THE FATTY (*Lep<sup>fa</sup>/Lep<sup>fa</sup>*) RAT

The mutation causing diabetes and obesity in the Fatty *Lep<sup>fa</sup>/Lep<sup>fa</sup>* rat was first described by Zucker and Zucker in 1961 (Zucker & Zucker. 1963). Similarly to the *Lep<sup>db</sup>/Lep<sup>db</sup>* mice, these rats also lack functional leptin receptors and this is manifested in an obese, hyperinsulinemic and hyperlipemic phenotype. The development of the phenotype is also similar to that of the *Lep<sup>db</sup>/Lep<sup>db</sup>* mice. Similarly to the other leptin signaling deficient animal models, the Fatty rat has elevated levels of NPY, low SNS tone and impaired BAT thermogenesis.

#### 2.4.2 MC signaling deficiency

Functional melanocortin signaling is essential for body homeostasis and involves the synthesis, processing and degradation of melanocortin peptides and the functional binding and activation of melanocortin receptors. Mutations in any of these steps can cause changes in body energy homeostasis.

##### 2.4.2.1 YELLOW OBESE (*A<sup>y</sup>/a*) MICE

The yellow obese mouse was one of the earliest obese laboratory animals described by Lataste in 1883 and by Cuneot in 1905 (Cuneot. 1905, Lataste. 1883). However, the gene was not cloned and characterized until 1992 when a mutation was identified on chromosome 2 in the agouti locus which encodes for agouti signaling peptide (ASIP) (Bultman, *et al.* 1992). As described in chapter 2.2.3, ASIP was found to control the relative amounts of eumelanin (black-brown) and pheomelanin (red-yellow) produced by hair follicles (Lu, *et al.* 1994) by antagonizing the MC1R. In the yellow obese mice, a 120 to 170 kbp deletion positions the ASIP gene under a ubiquitous promoter and this causes the coat to take on a yellow appearance. Normally ASIP is only expressed in the periphery, however, in the Yellow obese mice (Duhl, *et al.* 1994, Michaud, *et al.* 1993) there is impaired melanocortin signaling in both peripheral and central compartment. In addition to the yellow coat color, the yellow mice develop mature-onset obesity, type II-diabetes, hyperleptinemia, increased linear growth (in contrast to *Lep<sup>ob</sup>/Lep<sup>ob</sup>* mice) and infertility. The characteristics of the yellow obese have been confirmed to involve the agouti loci by creating using transgenic mice that have been engineered to ubiquitously overexpress the gene (Klebig, *et al.* 1995).

Heterozygous yellow obese mice have a somewhat milder obesity phenotype but the homozygous *A<sup>y</sup>/A<sup>y</sup>* mutation is lethal in the embryonic stage. The body weight increases linearly after puberty (8-12 weeks) and gradually reaches as high as 40 g (Carpenter &

Mayer. 1958, Castle. 1941, Dickie & Woolley. 1946). Increased adiposity is linked to increased fat cell size with only minor hyperplasia (Johnson & Hirsch. 1972). Obesity is significantly increased if the animals are fed obesogenic diets (Carpenter & Mayer. 1958). Plasma insulin is increased as a consequence of the increased obesity and decreased overall metabolic rate, although oxygen consumption is identical to that found in wild-type littermates (Bartke & Gorecki. 1968). The yellow mice have a reduced thermogenic capacity and are unable to maintain core body temperature when exposed to cold environments. Furthermore, locomotor activity is reduced in both young and in old  $A^Y/a$  mice (Dickerson & Gowen. 1947).

#### 2.4.2.2 CARBOXYPEPTIDASE E-DEFICIENT MICE

Carboxypeptidase E (CPE) is required to remove the basic residues from the intermediate products of prohormone processing in order to produce a bioactive hormone. CPE is involved in the processing of several different hormones; initially it was described as an enkephalin convertase (Fricker & Snyder. 1982, Hook, *et al.* 1982). CPE is required for the biological activity of  $\alpha$ -MSH and the CPE-deficient mice resemble obese leptin signaling deficient animals, being both hyperphagic and infertile. This animal model has revealed CPE's role in bone modeling, neuroprotection and in emotional responding. The spontaneous mutation of the *fat/fat* mouse (Coleman & Eicher. 1990) is in fact located in the near proximity of the CPE locus on chromosome 8, hence the name  $CPE^{fat/fat}$ . Later, a KO mouse lacking both exons 4 and 5 of the CPE gene was created in order to elucidate that the genetic traits of the  $CPE^{fat/fat}$ -mouse were a consequence of a non-functional CPE gene (Cawley, *et al.* 2004).

The CPE deficiency manifests as severe obesity in all backgrounds. Although, CPE-KO mice are born small as compared to their wild-type littermates, by week eight they are already significantly heavier (Cawley, *et al.* 2004, Leiter, *et al.* 1999). Interestingly, the mice continue to gain weight up to one year of age when both males and females can be as large as two or even three times the size of heterozygous or wild type littermates. Weight gain is dependent on the increase in fat mass alone and contributes to approximately 50% of body weight in CPE-KO of both genders, although female mice are slightly leaner. The substantial increase in weight has been attributed to hyperphagia in the adult mice; these can reach up to 70-80 grams of weight (Leiter, *et al.* 1999, Yuan, *et al.* 2004). The CPE-deficient animals also show a decreased metabolic rate and reduced spontaneous locomotor activity (Leiter, *et al.* 1999). The CPE-deficient mice develop diabetes with a slight variation in the progression depending on background (Cawley, *et al.* 2004, Leiter, *et al.* 1999, Naggert, *et al.* 1995).

The CPE-KO females develop both severe hyperglycemia, glucose intolerance and later also insulin-resistance whereas the male mice are less severely affected (Cawley, *et al.* 2004). The  $CPE^{fat/fat}$  females do not develop the hyperglycemia encountered in the male mice (Leiter, *et al.* 1999). One interesting feature is that proinsulin levels are exceptionally high in both models, which is due to a secretory and processing defect in the  $\beta$ -islets of the pancreas (Irminger, *et al.* 1997, Leiter, *et al.* 1999).

### 2.4.2.3 MC3R-KO

The mutant mice which are deficient in functional MC3Rs present a unique metabolic phenotype. At first glance, the obesity observed in MC3R-KO animals fed on a standard diet is only modest, with no apparent differences in total body weight compared to wild-type animals (Butler, *et al.* 2000, Chen, *et al.* 2000) and with no published evidence for hyperphagia in the backgrounds in mice consuming either in normal or high fat diets (Butler, 2006). Although the contribution of the MC3R in metabolic regulation has been unclear, recent data obtained using the MC3R-KO mice has indicated a critical role of MC3R in the adaptation to food intake and in the maintenance of glucose homeostasis during periods of restricted feeding (Sutton, *et al.* 2010). Furthermore, there is also a report that the MC3R displayed significant importance in salt-sensitive hypertension, as functional MC3R are important mediators of salt-induced natriuresis (Humphreys, *et al.* 2011).

When consuming a standard diet, the MC3R-KO mice are indistinguishable from WT and heterozygous animals. However, if the animals are weaned to a low fat chow and then presented with a high fat chow diet for six weeks they exhibit a modest weight gain (Butler, *et al.* 2000). Interestingly, the acquired weight is attributable entirely to an increase in fat mass (40%) and a modest decrease in fat free mass when fed regular chow (Butler, *et al.* 2000, Butler, 2006). Although the increase in adiposity might be dependent on a decreased spontaneous physical activity measured only during nighttime in wheel cages or using the photobeam system, it is more probably explained by an overall increase in obesity (Butler, *et al.* 2000, Butler, 2006, Thorburn & Proietto, 2000). More significantly, the increase in adiposity has been explained as being due to a disproportion in substrate utilization. In fact, the respiratory exchange ratio (RER) of MC3R-KO on the B6 background is significantly increased reflecting a difference of 12-14% in substrate utilization (Butler, *et al.* 2000, Butler, 2006, Elia & Livesey, 1988). Although there is no difference in the carbohydrate balance, there is an estimated 7 kJ/day imbalance in fat intake and fat oxidation also seen in MC3R-KO female mice (Butler, 2006). A sexual dimorphism has been observed since only the female MC3R-KO mice are prone to gain weight on a chow with a modest fat content (25% kJ/fat) and have a increased weight gain even in comparison to their male counterparts fed a high fat diet (60%kJ/fat) (Chen, *et al.* 2000). Recent data has shown that MC3Rs' are important in the adaptation to metabolic conditions. If feeding is restricted only to the daytime, the MC3R-KO mice are unable to efficiently produce and use glucose as reflected in decreased activity of gluconeogenic genes and increased lipogenic enzymes in the liver (Sutton, *et al.* 2010). In fact, the increased levels of lipogenic enzymes during restricted feeding suggest that MC3R-KO mice might convert carbohydrates into fatty acids and further into ketone bodies in the liver pointing to an important role of MC3R in regulating the rhythmicity of liver metabolism (Sutton, *et al.* 2010). Furthermore, the MC3R deficient mice show significantly reduced activity and wakefulness around food presentation and decreased expression in the genes involved in the regulation of rhythmic clock genes (Sutton, *et al.* 2008). Recent data has shown that MC3R-deficient mice have decreased lipolysis in WAT and decreased central mRNA levels of AGRP and NPY during fast and impaired fasting induced re-feeding (Renquist, *et al.* 2012). In addition to the regulation of excess sodium excretion and to the maintenance of normal blood pressure under high salt conditions,

the MC3R is also involved in regulating mechanisms governing glucose homeostasis under exceptional conditions such as in salt-induced hypertension (Humphreys, *et al.* 2011). The MC3R-KO mice exhibit mild insulin resistance on a HFD, however, they develop fasting hyperglycemia and hyperinsulemia associated with hypertension if consuming high sodium diets (Butler, 2006, Chen, *et al.* 2000, Ni & Humphreys, 2008). The abnormal glucose homeostasis and insulin resistance seen in the MC3R-KO mice has been assumed to involve increased sympathetic outflow and a decreased blood flow to skeletal muscle (Humphreys, *et al.* 2011). Interestingly, the phenotype of MC3R-deficient mice closely resembles the symptoms associated with Cushing's syndrome as also corticosterone levels are elevated in this mouse model (Renquist, *et al.* 2012).

#### 2.4.2.4 MC4R-KO

The development of the MC4R-KO mice represented a turning point in melanocortin research. These mice displayed many of the same characteristics as encountered in the leptin signaling deficient mouse models (Lep<sup>ob</sup>/Lep<sup>ob</sup> and Lepr<sup>db</sup>/Lepr<sup>db</sup>) and the agouti yellow mouse (A<sup>Y</sup>/a). Similarly to the Lepr<sup>db</sup>/Lepr<sup>db</sup> mouse lacking functional leptin receptors, the MC4R-KO mice were unresponsive to the effects of both peripheral and central administrations of leptin and thus they demonstrated the importance of melanocortin receptors as key mediators of leptin signaling in the central nervous system (Marsh, *et al.* 1999). The MC4R deficient mice are grossly obese and hyperphagic with a significantly increased lean mass and nose to anus length when fed energy rich diets. Furthermore, both insulin and leptin levels are increased and glucose levels are elevated only in male homozygous mice, whereas levels remained unchanged in female mice (Huszar, *et al.* 1997).

Although the MC4R-KO is maintained on different backgrounds, the phenotype of these is almost identical. On the standard rodent chow, hyperphagia is observed in the homozygous MC4R-KO mice as early as 3-5 weeks of age. Both lean mass (20%) and longitudinal length (10-12%) are increased, which is also observed in humans carrying MC4R mutations (Albarado, *et al.* 2004, Coll, *et al.* 2004, Hinney, *et al.* 2013, MacKenzie, 2006). The introduction of high fat or more palatable diets markedly augments hyperphagia in MC4R-KO mice similarly to the agouti yellow A<sup>Y</sup>/a mice (Butler, *et al.* 2000, Xu, *et al.* 2003). The sensitivity of both the A<sup>Y</sup>/a and the MC4R-KO to palatable or high fat containing diets has been linked to the centrally expressed brain-derived neurotrophic factor (BDNF), which is decreased in the ventromedial hypothalamus (VMH) in both models and in food deprived mice (Xu, *et al.* 2003). The effect of BDNF is particularly noticeable in the consumption of high fat diets as administration of BDNF to A<sup>Y</sup>/a mice reduces food consumption only when the animals are fed a high fat diet (Xu, *et al.* 2003). Peripheral or central administration of the non-selective melanocortin agonists does not reduce food intake in the MC4R-KO mice suggesting that the MC4R is the main regulator of feeding rather than the MC3R (Chen, *et al.* 2000, Kumar, *et al.* 2009, Marsh, *et al.* 1999). Interestingly, a reduction in food intake can be observed if young lean or pair-fed MC4R-KO mice are treated with leptin pointing to the involvement of alternative routes for leptin signaling besides the MC4R (Butler, 2006, Marsh, *et al.* 1999). The phenotype of MC4R-KO mice on the B6 background, which

is a known model used for the development of diet-induced obesity in mice, reveals a sexual dimorphism in hyperphagia. Female MC4R-KO on the B6 background are more sensitive towards hyperphagia when fed a high fat diet and they also display a higher caloric intake than either wild-type or Lep<sup>ob</sup>/Lep<sup>ob</sup> mice (Albarado, *et al.* 2004). On the other hand male mice on the B6 background are not hyperphagic when presented low fat chow (Fan, *et al.* 2004). MC4R-KO mice on the B6 background are also insensitive to the administration of cholecystokinin (CCK), which suggests that functional MC4R are required for the effects of the gut derived CCK to mediate satiety (Butler. 2006, Fan, *et al.* 2004). Pair-feeding MC4R-KO mice according to the food consumed by wild-type littermates reduces weight gain and adiposity, however, it does not completely prevent it (Marsh, *et al.* 1999, Ste Marie, *et al.* 2000). The MC4R-KO mice display reduced energy expenditure due to a reduction in the sympathetic activity (Rahmouni, *et al.* 2003, Sohn, *et al.* 2013) and physical activity (Butler. 2006, Chen, *et al.* 2000, Ste Marie, *et al.* 2000). Diet induced thermogenesis (DIT) normally associated with an increase of 10-20% in oxygen consumption is not present in MC4R deficient mice, evidence of a maladaptation to dietary changes and an increase in feeding efficiency (Butler. 2006). Furthermore, the reduced fatty acid oxidation together with a decreased DIT in the MC4R-KO mice is indicative of an increase in the respiratory exchange ratio (RER) (Albarado, *et al.* 2004). Indeed, higher RER values have been observed in both MC4R-KO males on standard low fat chow and in females on a purified high fat diet on the B6 background (Albarado, *et al.* 2004, Butler. 2006).

#### 2.4.2.5 POMC-KO

The POMC-KO mouse was created by deletion and replacement of exon 3 of the murine *Pomc1* gene with a neomycin cassette (Yaswen, *et al.* 1999). The POMC-deficient mice share many of the same characteristics of mice with dysfunctional melanocortin signaling, although a distinct feature of the model is a total adrenal deficiency due to the lack of ACTH (Yaswen, *et al.* 1999).

The POMC-KO mice are hyperphagic, have an increased weight gain both when fed a normal or a high fat diet and have increased longitudinal growth similarly to MC4R-KO and A<sup>y</sup>/a mice (Butler, *et al.* 2000, Yaswen, *et al.* 1999). The weight of POMC-KO mice is increased after weaning and continues to accumulate until the age of four months, when they can be twice the weight of wild-type animals (Yaswen, *et al.* 1999). Leptin levels remain high and glucose and insulin levels remain normal (Yaswen, *et al.* 1999). POMC-KO animals show a maladaptation to energy rich diets because of a higher caloric intake and decreased energy expenditure, which exaggerates their obesity in comparison to wild-type littermates (Yaswen, *et al.* 1999). In line with the red hair color presents in human subjects with POMC deficiency, the POMC-KO mice have a slightly yellow coat color, which becomes more prominent in older animals (Yaswen, *et al.* 1999). Similarly to MC5R-KO mice, the POMC-KO mice have a decreased ability to shed water from their fur and are therefore unable to normally regulate their body temperature (Chen, *et al.* 1997, Yaswen, *et al.* 1999). The adrenal insufficiency affects both corticosterone and aldosterone concentrations which fall below detectable level (Yaswen, *et al.* 1999). Plasma catecholamine levels are less affected since only adrenaline levels show a small decrease, and dopamine levels may show a marginal increase due to a compensatory effect (Yaswen, *et al.* 1999). The deficiencies of POMC also lead to

a severe underdevelopment of adrenal glands although these are not macroscopically detectable (Yaswen, *et al.* 1999).

### 2.4.3 Elevation of melanocortin tone

Increasing the melanocortin tone in transgenic animals has been implemented in only a handful of studies. Ubiquitous overexpression of  $\alpha$ - and  $\gamma_3$ -MSH in both lean and obese mice has resulted in a weight reduction without changes in food intake. However, the results show gender differences between the different backgrounds (Savontaus, *et al.* 2004). Inactivation of the  $\alpha$ -MSH degrading enzyme, PRCP, produces a lean phenotype with a shorter nose-to-anus length and resistance to high-fat diet (HFD)-induced obesity (Wallingford, *et al.* 2009).

#### 2.4.3.1 MSH-OE

The MSH-OE mouse has been produced in three different genetic backgrounds; lean (C57BL/6J.129- $A^{wJ}$   $db^{3J}$ ), in  $db^{3J}/db^{3J}$  and in  $A^Y/a$  mice. Although there were some gender differences in all backgrounds, the transgene overexpression caused significant reductions in weight development in mice in the obese  $Lepr^{db}/Lepr^{db}$  background (Savontaus, *et al.* 2004). In addition, transgenic mice on the C57BL/6J.129- $A^{wJ}$   $db^{3J}$  background have attenuated weight gain in the absence of feeding effects and display higher energy consumption and nutrient partitioning when feeding on a high fat diet (Lee, *et al.* 2007).

The MSH-OE mouse was created by insertion of a gene segment including both  $\alpha$ - and  $\gamma_3$ -MSH under the general CMV-promoter into fertilized C57BL/6xCBA F2 oocytes. The founders were then mated with agouti-colored mice from a B6 strain (Chua, *et al.* 2002, Kowalski, *et al.* 2001) in order to facilitate the visualization and selection of transgene expression. The selected transgenic mice were mated with both  $db^{3J}/db^{3J}$  and  $A^Y/a$  mice (Savontaus, *et al.* 2004). Transgene expression was detected centrally in the hypothalamus, brain stem and cerebellum, whereas peripheral expression was detected in the adrenal glands, skin, muscle, liver, kidney, heart, stomach and intestine. The levels of  $\alpha$ - and  $\gamma_3$ -MSH in brain areas important for metabolic regulation were increased 1.5- to 2-fold in the mediobasal hypothalamus (MBH) and by 2- to 4-fold in the brain stem. Lean MSH-OE mouse are readily distinguishable from the agouti-colored WT mice by their black coat-color, which is a result of a stimulatory effect of melanocortins on the melanin production in the skin. The weight gain is significantly reduced in both male and female mice on the  $db^{3J}/db^{3J}$ -background, however, adiposity was only decreased in male mice. There was no difference in nose-to-anus length (NAL), food intake or in glucose metabolism in these mice. Adiposity and food intake were similar, however, there were significant differences in glucose metabolism. Some gender-related differences were observed in the lean mice and on the  $A^Y$ -background. Weight gain was significantly reduced in obese lean male mice starting from 7-weeks of age, whereas this effect is only apparent in female mice on the  $A^Y$ -background starting from the same age. Only the lean male mice displayed shorter NAL and exhibited reduced adiposity in comparison to

control. Conversely, only female mice on the  $A^Y$ -background were shorter at three months of age. Both fed and fasted plasma insulin levels were reduced in both male and female lean mice, however, there was no difference in plasma glucose levels. However, the fasted and stimulated insulin levels were significantly decreased only in female mice on the  $A^Y$ -background. When the effects of dietary fat content was analysed in transgenic mice on the C57BL/6J.129-A<sup>wj</sup> db<sup>3j</sup> background, they displayed higher oxygen consumption and respiratory quotient only on a high fat diet (Lee, *et al.* 2007). These findings were consistent with the displayed modest reduction in weight gain in the absence of a feeding effect (Lee, *et al.* 2007). In addition, the HFD attenuated the increase in corticosterone levels in the transgenic mice (Lee, *et al.* 2007). The hemodynamic characteristics of lean MSH-OE mice have been evaluated revealing an improved baroreflex control of heart rate (Rinne, *et al.* 2008, Rinne, *et al.* 2013).

The effects of central overexpression of the complete precursor of MSH peptides have previously been studied using POMC-adenovirus associated virus (POMC-AAV) in rats. POMC-overexpression in the ARC of the hypothalamus has been associated with decreased hyperphagia in both leptin deficient and in aged obese rats (Li, *et al.* 2003, Li, *et al.* 2005), but failed to reduce the weight gain if animals were fed a high fat diet (Zhang, *et al.* 2010). In addition, a parallel study showed that the treatment could also increase weight gain and total caloric intake if treated animals first received standard rodent chow, which was later changed to a high-fat diet (Li, *et al.* 2007). The effects of POMC-overexpression in the NTS of the brain stem and the VTA in the tegmentum have also shown to reduce weight gain in diet-induced obesity (Andino, *et al.* 2011, Zhang, *et al.* 2010).

#### 2.4.3.2 PRCP-KO

Extracellular  $\alpha$ -MSH is regulated by a specific degrading enzyme, PRCP, which degrades the active form of  $\alpha$ -MSH. The PRCP-KO mouse lacks functional PRCP and has almost 60% higher hypothalamic levels of the active  $\alpha$ -MSH<sub>1-13</sub> (as opposed to the inactive  $\alpha$ -MSH<sub>1-12</sub>) (Wallingford, *et al.* 2009). The mice lacking functional PRCP are significantly leaner and have decreased food intake, adiposity and NAL length (Wallingford, *et al.* 2009). Expression analysis of PRCP showed abundant localization centrally in the cortex, brain stem, hippocampus and the hypothalamus. High levels of PRCP were found in the lateral-perifornical area, *zona incerta* and the dorsomedial nucleus of the hypothalamus, whereas in the ARC, the expression was significantly lower (Jeong & Diano. 2014). PRCP was found mostly opposite to or in the close proximity of neuronal POMC axon terminals, suggesting that PRCP is responsible for inactivating  $\alpha$ -MSH at the release sites (Wallingford, *et al.* 2009). Obesity is also attenuated in PRCP-KO mice when the animals were exposed to a high fat diet (45% fat). The observed decrease in weight was significant starting from the first week and lasten to the end of the 18-week experiment. It is also known that PRCP also regulates the thyroid axis as PRCP-deficient mice have higher levels of thyrotropin-releasing hormone (TRH) levels and administration of triiodothyronine (T<sub>3</sub>) can normalize the abnormal TRH levels (Jeong, *et al.* 2012).

## 2.5 THE CNS AS A TARGET FOR PEPTIDE AND GENE DELIVERY

The CNS is regulated by a multitude of different factors. The general conductors of the CNS are the major neurological circuits composed of neurotransmitters and a multitude of different neuropeptides. A considerable amount of effort has been expended in attempts to understand the way the CNS is regulated, however, much still remains unknown. Electrophysiological measurements are conducted on *ex vivo* tissue slices in order to determine neuronal connections. One way to study the different physiological functions of neuropeptides has been to deliver them or their analogues to the anatomically distinct areas or nuclei of the CNS in order to clarify site-specific effects or into the ventricular spaces in order to examine the general central effect of neuropeptides.

The function of ventricles in the CNS is to sustain buoyancy, protection, and chemical stability. The ventricles are filled with cerebrospinal fluid (CSF), which is produced by the choroid plexus and epidymal cells. Many neuropeptides are found in CSF and the ventricular space can therefore be considered as one of the natural delivery pathways of neuropeptides. Although the ventricular space cavity connects the CNS and the spinal chord, it can also be divided anatomically to distinct parts. The two lateral ventricles occupy the cerebral hemisphere and a third ventricle is connected to the lateral ventricles by a passage (*interventricular foramina*). The fourth ventricle is connected to the third ventricle by a narrow passage (cerebral aqueduct) and by the preceding central canal that continues down to the spinal chord. Additionally, CSF fluid passes to the subarachnoid space via openings in the fourth ventricle. The choroid plexus is a bundle of small capillaries surrounding epidymal cells, which forms the blood-brain barrier (BBB) by allowing only the passage of blood plasma into the CSF. Moreover, the BBB is considered to be semipermeable particularly at the ARC of the hypothalamus and where it permits the controlled, selective transport of various nutrients and energy signals such as leptin (Banks, 2006). CSF circulates from the lateral to the third ventricle continuing to the fourth ventricle and further to the spinal chord. In the arachnoid space, CSF returns to the blood through villi located in the dural sinuses of the meninges (Kandel, *et al.* 2000).

The anatomy of the CNS has been outlined and each divided into functionally distinct parts. Previously, the specific nuclei and existing neuronal projections have been characterized using mechanical disruption and direct delivery of neuropeptides and analogues, whereas the techniques used today involve knocking out distinct populations of neurons and receptors or by genetic rescue or overexpression of neuropeptides or their receptors in specific loci using gene delivery vectors. The information gathered in these studies together with illustrative histological data have been combined into anatomical maps. The specific locations of the CNS in these maps are defined by the anatomy of the skull bone, which is used in the stereotaxic delivery of neuropeptides and genes.

Stereotaxis is used in single or continuous delivery to the CNS. With both approaches, the anatomy of the skull bone is used in order to target specific areas or ventricles of the CNS. The parietal bone structures of the skull are divided into several different anatomical parts by a connective tissue joints (sutures). The meeting points of the sagittal and the coronal sutures are termed bregma (and additionally an interaural line in rodents), which is defined in coronal brain anatomy as the middle or zero point. This bregma-related line

is by definition invariable between vertebrates of the same genetic strain and is therefore useful in defining the anatomy of the CNS.

## 2.6 GENE DELIVERY VECTORS

Gene delivery is useful in the study of the acute and long-term effects of genes *in vitro* and *in vivo* and in the targeting and destruction of unwanted cells, such as cancer cells (Vile & Russell. 1994). Viral gene delivery vectors that produce stable over-expression have been proven to be effective in the characterization of neuronal networks and for analyzing the physiological effects of therapeutics and endogenous peptides in different anatomical locations of the CNS and for treating human diseases (Ridet & Privat. 1995). A gene delivery vector artificially carries foreign genetic material in the form of DNA or RNA into a cell, where it can be either be integrated into the host genome allowing long-term expression or transiently expressed. Viral gene delivery vectors exploit the specialized molecular mechanisms of naturally occurring viruses to efficiently transport their target genomes inside the cells that they infect. The subsequent infection and delivery of the genetic material is termed transduction and the infected cells are defined as having been transduced. Viral vectors can be divided into integrating or non-integrating classes. Furthermore, the non-integrating viruses may also replicate. The main classes of viral vectors are different retroviruses such as the integrating and non-replicating lentiviruses, the non-integrating and replicating adenoviruses and integrating adeno-associated viruses. Lentiviruses use the genes of the human immunodeficiency virus (HIV) to integrate to the genome of many types of cells (Trono. 2000). The lentiviral vectors have been rendered non-replicative by removing the genes responsible for the production of new viral particles from the vectors themselves. The target genes of lentiviruses integrate into the host genome by using retroviral reverse transcriptase and recombination processes. This molecular event is random and previously it has resulted in the activation of oncogenes in human trials using lentiviruses. Moreover, non-integrating adenoviruses are used to eliminate specific cells (such as cancer cells), since infection by adenoviruses results in the production of new viral particles and ultimately results in the bursting and destruction of the infected cells (Barry, *et al.* 2012). The characteristics of adenoviruses can be modified and targeted to specific cells by changing the characteristics of their core proteins. There are several different strains of adenoviruses and these can be combined and redesigned in order to match the specific target cells. Adeno-associated viruses (AAV) are viruses that resemble adenoviruses, however, they function more like retroviruses. The AAV does not evoke an immunological response and in that respect it differs from the adenoviruses and there are no known adverse effects in terms of integration of genes into the host genome, which is one reason why they have proven useful in human gene therapy (Grieger & Samulski. 2012).

### 3. AIMS OF THE STUDY

The current study is an investigation of the central effects of POMC-derived melanocortin peptide overexpression in obesity. There is compelling evidence indicating that the melanocortin system is essential for the regulation of energy metabolism.  $\alpha$ -MSH decreases obesity effects, but elevates sympathetic nervous system activity in the short term and the specific role of  $\gamma$ -MSH is still unclear. Transgenic mice overexpressing  $\alpha$ - and  $\gamma$ -MSH show attenuated weight gain, however, no conclusion about the specific effects of each MSH peptides or the target area could be made. In addition, rats with targeted central overexpression of the propeptide, POMC show similar effects. The main objectives of this study were to determine the site-specific long-term effects of  $\alpha$ -MSH or  $\gamma$ -MSH overexpression only in key areas of metabolic regulation in the CNS. The specific tasks investigated in this thesis were:

1. To develop lentiviral gene delivery vectors overexpressing  $\gamma$ - and  $\alpha$ -MSH and to demonstrate that the gene delivery vectors integrate and produce stable expression and biologically active peptides *in vitro* and *in vivo*
2. To determine the long-term anti-obesity effects of  $\alpha$ -MSH-OE in the ARC of the hypothalamus in diet induced obese mice.
3. To determine the anti-obesity effects of long-term  $\alpha$ -MSH-OE in the NTS of the brain stem in diet induced obese mice and to investigate if the treatment would cause any elevation in SNS tone.
4. To elucidate the effects of  $\gamma$ -MSH-OE in hypothalamus in the regulation of feeding and body metabolism in mice feeding on different diets and in the treatment of diet induced obesity.

## 4. MATERIALS AND METHODS

### 4.1 LENTIVIRUSES

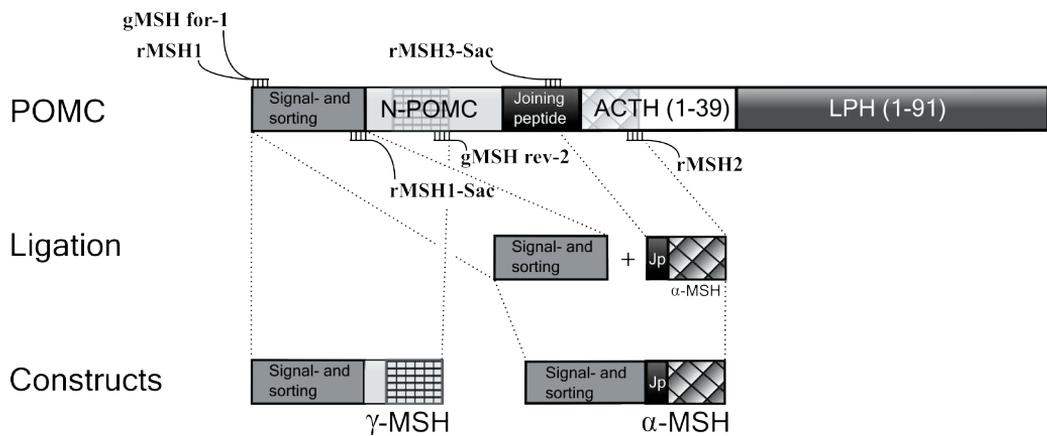
#### 4.1.1 DNA constructs

The  $\alpha$ -MSH gene construct used the signal- and sorting peptides of the mouse POMC pro-peptide followed by the  $\alpha$ -MSH sequence starting with the endogenous endoprotease cleavage site and ending in the C-terminal glycine allowing for amidation and an inserted stop codon (Schafer, *et al.* 1992) (Figure 3). The construct was generated by amplifying two separate fragments from the MSH-L construct described earlier (Savontaus, *et al.* 2004) and included a part of the 5' untranslated region, the signal sequence, the sorting sequence, the joining peptide and  $\alpha$ -MSH. The codon for the C-terminal glycine is immediately followed by a stop codon. The first fragment encodes the signal sequence and the sorting sequence and second part of the joining peptide sequence and  $\alpha$ -MSH (Figure 3). The fragments are amplified with primer-pairs rMSH1 and rMSH1-Sac, and rMSH3-Sac and rMSH2 (Table 4). Both amplified products include a Sac II restriction site aiding in the ligation of fragments to produce the DNA construct, which is identical to both rat and mouse  $\alpha$ -MSH (Figure 3).

**Table 4.** Primers used for the generation of constructs. Restriction sites (underlined) Sac II used for the generation and ligation of  $\alpha$ -MSH construct and Mlu I and Sal I for  $\gamma$ -MSH. Mutations (bold) were used to generate stop codon in  $\gamma$ -MSH template.

$\alpha$ -MSH		
Template DNA	Origin: MSH-L plasmid (Savontaus E. et al 2004)	Restriction site
Primers	rMSH1 5'-GTC CTC AGA AAG CTT CCT TTC CGC-3'	-
	rMSH1-Sac 5'-CGT TGC CTG GAA <u>ACC GCG GCG</u> TCT C-3'	Sac II
Primers	rMSH3-Sac 5'-AGC CAA GTC <u>CGC GGA</u> GGG CAA GC-3'	Sac II
	rMSH2 5'-CAC AGG GCG AAG CTT CTA GCC CAC CGG-3'	-
$\gamma$ -MSH		
Template cDNA	Origin: Mouse hypothalamic mRNA	Restriction site
Primers	gMSH for-1 5'-TGC CTT <u>TAC GCGTCA</u> GGG GT-3'	MluI
	gMSH rev-2 5'- <b>cta t</b> <u>GT CGA CTC</u> TTC CTC CGC ACG <b>CTA</b> CTG C-3'	SalI

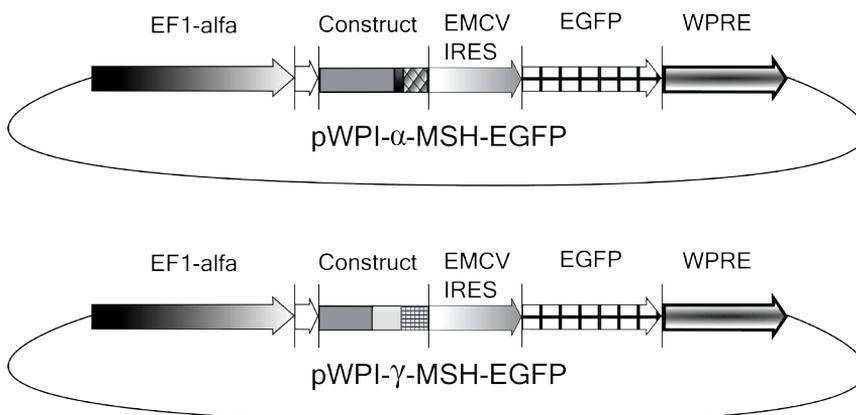
Mouse hypothalamic cDNA was used as a template to create the  $\gamma$ -MSH construct. The construct includes the signal- and sorting-sequences of POMC and the endogenous cleavage sites for appropriate intracellular processing (Figure 3). The  $\gamma_3$ -MSH sequence was amplified using primers (forward and reverse, respectively) gMSH for-1 and gMSH rev-2 (Table 4). The forward primer includes an MluI restriction (underlined) site achieved by changing two bases (bold) and the reverse primer had a SalI restriction site and extra codons for aiding restriction in the 5'-end (underlined and bold) and a stop codon (bold) in 3'-end (Table 4).



**Figure 3.** Generation of MSH constructs from POMC sequence.  $\alpha$ -MSH sequence was amplified from a DNA plasmid including the N-terminal POMC and ATCH sequences together with the signal and sorting sequences, which were ligated together. The  $\gamma$ -MSH sequence was amplified from mouse hypothalamic mRNA.

#### 4.1.2 Lentiviral constructs

In the production of the second-generation lentiviruses, the  $\alpha$ -MSH and  $\gamma$ -MSH constructs were ligated to the lentiviral vector plasmid pWPI-EGFP (LVi-EGFP) to produce pWPI- $\alpha$ -MSH-EGFP and pWPI- $\gamma$ -MSH-EGFP plasmids, respectively (Figure 4). In the bicistronic pWPI vector, the gene construct precedes the Encephalomyocarditis virus internal ribosomal entry site (EMCV IRES) and EGFP, which allows for the simultaneous expression of the transgene and the reporter gene (Jang, *et al.* 1988, Pelletier & Sonenberg. 1988). The pWPI vector plasmids use the EF1- $\alpha$  promoter, which is a general promoter (Lee, *et al.* 1992). In addition, the plasmids also include the WPRE (woodchuck hepatitis post-transcriptional regulatory element), which has been shown to enhance the expression of genes in different cell lines (Klein, *et al.* 2006).



**Figure 4.** The  $\alpha$ -MSH and  $\gamma$ -MSH gene constructs were subcloned into pWPI plasmid to produce pWPI- $\alpha$ -MSH-EGFP and pWPI- $\gamma$ -MSH-EGFP.

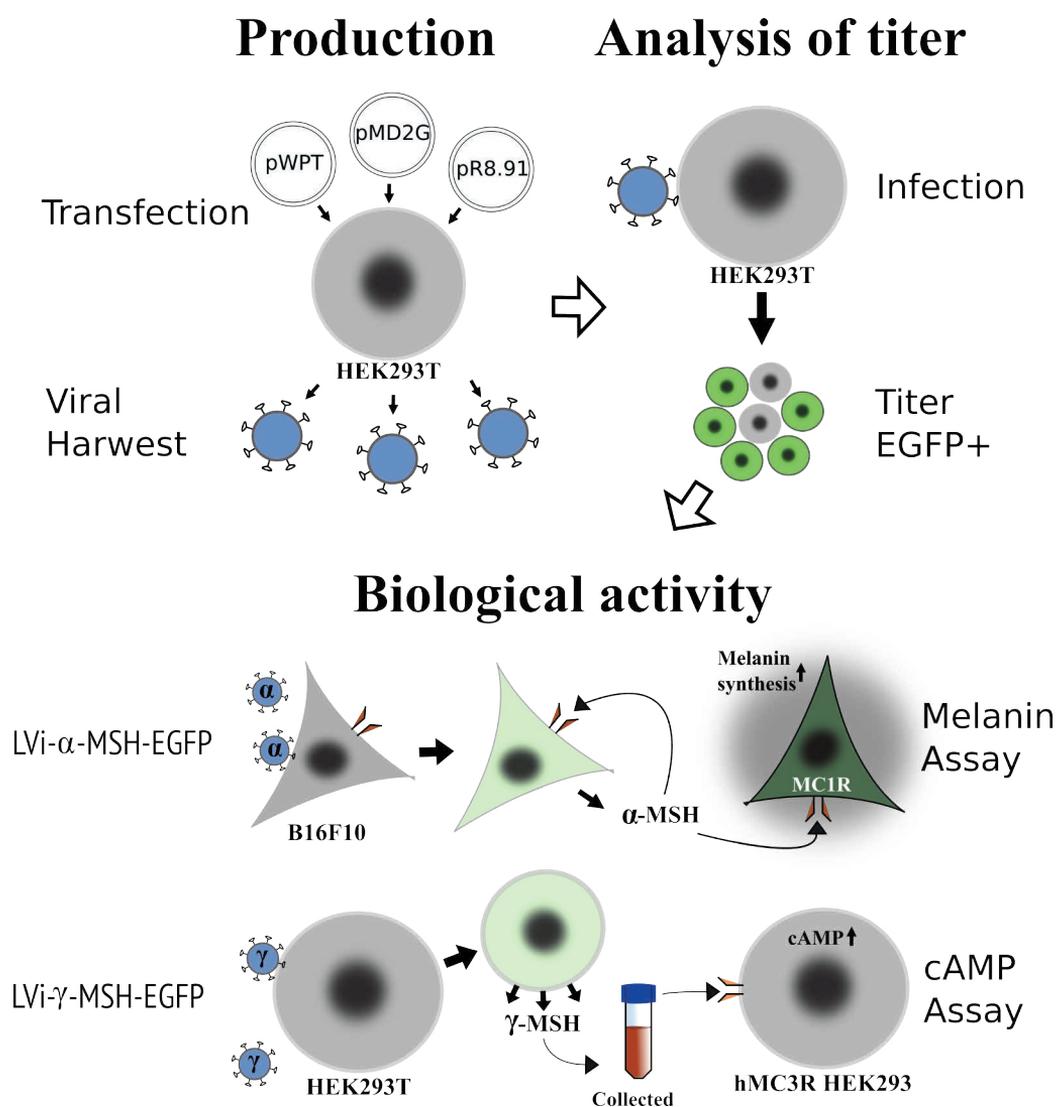
### 4.1.3 Generation of lentiviruses

Lentiviruses were produced in human embryonic kidney cells (HEK293T) that were grown in Dulbecco's modified Eagle's medium (DMEM) with 10% fetal bovine serum (LVi- $\alpha$ -MSH-EGFP) or advanced DMEM (LVi- $\gamma$ -MSH-EGFP) with 2% fetal bovine serum supplemented with 2 mM L-glutamine (1.5 g/l sodium bicarbonate and 4.5 g/l glucose), penicillin (100 U/ml), and streptomycin (100  $\mu$ g/ml) (Sigma-Aldrich Co., St. Louis, MO, USA) and with the LVi- $\gamma$ -MSH-EGFP also 0.03 mM cholesterol (Sigma-Aldrich Co., St. Louis, MO, USA). Addition of cholesterol to the growth medium of transfected cells aids the budding of cells (Mitta, *et al.* 2005). Normal cell culture conditions in cell culture incubators (37° C and 5% CO<sub>2</sub>) were used for the production of all viruses. First, 2.5 million low passage HEK293T cells (passage < 7) were plated on 10 cm cell culture plates and grown until 50 % confluency. Viral particles were produced by calcium phosphate transient co-transfection of the HEK293T cells with the lentiviral vector plasmid (pWPI- $\alpha$ -MSH-EGFP or pWPI- $\gamma$ -MSH-EGFP and pWPI-EGFP) and two helper plasmids: pCMV-pR8.91 (a packaging plasmid) and pMD2G (an VSV-G envelope plasmid) (Figure 5). The viruses were collected and filtered (0.45  $\mu$ m) and then concentrated by ultracentrifugation in 50000 x G (LVi- $\alpha$ -MSH-EGFP) or 20000 x G (LVi- $\gamma$ -MSH-EGFP) in 33 ml conical ultracentrifuge tubes (Beckman Coulter, Inc., CA, USA). A lower concentration speed has been shown to improve titers (al Yacoub, *et al.* 2007). Viral pellets were resuspended in sterile PBS solution (Sigma-Aldrich Co., St. Louis, MO, USA).

### 4.1.4 Analysis of lentiviruses

Titers (transducing units/ml (TU/ml)) were determined by fluorescence based flow cytometry (Dittrich & Gohde. 1969, Göhde. 1968) (Figure 5). First, thawed viral suspension was added in a 1:5 dilution series to a known number of cells on a 24-well plate. Since the viruses induce EGFP expression, the relative amounts of EGFP-positive (EGFP+) cells were assessed in each well by fluorescence based flow cytometry. Titers were calculated from wells with dilution series showing 10-20 % EGFP+ cells by the equation:  $TU = N \times (EGFP+) \times DF$  (N = cells at infection, EGFP+ = percent EGFP+ cell in well, DF = dilution factor):

The ability of the LVi- $\alpha$ -MSH-EGFP virus to produce biologically active  $\alpha$ -MSH was tested in a modified melanin in vitro assay by measuring melanin production in B16F10 melanocytes that express MC1-R (Siegrist & Eberle. 1986). The lentivirus vectors were analyzed by first plating 5000 B16F10 on 96-well plates in Dulbecco's modified Eagle's medium supplemented with 10% fetal bovine serum, 4 mM L-glutamine (1.5 g/l sodium bicarbonate and 4.5 g/l glucose), penicillin (100 U/ml), and streptomycin (100  $\mu$ g/ml). On the following day, the cells were infected with a MOI 100 (Multiplication of infectivity x 100) of the LVi- $\alpha$ -MSH-EGFP or LVi-EGFP virus and compared with untreated control cells. The concentration of melanin in the growth medium was determined by absorbance measurement at 405 nm 72 hours after the infection (Figure 5).



**Figure 5.** Schematic presentation of the LVi-EGFP, LVi- $\alpha$ -MSH-EGFP and LVi- $\gamma$ -MSH-EGFP lentivirus, titer determination and biological activity analysis protocol.

The ability of the LVi- $\gamma$ -MSH-EGFP virus to produce biologically active  $\gamma$ -MSH was tested by stimulation of a HEK293 cell line expressing human MC3R (hMC3R-cells) (Grieco, *et al.* 2002) and by measuring the elevation in intracellular cAMP levels using a commercially available kit (Perkin Elmer) according to manufacturer's instructions. The main goal of this method was to infect a separate cell line (HEK293T) using the LVi- $\gamma$ -MSH-EGFP in order to produce  $\gamma$ -MSH peptide in the cell growth medium, which was used to stimulate the hMC3R cell line in a cAMP assay (Figure 5). First, a HEK293T cell line was infected with a MOI 100 of the LVi- $\gamma$ -MSH-EGFP or LVi-EGFP. After this, 100 000 infected and non-infected cells were plated on 24-well plates and grown until confluency. Subsequently, the growth mediums of the cells were collected, pooled and stored in -80 C until later use. For the cAMP measurements, 10000 hMC3R cells grown

in Minimum essential media (Gibco® MEM, Thermo Fisher Scientific Inc, MA, USA), 10% fetal bovine serum, 4 mM L-glutamine (1.5 g/l sodium bicarbonate and 4.5 g/l glucose), penicillin (100 U/ml), streptomycin (100 µg/ml) and 50 µM of G418 (Sigma-Aldrich, MI, USA) were added to the wells of a 96-well plate and incubated with an equal amount of growth medium from non-infected HEK 293T cells (control medium), different concentrations of synthetic  $\gamma$ -MSH peptide (Tocris Biosciences Cat. No. 4272, Bristol, United Kingdom) diluted in control medium or the growth medium from LVi-EGFP and LVi- $\gamma$ -MSH-EGFP infected cells. The assay measured the amount of bound intracellular cAMP, which negatively correlated with unbound cAMP using Eu-labeled antibodies.

## 4.2 ANIMALS (I-III)

Two-month-old C57BL/6N male mice were obtained either from the local laboratory animal facilities (University of Turku) (I) or from Harlan Laboratories B.V. (Venray, The Netherlands) (I-III). The mice were kept in an animal room maintained at  $21 \pm 1^\circ\text{C}$  with a fixed 12-h light/12-h dark cycle. Food and water were available *ad libitum*, except when experiments with pair-feeding were being conducted (I).

### 4.2.1 Anesthesia and analgesia

In the stereotactic operations for analgesia either ketamine (75mg/kg) (Pfizer Inc, NY, NY, USA) (I-II) or buprenorphine (0.1 mg/kg) (Temgesic® Schering-Plough, New Jersey, USA) (III) was administered intraperitoneally 20 min prior to the injections and the animals were anesthetized using isoflurane. In addition, intraperitoneal or subcutaneous buprenorphine was administered if animals showed any signs of pain (immobilization etc.). At the end of the experiments, the mice were sacrificed in deep terminal sodium-pentobarbital (60 mg/kg) Mebunat Vet® (Orion Co. Espoo, Finland) (I, II) or ketamine (Ketalar®, Pfizer Inc. New York, USA) plus medetomidine (Domitor®, Orion Co. Espoo, Finland) (III) anesthesia in combination with intracardiac puncture.

### 4.2.2 Ethical aspects

Animal care was in accordance with the guidelines of the International Council of Laboratory Animal Science (ICLAS) and with the European Community Council Directive 2010/63/EU, and all experimental procedures were approved by the national animal care and use committee. Experiments were designed in order to minimize the number of animals used.

### 4.2.3 Diets

Standard rodent chow (SDS, Essex, UK) was used unless stated otherwise. Special diets obtained from Research Diets (New Brunswick, NJ) were used to induce obesity and are listed in detail in Table 5. A high-fat Western type diet (D12451) was used in study I and in the pair-feeding study. A Western diet including a moderate level of fat (D05022804) was used in study II and normal Western diet (D12079B) was used in study III. Standard rodent chow was used mainly in study III.

**Table 5.** Information about the main components of the diets used in each study.

Study (I-III) Product	Standard Chow		I D12451		II D05022804		III D12079B	
	g%	kcal%	g%	kcal%	g%	kcal%	g%	kcal%
Protein	21	17.5	24	20	18	17	20	17
Carbohydrate	90	75.1	41	35	62	58	50	43
Fat	3.7	7.4	24	45	12	25	21	40
Total		100		100		100		100
kcal/g	3.52		4.73		4.25		4.68	
Cholesterol	-		-		1.5		1.5	

### 4.2.4 Study design

In studies I-II, control groups were included for both the stereotaxic operation (non-treated control) and the lentivirus vector (saline) (Table 6). Since both saline and non-treated controls did not show significant differences in both studies I-II, they were excluded from the last experiment in order to reduce the numbers of animals needed.

**Table 6.** Information about the number of treated animals in addition to the number of animals left at the end and the number used for statistics in each study. In study I; One mouse in the LVi-EGFP died from operative trauma and five mice in the LVi-EGFP and three mice in the LVi- $\alpha$ -MSH-EGFP were euthanized before the end of the experiment due to other complications. Study I was divided into two separate experiments of which the other was a pair-feeding study where LVi-EGFP PF were fed similarly to matched pair in the LVi- $\alpha$ -MSH-EGFP group. Due to an unexplained cause in the pair-feeding study, there was an outbreak of dermatitis. Ultimately, two mice in LVi- $\alpha$ -MSH-EGFP and three mice in the LVi-EGFP PF groups had to be euthanized because of severe complications related to the dermatitis, although all treatment groups were severely compromised. In study II, one animal in the LVi-EGFP died from operative trauma and one LVi- $\alpha$ -MSH-EGFP treated animal suffered from a hematoma. In addition, one LVi- $\alpha$ -MSH-EGFP died after telemetric implantation. In study III, one animal in the LVi-EGFP group died from operative trauma and one animal in each treatment group died of other causes.

Experimental setups		I			
Treatment Group		LVi-EGFP	LVi- $\alpha$ -MSH-EGFP	Saline	Non-treated
Use of Animals	Start	12	12	6	6
	End	7	9	6	6
Animals included in statistics		4	4	5	6
I (pair-feeding)					
Treatment Group		LVi-EGFP	LVi- $\alpha$ -MSH-EGFP	LVi-EGFP PF	
Use of Animals	Start	13	13	14	
	End	13	11	11	
Animals included in statistics		7	7	7	
II					
Treatment Group		LVi-EGFP	LVi- $\alpha$ -MSH-EGFP	Saline	Non-treated
Use of Animals	Start	16	16	6	6
	End	15	16	6	6
Animals included in statistics		10	9	5	6
Telemetric Implantation		4	5	-	-
III					
Treatment Group		LVi-EGFP	LVi- $\gamma$ -MSH-EGFP		
Use of Animals	Start	20	20		
	End	18	19		
Animals included in statistics		17/15	16/13		

### 4.3 EXPERIMENTAL PROTOCOLS

#### 4.3.1 *Stereotaxis (I-III)*

Analgesia was administered 20 min prior to each operation intraperitoneally and the animals were anesthetized with isoflurane. Saline,  $2.1 \times 10^5$  TU (I-II) or  $6 \times 10^5$  TU (III) of LVi-EGFP, and LVi- $\alpha$ -MSH-EGFP (I-II) or LVi- $\gamma$ -MSH-EGFP (III) in similar volume was delivered bilaterally either to the ARC (I, III) or NTS (II) by stereotaxis. Before each injection, the animals were carefully positioned to a mouse adaptor in a stereotaxic frame from Stoelting (Stoelting Co., Wood Dale, IL, USA). A Stoelting QSI injector was

used to deliver a total volume of 1  $\mu$ l of the viral suspension at 0.1  $\mu$ l /min. The needle was withdrawn slowly 5 (I-II), 10 (I PF, III) after infusion.

The stereotaxic coordinates or the point of the injection according to the Bregma for the ARC were Anterior-Posterior (AP) 1.70 mm, Dorsal-Ventral (DV) -6.00 mm and Medial-Lateral (ML)  $\pm$  0.05 mm (I) and AP 1.70 mm, DV -5.90 mm and ML  $\pm$  0.13 mm at a 10° angle towards the midline (III) The stereotaxic coordinates or the point of the injection according to the Interaural structure for NTS injections were Anterior-Posterior (AP) - 3.50 mm, Dorsal-Ventral (DV) - 4.50 mm and Medial-Lateral (ML)  $\pm$  0.05 mm (II). Stereotaxic coordinates were obtained from Franklin & Paxinos. 1997 “The Mouse Brain: In Stereotaxic Coordinates”-atlas and refined using methylene blue test injections (Franklin & Paxinos. 1997).

#### **4.3.2 Exclusion criteria (I-III)**

At the end of first two studies, the coronal brain sections of both LVi- $\alpha$ -MSH-EGFP and LVi-EGFP injected animals were analyzed for EGFP expression to define the site of injection. Mice with detectable EGFP in the ARC inside the region of Bregma AP -1.45 to -2 mm according to Franklin and Paxinos at least unilaterally were included in the final results. EGFP expression in the ventricular space was an exclusion criterion, since this was considered as evidence of a ventricular administration or leakage of the viral suspension. In study I, four mice out of a total of seven LVi-EGFP injected and four out of nine LVi- $\alpha$ -MSH-EGFP injected mice showed EGFP in the ARC including one bilaterally (Table 6). In the pair-feeding experiment of study I, seven mice in each treatment group displayed EGFP in the ARC with two LVi- $\alpha$ -MSH-EGFP and one pair-fed LVi-EGFP treated mice bilaterally (Table 6). In study II, mice with injections that entered the fourth ventricle or that were located outside the NTS region of Interaural AP -3.20 to -3.80 mm (Franklin & Paxinos. 1997) were excluded from the final results (n = 5 in the LVi- $\alpha$ -MSH-EGFP and n = 3 in the LVi-EGFP group). Overall ten mice in the LVi-EGFP group and nine in the LVi- $\alpha$ -MSH-EGFP group were included in the final results (Table 6). Exclusion criteria in study III were based on unresponsiveness to diets and thus low weight gain in DIO sensitive mice consuming the Western diet for 13-weeks (one LVi-EGFP and three LVi- $\gamma$ -MSH-EGFP) and weight loss resistant mice (two LVi-EGFP and three LVi- $\gamma$ -MSH-EGFP) were excluded from experiment (Table 6).

#### **4.3.3 Body weight and food intake assessments (I-III)**

Body and food weights were measured biweekly (I, II) or weekly (I, III) in the first experiment, and daily food intake was calculated from the change in food weight divided by the number of days. In the pair-feeding experiment, the mice and food were weighed daily, and mice in the pair-fed LVi-EGFP treated group were given the amount of food consumed by a weight matched pair in the LVi- $\alpha$ -MSH-EGFP treated group during the corresponding experimental day. Food spillage was accounted for in all measurements by carefully checking the bedding (Tapvei aspen) for fallen red (I), blue (II), yellow (III) or brown-colored (chow) food crumbs and including the crumbs into the remaining food. In study III, fasting and re-feeding were also assessed. The experiments include measurements

of *ad libitum* feeding during the first two hours of the dark period 24 hours before the re-feeding analysis. Animals were fasted during the light period (12 hours) prior to re-feeding. Food was weighed manually two-, twelve- and 24-hours from the beginning of re-feeding.

#### 4.3.4 Basal glucose and glucose tolerance test (I-III)

For basal blood glucose level and the glucose tolerance test (GTT), the mice were administered intraperitoneally with glucose (5% [wt/vol], 1 g/kg body weight) after a four-hour fast. Tail vein blood samples (5  $\mu$ L) were withdrawn by incision at 0, 20, 40, 60, and 90 minutes from mice restrained shortly. Glucose concentration was measured with the Precision Xtra Glucose Monitoring Device (Abbott Diabetes Care, Abbott Park, IL).

#### 4.3.5 Estimation of energy expenditure (II)

The assessment of Total energy expenditure ( $TEE_{bal}$ ) was calculated according to the energy obtained from consumed food together with the relative gain or loss of energy from lean and fat mass change over time according to the following equation:  $TEE_{bal} = EI - (\Delta\text{somatc fat energy} + \Delta\text{somatc fat-free energy})$ , where EI = total energy intake (kcal),  $\Delta\text{somatc fat energy} = \text{change in fat mass (g)} \times 9.0 \text{ kcal / g}$  for negative change or 12.3 kcal/g for positive change,  $\Delta\text{somatc fat-free energy} = \text{change in lean mass (g)} \times 1.0 \text{ kcal / g}$  for negative change or 2.2 kcal / g for positive change. The estimation technique has been validated and shows a high correlation with total energy expenditure as measured with indirect calorimetry (Ravussin, *et al.* 2013).

#### 4.3.6 Hemodynamic parameters (II)

##### 4.3.6.1 BLOOD PRESSURE BY TAIL-CUFF

Systolic blood pressure (sBP) and heart rate (HR) were measured in conscious restrained animals optically using the tail-cuff system (TSE System International Group, Bad Homburg, Germany). The sBP and HR were assessed on day three after an acclimation for two consecutive days. The mean of 6-10 measurements from each mouse was recorded.

##### 4.3.6.2 BLOOD PRESSURE TELEMETRY AND PHARMACOLOGICAL TESTING

sBP and HR were measured in conscious, unrestrained mice using a radiotelemetry system (TA11PA-C10 and Dataquest software, Data Sciences International) as previously described (Rinne, *et al.* 2008, Rinne, *et al.* 2013). Baseline values for hemodynamic parameters during the first recovery week were recorded for three consecutive days and the results are given as 12 h means over non-active light and active dark periods. At the end, autonomic control of BP and HR was assessed pharmacologically using muscarinic blockade by atropine (2 mg/kg),  $\beta$ 1-adrenergic blockade by metoprolol (4 mg/kg) and  $\alpha$ <sub>1</sub>-adrenergic blockade with prazosin (1 mg/kg) comparing to saline (10 mL/kg) as described earlier (Rinne, *et al.* 2013).

#### **4.3.7 Body composition (II-III)**

Body composition (fat tissue and lean tissue in grams) was assessed utilizing an EchoMRI-700 quantitative nuclear magnetic resonance whole body composition analyzer (Echo Medical Systems, Houston, TX). Awake mice were placed in the holder for a duration of 1-3 minutes in this measurement.

#### **4.3.8 Metabolic cage and home cage assessments (II-III)**

Mice were weighed and placed into metabolic cages (Harlan Laboratories Inc, Indianapolis, Ind, USA) allowing the collection of urine and feces for over a period of 24 hours. Water and food consumption was measured and the fecal stool and total urine were weighed and collected for further analysis. In the home cage water intake assessment, water bottles were first filled and weighed and then added to each cage carefully. The water intake was measured for 72-hours and 24-hour water intake was calculated as a three-day average of the total amount of water consumed by the animal.

#### **4.3.9 Voluntary running wheel activity (III)**

Running wheel activity was measured prior to and three weeks after the treatments and three weeks after the beginning of the Western diet. Low-Profile wireless running wheels for mice (Med Associates, Inc. Vermont, USA) were used to measure 24-hour running wheel activity in the home cage. Weight change and food intake during the 24-hour analysis were also measured.

#### **4.3.10 Tissue collection and preparation (I-III)**

At the end of experiments, the mice were sacrificed after a four-hour fast. Blood samples were collected with terminal intracardiac puncture under deep pentobarbital sodium (70 mg/kg) anesthesia (I) or by decapitation (I PF). A total of 500 $\mu$ L blood per mice was collected in serum separation tubes (CAPIJECT® T-MG) (Terumo Medical Corporation, Elkton, MD, USA).

Whole brain samples were collected, rinsed in ice-cold PBS solution (pH 7.4), dried and frozen with isopentane in O.C.T solution (Sakura Finetek, Torrance, CA, USA). Brain sections were collected with a Leica CM-3050S cryostat in 10  $\mu$ m sections (Leica Microsystems GmbH, Wetzlar, Germany) and samples were stored isolated from air at -80°C (I-III).

In study I; subcutaneous, epididymal, mesenteric, and retroperitoneal white adipose tissue (WAT), and interscapular brown adipose tissue (BAT) depots were collected and weighed at sacrifice. In addition liver, heart and kidney were collected and weighed. In study II; mesenteric and retroperitoneal WAT and interscapular BAT depots, liver, heart and kidney were collected and weighed. In study III; a single lobe of intrascapular BAT and adrenal gland were collected, snap frozen and stored at -80 until analysis of mRNA.

## 4.4 BIOCHEMICAL ANALYSIS

### 4.4.1 Immunohistochemistry (I-II)

Immunohistochemistry (IHC) was performed using the avidin–biotin–peroxidase method. Briefly, samples were post-fixed in 4 % paraformaldehyde-PBS solution for 5 minutes and incubated for 20 minutes in 3% H<sub>2</sub>O<sub>2</sub> in methanol in order to inactivate endogenous peroxidase. 10% normal horse serum in PBST 0.1 % solution was used to block Fc receptors. The  $\alpha$ -MSH antibody (Phoenix Pharmaceuticals, Inc. catalogue number: H-043-01) was incubated at a concentration of 1/1000 overnight in 4°C in PBST 0.1 % solution. Subsequently, the sections were incubated with a biotinylated horse anti-rabbit IgG antibody (1/300) (Vector Laboratories, CA, USA) 1 h at room temperature in PBS solution. VectorElite ABC (Vector Laboratories, CA, USA) was used to amplify the signal and visualized using 3,3-diaminobenzidine (DAB). The tissue was then counter-stained using cresyl violet in order to visualize cell nuclei. The antibody used in IHC was specific to  $\alpha$ -MSH as incubation of primary antibody solution and 100 mM of synthetic  $\alpha$ -MSH (Tocris Bioscience, Bristol, United Kingdom Cat. No. 3013) abolished all immunoreactivity.

### 4.4.2 Image analysis and quantification (I-II)

Brain samples were examined with a Leica DM R microscope (Leica Microsystems GmbH, Wetzlar, Germany) under fluorescence filters or visible light fluorescent images were acquired from samples post-fixed in 4% PFA-PBS solution, dried and mounted with a fluorescent preserving hardening mounting medium with DAPI (Vector Laboratories Inc, Burlingame, CA, USA) using an Olympus DP70 camera and DP software (Olympus Co., Japan) (I) or a Zeiss Axioimager M1 and ZEN 2012 software (Carl Zeiss Microscopy LLC, New York, USA) (II). DAB stained sections were visualized using a BestScope BUC4-500C camera (BestScope International Limited, Beijing, China) and IScapture 2.6 software (Fuzhou Xintu Photonics Co., Fujian, China). The image series were then merged together using Windows Ice 1.3.3.0 software (Microsoft Co., USA). Pictures were analyzed using Adobe Photoshop 8.0 (Adobe Systems Inc., USA).

Coronal sections covering the ARC (I) or NTS (II) in 100  $\mu$ m increments were immunostained for  $\alpha$ -MSH and positive DAB staining was quantified manually (I) or by using automated DAB calculations (II). The ARC and NTS regions were cropped from the images according to Franklin and (Franklin & Paxinos. 1997). In study I, quantification was carried out by counting the number of neurons with detectable levels of  $\alpha$ -MSH in the ARC region. The researcher was blinded to the treatment group, the mean of three counts per sample was used with an n of 6 in each group. In study II, cropped images were analyzed with ImageJ 1.47 software (Rasband. 1997-2012), brown DAB staining was isolated and the pixel count of specific DAB staining calculated automatically using the color\_deconvolution/H&E DAB-program (Ruifrok, *et al.* 2003). Pixel counts were acquired from both hemispheres separately with four mice per group and from one hemisphere only in three additional mice in the LV $\alpha$ -MSH-EGFP group. The results include 3-8 samples per rostrocaudal segment in each group. Areas under the

curve (AUC) for the mean pixel count curves in Figure 9 were calculated and used to estimate the relative  $\alpha$ -MSH levels in the whole NTS area.

#### **4.4.3 Liver and serum lipids (I-III)**

Liver lipid contents were isolated and purified with the Folch method (Folch, *et al.* 1957) (I). Serum and liver triglycerides were quantified with Free Glycerol Reagent (F6428) and Triglyceride Reagent (T2449; Sigma Diagnostics). The non-esterified free fatty acids (NEFA) were determined with NEFA-C Reagent set (Wako Chemicals GmbH, Neuss, Germany).

#### **4.4.4 Cholesterol levels and non-esterified fatty acids (I-III)**

Serum total cholesterol levels were measured with Cayman Cholesterol Assay Kit (Cayman Chemical Company, MI, USA) (I) and the levels of non-esterified free fatty acids (NEFA) were determined from serum with NEFA-C Reagent set (Wako Chemicals GmbH, Neuss, Germany) (I-III).

#### **4.4.5 Serum insulin and glucose (I-II)**

The serum insulin concentration was measured using Mercodia Ultrasensitive Mouse Insulin ELISA Kit (Mercodia AB, Uppsala, Sweden). Serum glucose levels were determined using Cayman Glucose Colorimetric Assay Kit (Cayman Chemical Company, MI, USA).

#### **4.4.6 Urinary creatinine (II)**

24-h urine samples were collected in metabolic cages and the specimens were stored at  $-80^{\circ}\text{C}$  until assayed with a creatinine assay (Cayman Chemical Company, Ann Arbor, MI) relying on the Jaffé reaction to estimate the creatinine concentration which was then multiplied with the 24-hour urine volume.

### **4.5 GENE EXPRESSION (II-III)**

#### **4.5.1 Quantitative polymerase chain reaction**

The mRNA levels of uncoupling protein 1 (UCP1) in BAT and tyrosine hydroxylase from adrenal gland were analyzed using quantitative real-time PCR (qPCR). Briefly, the mRNA was first extracted and converted to cDNA using a High Capacity RNA-to-cDNA Kit (Applied Biosystems, CA) according to the manufacturer's instructions on a GeneAmp PCR System 9600 (Perkin Elmer). BAT mRNA was isolated using Qiazol (Chomczynski & Sacchi. 2006) and adrenal gland mRNA using a RNeasy Micro Kit

according to the manufacturer's instructions (Qiagen N.V. Venlo, Netherlands). Target genes uncoupling protein 1 (UCP1) and tyrosine hydroxylase (TH) were quantitated with 7300 Real-Time PCR System (Applied Biosystems) relative to the housekeeping genes: Ribosomal protein s29 (Rps29) (II) or  $\beta$ -actin (Mouse ACTB) (III) using the SYBR-Green method (Kapa Biosystems, Woburn, MA). The primer pairs are presented in Table 7.

**Table 7.** Primer-pairs used in assessment of mRNA levels of genes. All results were correlated according to known and commonly used house-keeping genes.

Houskeeping genes:	
<b><math>\beta</math>-actin</b>	Sequence
Upstream	5'-GGC CTC TAC GAC TCA GTC CA-3'
Downstream	5'-TAA GCC GGC TGA GAT CTT GT-3'
<b>Rps29</b>	Sequence
Upstream	5'-ATG GGT CAC CAG CAG CTC TA-3'
Downstream	5'-AGC CTA TGT CCT TCG CGT ACT-3'
Target genes	
<b>UCP1</b>	Sequence
Upstream	5'-ACT GCC ACA CCT CCA GTC ATT-3'
Downstream	5'-CTT TGC CTC ACT CAG GAT TGG-3'
<b>TH</b>	Sequence
Upstream	5'-CCC AAG GGC TTC AGA AGA G-3'
Downstream	5'-GGG CAT CCT CGA TGA GAC T-3'

#### 4.6 STATISTICAL METHODS

Weight development, food intake, body composition, telemetric measurements over time, glucose tolerance test and voluntary running wheel activity were analyzed using two-way ANOVA. Whenever the interaction was significant, the treatment effects were compared at different time points with Bonferroni post-hoc analysis. The parametric unpaired t-test was used for comparing normally distributed single-parameters and Mann–Whitney test for parameters with small numerical nomenclature between LVi- $\alpha$ -MSH-EGFP or LVi- $\gamma$ -MSH-EGFP and LVi-EGFP control treatments. Areas under the curves were calculated with the trapezoidal method. Statistical analyses were carried out with GraphPad Prism 6.0. Data are presented as means  $\pm$  SEM. The results were considered statistically significant at  $P < 0.05$ .

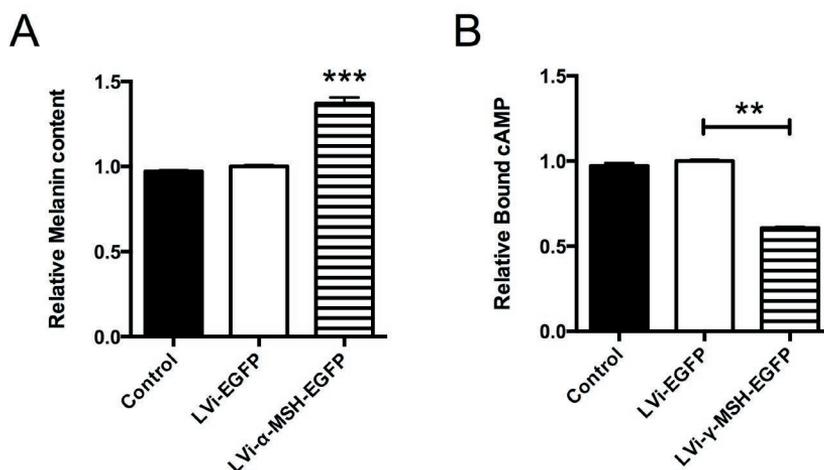
## 5. RESULTS

### 5.1 LENTIVIRAL VECTORS

#### 5.1.1 Biological activity of viruses

The ability of the LVi- $\alpha$ -MSH-EGFP to generate biologically active  $\alpha$ -MSH was tested in B16F10 melanocyte cells, which are known to express MC1R. As a result of MC1R-receptor activation, the LVi- $\alpha$ -MSH-EGFP infected melanocytes produced significantly more melanin than cells infected with the LVi-EGFP control virus and uninfected control cells indicating that the virally produced  $\alpha$ -MSH is biologically active (Figure 6 A). Furthermore, the lentiviruses induced  $71.7 \pm 1.4$  % infectivity in the B16F10 cells with a MOI100, which demonstrated the capability of the lentiviral vectors to induce viral transduction.

The ability of the LVi- $\gamma$ -MSH-EGFP to produce biologically active peptides was analyzed by using the growth medium of HEK293T cells infected with the LVi- $\gamma$ -MSH-EGFP. The cell growth medium of LVi- $\gamma$ -MSH-EGFP infected HEK293T cells resulted in significantly smaller levels of bound cAMP as compared with cells infected with the LVi-EGFP control virus (Figure 6 B).

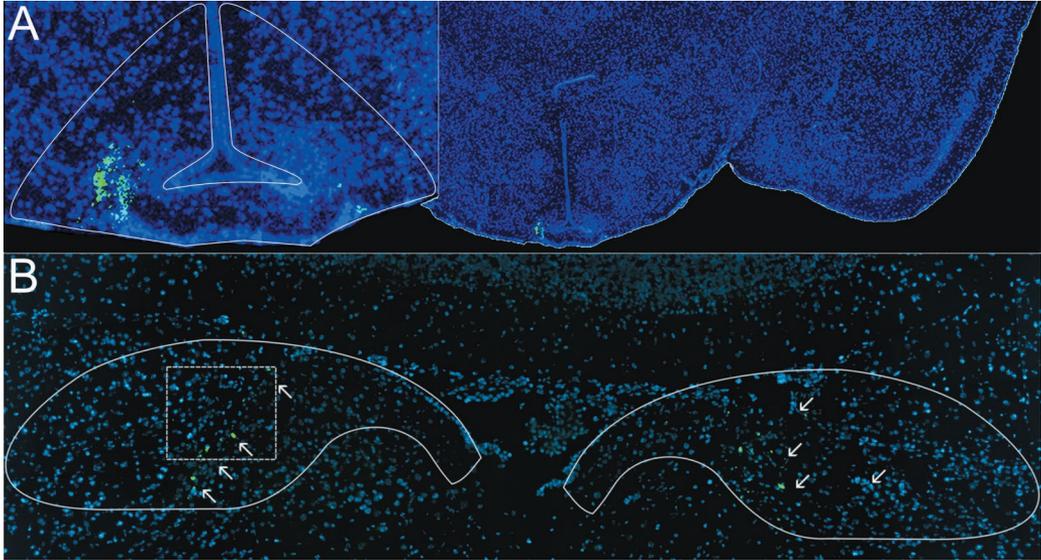


**Figure 6.** *In vitro* biological activity of LVi- $\alpha$ -MSH-EGFP and LVi- $\gamma$ -MSH-EGFP lentiviruses. A: The relative amount of melanin produced by the LVi- $\alpha$ -MSH-EGFP (n = 11) lentiviral vector compared to LVi-EGFP (n = 12) and non-infected control (n = 6) in B16F10 cells. B: The relative stimulatory capacity of the growth medium of non-infected control (n = 5) and LVi-EGFP (n = 5) or LVi- $\gamma$ -MSH-EGFP infected (n = 6) HEK293T cells to induce the release of bound cAMP in hMC3R cells \*\*\*P < 0.001, \*\*P < 0.01, one-way ANOVA followed by Kruskal-Wallis post-hoc test

## 5.2 IN VIVO GENE EXPRESSION ANALYSIS

### 5.2.1 EGFP expression

Coronal brain sections of animals injected with LVi-EGFP and LVi- $\alpha$ -MSH-EGFP lentiviruses in studies I-II were analyzed for the exact position of EGFP expression visually in DAPI stained sections in a fluorescent microscope. EGFP expression was found in the medial and basal region of the hypothalamic ARC (Figure 7 A) and in the medial and dorsal regions of the NTS in the brain stem (Figure 7 B).

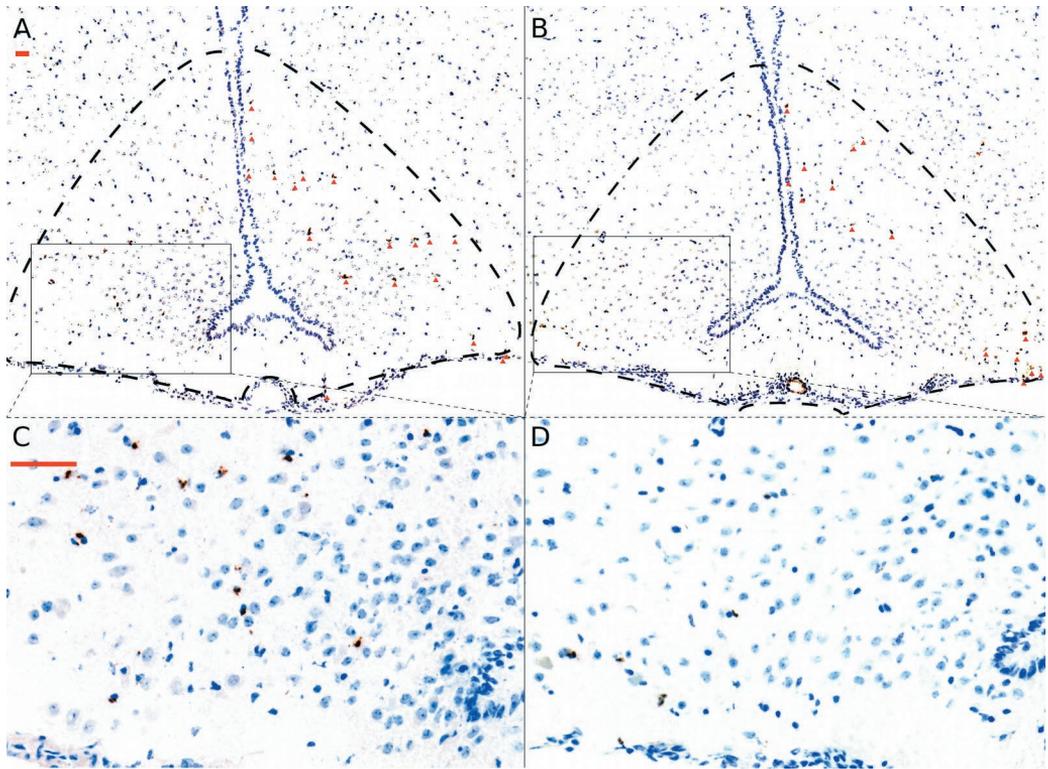


**Figure 7.** Location of lentivirally induced EGFP expression (green) in A: ARC injections and in B: NTS injections. Figure on the left in A is a magnification of the background coronal section. Marked area represents the corresponding target brain area and the white square in B indicated the location of DAB staining of  $\alpha$ -MSH immunoreactivity (Figure 9 D). DAPI (blue) is a nuclear stain. Arrows indicate location of EGFP transgene expression in the NTS.

### 5.2.2 Transgene and $\alpha$ -MSH immunostaining

#### *Hypothalamus*

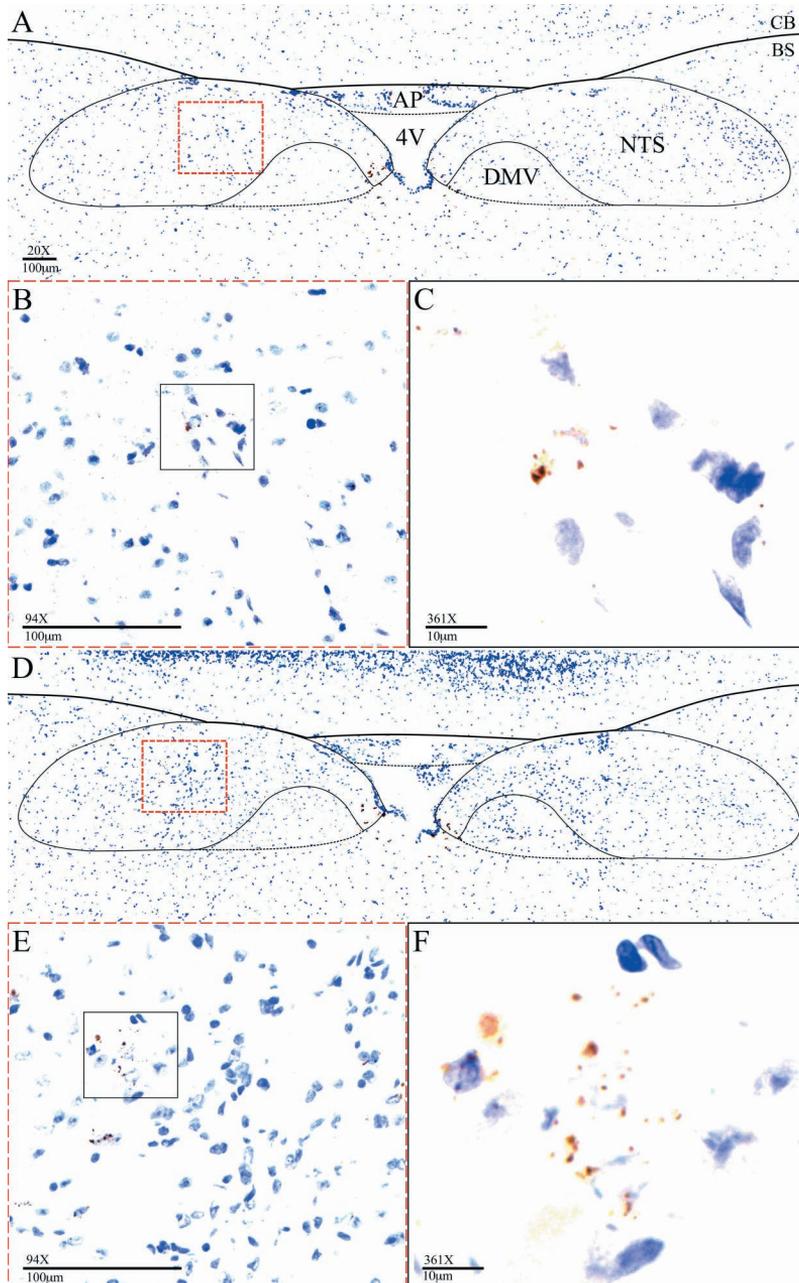
The level of  $\alpha$ -MSH overexpression in the ARC was semiquantified using immunohistochemistry. There was a 62 % increase in the number of  $\alpha$ -MSH stained neurons in the ARC in LVi- $\alpha$ -MSH-EGFP compared with LVi-EGFP injected mice ( $42 \pm 6.0$  vs.  $26 \pm 2.3$ , \* $P < 0.05$ ) (Figure 8).



**Figure 8.** Immunohistochemical staining in study I of  $\alpha$ -MSH in the ARC of the hypothalamus of representative samples of A: LVi- $\alpha$ -MSH-EGFP and B: LVi-EGFP treated animals. Positive DAB (brown) staining highlighted in the right hemisphere with red cones (A and B). High-resolution images of staining close to the third ventricle on the left hemisphere of C: LVi- $\alpha$ -MSH-EGFP and D: LVi-EGFP treated animals. Scale bar (red) indicates a distance of 50  $\mu$ m.

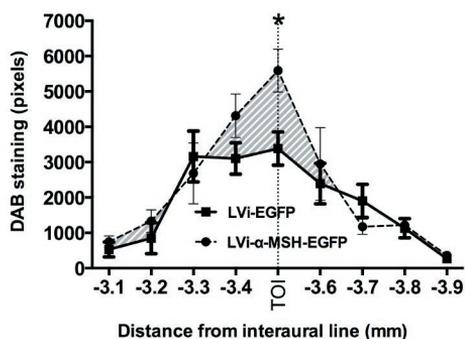
### ***Brain stem***

The  $\alpha$ -MSH immunoreactivity in NTS injections was determined in coronal sections using immunohistochemistry of LVi-EGFP and LVi- $\alpha$ -MSH-EGFP treatments groups. The  $\alpha$ -MSH immunoreactivity in the LVi-EGFP control group was mostly located in the close proximity of the fourth ventricle or the central canal in the commissural NTS with minor positive locations in the dorsal and medial NTS (Figure 9 A-C). In contrast,  $\alpha$ -MSH immunoreactivity in the LVi- $\alpha$ -MSH-EGFP samples was evident as a more intense and widespread staining descending from dorsolateral regions and dorsomedial to the medial NTS (Figure 9 D-E) and spreading on average over an area of  $255 \pm 14 \mu\text{m}$  in width ( $n = 5$ ).

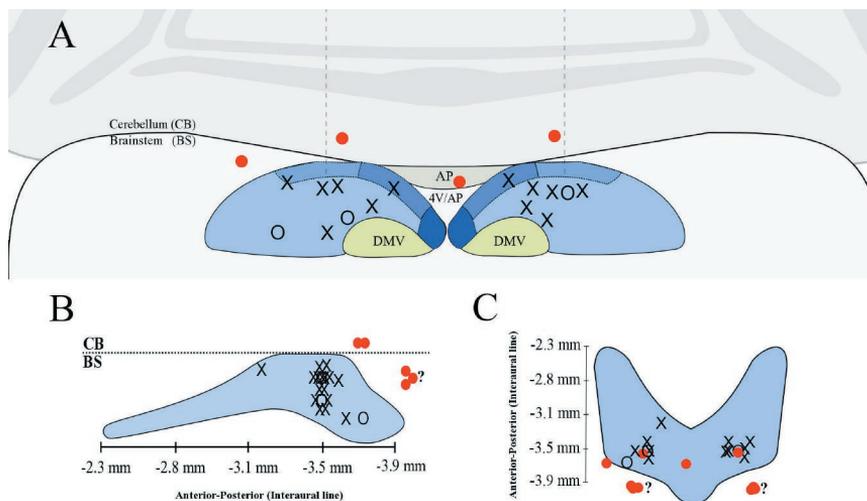


**Figure 9.** Representative images from study II of  $\alpha$ -MSH immunoreactivity in the coronal sections of the brain stem in the interaural -3.5 mm position of LVi-EGFP (A-C) and LVi- $\alpha$ -MSH-EGFP (D-F) injected mouse. A, D: 20x image of the nucleus tractus solitarius (black outline) and infection site (red box). B, E: 40x image of the injection site. C, F: Magnified 63x image of the black box in B and E. Cresyl (blue color) indicates nuclei and DAB (brown color) the location of  $\alpha$ -MSH immunoreactivity. Scale bar and magnification factor located in the lower left corner of each image. The white dotted box indicates the injection site and white arrows point to EGFP. AP = area postrema, BS = brain stem, CB = cerebellum, DMV = dorsal motor nucleus of the vagus, NTS = nucleus tractus solitarius, 4V = the fourth ventricle.

The data obtained from IHC-staining analysis was used in order to measure the major location of  $\alpha$ -MSH overexpression in the brain stem (Figure 10) and to compare this data to the determined target site. The quantification results indicate a significant 65 % increase in  $\alpha$ -MSH immunoreactivity in the interaural -3.5 mm sections in accordance with the coordinates used in the injections and the actual sites of successful injections (Figure 10). The overall  $\alpha$ -MSH immunoreactivity in the NTS as estimated by comparing the AUC values of the mean pixel count curves (Figure 10) was 31% more in the LVi- $\alpha$ -MSH-EGFP mice (AUC: 1288 vs. 983 pixels x section). In addition, NTS injections were plotted schematically (Figure 11) according to both EGFP and  $\alpha$ -MSH immunoreactivity in order to visualize the target sites and confirm the results obtained from semiquantification.



**Figure 10.** Semiquantification of  $\alpha$ -MSH immunoreactivity in study II (DAB stained pixels) in the NTS -3.9 to -3.1 mm from the interaural structure in LVi-EGFP (n = 4) and LVi- $\alpha$ -MSH-EGFP (n = 6) treated animals. TOI = Target of infection. \* P < 0.05, Mann-Whitney.



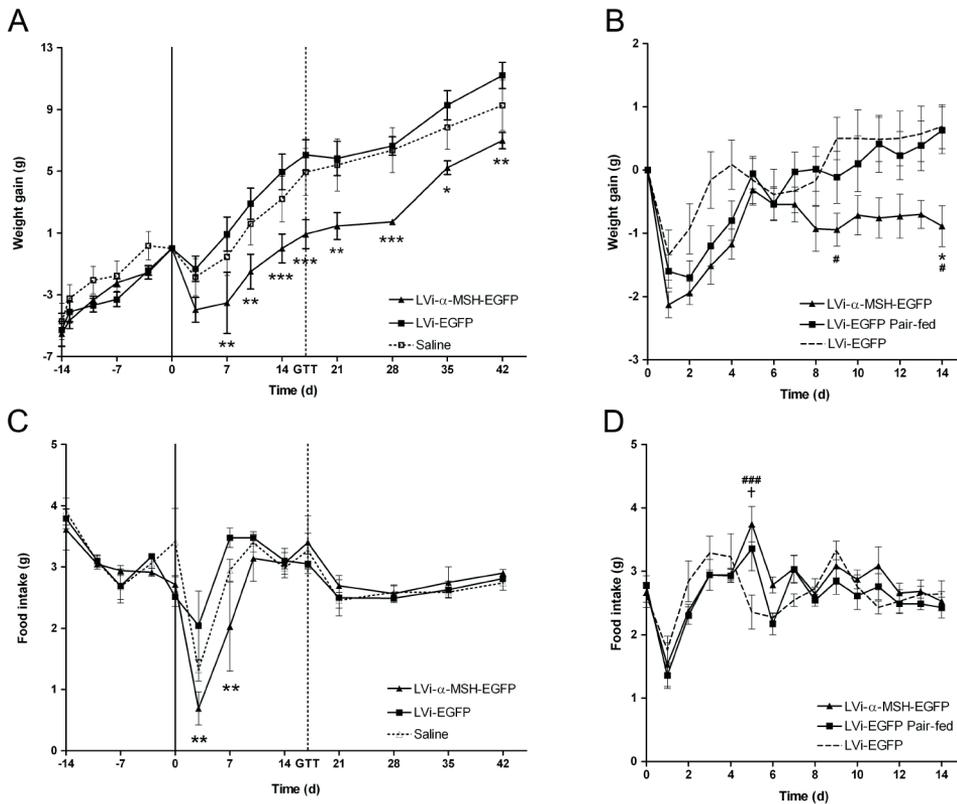
**Figure 11.** A: Schematic figure of coronal brain section in study II including injection sites, X = bilateral injection pair, O = unilateral hit, Red dot = injection missed NTS, AP = area postrema, DMV = dorsal motor nucleus of vagus, 4V = fourth ventricle, CC = central channel, NTS divided into; commissural (closest to 4V/CC), medial (middle of NTS), dorsomedial (next to commissural NTS) and dorsolateral (next to dorsomedial). B: Schematic figure of sagittal view in (A), C: Schematic figure of superior view in (A).

## 5.3 THE EFFECTS OF $\alpha$ -MSH OR $\gamma$ -MSH OVEREXPRESSION ON WEIGHT AND FOOD INTAKE

### 5.3.1 In the hypothalamus

#### 5.3.1.1 $\alpha$ -MSH

The first *in vivo* experiment in study I assessed the metabolic effects of LVi- $\alpha$ -MSH-EGFP compared with LVi-EGFP treated mice over six weeks after the injections. LVi- $\alpha$ -MSH-EGFP treated mice gained significantly less weight ( $8.4 \pm 0.4$  g) compared to LVi-EGFP treated mice ( $12.3 \pm 0.6$  g,  $P < 0.05$ ) during the experiment. The body weight gain was statistically significantly reduced in the LVi- $\alpha$ -MSH-EGFP group starting from day 7 (Figure 12 A). The LVi- $\alpha$ -MSH-EGFP treated mice consumed less food over the first week than the LVi-EGFP treated mice, but subsequently feeding increased to the same level and remained there until the end of the experiment (Figure 12 C). Viral infection *per se* had no effect on weight gain or food intake, as there were no differences between LVi-EGFP injected and saline injected animals (Figure 12 A, C).



**Figure 12.** A: Weight change and C: daily food intake of mice injected to the arcuate nucleus with lentiviral vectors LVi- $\alpha$ -MSH-EGFP ( $n = 4$ ) and LVi-EGFP ( $n = 4$ ) or saline ( $n = 5$ ) in study I. B: Weight change and D: daily food intake of weight matched LVi- $\alpha$ -MSH-EGFP treated group ( $n = 7$ ), pair-fed LVi-EGFP treated group ( $n = 7$ ) and *ad libitum* fed LVi-EGFP treated control group ( $n = 7$ ). LVi- $\alpha$ -MSH-EGFP compared to pair-fed LVi-EGFP (\*), and LVi-EGFP control (#), pair-fed LVi-EGFP compared to LVi-EGFP (†): \*\*\* $P < 0.001$ , \*\* $P < 0.01$ , \* $P < 0.05$ , #### $P < 0.001$ , # $P < 0.05$ , † $P < 0.05$ .

The aim of the pair-feeding experiment of study I was to define the role of feeding in the weight development of LVi- $\alpha$ -MSH-EGFP treated mice by pair-feeding a group of LVi-EGFP treated mice to the level of LVi- $\alpha$ -MSH-EGFP treated mice and comparing their weight gain. Although food intake was not significantly decreased in LVi- $\alpha$ -MSH-EGFP mice in this experiment, the weight gains between LVi- $\alpha$ -MSH-EGFP and LVi-EGFP groups were significantly different over the two week period after the injections (interaction of treatment and time:  $P < 0.0001$  and  $P = 0.0002$ , respectively, Figure 12 B, D). Food intake and weight gain tended to be lower on the first days after the injections in LVi- $\alpha$ -MSH-EGFP treated and pair-fed mice compared to LVi-EGFP treated *ad libitum* fed mice (Figure 12 B, D). Subsequently, food intake increased to the level of LVi-EGFP treated mice. Despite the similar food intake in all three groups after day 5, the LVi- $\alpha$ -MSH-EGFP group continued to gain less weight in comparison to both LVi-EGFP treated groups (Figure 12 B, D).

### 5.3.1.2 $\gamma$ -MSH

The *in vivo* experiment of study III aimed at defining the metabolic role of the  $\gamma$ -MSH over-expression period of 26 weeks, which was divided into an initial six-week chow diet, followed by a 13-week Western diet and a final seven-week chow diet intervention.

#### **Post-treatment chow diet period**

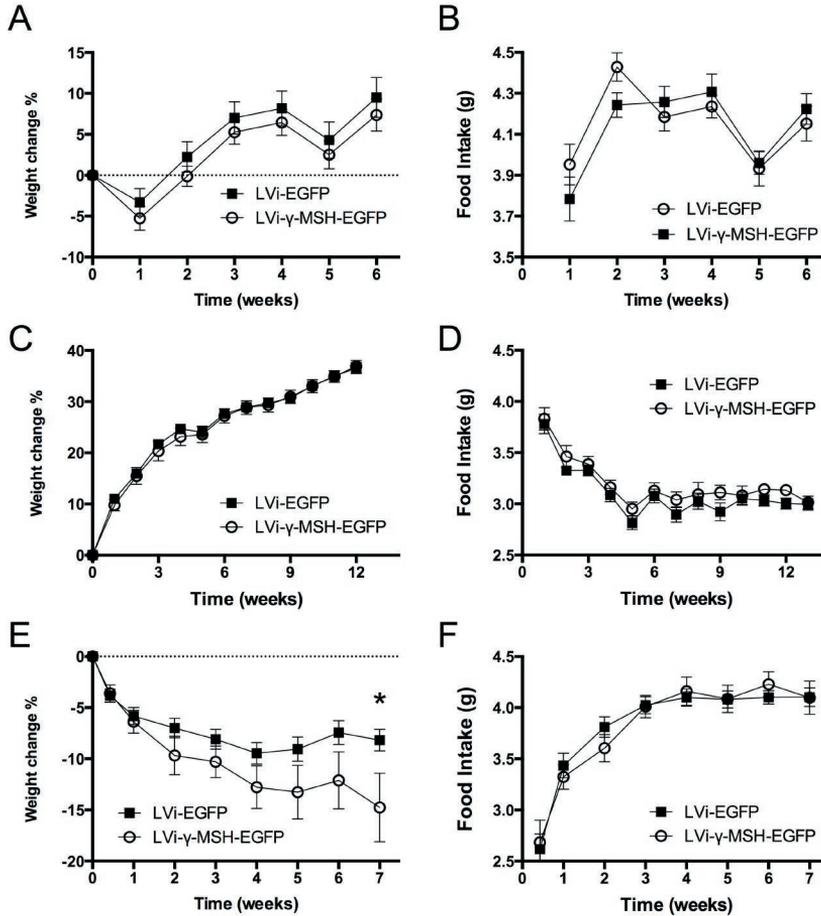
The LVi- $\gamma$ -MSH-EGFP treatment decreased the cumulative food intake during the first two weeks after stereotaxic delivery of lentiviral treatments compared to control ( $55.8 \pm 0.9$  vs.  $58.7 \pm 0.9$  g \* $P < 0.05$ ), but the weekly measurements were not significantly different (Figure 13 B). There were no differences in the total food intake over the course of the post-treatment chow period ( $169.5 \pm 2.0$  vs.  $170.1 \pm 2.0$  g  $P = \text{NS}$ ). Pre-treatment weight was regained within two weeks in both groups and overall weight development was similar in both groups during the six-week chow period (Figure 13 A). The weight reduction during the 12-hour fast prior to re-feeding was similar in both groups ( $-1.1 \pm 0.1$  vs.  $-1.2 \pm 0.1$  g  $P = \text{NS}$ ). There was no difference in the acute feeding (2h) after fasting ( $0.77 \pm 0.05$  vs.  $0.75 \pm 0.04$  g  $P = \text{NS}$ ) or under *ad libitum* conditions after the beginning of the dark period ( $0.63 \pm 0.03$  vs.  $0.61 \pm 0.04$  g,  $P = \text{NS}$ ). However, the treatment increased food intake over 24 hours time in LVi- $\gamma$ -MSH-EGFP animals after reintroduction to food ( $4.26 \pm 0.10$  vs.  $4.54 \pm 0.10$  g \* $P < 0.05$ ).

#### **Diet induced obesity period**

The relative weight change (Figure 13 C), daily food intake (Figure 13 D) and cumulative food intake during the first two weeks ( $51.1 \pm 1.4$  vs.  $49.7 \pm 0.9$  g  $P = \text{NS}$ ) and total food intake during the Western diet period ( $290.7 \pm 5.1$  vs.  $282.4 \pm 4.1$  g  $P = \text{NS}$ ) were similar between the LVi-EGFP and LVi- $\gamma$ -MSH-EGFP treatment groups. The weight tended to decrease more in the LVi- $\gamma$ -MSH-EGFP group during the 12 hour fast before re-feeding ( $-1.54 \pm 0.09$  vs.  $-1.30 \pm 0.08$  g  $P = 0.06$ ). Similarly to chow re-feeding assessment, there was no difference in the acute re-feeding ( $0.60 \pm 0.06$  vs.  $0.50 \pm 0.04$  g  $P = \text{NS}$ ) or normal feeding ( $0.49 \pm 0.06$  vs.  $0.48 \pm 0.06$  g,  $P = \text{NS}$ ). However, in contrast to the results on chow there was no differences in the 24-hour food intake between the treatments after re-access to food ( $3.55 \pm 0.10$  vs.  $3.36 \pm 0.10$  g  $P = \text{NS}$ ).

### Weight loss with chow diet

After the 13-week Western diet period, the diet was reverted back to standard rodent chow for a duration of seven weeks. The LVi- $\gamma$ -MSH-EGFP treated mice had a significantly increased relative weight loss compared to control (Figure 13 E). Food intake was similar in both treatment groups during this period (Figure 13 F).



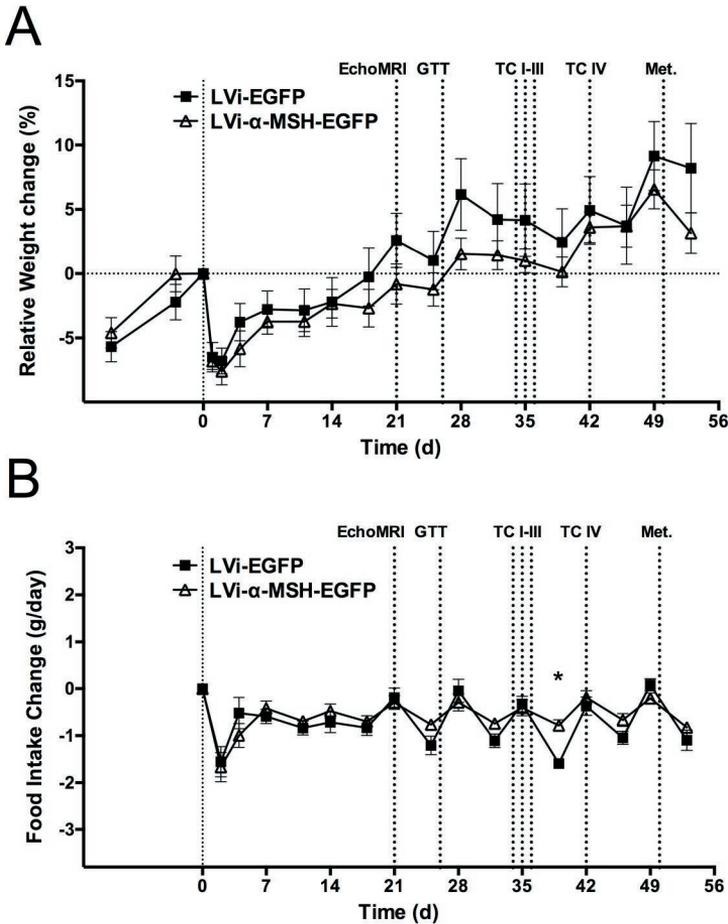
**Figure 13.** Relative weight change and food intake from all three parts of study III. Data from the initial chow period, A: Relative weight change, B: Food intake and the DIO Western diet period, C: Relative weight change and D: Food intake of LVi-EGFP (n = 17) and LVi- $\gamma$ -MSH-EGFP (n = 16) injected mice. E: Relative weight change and F: Food intake during the seven-week weight loss with chow diet-period in LVi-EGFP (n = 15) and LVi- $\gamma$ -MSH-EGFP (n = 13) injected mice \*P < 0.05.

### 5.3.2 In the brain stem

#### 5.3.2.1 $\alpha$ -MSH

There was no difference in relative body weight change between the treatments over time until day 53 (Figure 14 A). In the end, LVi- $\alpha$ -MSH-EGFP treated mice weighed significantly less than the LVi-EGFP mice ( $35.3 \pm 0.9$  vs.  $38.5 \pm 0.9$  g \*P < 0.05). The operation needed for viral injections caused a decrease in the body weights in both

groups, and the initial weight was achieved in the LVi-EGFP group by day 21 and in the LVi- $\alpha$ -MSH-EGFP group by day 28. On day 39 after three consecutive days of tail-cuff measurements, there was a difference in the feeding relative to baseline food intake and in total food intake (LVi-EGFP:  $2.3 \pm 0.1$  vs. LVi- $\alpha$ -MSH-EGFP:  $2.8 \pm 0.1$  g  $**P < 0.01$ ). The fluctuation in food intake in both treatment groups might have been related to weekly routines in the animal facilities or to the disturbed weight development after the experimental procedures.



**Figure 14.** Results from study II. A: Relative weight change, B: food intake change from baseline in food intake of mice injected to the NTS with lentiviral vectors LVi- $\alpha$ -MSH-EGFP ( $n = 9$ ) or LVi-EGFP ( $n = 10$ )  $*P < 0.05$ , Two-way-ANOVA followed by Bonferroni post-test. Time points of body composition analysis (EchoMRI), glucose tolerance test (GTT), tail-cuff blood pressure training and measurements (TC) and urine and fecal collections in the metabolic cages (Met.) are indicated as dotted vertical lines.

## 5.4 THE EFFECTS OF $\alpha$ -MSH OR $\gamma$ -MSH OVEREXPRESSION ON BODY COMPOSITION, ADIPOSITY AND TISSUE WEIGHTS

### 5.4.1 In the hypothalamus

#### 5.4.1.1 $\alpha$ -MSH

After sacrifice, liver, heart and the fat depots were individually weighed. The weight of the mesenteric fat depot was significantly decreased and the retroperitoneal fat depot showed a tendency to decrease in LVi- $\alpha$ -MSH-EGFP group compared with the LVi-EGFP group (Table 8), but there were no differences in subcutaneous, epididymal, or interscapular brown fat weights between treatments (Table 8). Moreover, there were no difference in heart weight, but the liver of the LVi- $\alpha$ -MSH-EGFP treated mice was significantly smaller (Table 8).

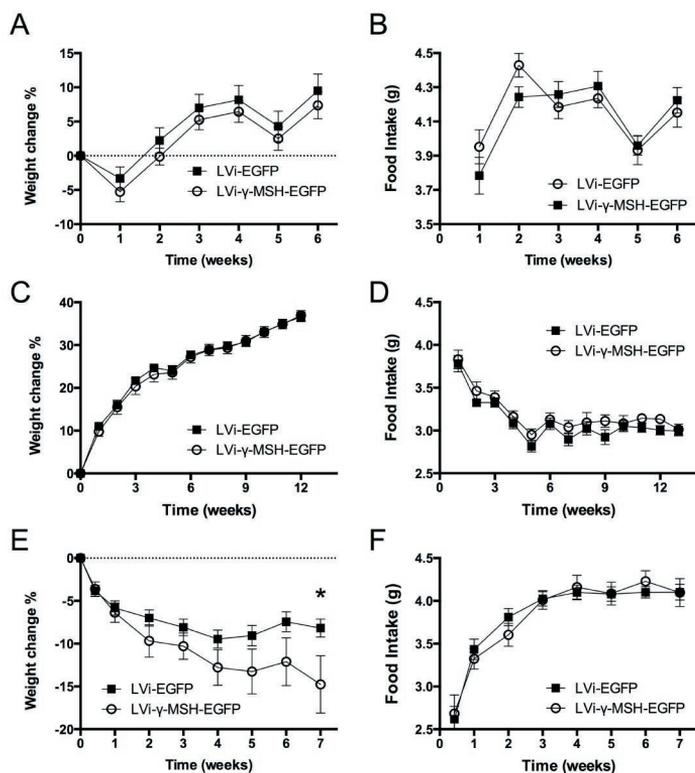
**Table 8.** Isolated tissues including fat depots from study I: LVi-EGFP (n = 4) and LVi- $\alpha$ -MSH-EGFP (n = 4), study II: LVi-EGFP (n = 10) and LVi- $\alpha$ -MSH-EGFP (n = 8) and study III: LVi-EGFP (n = 15) and LVi- $\gamma$ -MSH-EGFP (n = 13). \*\*P > 0.01 \*P > 0.05, non-parametric t-test was used in Study I and parametric t-test in Studies II and III.

Tissue		LVi-EGFP	LVi- $\alpha$ -MSH-EGFP
STUDY I	Subcutaneous fat (mg)	429 $\pm$ 27	461 $\pm$ 105
	Epigonadal fat (mg)	1343 $\pm$ 70	1243 $\pm$ 82
	Retroperitoneal fat (mg)	385 $\pm$ 21	195 $\pm$ 54
	Mesenteric fat (mg)	993 $\pm$ 96	729 $\pm$ 64 *
	Interscapular BAT (mg)	156 $\pm$ 34	143 $\pm$ 13
	<b>Sum of fat depots (mg)</b>	<b>5308 <math>\pm</math> 168</b>	<b>4525 <math>\pm</math> 445</b>
	Liver (mg)	1942 $\pm$ 35	1562 $\pm$ 42 *
	Heart (mg)	132 $\pm$ 7	146 $\pm$ 9
Tissue		LVi-EGFP	LVi- $\alpha$ -MSH-EGFP
STUDY II	Retroperitoneal fat (mg)	335 $\pm$ 18	256 $\pm$ 27 *
	Mesenteric fat (mg)	807 $\pm$ 69	552 $\pm$ 38 **
	Interscapular BAT (mg)	247 $\pm$ 14	188 $\pm$ 17 *
	Liver (mg)	2109 $\pm$ 116	2075 $\pm$ 158
	Heart (mg)	148 $\pm$ 3	149 $\pm$ 7
	Kidney (mg)	214 $\pm$ 5	208 $\pm$ 9
Tissue		LVi-EGFP	LVi- $\gamma$ -MSH-EGFP
STUDY III	Subcutaneous fat (mg)	651 $\pm$ 43	565 $\pm$ 82
	Epigonadal fat (mg)	1259 $\pm$ 82	1054 $\pm$ 121 (P= 0.09)
	Retroperitoneal fat (mg)	600 $\pm$ 47	502 $\pm$ 70
	Mesenteric fat (mg)	868 $\pm$ 46	741 $\pm$ 88 (P= 0.10)
	Inguinal fat (mg)	620 $\pm$ 40	491 $\pm$ 73 *
	Interscapular BAT (mg)	290 $\pm$ 17	269 $\pm$ 27
	<b>Sum of fat depots (mg)</b>	<b>5681 <math>\pm</math> 295</b>	<b>4525 <math>\pm</math> 445 (P= 0.08)</b>
	Liver (mg)	1851 $\pm$ 110	1764 $\pm$ 110
	Heart (mg)	142 $\pm$ 4	151 $\pm$ 5
Kidney (mg)	205 $\pm$ 7	213 $\pm$ 7	

5.4.1.2  $\gamma$ -MSH

Body composition was analyzed before treatments and at three-week intervals from the beginning of each diet period. During the post-treatment chow diet period the increase in fat mass to lean mass ratio was attenuated significantly at week six in the LVi- $\gamma$ -MSH-EGFP group ( $25 \pm 12$  vs.  $70 \pm 18$  % \* $P < 0.05$ ). There was no significant difference in fat mass (Figure 15 A), but lean mass tended to be increased compared to control (Figure 15 B). During the diet induced obesity period, the increases in both fat and lean mass were similar (Figure 15 C, D) nor were there any differences in total fat mass ( $19.4 \pm 0.8$  vs.  $19.5 \pm 0.9$  g  $P = \text{NS}$ ) or total lean mass ( $22.2 \pm 0.3$  vs.  $22.6 \pm 0.4$  g  $P = \text{NS}$ ) at the end of the Western diet in LVi-EGFP and LVi- $\gamma$ -MSH-EGFP treated mice respectively. However, during the weight loss with the chow diet-period the LVi- $\gamma$ -MSH-EGFP treatment significantly decreased fat mass at week six (Figure 15 E), however, lean mass was similar between the treatments during the period (Figure 15 F).

Liver, heart, kidney and adipose tissue depots were weighed at the end of study III and the inguinal fat depot was significantly decreased and epigonadal, mesenteric and total fat depot weights tended to be decreased in the LVi- $\gamma$ -MSH-EGFP treated mice compared to LVi-EGFP control (Table 8). There was no difference in the weight of subcutaneous, retroperitoneal or BAT between the treatments. In addition, the weights of liver, heart and kidney were similar between the treatments (Table 8).

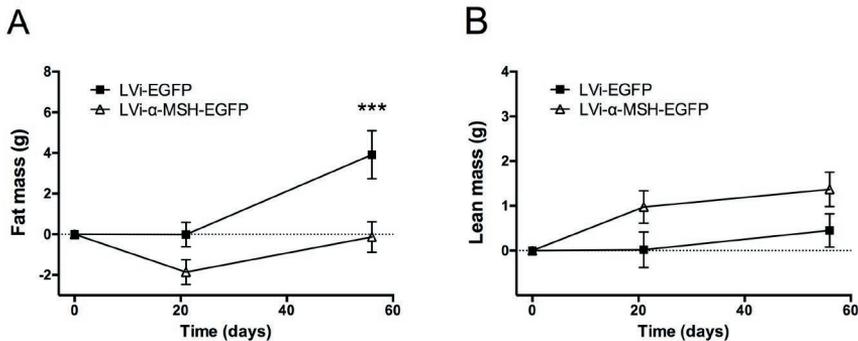


**Figure 15.** Body composition measurements from Study III. A: Fat mass and B: lean mass from post-treatment chow diet period in LVi-EGFP ( $n = 17$ ) and LVi- $\gamma$ -MSH-EGFP ( $n = 16$ ) injected mice. C: Fat mass and D: lean mass during the diet induced obesity period. E: Fat mass and F: lean mass on the weight loss with chow diet-period in LVi-EGFP ( $n = 15$ ) and LVi- $\gamma$ -MSH-EGFP ( $n = 13$ ) treated mice. \* $P < 0.05$  post-hoc test.

## 5.4.2 In the brain stem

### 5.4.2.1 $\alpha$ -MSH

The LVi- $\alpha$ -MSH-EGFP treated animals showed a significantly lower absolute fat mass ( $7.3 \pm 0.6$  vs  $9.8 \pm 0.6$  g  $***P < 0.001$ ) and change in fat mass 56 days after the injection (Figure 16 A). There were no significant differences in lean mass ( $24.2 \pm 0.4$  vs.  $24.3 \pm 0.4$  P = NS) or lean mass change (Figure 16 B) between the groups over time.



**Figure 16.** Body composition measurement in LVi-EGFP (n = 10) and LVi- $\alpha$ -MSH-EGFP (n = 9) treated mice in study II. A: Fat mass change and B: lean mass change  $***P < 0.001$  two-way anova post-hoc test.

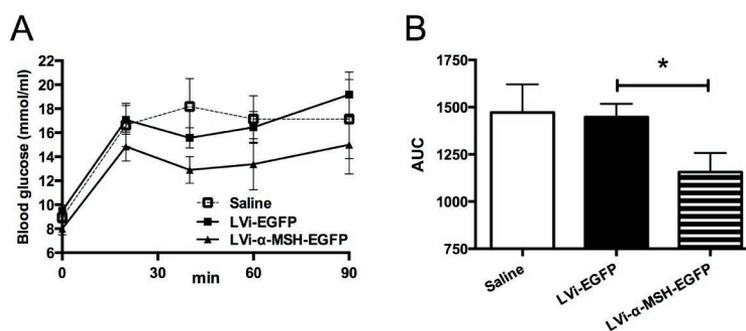
The weights of mesenteric and retroperitoneal WAT, and interscapular BAT depots were significantly smaller in the LVi- $\alpha$ -MSH-EGFP injected group as compared to the LVi-EGFP group at the end of study II (Table 8).

## 5.5 THE EFFECTS OF $\alpha$ -MSH OR $\gamma$ -MSH OVEREXPRESSION ON GLUCOSE METABOLISM

### 5.5.1 In the hypothalamus

#### 5.5.1.1 $\alpha$ -MSH

Intraperitoneal glucose tolerance test performed three weeks after the injections in study I showed that LVi- $\alpha$ -MSH-EGFP treated mice cleared blood glucose faster than to the LVi-EGFP group (Figure 17 A, B), but there was no difference in fasted glucose concentrations. Viral infection had no effect on glucose tolerance, as there were no differences between LVi-EGFP and saline treated groups.



**Figure 17.** Blood glucose data in A: GTT and B: are under the curve (AUC) of (A) in LVi-EGFP (n = 4) and LVi-α-MSH-EGFP (n = 4) treated mice of study I. \*P > 0.05 t-test

### 5.5.1.2 $\gamma$ -MSH

Basal glucose levels assessed week three after injections on the standard chow diet and were similar in both groups ( $8.1 \pm 0.3$  vs.  $7.8 \pm 0.3$  mmol/L, P = NS). The levels were also similar between the groups during the Western diet-period and during the weight loss with the chow diet-period (data not shown). GTT was assessed six weeks after the last diet change on the weight loss period, but there were no differences between the treatment groups (data not show).

## 5.5.2 In the brain stem

### 5.5.2.1 $\alpha$ -MSH

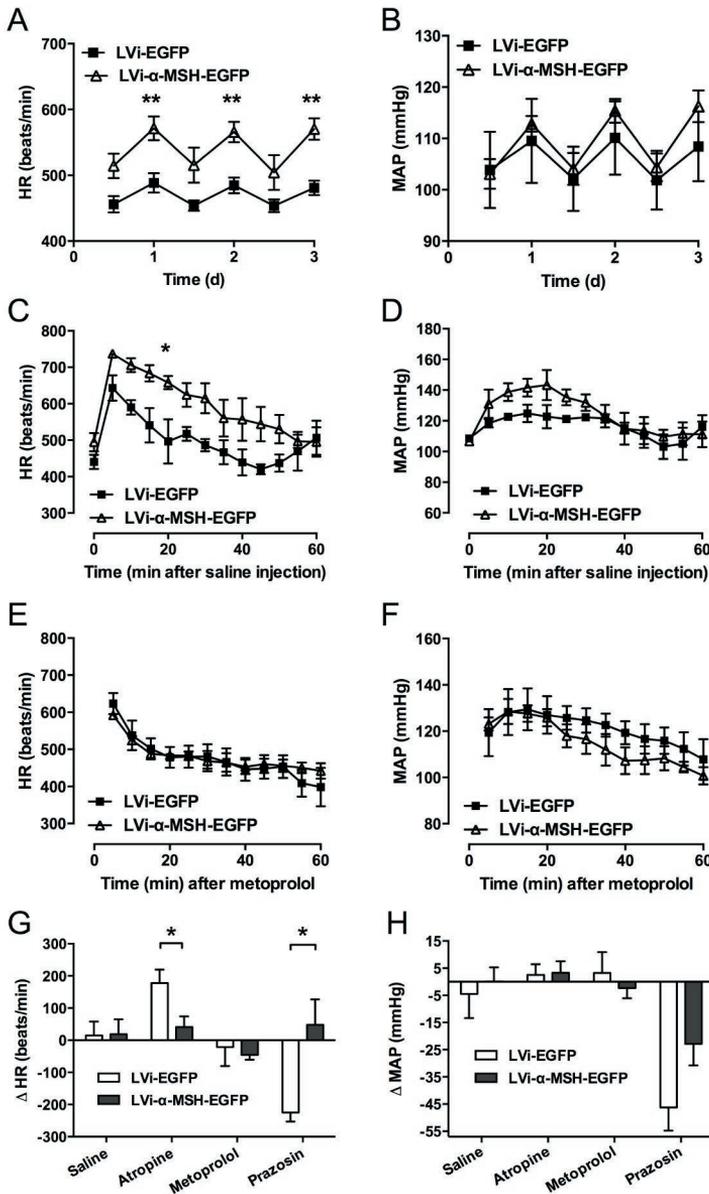
In study II, there was no significant difference in serum glucose levels after a four hour fasting period or after glucose load in GTT analyzed over time (data not shown) or in the area under the curve (LVi-EGFP:  $627 \pm 48$  vs. LVi-α-MSH-EGFP:  $638 \pm 31$  minutes x mmol/L). There were no differences in serum insulin levels at the end between the treatments (Table 10).

## 5.6 THE CARDIOVASCULAR EFFECTS OF $\alpha$ -MSH OVEREXPRESSION

### 5.6.1 In the brain stem

Study II assessed systolic blood pressure (sBP) and heart rate (HR) using the tail-cuff method, which showed no significant differences in HR and sBP in the LVi-α-MSH-EGFP ( $701 \pm 21$  b.p.m. and  $130 \pm 4$  mmHg) compared with the LVi-EGFP group ( $712 \pm 15$  b.p.m. and  $119 \pm 5$  mmHg, P = NS and P = 0.15, respectively). In the radiotelemetric assessments, the baseline HR was consistently higher in the LVi-α-MSH-EGFP group during the active dark cycle, but no changes were noted in MAP (Figure 18 A, B). To study autonomic control of cardiac function, acute cardiovascular responses to autonomic

blocking agents were monitored. The HR response to a control injection with saline was enhanced in the LVi- $\alpha$ -MSH-EGFP group without any significant effect on MAP (Figure 18 C, D). This difference was abolished when the mice were treated with metoprolol (Figure 18 E, F) evidence of increased sympathetic activity in the LVi- $\alpha$ -MSH-EGFP-treated mice. Furthermore, HR responses to muscarinic blockade with atropine were attenuated in the LVi- $\alpha$ -MSH-EGFP group (Figure 18 G), indicating lower cardiac vagal activity. Interestingly, the compensatory increase in HR as a response to vasodilatation induced by the  $\alpha_1$ -adrenergic receptor antagonist prazosin was enhanced in the LVi- $\alpha$ -MSH-EGFP group (Figure 18 G). These altered HR responses to autonomic blocking agents occurred without there being any significant differences in MAP responses between the groups (Figure 18 H).



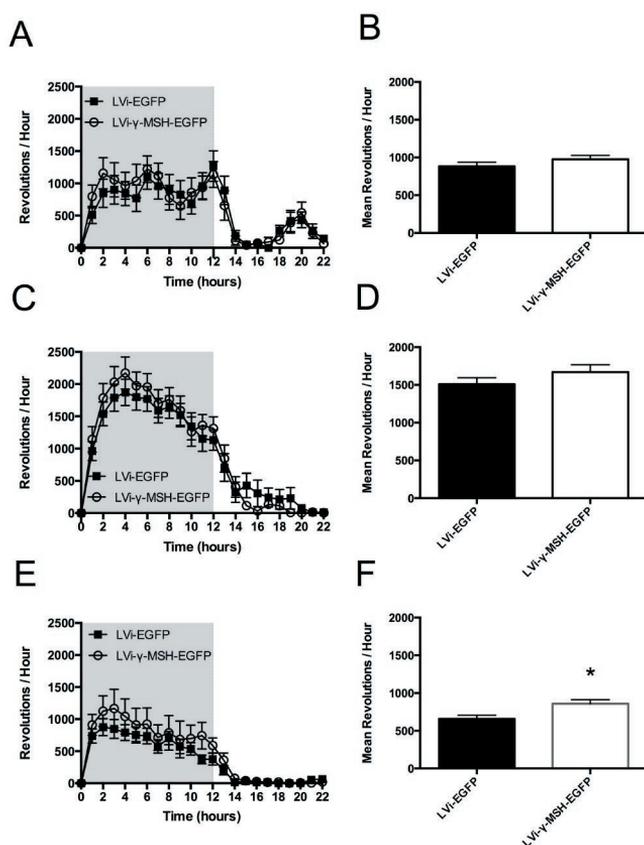
**Figure 18.** Telemetric cardiovascular measurements of LVi-EGFP ( $n = 4$ ) and LVi- $\alpha$ -MSH-EGFP ( $n = 4$ ) treated mice in study II. A: Mean arterial pressure (MAP) and B: Heart rate (HR). Effects of saline injection on C: MAP and D: HR. Effects of metoprolol injection on E: HR and F: MAP. \* $P < 0.05$ , \*\* $< 0.05$ ; two-way ANOVA followed by Bonferroni posttest. The change from baseline in G. MAP and H. HR 45-60 minutes after the administration of saline or autonomic nervous system blocking agents, atropine, metoprolol or prazosin. \* $P < 0.05$ ; Mann-Whitney.

## 5.7 THE EFFECTS ON LOCOMOTION

### 5.7.1 In the hypothalamus

#### 5.7.1.1 $\gamma$ -MSH

Voluntary running wheel activity in study III was assessed a week before and four weeks after the treatments on the standard rodent chow and four weeks after the shift to the Western diet. The pre-treatment assessment served as an introduction to the running wheels and was characterized by several peak activity points (revolutions/hour) during the dark period (Figure 19 A). The animals were divided into treatment groups based on total running wheel activity such that the mean activity during the dark period was similar (Figure 19 B). There was no difference in the running wheel activity between the groups during the post-treatment chow diet period assessment (Figure 19 C) and the mean running wheel activity during the dark period was also similar between the treatment groups (Figure 19 D). Consumption of the Western diet markedly reduced running wheel activity in both treatment groups but the activity of LVi- $\gamma$ -MSH-EGFP was slightly higher as compared to control at the beginning and during the last hour of the dark period (Figure 19 E). Interestingly, the running wheel activity was completely abolished in both groups after the dark period (Figure 19 E). The LVi- $\gamma$ -MSH-EGFP treated mice displayed a significantly higher mean running wheel activity during the dark period (Figure 19 F).

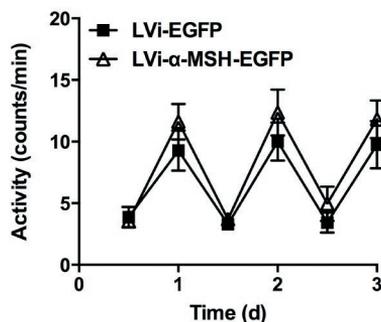


**Figure 19.** A: Running wheel activity prior to injections, B: Pre-treatment-mean running wheel activity per hour during dark cycle, C: Post-treatment chow diet-running wheel activity four weeks after injections, D: Post-treatment chow diet period-mean running wheel activity during dark period, E: Western diet-running wheel activity, F: Western diet-mean running wheel activity during dark period in LVi-EGFP (n = 17) and LVi- $\gamma$ -MSH-EGFP (n = 16) injected mice \*P < 0.05.

## 5.7.2 In the brain stem

### 5.7.2.1 $\alpha$ -MSH

Locomotion was assessed in mice implanted with radiotelemetric devices in study II, but there were no differences between the treatment groups during the assessment period (Figure 20).



**Figure 20.** Physical activity showing mean values for 12-hour light and dark periods over a three-day baseline measurements in LVi-EGFP (n = 4) and LVi- $\alpha$ -MSH-EGFP (n = 4) treated mice.

## 5.8 METABOLIC EFFECTS

### 5.8.1 In the hypothalamus

#### 5.8.1.1 $\gamma$ -MSH

In study III, the 24-hour food intake, water intake, urine volume and stool weights were assessed in metabolic cages. The 24-hour water intake was significantly smaller in the LVi- $\gamma$ -MSH-EGFP (Table 9). The 24-hour food intake, weight loss, total urine volume and total feces weight were similar in both groups (Table 9). The average 24-hour home cage water intake assessed over 72-hours was similar in the two groups ( $3.30 \pm 0.25$  vs.  $3.20 \pm 0.28$  mL P = NS).

### 5.8.2 In the brain stem

#### 5.8.2.1 $\alpha$ -MSH

In study II, the LVi- $\alpha$ -MSH-EGFP treated animals had lower 24-hour urine volume as compared to the LVi-EGFP treated group (Table 9). The levels of 24-hour creatinine excretion did not differ, indicating that there was no difference in their renal function (Table 9). There were no significant differences in water and food intake or the weight of the stool (Table 9).

**Table 9.** Parameters from the 24-hour metabolic cage assessment in both study II and III. In study II: LVi-EGFP (n = 10) was compared to LVi- $\alpha$ -MSH-EGFP (n = 9) and in study III: LVi-EGFP (n = 15) was compared to LVi- $\gamma$ -MSH-EGFP (n = 13) \*P < 0.05 non-parametric in study II and parametric in study III.

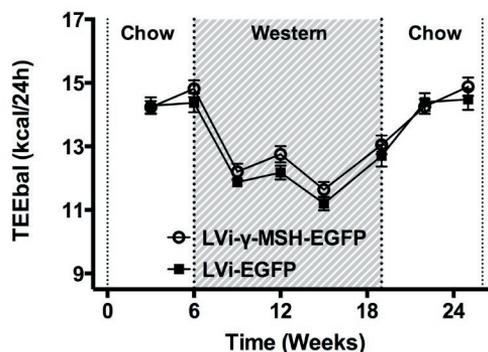
		LVi-EGFP	LVi- $\gamma$ -MSH-EGFP
Study III	Food (g/24h)	3.32 $\pm$ 0.11	3.26 $\pm$ 0.14
	Feces (g/24h)	0.30 $\pm$ 0.01	0.28 $\pm$ 0.02
	Water (mL/24h)	4.24 $\pm$ 0.56	2.92 $\pm$ 0.29 *
	Urine (mL/24h)	0.26 $\pm$ 0.04	0.28 $\pm$ 0.04
		LVi-EGFP	LVi- $\alpha$ -MSH-EGFP
Study II	Food (g/24h)	3.85 $\pm$ 0.32	3.65 $\pm$ 0.27
	Feces (g/24h)	0.36 $\pm$ 0.03	0.37 $\pm$ 0.03
	Water (mL/24h)	3.03 $\pm$ 0.38	2.36 $\pm$ 0.36
	Urine (mL/24h)	0.97 $\pm$ 0.14	0.47 $\pm$ 0.11 *
	Creatinine ( $\mu$ g/24h)	391 $\pm$ 36	388 $\pm$ 148

## 5.9 THE EFFECTS ON ENERGY EXPENDITURE

### 5.9.1 In the hypothalamus

#### 5.9.1.1 $\gamma$ -MSH

Energy expenditure was calculated by assessing the total energy gained from the change in lean and fat mass and reducing it from total energy intake. Energy expenditure was similar in both LVi-EGFP and LVi- $\gamma$ -MSH-EGFP treated mice over the three diet periods in study III (Figure 21).



**Figure 21.** Energy expenditure estimate (TEE<sub>bal</sub>) over time in mice treated with LVi-EGFP (n = 17/15) and LVi- $\gamma$ -MSH-EGFP (n = 16/13) in study III.

## **5.9.2 In the brain stem**

### **5.9.2.1 $\alpha$ -MSH**

In study II, there were no differences in the calculated energy expenditure ( $TEE_{bal}$ ) between the treatment groups from day 21 to 56 (LVi-EGFP:  $11.8 \pm 0.2$  kcal/24h vs. LVi- $\alpha$ -MSH-EGFP:  $12.1 \pm 0.4$  kcal/24h).

## **5.10 GENE EXPRESSION AND BIOCHEMICAL ASSAYS**

### **5.10.1 In the hypothalamus**

#### **5.10.1.1 $\alpha$ -MSH**

At the end of study I, it was decided to assess liver triglyceride content, serum levels of total cholesterol and triglycerides, but there were no differences detected between the LVi-EGFP and LVi- $\alpha$ -MSH-EGFP treatments (Table 10).

#### **5.10.1.2 $\gamma$ -MSH**

In study III, quantitative assessment of UCP1 mRNA levels in BAT and adrenal TH did not reveal any differences between the LVi-EGFP and LVi- $\gamma$ -MSH-EGFP treatments (Table 10). Moreover, the non-esterified fatty acids (NEFA) in the serum of LVi- $\gamma$ -MSH-EGFP tended to be lower than the corresponding value in the LVi-EGFP mice, but there were no differences in the serum triglyceride content (Table 10).

### **5.10.2 In the brain stem**

#### **5.10.2.1 $\alpha$ -MSH**

Study II assessed serum levels of NEFA, cholesterol and insulin but there were no differences observed between the LVi-EGFP and LVi- $\alpha$ -MSH-EGFP treatments. Despite the lower BAT weight (Table 8), the thermogenic capacity assessed as UCP1 mRNA level was also similar (Table 10).

**Table 10.** Results from biochemical assays and mRNA quantifications in Study I-III. Study I: LVi-EGFP (n = 4) was compared to LVi- $\alpha$ -MSH-EGFP (n = 4). Study II: LVi-EGFP (n = 10) was compared to LVi- $\alpha$ -MSH-EGFP (n = 9). Study III: LVi-EGFP (n = 15) was compared to LVi- $\gamma$ -MSH-EGFP (n = 13). NEFA, non-esterified fatty acids; BAT, brown adipose tissue; BAT UCP1, Brown adipose tissue uncoupling protein 1, TH, tyrosine hydrolase.

	Sample	LVi-EGFP	LVi- $\alpha$ -MSH-EGFP
—	Serum NEFA mmol/l	0.26 $\pm$ 0.03	0.25 $\pm$ 0.04
	Serum Cholesterol (mg/ $\mu$ l)	2.87 $\pm$ 0.17	2.10 $\pm$ 0.43
	Liver Triglycerides mmol/l	5.54 $\pm$ 0.97	5.18 $\pm$ 0.32
	Sample	LVi-EGFP	LVi- $\alpha$ -MSH-EGFP
=	Serum NEFA (mmol/L)	0.37 $\pm$ 0.03	0.35 $\pm$ 0.04
	Serum Cholesterol (mg/mL)	2.63 $\pm$ 0.17	2.97 $\pm$ 0.29
	Serum Insulin ( $\mu$ g/L)	0.77 $\pm$ 0.22	1.02 $\pm$ 0.24
	BAT UCP1 mRNA	1.06 $\pm$ 0.13	1.01 $\pm$ 0.16
	Sample	LVi-EGFP	LVi- $\gamma$ -MSH-EGFP
≡	Serum NEFA (mmol/L)	0.41 $\pm$ 0.03	0.35 $\pm$ 0.02 (P = 0.08)
	Serum Triglycerides (mmol/L)	1.33 $\pm$ 0.09	1.29 $\pm$ 0.12
	BAT UCP1 mRNA	1.00 $\pm$ 0.08	0.93 $\pm$ 0.06
	adrenal TH mRNA	1.00 $\pm$ 0.16	1.07 $\pm$ 0.14

## 6. DISCUSSION

### 6.1 METHODOLOGICAL CONSIDERATIONS

#### 6.1.1 *Gene therapy*

The introduction of genes to cells using gene delivery vectors is a well-established method and gene delivery has been attempted in humans to cure rare genetic disorders with some success. In contrast to pharmacological approaches, viral gene delivery provides a benefit of anatomically targeted treatment and long-term expression when used in animal studies to investigate the role of genes in the CNS. Melanocortin peptides are locally expressed and since these neuropeptides have a short half-life, central infusion was not considered as an alternative in this study. Therefore lentiviral vectors were chosen since these have been shown to induce long-term site-specific overexpression in the CNS. Genetically engineered transgene animal models are a well-characterized and reliable way to study the impact of genes. The insertion or removal of genes using recombination with the CRE-LOX system (Sauer, 1987, Sauer & Henderson, 1988) has been useful for the development of transgene or knock-out animals with region or tissue specific genetic modifications. Knock-out or transgenic animals are extremely useful when characterizing the general phenotype of abolishment or over-expression of a target gene, respectively. However, the development and characterization of TG-animals are often laborious, time-consuming and expensive.

#### 6.1.2 *Animal models*

The study of obesity in laboratory rodents extends back to the very beginning of the development and characterization of animal models intended for research. The spontaneous mutations that generated obesity in these early animal models have later been established and many have also been recognized in humans. Although laboratory rodents such as mice have been proven useful models in obesity research and since the genes that govern energy intake and energy metabolism are highly conserved between species, there are still questions that need to be considered. Mice are exceptionally resistant to the effects of obesity and the emotional elements, which are highly influential in human obesity, are different and challenging to interpret in mice. Another disadvantage in metabolic research is that within a population of genetically identical animals and presumably in humans, there will be a sub-population of low- and high-gainers making interpretation of results challenging (Bouchard, 1991). Closer examination of these subpopulations has revealed a variation in the genetic expression profiles, which has been linked to epigenetic and prenatal remodeling (Koza, *et al.* 2006). The C57BL/6N mice used in all of these studies are one of the most commonly used mouse strains and develop obesity when fed *ad libitum* with both normal and especially on high-fat diets (Collins, *et al.* 2004). In addition, the C57BL/6N strain also develops atherosclerosis when fed a high fat diet (Schreyer, *et al.* 1998). In summary, the C57BL/6N strain is highly suitable for obesity related studies.

In order to accelerate obesity in mouse strains, special rodent diets were used. In comparison to the standard rodent chow diet, these obesogenic diets mimic the highly processed Western type foods including a high animal based fat and sugar content and relatively small amount of dietary fiber. These diets rapidly induce obesity in both mice and rats; however, some individuals still remain resistant to obesity and this is a factor which must be taken into account (Bouchard. 1991). Pair-feeding of a control group with the group receiving the treatment may help elucidate food intake dependence. When the effects of  $\alpha$ -MSH overexpression were investigated in the hypothalamus, pair-feeding of the treatment groups was conducted in order to investigate the acute effects of feeding on weight development.

### 6.1.3 *Lentiviral constructs*

The basis for this thesis was to utilize the potential of lentiviral gene delivery vectors for the generation of a local overexpression of MSH peptides in the CNS. Lentiviral vectors are easily adaptable to suit different target tissues due to the use of different promoters, but have shown exceptional potential in numerous studies involving the CNS. Therefore, we chose a second-generation lentiviral construct including a general neuronal EF1- $\alpha$  promoter and VSV-G core protein was chosen since this has been shown to be transduced almost exclusively neurons in the long-term (Jakobsson, *et al.* 2003). The genome of the second-generation of lentiviral vectors is divided into three different plasmids in the production phase in order to eliminate the possibility of a theoretical multi-recombination event resulting in a self-replicative vector. The production and measurement of lentiviral concentration were determined using validated methods (Trono. 2000, Wiznerowicz & Trono. 2005). A clear disadvantage with the method used in this thesis is that over-expression is not confined to specific neuronal populations in the target area. In addition, we are not able to exclude the possibility of off-target effects related to neuronal projections to other brain regions. The combination of genetically modified mice with Cre-recombinase confined to certain neuronal populations such as POMC neurons with gene delivery vectors including LoxP-flanked gene expression cassettes would offer superior specificity over the use of “normal” overexpression vectors.

It is highly relevant to show that gene delivery vectors expressing peptides are able to produce biologically active compounds. Defective peptides may bind receptors without causing activation and thus act as antagonists of endogenous receptors or affect the binding of endogenous compounds. Therefore, it was considered important to decisively demonstrate the biological activity of each viral vector before *in vivo* studies. Both the  $\alpha$ -MSH (LVi- $\alpha$ -MSH-EGFP) and  $\gamma$ -MSH lentiviral vector (LVi- $\gamma$ -MSH-EGFP) were shown to efficiently activate melanocortin receptors *in vitro*. Moreover, the *in vivo* studies showed that the lentiviruses induced long-term moderate overexpression of the MSH peptides.

The use of fluorescent reporter genes such as the GFP and EGFP have proven useful in the investigation of gene expression (Chalfie. 1995, Inouye & Tsuji. 1994) and also in the validation of the location of gene expression by lentiviral transduction in our studies.

Although GFP and EGFP are readily used in research, there is a disadvantage when using green fluorophores. In fact, GFP and EGFP have fairly low penetration in tissue due to a moderately high energy and shorter wavelength compared to fluorophores of the far-red spectrum. Another disadvantage in the use of fluorophores is the bleaching factor or destruction of the peptide responsible for emitting the light. In order to minimize the effects of bleaching, analysis of EGFP expression in the *in vivo* studies was conducted immediately following sectioning and the effects of light and oxygen exposure were avoided.

#### 6.1.4 Stereotaxic delivery

In order to determine the effects of neuropeptides in specific locations of the CNS, stereotaxis was used to deliver the MSH overexpressing lentiviral vectors in mice. Although stereotaxis is a well-utilized method in research, the literature associated with methodology is scarce. Target area coordinates are predominantly obtained from brain maps and optimized by using dyes (Franklin & Paxinos, 1997).

Delivery to specific nuclei in the CNS of small rodents such as mice represents a major challenge. Firstly, the target nuclei in the mouse CNS are tiny and are very challenging to target. Secondly, the accuracy of the method is highly dependent on the anatomy and size of the skull, which vary significantly even between mice of the same species, size and gender. Correct positioning of an animal in the frame is essential and ultimately relies on visual cues, which are analyzed subjectively by the operator. The margin of error is significant if positioning is not corrected between each animal and this variance between individuals increased the number of animals needed for each study. A laser-guide was developed in order to correct the inexact method of visual analysis of positioning the animal onto the stereotaxic frame. The laser is attached to a specialized holder and is aimed onto the skull bone. The method involves positioning of the animal according to the laser, which is reflected from skull bone onto a set target. The hypothesis was that this surface would be a more homologous target and would provide an accurate determination of head position as opposed to the fastening points of the ear cavities and incisors of the upper jaw. Indeed, it was possible to increase the success rate of the injections with this system.

The methodology involved in stereotaxic drug administration is rather invasive and ultimately includes the penetration through brain tissue in order to reach the target areas. For instance, in intrahypothalamic injections it was necessary to penetrate the hippocampus, thalamus and the medial hypothalamus and in intrabrainstem injection also the cerebellum. In fact, mechanical disruption of brain tissue was previously used to analyze the physiological function brain areas. The needle tract of the injection represents a relatively small disturbance of the brain tissue reaching to target sites, but it was not possible to determine whether the injections caused any disruption of specific neuronal projections. Animals were excluded from experiments if the injections penetrated into the ventricles or produced hematomas in the CNS. In intrahypothalamic injections, there was also a comparison made of the weight and food intake of non-treated versus saline injections. The saline injected animals had a similar weight development as compared

to non-treated control after recovery from operations and showed that the injection did not cause significant damage in the treated animals. Although the protrusion of CNS did not significantly impact the development of the studied animals, all results represent the difference between animals treated similarly with a lentivirus and the only variable in the final results was the presence or lack of the target gene.

### ***6.1.5 Characterization of obesity and hemodynamic changes***

The development of obesity involves many different parameters and the timescale in which these occur varies. For instance, the accumulation of fat mass is an essential parameter in obesity for instance compared to weight gain or food intake. Increased fat mass in metabolically active peritoneal fat deposits is the initial sign in the development of obesity. After there was an increase in fat mass, then other factors such as disturbed glucose metabolism could be detected.

The development of obesity was assessed with a battery of different methods. Weight and food intake measurements were the primary parameters in the characterization of changes in body metabolism. Since both parameters were manually assessed on normal laboratory scales, there will automatically be a small variance in the results in addition to the daily fluctuations in the normal weight of mice. However, these variations are corrected over time and by increasing the number of treatment subjects. Body composition including fat mass, fat-free mass and free water were analyzed with commercially available and standardized quantitative nuclear magnetic resonance (NMR). The assessment of body composition using NMR is highly dependent on the level of immobilization in the target subject and small movements can cause large variations in the results. The variation eventually leads to repetition of the assessments. Analysis of glucose metabolism (glucose and insulin tolerance) was an important face of the study, however, the method is rather stressful for the animals and may interfere with weight and fat development. End-point data include a large subset of both commercially available and in house methods. Many of the methods involved in the assessment of serum and tissue parameters are now more sensitive than before and require smaller sample volumes. In the case of small rodents such as mice, small sample volumes are critical in order to reduce the requirements of animals for each experiment. Different metabolic parameters are obtained from the blood, tissues, urine and feces. Serum levels of glucose, insulin, cholesterol, triglycerides and non-esterified free fatty acids and triglycerides from liver in addition to urine creatinine and catecholamine levels. BAT activity and adrenal gland activity were determined by analyzing mRNA levels and information about lipid content different tissues homogenates and in feces were obtained using commercial kits. However, there is a certain degree of variance in the results obtained from these measurements, which often leads to non-significance in the statistical evaluation of the final results. Information about locomotor activity and voluntary running wheel activity were measured using commercially available light beam cages and running wheels. However, some animals did not acclimatize to the presence of running wheel devices in the home-cage and exhibited low running activity. Blood pressure was assessed using the tail-cuff method. However, this method has some limitations since the animals may be subjected to slight stress. Therefore, the less stressful method of radiotelemetry was

also included, as this has been assessed as being the benchmark method for the study of hemodynamic parameters in mice (Rinne, *et al.* 2008).

## 6.2 THE EFFECTS OF LONG-TERM CENTRAL $\alpha$ - AND $\gamma$ -MSH OVEREXPRESSION

**Table 11.** Summary of the main findings in studies I-III

Study	Viral vector	CNS Target Area	Diet	Main outcomes				
				Food intake	Body composition (Adiposity)	Hemodynamic and SNS effects	Glucose metabolism	Locomotion
I	$\alpha$ -MSH	ARC	45% Fat	NS	na	na	↑	na
II	$\alpha$ -MSH	NTS	10% Fat	NS	↓	↑	NS	NS
III	$\gamma$ -MSH	ARC	Chow / 40% Fat	↑ (Fasting)	↓ (Chow)	NS	NS	↑ (Chow)

↑ = Increase ↓ = Decrease NS = non significant NA = Not analyzed

### 6.2.1 Food intake and weight development

The present studies showed that chronic  $\alpha$ -MSH overexpression in the hypothalamus attenuated weight development in mice on a high-fat diet without affecting food intake. The  $\alpha$ -MSH treatment in the brain stem was unable to significantly impact on weight or food intake during experiment. On the other hand,  $\gamma$ -MSH overexpression in the hypothalamus decreased the weight of obese mice when they were returned to the low-fat chow diet without affecting food intake. In addition, fasting for 12 hours increased the 24-hour feeding in the  $\gamma$ -MSH treatment group.

The acute and chronic effects of melanocortins are distinct and the reduction of certain effects over time is the result of desensitization caused by receptor internalization and other compensatory mechanisms (Shinyama, *et al.* 2003). Acutely,  $\alpha$ -MSH administration to the ventricular cavity and directly to the paraventricular nucleus of the hypothalamus has decreased food intake (Kask, *et al.* 2000, McMinn, *et al.* 2000, Soos, *et al.* 2010, Wirth, *et al.* 2001, Zhang, *et al.* 2010).  $\alpha$ -MSH is synthesized in first-order neurons in the ARC, which project to second-order neurons in PVN, LHA and also to the NTS of the brain stem (Berthoud, *et al.* 2006, Elmquist, *et al.* 1999, Williams, *et al.* 2000, Zheng, *et al.* 2005) (Figure 22). The primary target of second-order neurons in the PVN is MC4R and animals deficient of MC4R do not respond to the anorexigenic effects of melanocortin agonists (Chen, *et al.* 2000, Marsh, *et al.* 1999). Hypophagia is among the effects that is diminished after prolonged exposure of MC3R/MC4R agonist, in genetic targeting of POMC and in the present studies (Kievit, *et al.* 2013, Li, *et al.* 2003, Li, *et al.* 2005, Li, *et al.* 2007, Zhang, *et al.* 2010).

The roles of  $\gamma$ -MSH and the activation of MC3R in food intake and weight development have remained unclear. As mentioned in previous sections, the MC3R-deficient mice represent an interesting metabolic phenotype with increased fat to lean mass ratio, impaired lipolysis under fast, decreased fasting induced re-feeding and defective circadian rhythm in food expectancy (see Butler. 2006). As compared to

$\alpha$ -MSH, there are very few studies characterizing the metabolic effects of  $\gamma$ -MSH. Infusion of a MC3R agonist directly to the hypothalamus and to the periphery was shown to increase food intake (Lee, *et al.* 2008, Marks, *et al.* 2006). Moreover, Cowley and colleagues (Cowley, *et al.* 2001) showed that  $\gamma$ -MSH could directly inhibit the electrophysiological activity in POMC neurons (Figure 22). By using lentiviral gene therapy, it was hoped to investigate the chronic effects of  $\gamma$ -MSH in the hypothalamus. During re-feeding measurements on the chow diet after a 12-hour fast, a small increase in food intake was also observed, which should de facto be related to an inhibition of anorexigenic activity after the acute re-feeding phase. Thus, the small increase in fasting induced re-feeding, which may in fact represent POMC auto-inhibition. Evidence seems to suggest that the mechanisms of  $\gamma$ -MSH in the hypothalamus are more complicated concerning food intake and weight development than has previously been thought since the treatment caused significant weight loss in the DIO mice that had been reintroduced to the standard low-fat diet.

### 6.2.2 *Body composition*

The present studies demonstrated that  $\alpha$ -MSH overexpression in the hypothalamus decreased obesity and the size of metabolically active fat depots, whereas the treatment attenuated body adiposity without significantly affecting weight development and food intake in the brain stem.  $\gamma$ -MSH was demonstrated to exert a positive modulatory effect on body composition, which was dependent on the ingestion of the low fat standard chow diet.

The central melanocortin system has been directly linked to peripheral lipid metabolism (Nogueiras, *et al.* 2007) and the long-term anti-obesity effects of melanocortins have been associated with increased SNS activity, which drives lipolysis and energy expenditure. The increase in energy expenditure by melanocortins is at least partly due to direct activation of SNS-mediated BAT thermogenesis. Recent data have directly linked the melanocortin system to peripheral lipid metabolism and one of the target sites of melanocortins, the PVN has been shown to directly innervate WAT (Bowers, *et al.* 2004, Nogueiras, *et al.* 2007, Shi & Bartness. 2001) (Figure 22). The MC4R has been shown to activate distinct SNS innervation to BAT and WAT (Brito, *et al.* 2007, Song, *et al.* 2005, Song, *et al.* 2008) and regulate both sympathetic and parasympathetic preganglionic neurons (Sohn, *et al.* 2013).

With respects to the brain stem, it was concluded that  $\alpha$ -MSH overexpression reduced fat mass without impacting on the weight under the observation period. Moreover, although food intake was transiently decreased over the first few days,  $\alpha$ -MSH overexpression in the NTS also increased SNS-activity without affecting BAT thermogenesis at the end of the experiment (Figure 22).

$\gamma$ -MSH overexpression in the ARC attenuated the increase in fat to lean mass ratio, but surprisingly only on the standard rodent chow diet. The modulation of body composition did not result in significant changes in weight or total food intake. Interestingly, when the diet was changed to a high-fat Western diet, the positive effects

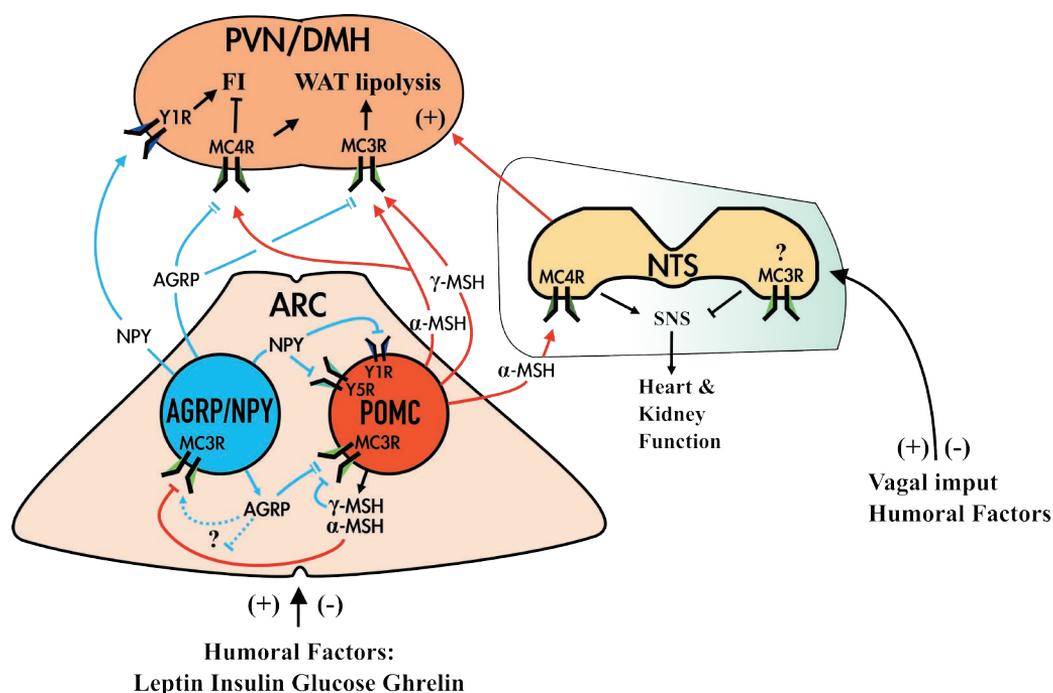
in body composition became attenuated. In an effort to clarify the effects of the diet in the  $\gamma$ -MSH treated animals, the high fat western type diet was changed to standard low-fat chow. The  $\gamma$ -MSH treatment decreased weight more than occurred in the controls and this reduction was dependent on a reduction in fat mass. These results indicate that central MC3Rs could indeed be involved in the lipolysis of WAT in the periphery (Figure 22). Moreover, the MC3R-deficient mice have increased respiratory exchange ratio (RER) and thus prefer carbohydrates as the main energy source (Butler & Cone, 2003). Overexpression of  $\gamma$ -MSH in the hypothalamus might shift the preference towards fat utilization.

### 6.2.3 *Metabolic, hemodynamic and other effects*

Glucose metabolism was assessed by GTT and analysis of serum glucose and insulin levels from the collected blood of sacrificed animals. Other parameters included analysis of serum lipids and activity assessment of BAT and adrenal gland. Urine was collected in metabolic cages to permit the measurement of excreted creatinine. Locomotor activity was assessed in voluntary running wheels and in telemetric cages. Hemodynamic parameters were analyzed using telemetric devices and tail-cuff measurements.

Hypothalamic  $\alpha$ -MSH overexpression improved glucose clearance, however, the other measured parameters were similar. Improved glucose clearance in the  $\alpha$ -MSH treated mice correlated with a decreased overall obesity. Assessment of hemodynamic parameters and SNS activity was not implemented because of the existing consensus about the effects of  $\alpha$ -MSH and analogues on hemodynamic regulation in the hypothalamus.

Mice treated with the LVi- $\alpha$ -MSH-EGFP virus displayed a significantly decreased urine secretion without affecting their drinking behavior. It appeared that renal function had been affected and it was hypothesized that in the brain stem,  $\alpha$ -MSH was either affecting renal SNS activity or decreasing blood pressure. It was possible to detect a tendency towards an increased blood pressure in the  $\alpha$ -MSH treated mice using the tail-cuff method, which eventually was the reason for resorting to telemetric implantation and a more accurate assessment of the hemodynamic effects using radiotelemetry. The  $\alpha$ -MSH treated mice exhibited increased heart rate during the recovery phase and acutely when mice were administered saline. Furthermore, the  $\alpha$ -MSH treated animals had attenuated tachycardic response when administered with both adrenergic and parasympathetic blockers suggesting increased sympathetic activity and decreased vagal tone in cardiac control. The expression of  $\alpha$ -MSH was localized in the brain stem, indicating an involvement of  $\alpha$ -MSH in this brain region in the increase in SNS activity and vagal tone (Figure 22). There were no differences in glucose metabolism, which was reflected in feeding behavior and in weight development.



**Figure 22.** Schematic presentation of the chronic effects of melanocortins in the regulation of body metabolism in the CNS. Orexigenic (blue), anorexigenic (red) projections and factors with positive (+) and negative role (-) involved in the regulation of food intake, energy expenditure, thermogenesis, body composition and SNS-activity. AGRP is an inverse agonist of MC-receptors, whereas NPY acts on Y-receptors to increase feeding and decrease energy expenditure.  $\gamma$ -MSH seems to act as an auto-receptor on POMC neurons in certain situations but the effect on AGRP/NPY neurons is unclear.  $\alpha$ -MSH modulates body composition by reducing fat mass, but have cardioaccelerator and renal effects related to increased SNS-activity modulated by the NTS.

We assessed the locomotion of mice treated with LVi- $\gamma$ -MSH-EGFP using voluntary running wheel activity in addition to basal glucose, glucose tolerance, BAT UCP1 mRNA and tyrosine hydroxylase mRNA levels in the adrenal gland in order to assess the level of SNS activity. As mentioned in section (6.2.1.2), the  $\gamma$ -MSH treatment increased voluntary running wheel activity on the high-fat Western-type diet. The contributing factor for this effect is not known, but it might relate to food seeking behavior, which has been speculated in some studies (Butler, 2006, Herwig, *et al.* 2013).  $\gamma$ -MSH treatment did not have any direct impact on glucose metabolism, although the mice displayed lower fat mass. Moreover, the UCP1 and TH levels were similar, suggesting that the overall SNS activity was unchanged.

We were unable to conduct hemodynamic analysis of LVi- $\gamma$ -MSH-EGFP mice. Nevertheless, the MC3R is involved in hemodynamic regulation both centrally and peripherally. MC3R-deficient mice have been reported to be more prone to salt-induced hypertension that is attributed to a decreased natriuretic action (Humphreys, *et al.* 2011). Furthermore,  $\gamma$ -MSH has been shown to both decrease and increase blood pressure (De Wildt, *et al.* 1994, Huang & Leenen, 2002, Li, *et al.* 1996, Nishimura, *et al.* 2000). The pressor effects associated with  $\gamma$ -MSH infusion centrally seem to be dependent on

the activation of FMRFamide-gated sodium channels, which causes sympathoexcitation (Ni, *et al.* 2006). Microinjection of  $\gamma$ -MSH to the NTS has been shown to decrease blood pressure, which suggest that  $\gamma$ -MSH may be involved in the regulation of baroreflex function (Humphreys, *et al.* 2011) (Figure 22). The chronic effects of  $\gamma$ -MSH on hemodynamic function centrally in the hypothalamus and brain stem are not known and would therefore be interesting targets of investigation with the LVi- $\gamma$ -MSH-EGFP lentivirus vector.

### 6.3 COMPLEXITY OF THE CNS

The melanocortin system indisputably plays an important role in the regulation of body metabolism and energy intake, but is also involved in an array of other functions both centrally and peripherally. Furthermore, the POMC mediated neuropeptides are accompanied by several other elements in the CNS, which include different neuronal subtypes and a multitude of different receptors and their effector molecules (for more information 2.1.1.5). Not only is the specific location of where the neuropeptides are released important, but also several different modulators can impact on the outcome. Moreover, both receptor expression and effector availability are regulated and in most cases by several non-related mechanisms. In addition, many functions in the CNS are tightly interconnected. When assessing body metabolism and food intake, the emotional and behavioral aspects must also be contemplated. Assimilation of this level of complexity is extremely demanding and contradicts the desire of researchers to simplify the mechanisms involved. At present, scientists are still only appreciating the level of overlap in the CNS and there needs to be an overwhelming consensus about each independent mechanism before they can be convincingly inter-related.

### 6.4 THERAPEUTIC ASPECT OF MELANOCORTINS

While melanocortins do seem to possess the therapeutic potential, there are several hurdles which need to be overcome. Firstly, the anti-obesity effects of melanocortins are centrally mediated and thus synthetic agonists of melanocortin receptors are required to penetrate through the BBB. Secondly, MC4R agonists increase sympathetic nervous activity, which leads to hemodynamic changes and this is a major cause for concern. Thirdly, the anti-obesity effects of MC4R agonists attenuate over time, due to receptor internalization and elevations in the levels of the degrading enzymes and in other opposing factors (Kumar, *et al.* 2009, Shinyama, *et al.* 2003, Wallingford, *et al.* 2009).

In 2009, Kumar and coworkers tested several newly developed melanocortin agonists in MC3R- and MC4R-deficient animals and revealed that their anti-obesity effects, including the reduction in food intake, were MC4R-dependent (Kumar, *et al.* 2009). The agonist that caused sustained anti-obesity effects, BIM-22493, was then taken to a pre-clinical trial in Rhesus macaques where it also decreased obesity, but also decreased blood pressure. BIM-22493 caused a transient decrease in food intake, which suggests that other factors contributed to the anti-obesity effects. These results also indicated that BIM-22493 did not cause receptor internalization and most importantly, it did not cause

adverse SNS-related effects. Since melanocortins are able to cause activation of several different intracellular signaling pathways, there is the possibility that BIM-22493 was able to cause activation in one or several cascades that were responsible for the anti-obesity effects, but not in those that cause SNS-activation. RM-493 (BIM-22493) is currently undergoing phase II trials.

The therapeutic potential of MC3R agonists have not been thoroughly investigated and the present studies revealed that an MC3R agonist could prove useful in diet intervention since the  $\gamma$ -MSH overexpressing lentiviral vector targeted to the hypothalamus decreased fat mass even when mice were consuming low-fat. Although the MC3R-deficient mice have helped to clarify many of the effects associated with MC3R action, there are only a few studies that have investigated the effects of exclusive stimulation of this single receptor subtype (Lee M. et al 2008; Marks DL et al 2006). Studies of chronic stimulation of MC3R/MC4R with  $\gamma$ -MSH have not been conducted and the results presented in this thesis are therefore novel. Previous studies in laboratory rodents have indicated MC3R agonists to be responsible for hyperphagia and inhibition of the anorexigenic POMC neurons (Cowley, *et al.* 2001, Lee, *et al.* 2008, Marks, *et al.* 2006) and thus have resulted in the conclusion that MC3R lacks therapeutic potential in combatting obesity. It was found that  $\gamma$ -MSH over-expression in the hypothalamus caused hyperphagia after fasting, but not under normal circumstances. Moreover, the treatment had no impact on weight gain or body composition when animals consumed the high-fat diet, but it did reduce fat mass with the standard low-fat diets. Since the phenotype of MC3R-deficient mice shares similar characteristics with the symptoms of patients suffering from Cushing's syndrome *e.g.* increased adiposity, decreased lean mass, decreased immune function, elevated corticosterone, defective fasting induced HPA-axis activation and increased sensitivity to salt-induced hypertension (Butler, *et al.* 2000, Chen, *et al.* 2000, Ellacott, *et al.* 2007, Ni, *et al.* 2003, Renquist, *et al.* 2012), it would be interesting to investigate the therapeutic potential of MC3R-agonists in the treatment of this syndrome.

In conclusion, although the therapeutic benefits of melanocortin receptor agonists have been questioned due to adverse effects, the true potential of the activation of both central and peripheral melanocortin agonist are still emerging. Recently, a selective MC4R agonist has been shown to lack adverse SNS effects and the present investigations of long-term central  $\gamma$ -MSH over-expression have shown that this compound can cause a decrease in adiposity without elevating SNS-activity. In summary, the melanocortins still hold potential as anti-obesity therapeutics.

## 7. SUMMARY AND CONCLUSIONS

Although  $\alpha$ -MSH is anorexigenic with acute administrations, the long-term effect on obesity was independent of food intake in the hypothalamus and brain stem. Treatment with  $\alpha$ -MSH decreased the fat mass and elevated SNS-activity in the brain stem. On the other hand, hypothalamic  $\gamma$ -MSH treatment reduced adiposity, but only when animals were fed the standard low-fat diet and in that situation it did not affect overall SNS activity. The main findings and conclusions of the thesis are presented below:

1. High titer lentiviral gene delivery vectors overexpressing  $\gamma$ - and  $\alpha$ -MSH were generated and shown to induce long-term expression of biologically active peptides in vitro and in vivo.
2. The anti-obesity effects of long-term  $\alpha$ -MSH overexpression in the arcuate nucleus of the hypothalamus in diet induced obese mice were shown to be independent of any reduction in food intake.
3. The long-term effects of  $\alpha$ -MSH-OE in the nucleus tractus solitarius of the brain stem in diet induced obese mice were decreased adiposity without significant effect on food intake during the course of the study. Radiotelemetric assessment showed that the treatment increased heart rate, which was attenuated by adrenergic blockade. In addition, the treatment decreased urine secretion, which together with hemodynamic assessment pointed towards SNS-activation.
4. The presence of  $\gamma$ -MSH-OE in arcuate nucleus of the hypothalamus improved adiposity without affecting weight development on the standard diet. However, feeding the high fat diet abolished this effect. The treatment decreased weight and fat mass in obese mice when the diet was changed back to the standard diet. In addition, the treatment also increased voluntary running wheel activity and re-feeding after fasting, two observations which are opposite to the findings observed in MC3R-deficient mice.

In conclusion, the outcome of the investigations conducted in this thesis indicates that central  $\alpha$ -MSH mediated food independent anti-obesity effects over the long-term. Furthermore, the results demonstrated a potential therapeutic role for  $\gamma$ -MSH in the obesity when combined with dietary intervention.

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