

## Hypothesis: *Musculin* is a hormone secreted by skeletal muscle, the body's largest endocrine organ.

Evidence for actions on the endocrine pancreas to restrain the  $\beta$ -cell mass and to inhibit insulin secretion and on the hypothalamus to co-ordinate the neuroendocrine and appetite responses to exercise

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**Abstract.** Recent studies indicate that skeletal muscle may act as an endocrine organ by secreting interleukin-6 (IL-6) into the systemic circulation. From an analysis of the actions of IL-6 and of additional literature, we postulate that skeletal muscle also secretes an unidentified hormone, which we have named *Musculin* (*Latin: musculus = muscle*), which acts on the pancreatic  $\beta$ -cell to restrain the size of the  $\beta$ -cell mass and to tonically inhibit insulin secretion and biosynthesis. It is suggested that the amount of *Musculin* secreted is determined by, and is positively correlated with, the prevailing insulin sensitivity of skeletal muscle, thereby accounting for the hyperinsulinemia that occurs in insulin resistant disorders such as type 2 diabetes mellitus, obesity, and the polycystic ovary syndrome. In addition, it is postulated that *Musculin* acts on the hypothalamus (arcuate nucleus, dorsomedial hypothalamic nucleus) to co-ordinate the neuroendocrine and appetite responses to exercise. However, the possibilities that *Musculin* may act on additional central nervous system sites and that an additional hormone(s) may be responsible for these actions are not excluded. It is suggested that a search be made for *Musculin*, since analogues of such a substance may be of therapeutic benefit in the treatment of the current global diabetes and obesity epidemic. ([www.actabiomedica.it](http://www.actabiomedica.it))

**Key words:** *Musculin*, skeletal muscle hormone, exercise, pancreatic beta cell, hypothalamus, growth hormone, adrenocorticotropin, prolactin

### Introduction

The concept that skeletal muscle may act as an endocrine organ has received credence from studies of the effects of exercise on plasma concentrations of interleukin-6 (IL-6) and IL-6 gene expression in skeletal muscle. IL-6 is a member of a family of cytokines that share a similar helical protein structure and a similar receptor subunit (1). IL-6 exerts its cellular effects by binding to membrane-bound or soluble IL-6 receptors and the liganded receptor(s) then associate(s) with the membrane-bound glycoprotein gp130 (2). The IL-6r-gp130 heterodimer activates members of the Janus-activated protein kinases (JAKs) which

then phosphorylate and activate the Signal Transducer and Activator of Transcription (STAT-3) in many cell types. As a result of STAT-3 activation, IL-6 activates a family of proteins including the Suppressor of Cytokine Signaling (SOCS) protein, SOCS-3 (3).

IL-6 is produced by cells of the reticuloendothelial and immune systems as well as keratinocytes, osteoblasts, adipose tissue, smooth muscle and skeletal muscle cells (1,4). Although skeletal myocytes produce IL-6 in response to those inflammatory stimuli that also release the cytokine from monocytes and cardiac myocytes, skeletal myocytes appear unique in their ability to release IL-6 in response to muscle contraction and in the absence of inflammation (5). The con-

traction-induced rise in IL-6 gene transcription seems predominantly localized to the type 2 fibers and may be mediated by a rise in cytosolic  $\text{Ca}^{2+}$  that occurs during the contractile process (6).

During exercise, glucose disposal increases but hypoglycemia is prevented by a concomitant increase in hepatic glucose production (HGP). The increased HGP that occurs during exercise of moderate intensity is thought to be mainly due to an increased portal venous glucagon:insulin ratio, although exercise of more severe intensity also stimulates the secretion of growth hormone (GH), epinephrine (EPI), and cortisol. Since the time course with which these counterregulatory factors increase cannot account for the rapid exercise-induced increase in HGP, it has long been suspected that an as yet unidentified factor released from skeletal muscle might contribute to the increased HGP. It now appears that IL-6 may partly, or wholly, fulfil the criteria of this so-called “work factor” (Figure 1) and since plasma levels of IL-6 positively correlate with exercise intensity, IL-6 may become an important stimulus of HGP as exercise intensity increases (7-12).

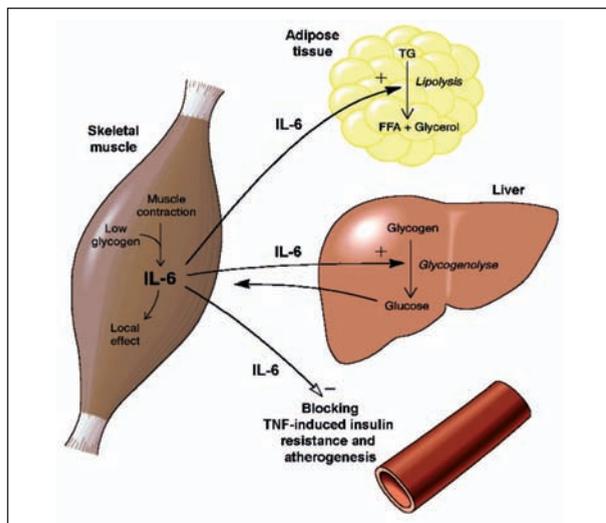
IL-6 acts as an insulin antagonist in the liver by inhibiting glycogen synthase activity and accelerating glycogen phosphorylase activity (13). The cytokine al-

so induces SOCS-3 expression in the liver *in vitro* and *in vivo* which inhibits hepatic insulin receptor autophosphorylation, insulin receptor substrate-1 (IRS-1) tyrosine phosphorylation, the association of IRS-1 with the p85 subunit of phosphatidylinositol (PI) 3-kinase and activation of serine/threonine protein kinase Akt (14). By contrast, when IL-6 is depleted in the leptin-deficient *ob/ob* mouse by immunoneutralization with an IL-6 antibody, hepatic insulin sensitivity is selectively increased (15). Although IL-6 acts as an insulin antagonist in the liver, it acts as an insulin sensitizer in skeletal muscle by enhancing the ability of insulin to stimulate muscle glycogen synthesis. These findings indicate that IL-6 exerts tissue-specific effects on insulin action (16).

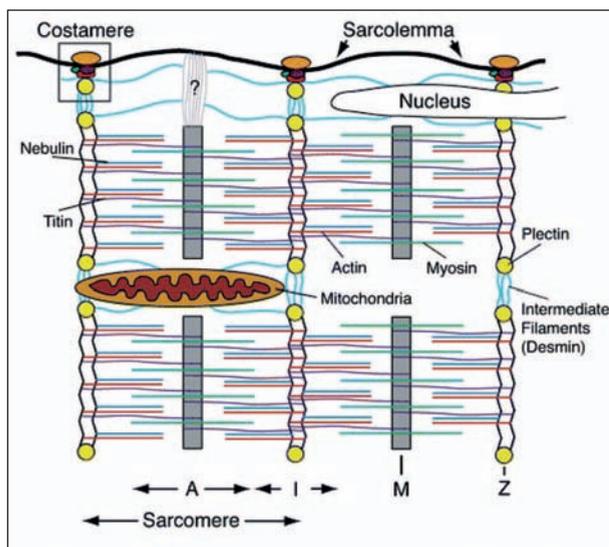
#### Skeletal muscle structure

The aforementioned studies therefore assign to skeletal muscle the status of an endocrine gland and, given its sheer size, it would appear to be the largest of its kind in the body. Skeletal muscle contains a large number of genes whose expression is regulated by that powerful modulator of muscle insulin sensitivity, physical exercise (17-28). In this section, we provide a brief outline of the major components of skeletal muscle in order that the reader may obtain a glimpse of the mechanisms by which muscular contraction may modify skeletal muscle gene expression (29-35).

The characteristic striated appearance of myofibrils as alternating light (I-band) and dark (A-band) bands results from the precise alignment of the filament systems of the sarcomere, the basic contractile unit of the myofibrils. The sarcomere is principally composed of parallel arrays of actin-containing thin filaments, the thick myosin-containing filaments, single titin molecules, and the giant protein, nebulin (Figure 2). The actin molecules have been implicated in diverse cellular functions such as motility, cytokinesis, and contraction and are anchored in the Z-disc and span the I-band. The I-region links the A-band, the region of active force generation, with the bordering Z-lines, and also contains part of the immense protein, titin. The actin filaments extend toward the middle of the sarcomere and, in the A-band, they interdigitate with the myosin-containing thick fila-



**Figure 1.** Schematic presentation of the biological effects of muscle-derived IL-6. TG, triglyceride; FFA, free fatty acid; TNF, tumor necrosis factor. (reproduced with permission from ref. 4)



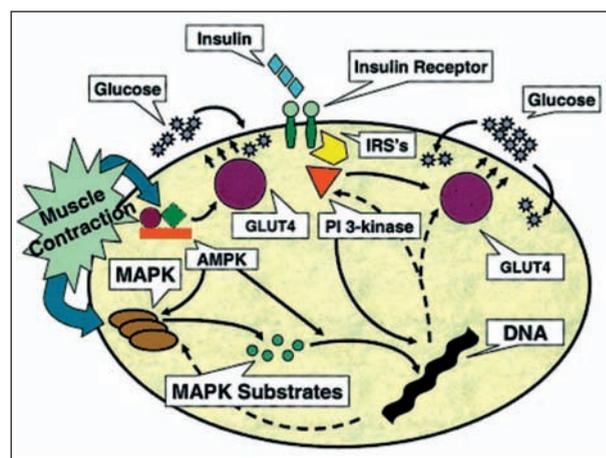
**Figure 2.** A schematic overview of cytoskeletal linkages in striated muscle. The sarcomeres contain four filament systems: actin-thin, myosin-thick, titin, and nebulin filaments. The borders of individual sarcomeres are the Z-lines, which are precisely aligned and laterally associated with intermediate filament proteins (such as desmin) and other cytoskeletal proteins (such as plectin). The intermediate filaments and associated proteins also may link the peripheral myofibrils to costameres at the sarcolemma (the muscle membrane), to mitochondria, and to the nuclear membrane. Although many of the detailed interactions are not yet known, these linkages are responsible for the mechanical integration and stability of myofibrils, organelles, and membrane components for effective force transmission. The microtubule system is not depicted in the schematic because it is unclear how they are arranged in striated muscle; however, they may be linked to myofibrils and intermediate proteins such as plakin family members (reproduced with permission from ref. 32)

ments. The M-line region is the anchoring site for the thick filaments and its appearance is considered to be the final step in myofibril assembly. The Z-lines define the lateral boundaries of the sarcomere, they are the anchoring sites for the thin, titin, and nebulin filaments, and are thus the primary means of transmission of the force generated by contraction.

The third filament system is made up of the huge modular protein, titin. The N-terminal ends of titin overlap in the Z-line, the titin molecules span the I- and A-bands and their C-terminal ends overlap in the M-line, thus forming a continuous filament system in the myofibrils. Titin possesses several distinct properties—first, it may function as a molecular spring

and thus determine myofibrillar stiffness; second, titin contains repeating motifs, it is assembled early in myofibrillogenesis and it interacts with several sarcomeric components, and may therefore stabilize the sarcomere; third, the titin C-terminal region contains a serine-threonine kinase domain which has been recently shown to control muscle gene expression and protein turnover (34). These findings provide a structural basis by which physical exercise may modify skeletal muscle gene expression, including key proteins of the insulin signaling pathway (Figure 3).

The fourth filament system is made up of another giant protein, nebulin, which spans the length of the actin filaments. The C-terminal end of nebulin is partially inserted into the Z-lines whereas its N-terminal end extends to the ends of the thin filaments. Nebulin is inextensible and may therefore specify the

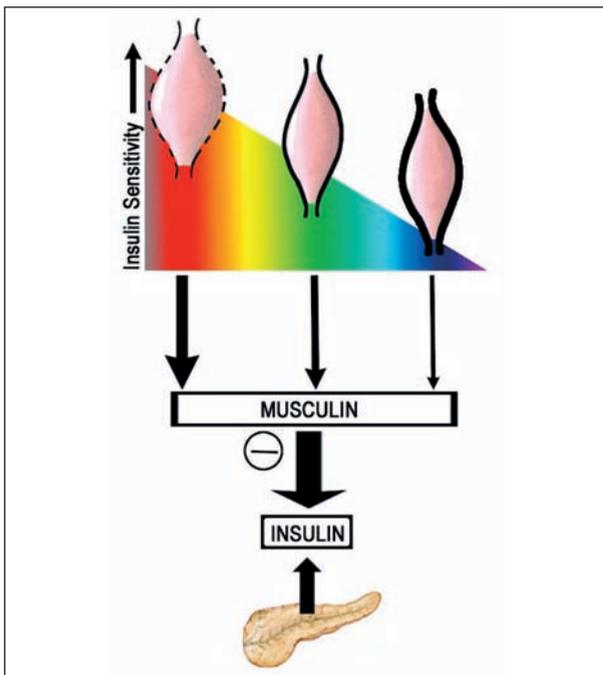


**Figure 3.** Exercise training-induced changes in insulin signaling in skeletal muscle. Insulin signal transduction through the insulin receptor, insulin receptor substrate (IRS)-1/2 and phosphatidylinositol 3-kinase (PI3-kinase) is enhanced in skeletal muscle in the hours after an exercise bout. These changes may enhance insulin sensitivity, as well as regulate gene expression after exercise. Immediately after exercise, mitogen-activated protein kinase (MAPK) signaling to downstream substrates is enhanced, providing a possible molecular mechanism for exercise-induced transcriptional regulation in skeletal muscle. Acute exercise also increases AMP-activated protein kinase (AMPK) activity, leading to changes in glucose uptake and gene expression. Exercise training is associated with changes in mRNA of several components of insulin and MAPK signaling cascades. The “master regulator(s)” of exercise-responses on gene expression has not been completely defined (reproduced with permission from ref. 61)

precise lengths of the thin filaments. Since physical exercise regulates skeletal muscle genes that code for proteins of both known and unknown functions, we postulate that:

- One of these unknown transcripts codes for a hormone which we have named *Musculin*.
- The amount of *Musculin* secreted is determined by, and is positively correlated with, the prevailing insulin sensitivity in skeletal muscle.
- *Musculin* acts on the endocrine pancreas to restrain the overall size of the  $\beta$ -cell mass and to tonically inhibit the  $\beta$ -cell's capacity to synthesize and secrete insulin.

These postulates are depicted schematically in Figure 4 and are discussed below.



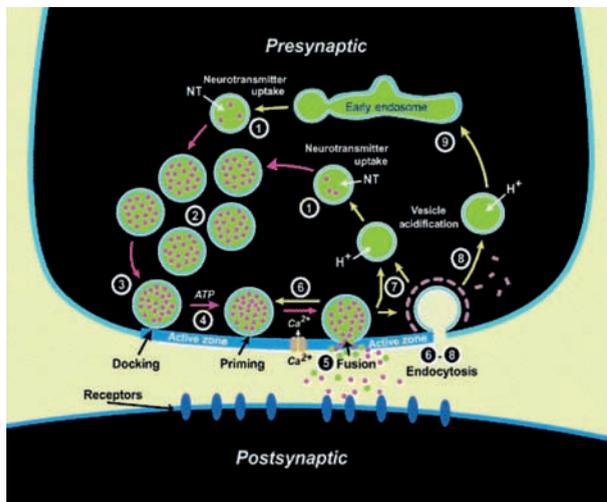
**Figure 4.** Schematic representation of the secretion of *Musculin* as a function of muscle insulin sensitivity. It is proposed that *Musculin* is a hormone released by skeletal muscle that acts on the pancreatic  $\beta$  cell to restrain  $\beta$ -cell mass and  $\beta$ -cell secretion of insulin. Furthermore, it is suggested that the amount of *Musculin* secreted is determined by, and positively correlated with, muscle insulin sensitivity. The lines around the periphery of each muscle designate insulin sensitivity. *Left*, increased insulin sensitivity (---); *Centre*, normal insulin sensitivity (—); *Right*, reduced insulin sensitivity (—). The width of the arrows leading from the skeletal muscles to the pancreas schematically depict the amount of the hormone *Musculin* that is secreted

#### *Evidence that skeletal myocytes contain the intracellular machinery required for hormone secretion*

The suggestion that skeletal muscle may function as an endocrine organ presupposes that the myocyte is capable of transporting hormones from their intracellular site of synthesis to the cell surface and of secreting these hormones into the systemic circulation. Intracellular proteins that are destined for secretion are usually transported to the cell surface in vesicles and this process has been most intensively investigated in presynaptic nerve terminals (36-39). A brief outline of the proteins involved in this 'Synaptic Vesicle Cycle' and a description of their skeletal myocyte counterparts is provided below.

When an action potential causes the opening of  $\text{Ca}^{2+}$  channels in a nerve terminal, the resulting  $\text{Ca}^{2+}$  transient stimulates synaptic vesicle exocytosis and neurotransmitter release (Figure 5, ref. 39). The steps in the trafficking cycle for synaptic vesicles can be enumerated as follows: (Step 1) Neurotransmitters are actively transported into synaptic vesicles and (Step 2) cluster in front of the active zone. They then dock at the active zone (Step 3), where they are primed (Step 4) to render them competent for  $\text{Ca}^{2+}$ -triggered fusion-pore opening (Step 5). The synaptic vesicles may be recycled by either of two fast pathways or one slower pathway. The fast pathways are preferentially used when the frequency of nerve stimulation is low, during which the vesicles either remain at the active zone and are refilled, or are locally recycled without clathrin-mediated endocytosis. The slower pathway involves clathrin-mediated endocytosis and is utilized at higher frequencies of nerve stimulation. The process of membrane fusion involves SNARE proteins that are characterized by an homologous 70-residue sequence termed the SNARE motif. The SNARE proteins are present on both fusing membranes before fusion and they associate into tight core complexes during fusion. Vesicle endocytosis is mediated by three SNARE proteins: i) Synaptobrevin (or Vesicle-Associated Membrane Protein, VAMP) on the synaptic vesicle, (ii) Syntaxin 1 and (iii) SNAP-25 located on the presynaptic cell membrane (Figure 6).

The scheme shown in Figure 6 proposes that the SNARE complex pulls the synaptic vesicle and plasma

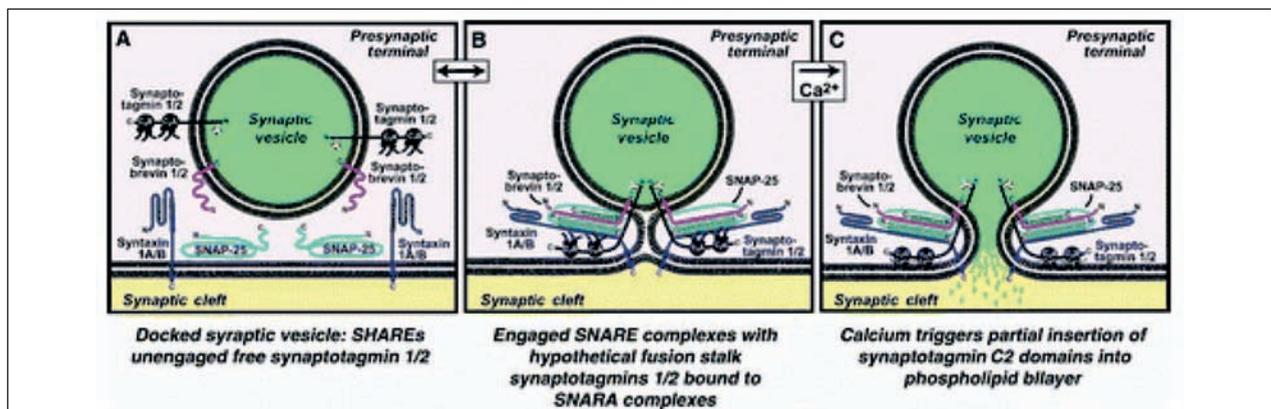


**Figure 5.** The synaptic vesicle cycle. Synaptic vesicles are filled with neurotransmitters by active transport (step 1) and from the vesicle cluster that may represent the reserve pool (step 2). Filled vesicles dock at the active zone (step 3), where they undergo a priming reaction (step 4) that makes them competent for  $\text{Ca}^{2+}$  triggered fusion-pore opening (step 5). After fusion-pore opening, synaptic vesicles undergo endocytosis and recycle via several routes: local reuse (step 6), fast recycling without an endosomal intermediate (step 7), or clathrin-mediated endocytosis (step 8) with recycling via endosomes (step 9). Steps in exocytosis are indicated by red arrows and steps in endocytosis and recycling by yellow arrows (reproduced with permission from ref. 39)

membranes close together and creates an unstable intermediate. The intermediate can either progress to a fusion pore or regress to the docked state of synaptic vesicles that do not contain engaged SNAREs. Complexins may then bind and stabilize the synaptic core complex which is essential for the proper positioning of synaptotagmin 1.

Synaptotagmins 1 and 2 are abundant synaptic vesicle proteins that act as  $\text{Ca}^{2+}$  sensors for fast exocytosis. Synaptotagmin 1 binds to the SNARE complex in the absence of  $\text{Ca}^{2+}$ , but switches to binding the phospholipid membrane when  $\text{Ca}^{2+}$  enters. This may then destabilize the fusion intermediate and open the fusion pore. Synaptotagmin 1 is part of a gene family containing 15 members, and it is possible that one or more of these other family members mediates  $\text{Ca}^{2+}$ -induced slow exocytosis. SNARE complex formation is also regulated by SM (Sec1/Munc18-like) proteins, tomosyn, amisyn and the synaptophysins. Synaptophysins are abundant synaptic vesicle proteins that bind synaptobrevin and may restrict its availability for fusion.

These observations are of relevance for skeletal muscle (and adipocyte) function since synaptobrevins 1 and 2, syntaxin 4, and VAMP 2 and 3 have been



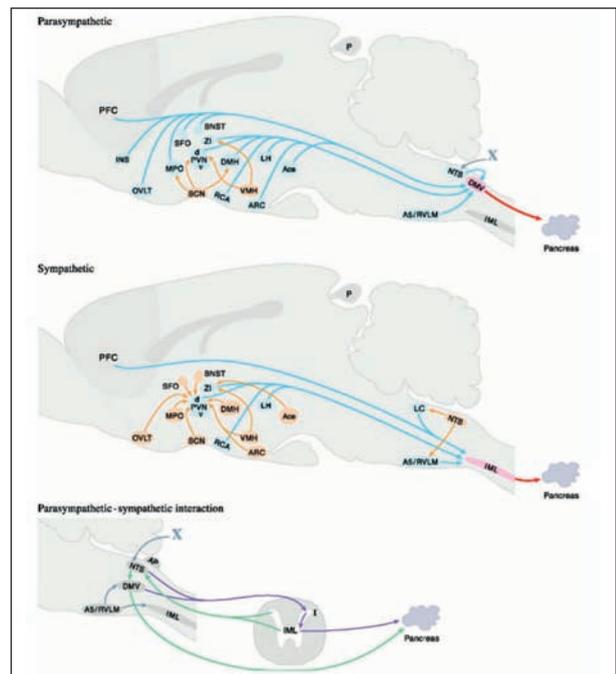
**Figure 6.** Model for the functions of SNARE proteins, complexins, and synaptotagmins 1 and 2 in synaptic vesicle exocytosis. In docked vesicles (*panel A*), SNAREs and synaptotagmins are not engaged in direct interactions. During priming (*panel B*), SNARE complexes form, complexins (green) are bound to fully assembled complexes, and synaptotagmins constitutively associate with the assembled SNARE complexes. The synaptic vesicle membrane and plasma membranes are forced into close proximity by SNARE complex assembly, which results in an unstable intermediate that is shown as a speculative fusion stalk.  $\text{Ca}^{2+}$  influx (*panel C*) further destabilizes the fusion intermediate by triggering the  $\text{C}_2$  domains of synaptotagmin to partially insert into the phospholipids. This action is proposed to cause a mechanical perturbation that opens the fusion pore. Note that the nature and stability of the putative fusion intermediate is unclear and that SNARE complex assembly in panel B is suggested to be reversible, whereas  $\text{Ca}^{2+}$  triggering is not (reproduced with permission from ref. 39)

found in skeletal myocytes and adipocytes, and VAMP5 has been isolated from C<sub>2</sub>C<sub>12</sub> myocytes during myogenesis. The findings therefore suggest that mechanisms for the intracellular trafficking of proteins, similar or identical to those described in synaptic nerve terminals, also exist in skeletal myocytes (and adipocytes, 40-49).

### *Insulin secretion in states of increased muscle insulin sensitivity*

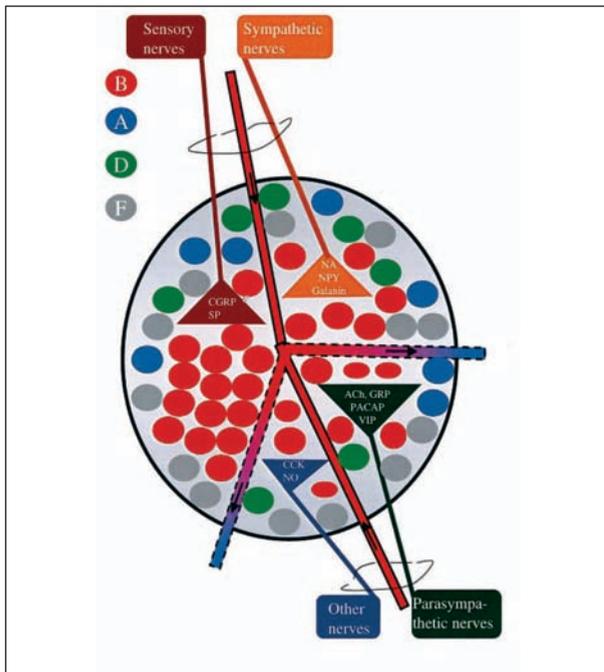
Although an increased sensitivity of skeletal muscle to the actions of insulin can be achieved in the mouse by deletion of the genes coding for the p85 $\beta$  subunit of phosphoinositide 3-kinase or the ganglioside GM3 (50, 51), the most physiological means of achieving this effect is by physical exercise. Indeed, numerous studies have shown that exercise causes an acute insulin-independent increase in glucose transport which is followed by an increase in skeletal muscle insulin sensitivity (52-65) that is mediated by translocation of more GLUT4 glucose transporters to the myocyte cell membrane (66-77). Exercise acutely reduces insulin secretion (62-64, 78-92) and increases glucagon secretion (93-102) and thus alters the portal venous insulin:glucagon ratio. The rise in portal venous glucagon is essential for the increased gluconeogenesis and HGP and the lowering of portal venous insulin concentration may restrain these effects of glucagon and prevent hyperglycemia.

Several mechanisms may contribute to these exercise-induced changes in islet hormone secretion, and one of these has been thought to be an exercise-induced alteration in autonomic nervous system function. The endocrine pancreas is innervated and regulated by both the parasympathetic nervous system derived from neurons in the dorsal motor nucleus of the vagus (DMV) and the sympathetic nervous system derived from cell bodies in the intermediolateral column (IML) of the spinal cord. Furthermore, these cell groups receive either direct or indirect inputs from second- and third-order neurons located in the prefrontal, piriform and gustatory cortices and several sub-cortical brain areas (Figure 7; 103-111). The parasympathetic cholinergic nerve fibers innervating the islets are postganglionic in origin, they originate from



**Figure 7.** Sagittal scheme of first-order projections to the pancreas (in red), second-order in blue, and third-order in yellow. It is clear by comparing the parasympathetic pattern against the sympathetic pattern that far more second-order cell groups are in control of the dorsal motor nucleus of the vagus than in control of the sympathetic neurons. The parasympathetic-sympathetic interaction illustrates the relationship between the cell groups that may influence the vagal output in green or the sympathetic output in pink. It is clear that both vagal and sympathetic output are influenced by each other. Abbreviations: A5/RVLM, rostral ventrolateral medulla; Ace, amygdala central part; AP, area postrema; ARC, arcuate nucleus; BNST, bed nucleus of the stria terminalis; DMH, dorsomedial nucleus of the hypothalamus; DMV, dorsal motor nucleus of the vagus; IML, intermediolateral column; INS, insular cortex; LC, locus coeruleus; LH, lateral hypothalamus; MPO, medial preoptic area; NTS, nucleus tractus solitarius; OVL, organum vasculosum of the lamina terminalis; PFC, prefrontal cortex; PVN, paraventricular hypothalamus; RCA, retrochiasmatic area; SCN, supra-chiasmatic nucleus; SFO, subfornical organ; VMH, ventromedial hypothalamus; ZI, zona incerta (reproduced with permission from ref. 110)

intrapancreatic ganglia, and terminate close to the islet endocrine cells (Figure 8). The intrapancreatic ganglia are in turn controlled by preganglionic fibers which originate in the DMV, traverse the vagus as part of the bulbar outflow tract, and enter the pancreas along the cranial and caudal pancreaticoduodenal arteries. The adrenergic nerves innervating the islets are also post-



**Figure 8.** Schematic view of the innervation of a pancreatic islet with the main branches of the autonomic nerves (parasympathetic nerves, sympathetic nerves, sensory nerves and other nerves) with their respective neurotransmitters. The four main types of islet endocrine cells are also illustrated with beta cells (B) forming the central islet portion, whereas an islet mantle zone harbors alpha cells (A cells, glucagon cells), delta cells (D cells, somatostatin cells) and F cells (pancreatic polypeptide (PP) cells). Afferent vessels (red) and fenestrated efferent vessels (red to blue) are also illustrated (arrows indicate blood flow direction). Ach = acetylcholine, NO = nitric oxide (reproduced with permission from ref. 122)

ganglionic and their nerve cell bodies are located in either the celiac ganglion or the paravertebral sympathetic ganglia. The postganglionic fibers then pass from the ganglia within the mixed autonomic nerves and enter the pancreas along its blood vessels.

It has been demonstrated that stimulation of the vagus (parasympathetic) and splanchnic (sympathetic) nerves can alter insulin and glucagon secretion. Stimulation of the vagus nerve increases insulin release by predominantly muscarinic mechanisms, and vagal non-muscarinic (possibly peptidergic) mechanisms may mediate changes in glucagon secretion. Stimulation of  $\alpha$ -adrenergic receptors inhibits insulin secretion and  $\beta$ -adrenergic stimulation increases insulin release, whereas both  $\alpha$ - and  $\beta$ -adrenergic stimulation

increases the secretion of glucagon (112-122). However, despite the wealth of literature dealing with the effects of autonomic neural stimulation on islet hormone secretion, it is intriguing to note that complete denervation of the canine pancreas has no effect on the *in vivo* insulin and glucagon responses to exercise (123). These findings indicate that although *in vitro* experimental stimulation of the parasympathetic and sympathetic nervous input to the pancreas does cause the aforementioned changes in insulin and glucagon secretion, the autonomic innervation does not appear essential for the *in vivo* generation of islet cell responses that occur during moderate exercise. Moreover, these islet cell responses to exercise are unlikely to be due to muscle-derived IL-6 since this cytokine has been shown to stimulate, rather than inhibit,  $\beta$ -cell secretion of insulin (124). To reconcile these observations, we propose that:

- *The acute changes in insulin and glucagon secretion during moderate exercise are hormonally mediated by an acute release of Musculin from exercising muscle.*
- *The autonomic nervous system may become increasingly important as a regulator of islet hormone secretion as exercise intensity increases.*

Studies of the acute effects of endurance exercise on the autonomic nervous system in man suggest that inhibition of cardiac vagal activity occurs very early after the onset of exercise, whereas sympathetic activation occurs later and becomes more pronounced as exercise intensity increases (125, 126). However, as judged by measurements of plasma catecholamines and whole-body norepinephrine (NE) spillover into plasma, prolonged endurance training actually reduces sympathetic nervous system activity (127-134). This reduction in sympathetic nervous system activity is likely to be a tissue-specific response and has been shown to occur in the kidney, but not in the heart (132). To our knowledge, no studies have directly determined the long-term effect of endurance exercise in animals or man on NE spillover into plasma from the pancreas but, based on the available evidence, it seems reasonable to suggest that it would be either reduced or unaltered, but not increased.

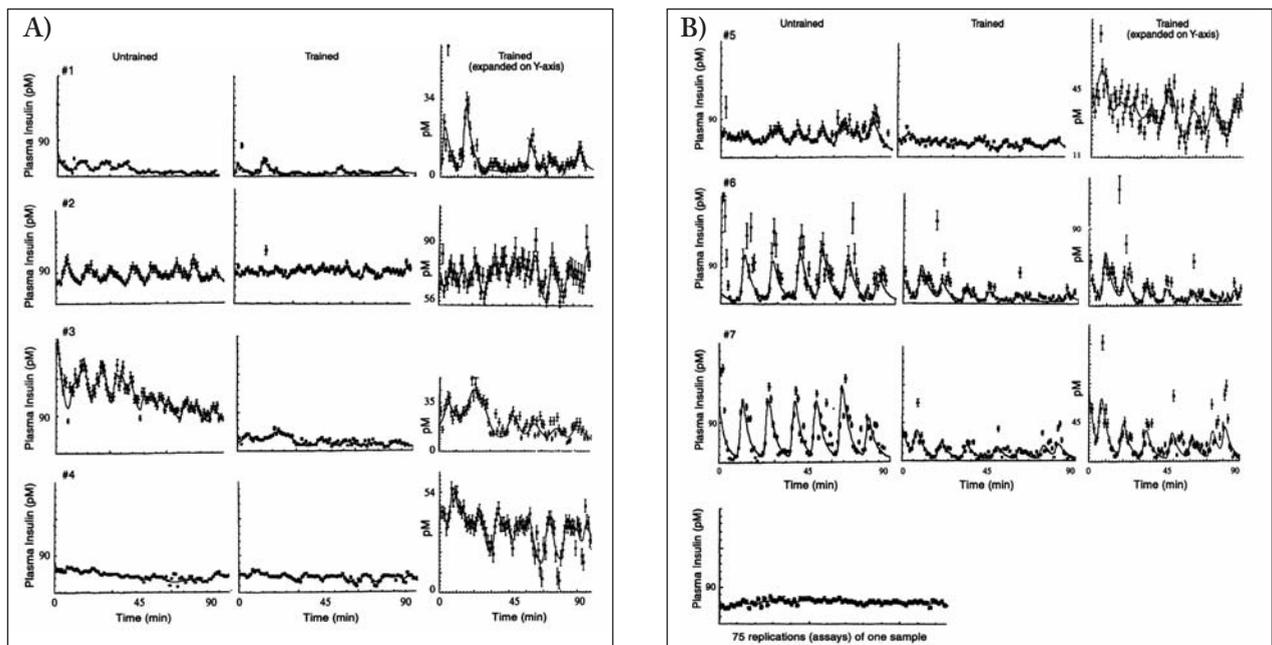
As noted previously, a number of studies have shown that long-term endurance exercise lowers plasma insulin concentrations. Like most, if not all, en-

ocrine tissues, the  $\beta$ -cell secretes insulin in a pulsatile fashion and Engdahl et al. (90) have shown that long-term endurance exercise reduces the mass of insulin secreted per burst, the burst height and insulin production rate, but has no effect on the interpulse interval or burst half-duration (Figure 9). If one was to ascribe these alterations in insulin secretion solely to an alteration in sympathetic nervous system activity, one would have to postulate that long-term endurance exercise had increased pancreatic sympathetic nervous system activity. However, since as noted above, there is currently no available evidence to suggest that long-term endurance activity increases NE spillover into plasma from any organ, this explanation would appear unlikely. Rather, we postulate that:

- Long-term endurance exercise may upregulate Musculin synthesis and secretion from skeletal myocytes.
- The resultant increase in serum Musculin concentrations may augment the tonic inhibitory regulation of the  $\beta$ -cell, thereby reducing the steady-state level of insulin in plasma.

### *Insulin secretion in states of decreased muscle insulin sensitivity*

The concept that resistance to the action of insulin may be pathophysiologically important in some patients with diabetes was first enunciated by Himsworth in the 1930s (135-138). The development of an insulin bioassay by Bornstein and Lawrence (139) and the ground-breaking insulin radioimmunoassay by Yalow and Berson (140) conclusively demonstrated that hyperinsulinemia was present in type 2 diabetic patients, and this finding was confirmed by others. Although the meaning of these observations was debated for some years, the measurement of insulin-mediated glucose disposal during a continuous infusion of insulin-glucose-epinephrine-propranolol (141), and subsequently by the hyperinsulinemic-euglycemic clamp technique (142), conclusively demonstrated the defective ability of insulin to increase tissue utilization of glucose in most patients with type 2 diabetes. It is now widely appreciated that insulin resistance may an-



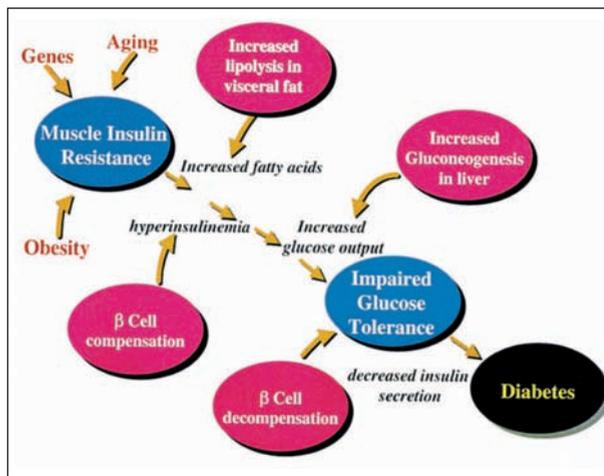
**Figure 9A and 9B.** Effect of long-term endurance training on pulsatile insulin secretion. Individual pulse profiles for 7 untrained and 7 trained men. Solid lines, best fit from deconvolution analysis. Nos. at upper left, subject no. for each pair of subjects whose data are shown side by side were assayed during the same assay. For purposes of comparison, right column shows same data as middle column; however, y-axis has been expanded so that pulses can be visualized. Note: ranges for insulin concentrations on y-axis are not the same as other panels. Single graph at bottom of panel B represents sample of blood that was assayed in duplicate 75 times during 1 assay (reproduced with permission from ref. 90)

tedate the development of diabetes by many years (144-147), and that the hyperinsulinemia *per se* may contribute to the development of dyslipidemia and hypertension, which in turn increases an individual's risk for the development of cardiovascular disease. In 1988, Reaven coined the term Syndrome X (143) to describe the association of insulin resistance, hyperinsulinemia, varying degrees of glucose intolerance and dyslipidemia, although with the inclusion of numerous other metabolic abnormalities, this nomenclature has given way to the term 'The Insulin Resistance Syndrome' (148). A schematic representation of the mechanisms leading from muscle insulin resistance to Impaired Glucose Tolerance and frank Diabetes is shown in Figure 10.

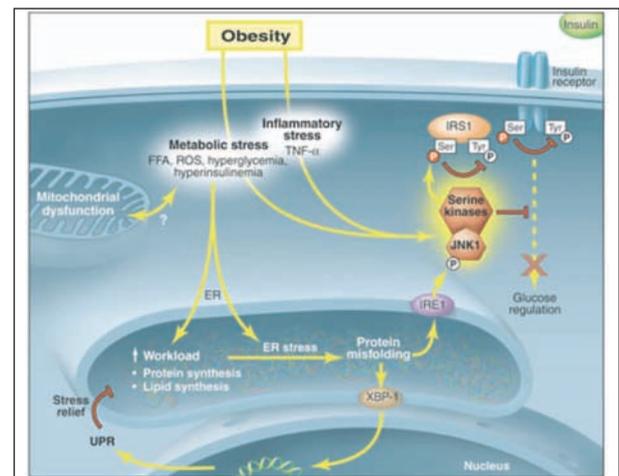
The molecular basis of insulin resistance in insulin target tissues has been the focus of intense research during the last decade (149-170). Studies by Hotamisligil and coworkers have demonstrated that obesity activates cellular stress signaling and inflammatory pathways in the adipocyte and it now appears that the

stress signals originate in the endoplasmic reticulum (ER) (151-153, 166, 167, 170). The ER is involved in the secretion and processing of membrane proteins, but biological insults such as infection, hypoxia, or exposure to excess lipids can disrupt ER function, causing unfolded or misfolded proteins to accumulate in the ER lumen. To compensate for this stress, the ER activates a transcriptional program termed the 'unfolded protein response' which slows protein synthesis and promotes protein degradation (Figure 11). This sequence of events impairs insulin receptor signaling in the adipocyte (and liver) of obese animals and results in insulin resistance in these tissues. However, ER stress seems not to be present in the skeletal muscle of obese animals (167), suggesting that alternative mechanisms must underly insulin resistance in this site.

Since skeletal muscle accounts for up to 80% of the total daily insulin-mediated glucose disposal in man, insulin resistance in skeletal muscle must contribute significantly to the insulin resistance defect in

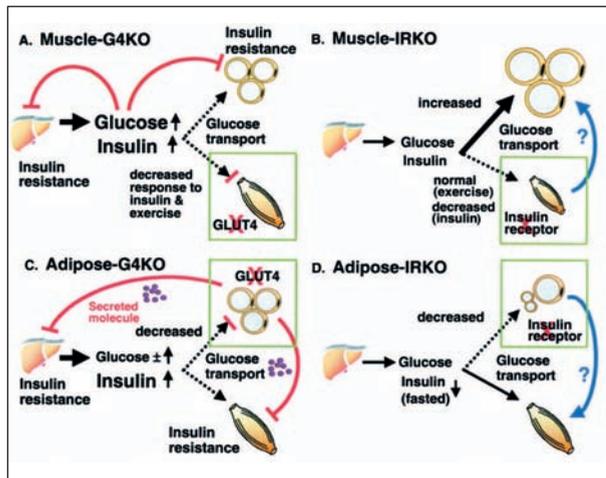


**Figure 10.** Metabolic Staging of Type 2 Diabetes. Type 2 Diabetes is characterized by a progressive decrease in insulin action, followed by an inability of the  $\beta$  cell to compensate for insulin resistance. Insulin resistance is the first lesion, due to interactions among genes, aging, and metabolic changes produced by obesity. Insulin resistance in visceral fat leads to increased fatty acid production, which exacerbates insulin resistance in liver and muscle. The  $\beta$  cell compensates for insulin resistance by secreting more insulin. Ultimately, the  $\beta$  cell can no longer compensate, leading to impaired glucose tolerance and diabetes (reproduced with permission from ref. 161)



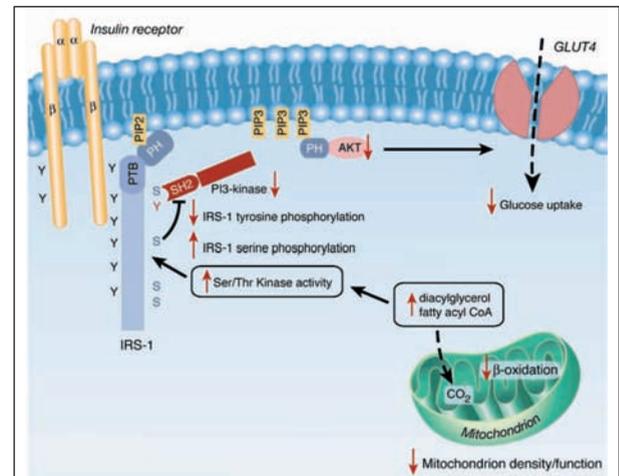
**Figure 11.** No stress relief for the Endoplasmic Reticulum (ER). The metabolic and inflammatory stresses of obesity disrupt the smooth operation of the ER and cause protein misfolding. The ER attempts to cope with stress by activating XBP-1, a transcriptional regulator of the unfolded protein response (UPR). If these responses fail to restore homeostasis, stress-induced IRE1 activates JNK1, a serine kinase that opposes insulin action. Impaired insulin signaling might serve to alleviate intracellular stress, but it does so at the expense of systemic glucose regulation. FFA, free fatty acids; ROS, reactive oxygen species (reproduced with permission from ref. 166)

most, if not all, patients with diabetes (142). Although insulin resistance can be selectively induced in skeletal muscle of laboratory animals by deletion of those genes coding for the GLUT4 glucose transporter and the insulin receptor (Figure 12), as well as PPAR $\gamma$  and caveolin-3 (154, 160, 162-164, 168), the studies of Shulman and coworkers point towards mitochondrial dysfunction as being perhaps the most important me-



**Figure 12.** Changes in glucose homeostasis and adiposity with muscle-specific or adipose-specific ablation of GLUT4 or IR. *A*, muscle-G4KO mouse. Ablation of GLUT4 from muscle (green box) decreases both insulin- and exercise-induced glucose uptake in muscle resulting in hyperglycemia, hyperinsulinemia, and secondary insulin resistance in the liver and adipose tissue. Insulin resistance in the liver and adipose tissue may be caused, at least partly, by glucose toxicity (red curves). *B*, muscle-IRKO (or MIRKO) mouse. Ablation of IR in muscle (green box) decreases muscle mass but does not change plasma glucose or insulin levels or glucose tolerance. Contraction-stimulated glucose uptake remains normal. Increased glucose uptake into adipose tissue increases adipose mass, serum triglycerides, and free fatty acids. Whether muscle releases a factor that directly acts on adipose tissue is unknown (blue curve). *C*, adipose-G4KO mouse. Ablation of GLUT4 in adipose tissue (green box) does not alter adipose mass, but results in insulin resistance in liver and muscle and systemic hyperinsulinemia. This is most likely due to altered secretion of an unknown molecule(s) from adipose tissue (red curves). Blood glucose is increased in some of the adipose-G4KO mice (symbol  $\pm$ ). *D*, adipose-IRKO (or FIRKO) mouse. In contrast to the adipose-G4KO mouse, ablation of IR in adipose tissue (green box) decreases adipose mass, lowers fasting insulin levels, and may increase energy expenditure. This may, in part, be driven by changes in adipocyte-secreted molecules (blue arrow). Red, insulin resistance; blue, insulin action or sensitivity (reproduced with permission from ref. 162)

chanism underlying common forms of skeletal muscle insulin resistance (150, 155, 156, 158, 165, 169, Figure 13). With the use of  $^{13}\text{C}$  NMR spectroscopy to measure the rate of  $[1-^{13}\text{C}]$ glucose incorporation into muscle glycogen, these investigators have demonstrated that muscle glycogen synthesis is the major pathway for glucose metabolism in both normal and diabetic individuals during steady-state hyperglycemic, hyperinsulinemic conditions and that muscle glycogen synthesis is  $\sim 50\%$  lower in diabetics. Furthermore, the data suggest that insulin-stimulated glucose transport, rather than defective hexokinase II activity, is the rate-limiting step for muscle glycogen synthesis and is reduced in diabetic subjects.



**Figure 13.** Potential mechanism by which mitochondrial dysfunction induces insulin resistance in skeletal muscle. In the depicted model, a decrease in mitochondrial fatty acid oxidation, caused by mitochondrial dysfunction and/or reduced mitochondrial content, produces increased levels of intracellular fatty acyl CoA and diacylglycerol. These molecules activate novel protein kinase C, which in turn activates a serine kinase cascade [possibly involving inhibitor of nuclear factor  $\kappa\text{B}$  kinase (IKK) and c-jun N-terminal kinase-1], leading to increased serine phosphorylation (pS) of insulin receptor substrate-1 (IRS-1). Increased serine phosphorylation of IRS-1 on critical sites (e.g. IRS-1 Ser<sup>307</sup>) blocks IRS-1 tyrosine (Y) phosphorylation by the insulin receptor, which in turn inhibits the activity of phosphatidylinositol 3-kinase (PI 3-kinase). This inhibition results in suppression of insulin-stimulated glucose transport, the process by which glucose is removed from the blood. PIP3 indicates phosphatidylinositol 3,4,5-trisphosphate; PTB, phosphotyrosine binding domain; PH, pleckstrin homology domain; SH2, src homology domain (reproduced with permission from ref. 169)

The finding of an inverse relationship between plasma free fatty acid concentrations, intramuscular triglyceride content and insulin sensitivity provides evidence for a causal relationship between altered fatty acid metabolism and insulin resistance in diabetes (156, 157). In the 1960s, Randle et al. (149) suggested that an increased supply of fatty acids competed with glucose for oxidation to increase intracellular levels of acetyl CoA and citrate. This was thought to lead to an inhibition of pyruvate dehydrogenase and phosphofructokinase which was thought to then increase intracellular glucose and glucose-6-phosphate concentrations, thereby resulting in reduced insulin-stimulated glucose uptake. This idea has essentially been refuted and it is now thought that fatty acids alter cellular activation of the protein kinase C isozymes, epsilon and theta, and cause serine phosphorylation of IRS-1, thereby abolishing insulin-stimulated IRS-1-associated PI-3 kinase activity and reducing glucose transport. Recently, insulin resistance in healthy, non-diabetic elderly individuals has also been shown to be due to increased intramyocellular fatty acid metabolites causing the aforementioned cascade of events (165). The findings may be due to an age-related reduction in mitochondrial oxidation and phosphorylation capacity, due either to a reduction in number and/or function of the mitochondria with advancing age.

Although, as stated above, the net effect of these changes in the intracellular milieu of the insulin-resistant adipocyte and myocyte is to reduce insulin-mediated glucose transport, tissue-specific differences in glucose transporter protein abundance in these cells have been reported (171-175). For example, the reduction in glucose uptake into the adipocyte is due in large part to decreased abundance of the GLUT4 protein consequent upon a reduction in GLUT4 mRNA expression in that tissue. In contrast, GLUT4 abundance and mRNA expression are not significantly altered in the myocyte, and the defect in glucose transport into that tissue may be largely due to defective trafficking of the GLUT4 protein from the cytosol to the cell membrane. This defect may be a consequence of alterations in levels (and/or function) of the vesicle transport proteins cellubrevin, VAMP-2, and syntaxin-4. Such alterations have been found in the ske-

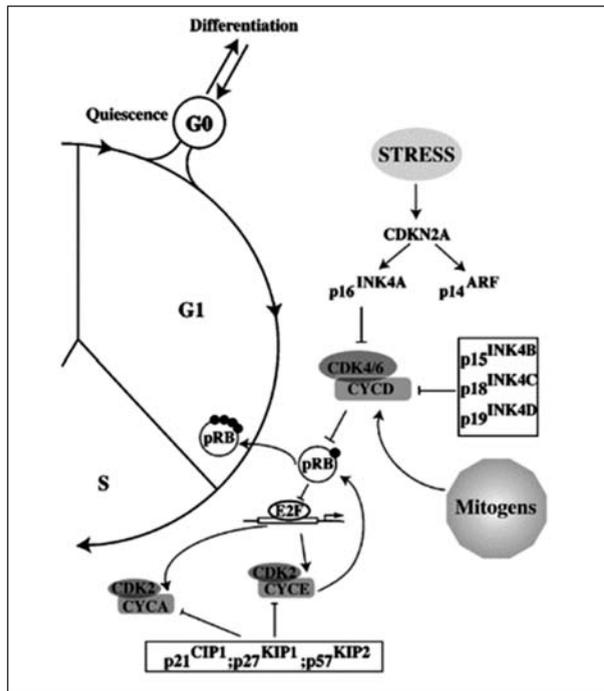
letal muscle of the Zucker diabetic fatty rat, a model of type 2 diabetes (49). Furthermore, the correction of these abnormal levels by the restoration of normoinsulinemia, and their absence in the streptozotocin-diabetic rat model of type 1 diabetes, suggests that hyperinsulinemia *per se*, rather than hyperglycemia, is responsible for these changes. From these observations, we postulate that:

- *Perturbations of the vesicular transport proteins in the insulin-resistant myocyte could contribute to defective transport to the cell surface of other intracellular myocyte proteins.*
- *These perturbations could provide a structural basis for the suggestion that Musculin secretion may be defective in insulin resistant states.*

#### *The regulation of the pancreatic $\beta$ -cell mass*

Although it was previously thought that the  $\beta$ -cell mass was static, it is now believed to be dynamic and, at any moment in time, total  $\beta$ -cell number is the result of a balance between neogenesis, replication, and apoptosis (176-180). For example, the first two weeks of the neonatal rat's life is characterized by marked  $\beta$ -cell mitosis and neogenesis which is followed by a wave of  $\beta$ -cell apoptosis from postnatal days 13 to 24. During the first three weeks of life,  $\beta$ -cell mass and body weight are not tightly correlated and, during this time, large fluctuations in the concentration of  $\beta$ -cell peptides have been observed (181-184). However, from day 24 onwards,  $\beta$ -cell mass and body weight are highly correlated, although the factors responsible for this tight regulation are unclear. The demonstration in the mouse that pre-existing, terminally differentiated  $\beta$ -cells, rather than pluripotent stem cells, are the major source of new  $\beta$ -cells formed during adult life and following partial pancreatectomy (185,186), implies a role for cell cycle regulation in this process.

The mammalian G1 cyclins and their associated kinases (cdk) integrate extracellular mitogenic signals and regulate the cell division cycle (187-192, Figure 14). The three D-type cyclins (D1, D2, and D3) bind to and regulate one of two cdk subunits, cdk4 and cdk6, as well as the E-type cyclins (E1 and E2) which, in similar fashion, govern the activity of a single



**Figure 14.** G1-to-S cell cycle control. Production of D-type cyclins and activation of cdk 4/5 in response to mitogens results in phosphorylation and inactivation of pRB (and family members) with consequent derepression of E2F-dependent transcription. This results in cyclin E and A synthesis, activation of cdk2 and further pRB phosphorylation. The activity of cdk 4/6 is opposed by p16INK4a, produced in response to stress, or by other members of the INK4 family, produced in response to differentiation signals. In a conceptually similar manner, the activity of cdk2 is opposed by members of the CIP/KIP family of inhibitors, also produced in response to stress and differentiation signals. In contrast to INK4 proteins, CIP/KIP inhibitors can act as assembly factors for cycD/cdk4(6) complexes, and can be titrated away from cdk2 by these D cyclin-containing complexes (reproduced with permission from ref. 192)

catalytic subunit, cdk2. Mitogen-induced signal transduction pathways promote the activation of cyclin D-cdk complexes which then inactivate two classes of cell cycle inhibitors. The cdk2 also phosphorylates Retinoblastoma (Rb) protein family members (Rb, p107, and p130) thus inactivating their transcriptional co-repressor activities. This process controls an E2F-dependent transcriptional program that activates a battery of genes whose products are required for DNA replication and metabolism.

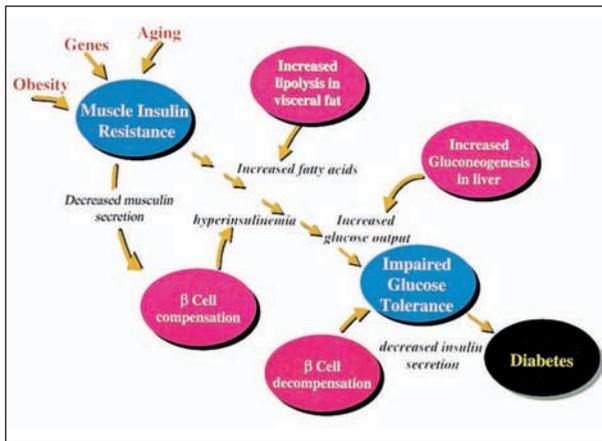
The relevance of this information is highlighted by the demonstration that cyclin D2 is expressed in

the nuclei of a subset of  $\beta$ -cells and that deletion of the cyclin D2 gene has revealed an essential role for cyclin D2 in the normal postnatal development of the  $\beta$ -cell mass. In addition, the  $\beta$ -cells of *cyclin D2*<sup>-/-</sup> mice are unable to upregulate expression of the remaining D-cyclins and eventually develop glucose intolerance. However, in all other respects, *cyclin D2*<sup>-/-</sup> mice are phenotypically indistinguishable from control animals (186). In addition, *Cdk4*<sup>-/-</sup> mice also display defective  $\beta$ -cell proliferation and develop insulin-deficient diabetes, indicating that Cdk4 acts in partnership with cyclin D2 to regulate cell cycle progression in  $\beta$ -cells (194). However, in contrast to *cyclin D2*<sup>-/-</sup> mice, *Cdk4*<sup>-/-</sup> animals are smaller than normal and infertile, indicating that Cdk4 may play a more general role in development.

In addition, studies in rodents and man have demonstrated that the  $\beta$ -cell mass increases in insulin resistant states, although the magnitude of the effect is far greater in the rodent. The generation of double heterozygous *IR/IRS-1*<sup>-/-</sup> mice causes severe muscle insulin resistance, a 2.6-fold rise in plasma insulin concentrations, a 2-30-fold (mean: 10-fold) increase in  $\beta$ -cell mass, and eventual diabetes (195). Moreover, an analysis of human pancreata obtained at autopsy has shown that the relative  $\beta$ -cell volume is increased by ~50% in obese versus lean nondiabetic individuals, an effect that is due to increased islet neogenesis, since the frequency of apoptosis did not differ significantly between the two groups (196). With these findings in mind, we postulate that:

- *A decline in Musculin secretion that occurs as a consequence of decreased skeletal muscle insulin sensitivity could stimulate  $\beta$ -cell neogenesis by upregulating  $\beta$ -cell cyclin D2 and/or Cdk4 gene expression (Figure 15).*

In this regard, it is noteworthy that a precedent for the hormonal regulation of Cyclin gene expression has been established by the studies of Sicinski et al (197) which have shown ovarian Cyclin D2 to be a follicle-stimulating hormone (FSH)-responsive gene. The finding that  $\beta$ -cell hyperplasia occurs in *IR/IRS*<sup>-/-</sup> mice before the development of hyperglycemia has led to the suggestion that a factor(s) in addition to glucose, is responsible for the expansion of the  $\beta$ -cell mass in the mouse (195), and the studies of Flier et al (198)



**Figure 15.** Metabolic Staging of Type 2 Diabetes. This figure is a modification of Figure 10 and proposes that the hyperinsulinemia that occurs as a consequence of skeletal muscle insulin resistance is due to a reduction in a tonic inhibitory regulation of insulin secretion and synthesis by the pancreatic  $\beta$ -cell. The inhibitory regulation is postulated to be due to secretion of a putative skeletal muscle hormone termed *Musculin* and decreased skeletal muscle insulin sensitivity (or increased skeletal muscle insulin resistance) is proposed to result in reduced secretion of the hormone

also lend support to this hypothesis. These authors transplanted wild-type (WT) islets under the kidney capsule of *IR/IRS-1<sup>-/-</sup>* and *ob/ob* mice and in both cases, the  $\beta$ -cell volume increased significantly, due to increased  $\beta$ -cell mitosis. In contrast, islets from *IR/IRS-1<sup>-/-</sup>* mice, when transplanted into WT recipients, displayed a reduced mitotic index. However, the authors were unable to specify the nature of this factor or ascertain its source. In previous studies, Kahn and colleagues (154, 199) have reported the effects of the conditional inactivation in mice of the insulin receptor in liver (LIRKO) or muscle (MIRKO), and noted marked islet hyperplasia in the LIRKO animals, but normal sized islets in the MIRKO mice. The authors therefore suggested that the findings did not lend support to the notion that this mitogenic factor was of skeletal myocyte origin, although whether the perturbation of the intracellular milieu that follows a complete loss of muscle insulin receptor function is identical to that which results from mitochondrial dysfunction causing the common form of human insulin resistance remains to be determined.

### Evidence that musculin may act on the hypothalamus to coordinate the neuroendocrine and appetite response to exercise

It has long been appreciated that acute exercise causes a neuroendocrine response that includes reproducible and robust increases in serum GH, adrenocorticotropic (ACTH), and prolactin and less marked increments in serum thyrotropin (TSH), FSH, oestradiol and progesterone (in women), and testosterone in men (200–245). In view of these findings and in the interest of space, only the possible mechanisms underlying the GH, ACTH, and prolactin responses to exercise are discussed below. Physical exercise also produces a change in appetite characterized by short-term anorexia (246–254). In order to facilitate an understanding of the possible mechanisms by which these adaptations are mediated, we firstly provide a brief outline of the hypothalamic regulation of anterior pituitary hormone secretion and of the anatomy and connections of the hypothalamic nuclei that are likely to be involved.

#### *The hypothalamic regulation of anterior pituitary hormone secretion*

##### *GH*

The two main hypothalamic neuropeptides that regulate GH secretion are GH-Releasing Factor (GRF) and Somatostatin (255, 256, Figure 16). A third important stimulatory input to GH secretion is provided by the peptide Ghrelin that is released from the stomach (257), but Ghrelin will not be further discussed in this manuscript since its plasma concentrations are unaffected by exercise (258). GH stimulates the hepatic production of Insulin-Like Growth Factor-1 (IGF-1) which then exerts a negative feedback on GH by stimulating the hypothalamic release of somatostatin and by decreasing GH secretion and gene expression in the anterior pituitary (259–262).

Human GRF is a 44-residue neuropeptide that was originally isolated from a human pancreatic tumor that caused acromegaly (263, 264). GRF is synthesized in the arcuate nucleus (ARC) of the hypothalamus and GRF axons abut the long portal vessels from whe-

re the peptide is secreted in a pulsatile manner into the hypophysial-portal circulation (265, 266). GRF binds to a specific receptor on the somatotrophic cell membrane and results in an increase in cyclic AMP and  $Ca^{2+}$  concentrations, an activation of protein kinase A, and a stimulation of GH secretion and GH gene expression (267-271).

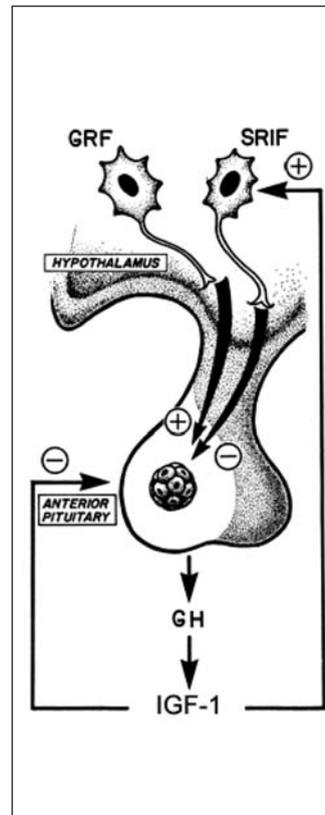
Somatostatin-14 (SRIF, SS-14) is present in several hypothalamic areas including the anterior periventricular area and the ARC, but it is only the anterior periventricular area which sends axons to the external zone of the median eminence from where the peptide enters the hypophysial-portal circulation (266, 272-274). SS-14 acts on specific receptor(s) on the somatotrope cell membrane and reduces  $Ca^{2+}$  concentrations, decreases GH secretion and suppresses the GRF-induced increase in GH gene transcription. However, SS-14 does not seem to exert an appreciable effect on basal GH gene transcription (275-278).

### ACTH

It has been traditionally thought that the hypothalamus only exerts a stimulatory influence upon the secretion and synthesis of ACTH and that this is mediated by the neuropeptides corticotropin-releasing factor (CRF), arginine vasopressin (AVP), and oxytocin (OT) which are secreted into the hypophysial-portal circulation (279-284, Figure 17). ACTH then stimulates the adrenocortical secretion of cortisol which exerts a negative feedback effect on ACTH release by acting on hypothalamic and extrahypothalamic brain sites as well as on the anterior pituitary corticotropes.

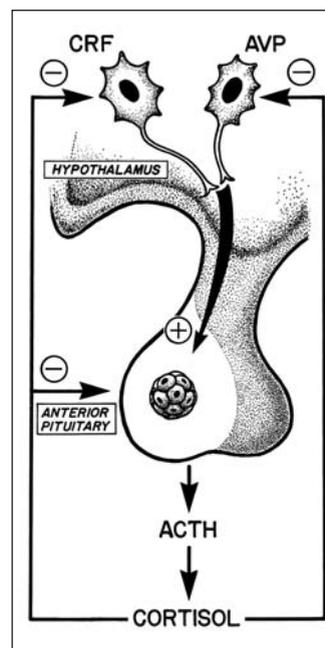
However, studies of the hypothalamic-pituitary-adrenal (HPA) axis in animals in which the pituitary has been surgically disconnected from the hypothalamus have suggested that the hypothalamus may exert both stimulatory and inhibitory regulation over ACTH secretion and proopiomelanocortin (POMC) biosynthesis, and the inhibitory regulation has been postulated to be mediated by a currently unidentified substance termed Corticotropin Release-Inhibitory Factor (282, Figure 18).

CRF is a 41-residue peptide that is the most potent ACTH secretagogue in the rat although its abi-

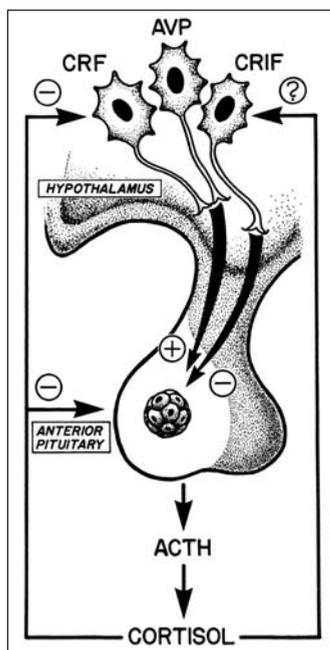


**Figure 16.** A schematic representation of the current model of the regulation of Growth Hormone secretion. The hypothalamus both stimulates and inhibits Growth Hormone (GH) secretion by secreting Growth Hormone-Releasing Factor (GRF) and Somatostatin (SRIF) into the hypophysial-portal circulation. GH then stimulates the hepatic production of Insulin-Like Growth Factor-1 (IGF-1) which exerts a stimulatory effect on hypothalamic SRIF release and an inhibitory effect at the level of the anterior pituitary to decrease GH release and biosynthesis. Although not shown in the diagram, GH release is also stimulated by the stomach-derived peptide Ghrelin which acts on a specific anterior pituitary receptor

lity to stimulate ACTH secretion is potentiated several-fold by agonists such as AVP, OT, angiotensin II, NE and EPI (285, 286). However, CRF may not be the most potent ACTH secretagogue in all species as



**Figure 17.** A schematic representation of the current model by which the hypothalamus is thought to regulate ACTH secretion. This model proposes that the hypothalamus only stimulates ACTH secretion by secreting neuropeptides such as CRF and AVP into the hypophysial-portal circulation. ACTH then stimulates the adrenocortical production of cortisol, which then restrains the secretion of ACTH by exerting negative feedback effects on the anterior pituitary, hypothalamus, and various extrahypothalamic brain sites (reproduced with permission from ref. 282)



**Figure 18.** A postulated bidirectional model of the way the hypothalamus may regulate ACTH secretion. This is a model that postulates that the hypothalamus may both stimulate and inhibit ACTH secretion. Moreover, it suggests that the hypothalamic inhibition of ACTH release is mediated by the secretion of a single CRIF. However, it is possible that several substances could cooperate to mediate the inhibition by acting in an analogous fashion to the stimulatory interaction of CRF and AVP (reproduced with permission from ref. 282)

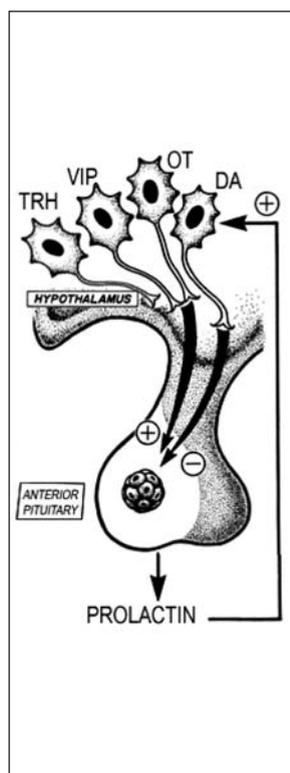
it appears to be equipotent with AVP in the bovine species and in the ovine species, AVP appears to be even more potent than CRF (287-289). In the rat, CRF is the only hypothalamic neuropeptide known to increase POMC biosynthesis, and none of the aforementioned ACTH secretagogues are able to potentiate this effect of the peptide (290-294). CRF exerts its effects on the anterior pituitary by binding to a specific adenylate cyclase-linked receptor. The binding of the hormone to the corticotrophic cell membrane results in increased intracellular concentrations of cAMP, an increased influx of extracellular  $Ca^{2+}$ , and an activation of protein kinase A and phosphorylation of a number of intracellular proteins (295-302).

AVP is also secreted into the hypophysial-portal circulation and acts on the anterior pituitary to stimulate ACTH release. AVP is a weak ACTH secretagogue in the rat and in man, although as noted above, this order of potency may not pertain in all species. AVP binds to the V1b receptor on the corticotrophic cell which is coupled to the PI signaling pathway and therefore hormone binding increases the production of inositol 1,4,5-trisphosphate ( $IP_3$ ) and diacylglycerol (DG). The DG is required for the activation of protein kinase C which phosphorylates a number of intracellular substrates. The  $IP_3$  causes the liberation of  $Ca^{2+}$  from intracellular stores and, together with the

influx of extracellular  $Ca^{2+}$ , causes the rise in  $Ca^{2+}$ ; that is required to mediate ACTH release.

### Prolactin

Prolactin is synthesized by the lactotropes of the anterior pituitary gland which possess a high intrinsic hormonal secretory activity and are under tonic hypothalamic inhibitory control mediated by dopamine (DA) in the hypophysial-portal circulation (320-324, Figure 19). Therefore, the ability of a given stimulus to reduce the tonic inhibitory effects of DA on the lactotrope is a cardinal, but not the sole, mechanism that increases prolactin secretion. The anterior pituitary lactotropic D2 DA receptor is coupled to  $G_{i-3}\alpha$  and DA binding causes inhibition of the adenylate cyclase and inositol phosphate metabolism, inhibition of  $Ca^{2+}$  channels, and excitation of voltage-sensitive  $K^+$  channels (325-328). However, DA withdrawal also leads to activation of protein kinase A which causes phosphorylation of intracellular substrates including  $Ca^{2+}$  channels, thereby increasing the probability of  $Ca^{2+}$  channels being open, and promoting the influx of extracellular  $Ca^{2+}$ . In this man-



**Figure 19.** A schematic representation of the regulation of prolactin secretion. The hypothalamic Tuberoinfundibular Dopamine neurons (TIDA) secrete Dopamine (DA) into the hypophysial-portal circulation which exerts a dominant inhibitory influence on the anterior pituitary lactotrophs to restrain prolactin secretion and synthesis. The activity of the TIDA neurons are in turn subjected to both positive and negative regulation by numerous hypothalamic amines and neuropeptides. The hypothalamus also stimulates prolactin secretion by secreting neuropeptides such as Thyrotropin-Releasing Hormone (TRH), Vasoactive-Intestinal Peptide (VIP) and Oxytocin (OT) into hypophysial-portal blood. Prolactin in turn restrains its own secretion by means of an ultra-short loop feedback effect that involves stimulation of TIDA neuronal activity

ner, DA potentiates the prolactin-releasing activity of secretagogues such as Thyrotropin-Releasing Hormone (TRH) which predominantly act by the protein kinase C pathway (329, 330). In contrast to GH and ACTH which stimulate the synthesis of additional hormones in peripheral target organs that in turn restrain their secretion by negative feedback effects on the pituitary and hypothalamus, prolactin regulates its own secretion by a positive short-loop feedback mechanism that involves activation of those tuberoinfundibular neurons that project to the external zone of the median eminence (331, 332). As alluded to above, additional regulatory inputs to prolactin secretion exist in the form of hypothalamic releasing factors, the best studied of which are TRH, vasoactive intestinal peptide (VIP) and OT.

TRH was initially isolated as a hypophysiotropic factor capable of stimulating TSH secretion from anterior pituitary cells but was subsequently found to stimulate prolactin release both *in vitro* and *in vivo*. TRH is secreted into the hypophysial-portal circulation and the TRH receptor is located in the anterior pituitary, specifically on lactotropes and thyrotropes (333-340). The binding of TRH to its receptor activates phospholipase C which initiates a cascade of intracellular signaling events that are similar, or identical, to those produced by the aforementioned binding of AVP to the anterior pituitary V1b receptor (341, 342). As noted above, several studies indicate that transient DA antagonism, or withdrawal, may augment TRH-stimulated prolactin secretion, although whether tuberoinfundibular neurons are ever truly quiescent under physiological conditions is open to conjecture.

VIP was initially isolated from porcine small intestine but VIP-immunoreactive(-ir) perikarya are also found in the hypothalamic paraventricular nucleus (PVH). VIP-ir is found in nerve terminals in the external zone of the median eminence from where the peptide is secreted into hypophysial-portal blood (343-346). VIP binds to a specific receptor on the anterior pituitary and causes an activation of the adenylate cyclase, a rise in  $Ca^{2+}_i$  and phosphorylation of a set of intracellular proteins that are distinct from those phosphorylated by TRH (347-351). Studies employing the technique of VIP immunoneutralization with specific VIP antisera have shown that VIP is entirely responsi-

ble for the ether stress-induced rise in prolactin. Moreover, VIP is required for the acute prolactin response to suckling and is one of the prolactin releasing factors required for maintenance of the hyperprolactinemia in continuously suckling animals (352).

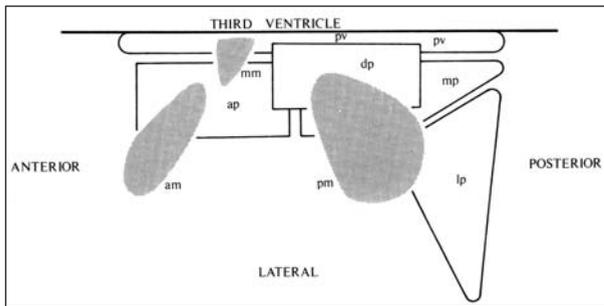
OT synthesized in the parvocellular part of the PVH as well as the periventricular nucleus (Pv) reaches the anterior pituitary by secretion into the long portal vessels. In addition, the OT synthesized in the magnocellular divisions of the PVH and the supraoptic nucleus (SON) is transported by axoplasmic flow to the posterior pituitary from where it may reach the adenohypophysis by means of the short portal vessels which connect the neural lobe with the inner zone of the anterior lobe (353-355). The oxytocinergic neurons in turn receive inhibitory inputs from VIP neurons originating in the suprachiasmatic nucleus (SCN). OT binds to a specific receptor on lactotropes and causes a dose-related increase in prolactin release *in vitro* and  $Ca^{2+}_i$  concentrations in these cells (356, 357). Studies employing specific OT antisera have shown that endogenous OT is likely to be one factor that mediates the prolactin response to suckling and studies with OT antagonists indicate that OT is required for the prolactin rise on the afternoon of proestrus, but is not involved in the prolactin response to ether stress (358, 359). Stimulation of the uterine cervix during mating also causes unique nocturnal and diurnal surges of prolactin secretion and a role for OT in mediating this response is demonstrated by the abolition of the afternoon rise in prolactin and OT by injection of VIP antisense oligonucleotides into the SCN (357).

Taken together, these findings indicate that multiple hypothalamic factors regulate the release of prolactin and that the various components of this system can be activated in a stimulus-specific manner.

### *The hypothalamic nuclei involved in the regulation of anterior pituitary hormone secretion and appetite*

#### *PVH*

The PVH lies on either side of the third ventricle and can be divided into at least eight clearly defined subdivisions (Figure 20).



**Figure 20.** A schematic diagram to show the major cell groups of the paraventricular nucleus of the hypothalamus in the rat, as viewed from above. The three parts of the magnocellular division are shown in *stipple* and are embedded in the parvocellular division, which consists of five parts. The abbreviations are as follows: am, anterior magnocellular; ap, anterior parvocellular; dp, dorsal parvocellular; lp, lateral parvocellular; mm, medial magnocellular; mp, medial parvocellular; pm, posterior magnocellular; pv, periventricular (reproduced with permission from ref. 282)

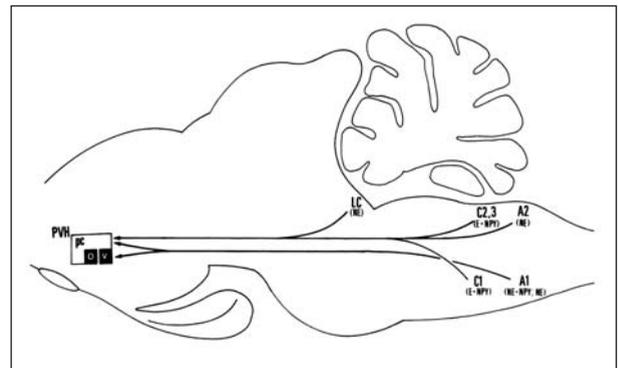
Three of these are magnocellular (anterior, medial, posterior) that project to the posterior pituitary and five are parvocellular (periventricular, anterior, medial, dorsal, lateral) which project to the external zone of the median eminence and are also interrelated with autonomic cell groups in the brain stem and spinal cord via bidirectional pathways (360-362). The PVH is also connected with a number of brain regions, and prominent among these are the forebrain, the limbic system and the brainstem. For example, the parvocellular part of the PVH receives moderately dense projections arising from all areas of the hypothalamus (except the SON, the medial and lateral mamillary nuclei, and the magnocellular division of the PVH), from the subfornical organ and the bed nucleus of the stria terminalis, but the magnocellular divisions receive relatively few inputs from these structures (363). The PVH is also densely innervated by aminergic and peptidergic axon terminals that arise from cell bodies located in brainstem nuclei. The aminergic terminals contain NE, EPI, DA, and serotonin and, of these, the noradrenergic and adrenergic projections have been subjected to the most detailed analysis.

#### *Aminergic innervation*

The noradrenergic input to the PVH arises almost exclusively from three interrelated cell groups in

the brainstem, namely the A2 region in the nucleus of the tractus solitarius (NTS), the A1 region in the ventrolateral medulla, and the A6 area in the locus ceruleus (364, Figure 21). The fibers from the A1 region are almost entirely directed toward the magnocellular divisions and preferentially terminate on vasopressinergic cell bodies. The projections arising from the A6 area are almost entirely distributed to the parvocellular PVH, and their most prominent input is localized in the periventricular zone, an area known to contain DA-, somatostatin- and TRH-stained neurons.

The ascending adrenergic projections to the PVH are also derived from three discrete brainstem cell groups (365), namely the C1 group (in the rostral ventrolateral medulla), the C2 group (in the rostral part of the NTS), and the C3 group (in the medial longitudinal fasciculus and nucleus prepositus hypoglossi). However, in contrast to the highly differentia-



**Figure 21.** The brainstem catecholaminergic and NPY-immunoreactive innervation of the PVH. Schematic drawing of a sagittal section through the rat brain to indicate the dominant biochemical makeup and distribution of catecholaminergic and NPY-immunoreactive inputs from the brainstem to the PVH. Adrenergic (E) projections arise from the C1, C2, and C3 regions, are distributed overwhelmingly to the parvocellular (pc) division of the nucleus, and generally stain positive for NPY immunoreactivity. Noradrenergic (NE) projections from the locus ceruleus and A2 cell groups are also distributed primarily to the parvocellular division, but are, for the most part, NPY negative. A heterogeneous input arises from the A1 region and is distributed to both the parvocellular division and preferentially to those parts of the magnocellular division in which vasopressinergic neurons (V) predominate over oxytocinergic ones (o). One component appears also to contain NPY immunoreactivity, whereas a second one does not (reproduced with permission from ref. 282)

ted noradrenergic projections of the PVH, the projections from each of the adrenergic cell groups are very similarly distributed within the PVH, and in each case, the most dense innervation is seen in the dorsal medial parvocellular part, an area that is rich in CRF-stained neurons.

#### *Peptidergic innervation*

The PVH is also innervated by peptidergic axon terminals such as those that stain for neuropeptide Y (NPY) and galanin (GAL).

NPY is a 36-residue peptide that was originally isolated from porcine brain and has a high degree of sequence homology with peptide YY and pancreatic polypeptide (366). NPY-stained perikarya and axon terminals are widely distributed within the brain and the PVH and ARC, respectively, contain the highest density of NPY-stained axon terminals and perikarya in the brain (367-372). NPY is extensively colocalized within brainstem adrenergic neurons that project to the PVH, while its expression in noradrenergic neurons appears limited to a subpopulation of cells in the A1 group. NPY-stained projections are most dense in the anterior and medial parvocellular parts of the PVH, and these areas are known to contain CRF- and TRH-stained neurons.

GAL is a 29-residue peptide that was first isolated from porcine intestine but is also widely distributed in the central nervous system (373-379). Within the hypothalamus, GAL-stained perikarya are found in the ARC where they coexist in a large proportion of tyrosine hydroxylase (TH)-positive cells, and in the magnocellular and parvocellular PVH, where a large proportion of cells stain for both GAL and AVP. GAL-ir perikarya are also found in the locus ceruleus (A6 area) and in the caudal part of the A2 area, where they coexist within a large number of the noradrenergic neurons. In addition, the rostral parts of the A2 and C1 areas also contain GAL-positive perikarya which do not stain for TH. GAL-ir perikarya are also found in a number of other brain areas which likely do not participate in the regulation of hypothalamo-hypophysial secretion. The PVH receives a prominent galaninergic input of fibers and rostrally the most prominent inputs are confined to the anterior and peri-

ventricular parts of the nucleus, whereas caudally the dorsal and ventral medial subdivisions are the most heavily innervated. These GAL-ir fibers arise from the A1 and A6 areas, the ARC, the dorsomedial nucleus (DMH), the LHA and the medial preoptic area (377).

#### *Neuropeptides synthesized in the PVH*

The PVH also contains a number of neuropeptides but for the purposes of this manuscript, we will limit our discussion to CRF, AVP, TRH, and VIP.

#### *CRF*

The rat brain contains about 2,000 CRF-stained perikarya distributed throughout all eight parts of the PVH, and most of these cells are found in the parvocellular division (380, 381). The medial, periventricular, and medial lateral parts of the parvocellular division contain about half of the total number of CRF-stained neurons, and these areas are known to send massive projections to the external zone of the median eminence. Furthermore the CRF neurons in the parvocellular division of the PVH may be subdivided into two populations that are distinguished by the colocalization of the AVP precursor (pro-AVP)-derived peptides AVP, the vasopressin-neurophysin (NP) or the pro-AVP C-terminal glycopeptide (382, 383). The CRF neurons receive axonal inputs that stain for NPY, TH, dopamine- $\beta$ -hydroxylase, Cocaine and Amphetamine-Regulated Transcript (CART), glutamate (GLU), Glucagon like peptide-1 and Pituitary Adenylate Cyclase-Activating Polypeptide (PACAP), indicating that they are subject to a wide variety of influences (370, 384-388, Figure 22). About 15% of the total CRF-stained population is found in those areas of the magnocellular division that predominantly contain oxytocinergic cells and in addition to the PVH, CRF-stained cells are also found in the basal hypothalamus, telencephalon, and brainstem, and these areas are involved in the functioning of the autonomic nervous system. Finally, CRF-stained cells are found scattered throughout the cerebral cortex where they are concentrated in layers II and III.

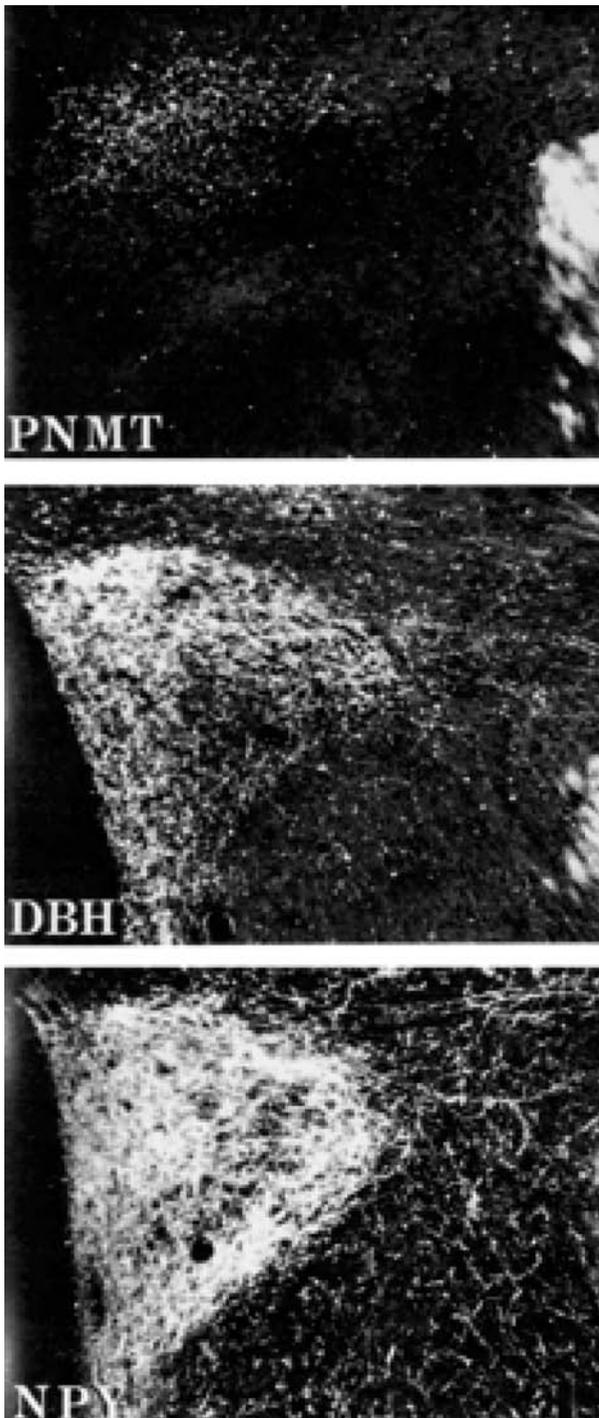


Figure 22. Innervation of the PVH by PNMT, DBH and NPY immunoreactive fibers. Darkfield photomicrographs of avidin-biotin immunoperoxidase preparations to show the distribution of fibers and varicosities stained for phenylethanolamine-*N*-methyltransferase (PNMT), dopamine- $\beta$ -hydroxylase (DBH), and neuropeptide Y (NPY) immunoreactivity at a similar level through the paraventricular nucleus (PVH; the third ventricle is at the extreme left of each micrograph). At this midcaudal level, basic similarities and differences in the density of each input may be appreciated, although in these thicker (30–35  $\mu$ M) sections, details of the distributions cannot necessarily be inferred. Note that the distribution of PNMT-stained elements is largely limited to a discrete part of the parvicellular division of the nucleus; few are seen in the magnocellular division. The DBH-stained projection encompasses and exceeds that localized with anti-PNMT, providing a prominent input to the magnocellular division, which is located at the right-hand margin of the nucleus at this level. The NPY-stained input encompasses and exceeds the distribution and density provided by DBH-immunoreactive inputs, providing perhaps the most prominent chemically specified input to the PVH yet described (reproduced with permission from ref. 282)

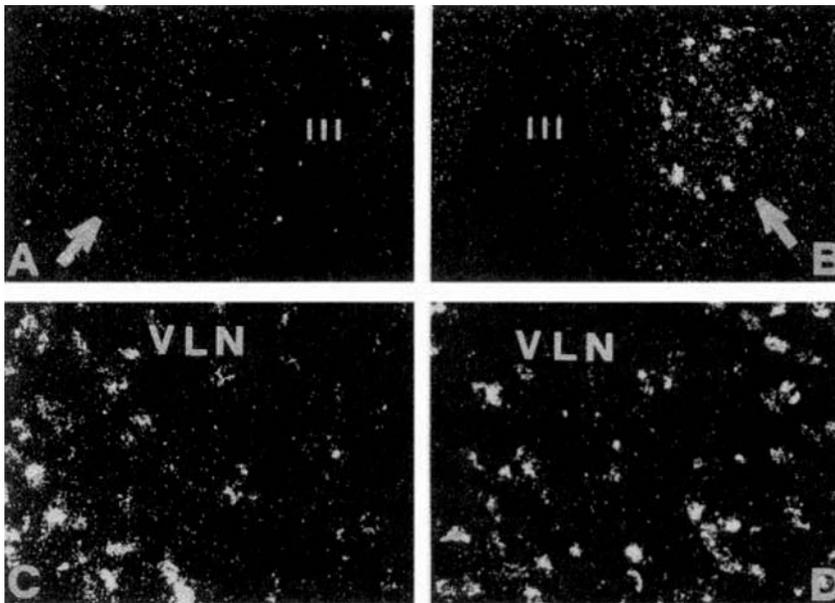
396). At least four different VIP systems exist within the brain – 1) an intracerebral cortical system; 2) one innervating the amygdala and bed nucleus of the stria terminalis; 3) a pathway originating in the SCN, and 4) another originating the midbrain central grey. VIP-stained perikarya can be visualized in the untreated animal in the limbic and neocortex, in the SCN and in the central grey of the midbrain. However, adrenalectomy and lactation combined with colchicine treatment results in the appearance of a large population of VIP-stained perikarya in the parvocellular part of the PVH and increases the number of VIP-stained fibers in the external zone of the median eminence (391). In addition, the induction of hypothyroidism also allows the detection of VIP mRNA in these PVH neurons (395, Figure 23). These findings provide an anatomical basis for the previously described role of VIP as a prolactin-releasing factor during lactation and indicate that VIP synthesis in the PVH is regulated by the thyroid status of the animal.

### VIP

VIP was originally isolated from hog small intestine and subsequently found to be widely distributed in the central and peripheral nervous systems (389–

### TRH

Within the hypothalamus, the TRH-producing neurons are found in the anterior, lateral, dorsal and medial parts of the parvicellular PVH, and in the an-



**Figure 23.** Effect of hypothyroidism on VIP mRNA. Darkfield photomicrograph of coronal sections through the hypothalamic paraventricular nucleus (PVN) (A,B) and thalamic ventrolateral (VLN) (C, D) nuclei on the same tissue sections. Sections were hybridized with a  $^{35}\text{S}$ -labeled rat VIP mRNA antisense probe. Note presence of hybridized cells in the PVN only in the hypothyroid animal (B) but conspicuous absence in the euthyroid control (A). Arrow denotes the PVN; III = third ventricle (reproduced with permission from ref. 395)

terior periventricular area. Moreover, these TRH neurons receive a variety of axonal inputs including those that stain for NPY, GAL, CART, Agouti-related protein (Agrp), and  $\alpha$ -melanocyte-stimulating hormone. These inputs originate from the ARC, the DMH, and the brainstem, indicating that TRH neurons are regulated in a highly complex manner (397-405). In addition, TRH-stained neurons are also found in the basal part of the anterior and lateral hypothalamus, the perifornical area and DMH, where they are likely to subservise functions other than the regulation of TSH and PRL secretion.

### ARC

The ARC surrounds the ventral part of the third ventricle and communicates primarily with the pituitary gland, hypothalamus, limbic system, midbrain periaqueductal gray and brainstem autonomic nuclei (406, 407). In addition, the ARC contains receptors for glucocorticoids, estradiol, insulin, leptin and GH (408-413) and in this way, it integrates emotional and sensory stimuli and peripheral signals relating to an individual's metabolic status, which it may then relay to the those brain areas concerned with the regulation of the endocrine and autonomic nervous systems.

### Neuropeptides synthesized in the ARC

At least fifteen neurotransmitters and neuropeptides have been found in arcuate perikarya but for the purposes of this review, we will focus on GRF and the Central Melanocortin System which includes those neurons which express NPY and Agrp, and POMC.

### GRF

As noted above, GRF perikarya are located in the ARC and the GRF staining in the ARC and external zone of the median eminence is obliterated by treatment of neonatal rats with the ARC toxin monosodium GLU, indicating that the ARC is the source of GRF that enters the hypophysial-portal circulation (265, 414-417). Neurotensin is colocalized within a subset of these GRF-ir neurons, but colocalization of GRF with  $\alpha$ -melanocyte stimulating hormone or ACTH (1-24) has not been demonstrated.

### The Central Melanocortin System

The mammalian central melanocortin system is defined as a collection of circuits that include (i) ARC neurons that express NPY and Agrp (NPY/Agrp) and POMC, (ii) POMC neurons originating in the NTS

in the brainstem and (iii) downstream targets of these neurons that express the melanocortin-3 and melanocortin-4 receptors (MC3-R and MC4-R) (418, 419).

#### *NPY/Agrp neurons*

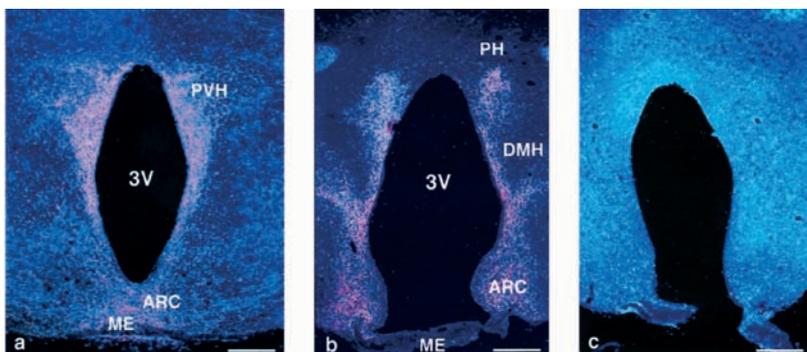
As stated above, the ARC contains the highest density of immunoreactive NPY perikarya of any area in the brain (367, 368). The ARC NPY neurons provide the major NPY-ir input to CRF-, AVP-, and TRH-stained neurons in the PVH (370, 401, 420), they project to the SON and form synapses with AVP-ir neurons (421), and they also provide ~50% of the NPY innervation to the gonadotropin-releasing hormone neurons in the medial preoptic area (422). These fiber projections provide the anatomic basis for the established roles of NPY in regulating the hypothalamic-pituitary-adrenal, -thyroid, and -gonadal axes. In addition, NPY is the most powerful orexigenic peptide known and its administration to experimental animals causes a robust and sustained increase in food intake, an effect that is partly mediated by the Y2 NPY receptor (423, 424). NPY also decreases the sympathetic outflow to brown adipose tissue in the rat and may thereby decrease the metabolic rate (425). The ARC NPY neurons are major targets for the action of insulin and leptin and these aspects are discussed below.

*Agrp* was isolated in 1997 and is a 132-residue peptide that is a homolog of the skin agouti peptide (426, 427). The skin agouti peptide is an antagonist of the MC1-R on melanocytes (428) whereas *Agrp* is an antagonist of brain MC3-R and MC4-R receptors (427, 429). *Agrp*-ir perikarya are found exclusively in the ARC where the peptide is colocalized within

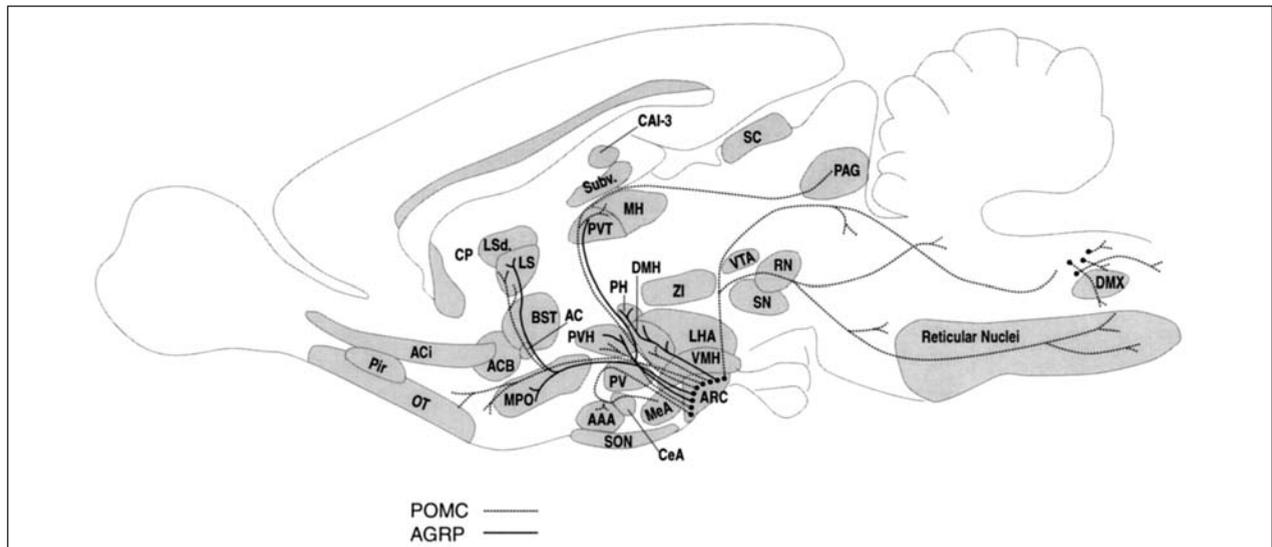
~95% of the NPY neurons (430, 431). The ARC sends dense fiber projections to the hypothalamus and septal region and within the hypothalamus, the most dense fiber staining is seen to proceed along the third ventricle as well as in the Pv nucleus, the parvocellular PVH, the DMH, and the rostral end of the posterior nucleus (432, Figure 24). Those hypothalamic areas devoid of *Agrp*-positive fibers include the magnocellular PVH, the SON, the SCN, the ventromedial nucleus and the compact zone of the DMH (Figure 25).

#### *POMC neurons*

The POMC gene codes for the 241-residue protein POMC and is expressed in the pituitary and in many non-pituitary tissues (433-439). POMC mRNA is most abundant in the pituitary, but its content in most of the non-pituitary tissues is extremely low and the generated mRNAs are truncated, non-functional transcripts that cannot be efficiently translated. POMC is a prototypical polypeptide precursor which contains eight pairs, and one quadruplet, of basic amino acids which are potential cleavage sites for processing enzymes (Figure 26), and the nature of the POMC products in any given tissue therefore reflects which cleavage sites are used. For example, only four of the cleavage sites are used in the anterior pituitary corticotrope and the peptides produced include N-terminal peptide (NT), joining peptide (JP), ACTH,  $\beta$ -lipotropin ( $\beta$ -LPH) and a small amount of  $\gamma$ -LPH and  $\beta$ -endorphin. The ARC also expresses the POMC peptide but, in this nucleus, all the cleavage sites are used and smaller peptides are produced – NT gives rise to the  $\gamma$ -melanocyte-stimulating hormones ( $\gamma$ MSHs), ACTH yields  $\alpha$ -MSH and CLIP (corticotropin-like intermediate lobe pepti-



**Figure 24.** Immunohistochemistry demonstrates dense hypothalamic neuronal fibers expressing AGRP in the diestrous rat. AGRP immunoreactivity is found in hypothalamic fibers projecting from the ARC as well as in the PVH (a) and DMH and PH nuclei (b). Preadsorption with the immunizing peptide AGRP-(83-132) blocks the staining reaction (c). Bars, 100  $\mu$ m (reproduced with permission from ref. 432)



**Figure 25.** Schematic diagram of a sagittal view of the rat brain, illustrating the comparative distributions of POMC and AGRP neurons. AAA, anterior amygdaloid area; AC, anterior commissure; ACB, nucleus accumbens; ACi, anterior commissure, intrabulbar; ARH, arcuate nucleus of the hypothalamus; BST, bed nucleus of the stria terminalis; CA1-3, field CA1-CA3 of the hippocampus; CeA, central nucleus of the amygdala; CP, caudate putamen; DMX, dorsal motor nucleus of the vagus; LHA, lateral hypothalamic area; LSd, lateral septal area, dorsal aspect; MeA, medial amygdala; MH, medial habenula; MPO, medial preoptic area; OT, olfactory tubercle; PAG, periaqueductal gray; PH, posterior hypothalamus; Pir, piriform cortex; PV, paraventricular nucleus of the hypothalamus; PVH, paraventricular nucleus of the thalamus; PVT, paraventricular nucleus of the thalamus; RN, red nucleus; SC, superior colliculus; SN, substantia nigra; SON, supraoptic nucleus; Subv, subiculum, ventral; VMH, ventromedial nucleus of the hypothalamus; VTA, ventral tegmental area; ZI, zona incerta. The locations of AGRP-immunoreactive fibers and cell bodies are based on data from the rat; fiber termini remain hypothetical. AGRP fiber distribution in the caudal brainstem was not examined in this study (reproduced with permission from ref. 432)

de), and  $\beta$ -LPH is processed to  $\beta$ -MSH,  $\beta$ -end<sub>(1-31)</sub>, and  $\beta$ -end<sub>(1-27)</sub>.  $\alpha$ -MSH is an agonist of both the MC3-R and MC4-R (440,441) and is regulated by both insulin and leptin.

The CART was originally identified as an mRNA that was upregulated in rat striatum and cerebellum by the administration of cocaine and amphetamine (442). In the rat, the CART gene encodes a peptide of either 116 or 129 residues which includes a leader sequence of 27 residues, thus resulting in a mature CART peptide of either 102 or 89 residues. In contrast to the rat which contains both the long and short CART peptides, only the short form exists in humans. CART mRNA and peptides are found in many hypothalamic nuclei including the ARC where it is coexpressed in most of the ARC POMC-positive cells and regulated by leptin.

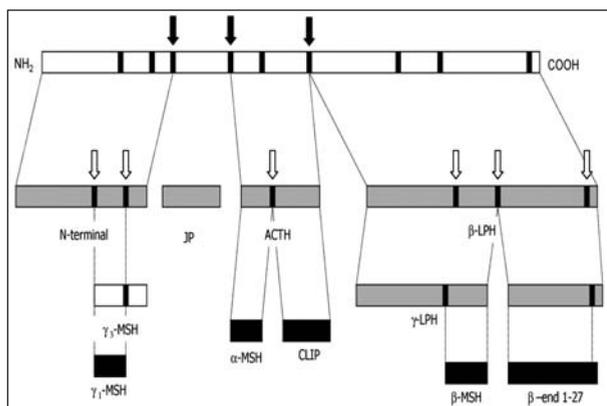
CART is a potent inhibitor of feeding and can completely override the feeding response induced by neuropeptide Y (443). CART-positive perikarya are

also found in the PVH, the SON, the lateral hypothalamic area (LHA), the DMH, the Pv nucleus, and the ventral premammillary nucleus (PMV), and CART-positive fibers are distributed throughout the hypothalamus. CART-positive fibers form synaptic contacts with TRH and CRF-stained neurons in the PVH and these findings provide the anatomical basis for the involvement of the peptide in the regulation of both the hypothalamic-pituitary-thyroid and hypothalamic-pituitary-adrenal axes (385, 444-449).

#### *Hormonal regulation of NPY/Agrp and POMC/CART neurons by insulin and leptin*

##### *Insulin*

Several lines of evidence indicate that insulin is a key peripheral hormonal signal that regulates food intake and body fat mass (450-452). First, the plasma  $t_{1/2}$  of insulin is 2-3 minutes, thus rendering the hor-



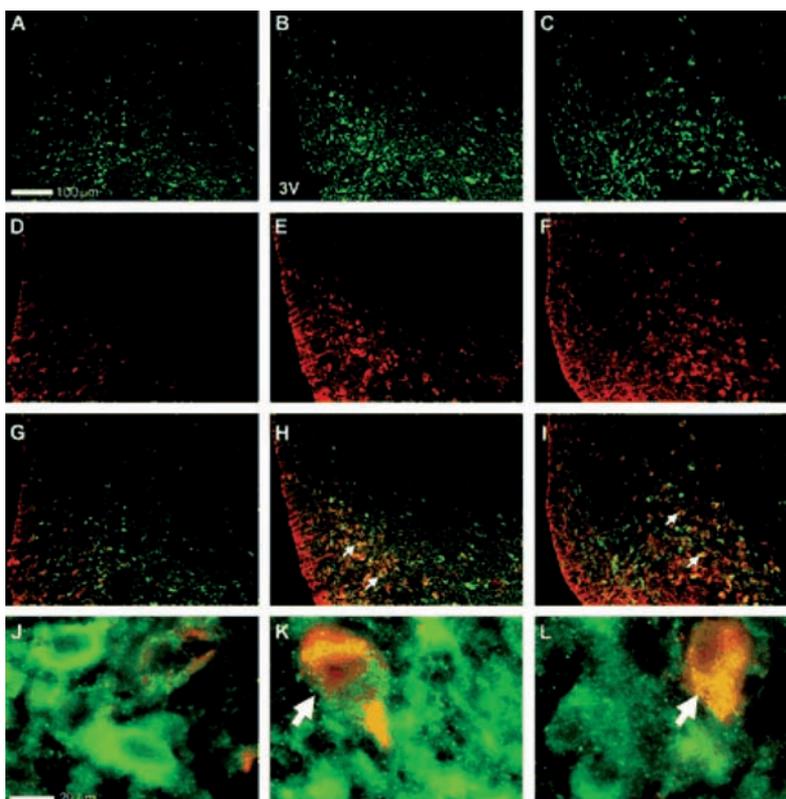
**Figure 26.** POMC posttranslational processing by PC1 (black arrow) and PC2 (clear arrow) at dibasic cleavage sites (solid line). Tissuespecific expression results in a different range of peptides produced in the anterior pituitary (■) compared with the hypothalamus (▀). (reproduced with permission from Coll AP, Farooqi IS, Challis BG, Yeo GS, O'Rahilly S: *J Clin Endocrinol Metab* 2004; 89:2557-2562)

mone capable of responding rapidly to changes in metabolism and providing the brain with minute-to-minute information of an individual's physiological state. Second, insulin receptors are widely distributed in the cen-

tral nervous system and are found in particularly high concentrations in those brain regions involved in the regulation of food intake and body weight (453, 454). Third, insulin gains entry into the brain via a saturable transport process that moves the hormone from the plasma into brain interstitial fluid (455). Fourth, the intracerebroventricular (icv) administration of insulin reduces food intake and this effect may be due to its ability to decrease NPY/AgRP and increase POMC gene expression in the ARC (456-458). The effects of insulin in the ARC are mediated by tyrosine phosphorylation of the insulin receptor, IRS-1 and -2, increased binding of activated IRS-1 and -2 to the regulatory subunit of PI3-kinase and activation of protein kinase B/Akt (459). It is noteworthy that the insulin-induced increase in PI3-kinase activity preferentially occurs in IRS-2-containing neurons and that its inhibitory effect on food intake is blocked by PI3-kinase inhibitors (Figure 27).

### Leptin

Leptin, a 167-residue peptide that is the product of the *ob* gene, is derived almost exclusively from adi-

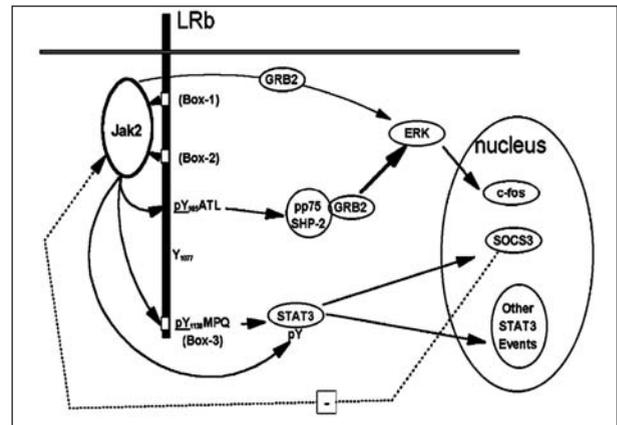


**Figure 27.** Insulin enhances PIP<sub>3</sub> immunoreactivity primarily in IRS-2-expressing arcuate nucleus neurons (A-I: x20 magnification, third ventricle at lower left of frame; J-L: x100 view of ARC neurons). Rats were treated with intracerebroventricular vehicle (A, D, G, and J), intracerebroventricular insulin (10mU, 5 min; B, E, H, and K), or peripheral insulin (5 units i.p., 15 min; C, F, I, and L); the sections of arcuate nucleus immunostained for IRS-2 (A-C) and PIP<sub>3</sub> (D-F); and the images merged at low (G-I) and high power (J-L). IRS-2 immunoreactivity was detected specifically in neurons of the arcuate nucleus with all treatments (A-C), and with no staining detected elsewhere. Insulin treatment, either intracerebroventricularly (E) or peripherally (F), induces increased PIP<sub>3</sub> immunoreactivity compared with vehicle treatment (D). Enhanced PIP<sub>3</sub> immunoreactivity occurs primarily in IRS-2-positive neurons (G-I). Especially at high magnification, PIP<sub>3</sub>/IRS-2 double-positive neurons are identified in insulin-treated arcuate nucleus neurons (K and L), whereas few if any are observed in vehicle-treated rats (J). 3V, third cerebral ventricle (reproduced with permission from ref. 459)

pose tissue and is secreted in a pulsatile manner into the systemic circulation (460, 461). Leptin is an important peripheral signal that regulates energy balance since both peripheral and icv administration of the hormone reduces food intake and body weight (462, 463).

The leptin receptor (ObR) belongs to the cytokine receptor class I super-family (464) and five alternatively spliced forms with different carboxy-terminal lengths (a-e) have been identified (465). The expression of the short leptin receptor isoform, ObRa, is highest in the choroid plexus and microvessels where it may be involved in receptor-mediated transport of the hormone across the blood-brain barrier and in the clearance of leptin from the cerebrospinal fluid (466-469). The long form of the leptin receptor, ObRb, is expressed in varying concentrations in several brain nuclei (470, 471). Within the hypothalamus, dense mRNA expression is found in the ARC, DMH, ventromedial hypothalamus (VMH), and ventral premamillary (PMV) nuclei, moderate expression is found in the Pv and LHA, and lower levels still are found in the PVH. Many of these areas are involved in the regulation of feeding behavior and animals bearing a selective neuron-specific deletion of the ObR develop obesity, indicating that most, if not all, of leptin's weight-reducing effects are due to its actions in the brain (472).

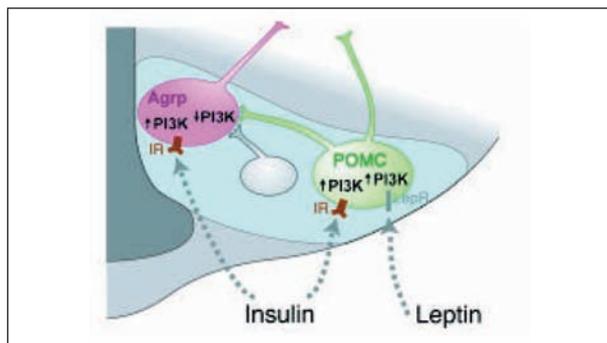
Activation of ObRb results in activation of the associated Jak2 tyrosine kinase and subsequent tyrosine phosphorylation of ObRb (473, 474). Two important tyrosine residues that are phosphorylated during receptor activation are Tyr<sup>985</sup> and Tyr<sup>1138</sup> which mediate distinct signaling pathways. Tyr<sup>985</sup> binds to the src homology 2 (SH2)-domain protein, SH2-domain phosphotyrosine phosphatase (SHP-2), and leads to activation of the extracellular signal-regulated kinase (ERK) and induction of *c-fos* expression. Tyr<sup>1138</sup> binds to STAT3 proteins which become tyrosine phosphorylated by Jak2, dissociate in the cytoplasm to form dimers, and finally translocate to the nucleus where they regulate gene transcription (Figure 28, 475). One of the genes induced by STAT3 is that which codes for SOCS3 which functions as a major feedback inhibitor of ObRb signaling (476). In addition, the effects of ObRb activation on food intake, body weight and the Jak-STAT pathway re-



**Figure 28.** Model of LRB signaling. Murine LRB contains three intracellular tyrosine residues (shown with surrounding amino acids) in addition to the conserved Box 1 and Box 2 motifs required for interaction with Jak2. Upon ligand stimulation, the associated Jak2 tyrosine kinase becomes activated, autophosphorylating and phosphorylating Tyr<sup>985</sup> and Tyr<sup>1138</sup> of the LRB. Phosphorylated Tyr<sup>1138</sup> recruits STAT3, which is then tyrosine-phosphorylated by Jak2, whereupon it translocates to the nucleus to mediate the transcription of *socs3* and other genes. SOCS3 ultimately feeds back upon and inhibits Jak2/LRB signaling (dotted line). Phosphorylated Tyr<sup>985</sup> recruits SHP-2, which is then tyrosine-phosphorylated by Jak2. Phosphorylated SHP-2 (identical to pp75) binds GRB-2 and mediates the majority of ERK activation during LRB signaling. An additional minor amount of GRB-2 binding and ERK activation is mediated directly by Jak2 (thin line). The activation of ERK results in the transcription and accumulation of *c-fos* message (reproduced with permission from ref. 475)

quire an intact PI3-kinase-phosphodiesterase 3B-cyclic AMP signaling pathway, since these effects are blocked by a phosphodiesterase 3 inhibitor (477, 478).

The weight-reducing effects of leptin are mediated by stimulation of the anorexigenic POMC neurons and inhibition of the orexigenic NPY/AgRP neurons in the ARC (479-485). Leptin increases the frequency of action potentials in POMC neurons by causing depolarization through a nonspecific cation channel and by reducing the inhibition exerted by local NPY/ $\gamma$ -aminobutyric acid neurons (484). As judged by its ability to activate PI3K, leptin increases the membrane accumulation of PI3K in POMC neurons but decreases PI3K accumulation in AgRP neurons (Figure 29, 485). Moreover, this latter effect of leptin on AgRP neurons is indirect, since it is blocked by



**Figure 29.** Unifying mechanism for leptin modulation of key arcuate nucleus neurons in which PI3K activity is a mediator and/or marker of neuronal activation and neuropeptide release in both AgRP (pink) and POMC (green) neurons. The effects of insulin on PI3K activity are direct in both neuronal subtypes, but the effects of leptin on PI3K activity in AgRP neurons require synaptic transmission from POMC or other (gray) inhibitory synaptic neurons. IR, insulin receptor; LepR, leptin receptor (reproduced with permission from ref. 485)

inhibitors of synaptic transmission. Although insulin, like leptin, increases PI3K accumulation in POMC neurons, it also increases PI3K accumulation in AgRP neurons and neither of these actions are affected by inhibitors of synaptic transmission.

These results provide a new model to explain how leptin may exert different effects on these two cell types and suggest that the parallel effects of leptin and insulin on energy balance could be integrated at the level of the POMC neuron.

## DMH

### Connections

The DMH has been associated in some way with almost every goal-directed behavior and visceral response associated with the hypothalamus. The DMH lies adjacent to the third ventricle caudal to the PVH, dorsal to the VMH, and ventral to the zona incerta. The majority of the inputs to the DMH arise in the hypothalamus, although there are a few significant inputs from the telencephalon and brainstem (Figure 30, 486). With the exceptions of the magnocellular preoptic nucleus, the magnocellular parts of the PVH, the SON, and the medial and lateral mamillary nuclei, each major hypothalamic nucleus and area provides inputs to the DMH. The major projections from the DMH are also intrahypothalamic and follow three distinct ascending pathways - a) *paraventricular*, b) *ventral*, and c) *lateral*. Within the hypothalamus, the most densely innervated areas are the dorsal and ventral medial parvocellular parts of the PVH, other dorsal regions of the periventricular zone, the preoptic SCN, and the parastriatal nucleus (487).

### Neuropeptides synthesized in the DMH

The DMH also contains neuropeptide perikarya and fibers but for the purposes of this discussion, we will only focus on CRF and NPY since their genes have been shown to be regulated by exercise.



**Figure 30.** General organization of projections to the DMH. Inputs primarily utilize three descending pathways: *periventricular* and *medial* (1) and *lateral* (2), and two major ascending pathways: *midbrain periventricular* (3) and *brainstem lateral* (4). Pathways that were observed in our control injections, or reliably reported in the literature, are represented by a solid line. Regions for which the pathway is uncertain are represented by a dashed line (reproduced with permission from ref. 486)

### CRF

Several studies have shown that food intake and body weight are significantly decreased when rats are allowed free access to a running wheel (488,489). In addition, 42 h of running wheel access augments CRF gene expression in cell bodies located in the dorsal aspect of the DMH, but has no effect on CRF gene expression in the PVH (Figure 31, 490). Since the icv administration of a CRF antagonist specifically prevents the effects of exercise on meal size (491), the findings suggest that exercise induces endogenous CRF release leading to a reduction in meal size and food intake. Although the PVH and central nucleus of the amygdala (CeA) are important sites that mediate some of the central actions of CRF, lesions of these nuclei have no effect on exercise-induced anorexia, indicating that these brain areas do not play a role in mediating this response (492, 493). To date, the exact mechanisms by which exercise initially activates CRF gene expression in the DMH remain unknown.

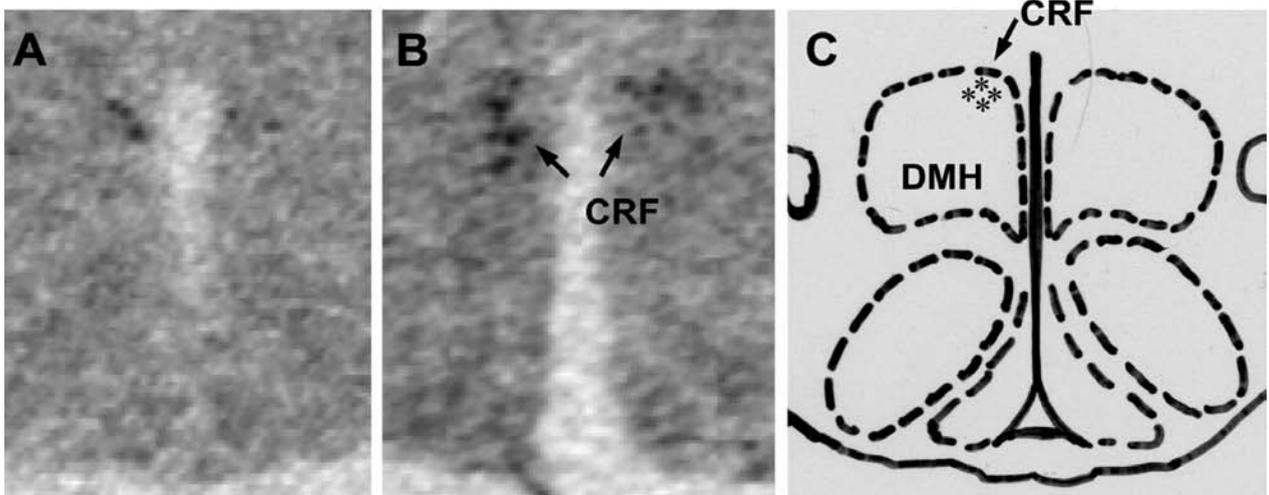
### NPY

Physical exercise also increases NPY mRNA expression in the DMH and ARC (400, 494), but in contrast to the time course with which running wheel

access increases DMH CRF gene expression, DMH NPY gene expression only increases after 7-days of exercise. Although DMH CRF gene expression is still elevated after 7-days of exercise, the CRF-mediated, exercise-induced anorexia subsides and the food intake in exercised animals closely approximates that seen in sedentary animals. It therefore appears that the increase in NPY gene expression seems to override the effect of CRF on food intake at this time.

### *Postulated mediation by Musculin of exercise-induced GH, ACTH and PRL secretion*

A number of studies in man have demonstrated that physical exercise has no discernible acute or chronic effects on serum leptin concentrations (495-499), suggesting that it is unlikely that leptin plays a significant role in mediating the effects of exercise on anterior pituitary secretion. Furthermore, although insulin may stimulate anterior pituitary hormone secretion indirectly by virtue of the hypoglycemia that results from excessive insulin production or administration, the occurrence of hypoglycemia implies an underlying pathophysiological state, and is not a usual concomitant of physical exercise. Moreover plasma insulin levels decline, rather than increase, during exercise, and taken together these findings also tend to exclude a significant role for



**Figure 31.** Effect of exercise on CRF gene expression in the DMH. In situ hybridization of CRF with  $^{35}\text{S}$ -labeled-CRF antisense riboprobe. CRF gene expression was detected very lightly in sedentary rats (*A*), CRF was highly expressed in the DMH in voluntary exercising rats (*B*), and the induction of DMH CRF expression was mainly localized to the dorsal region of the DMH (*B* and *C*) (reproduced with permission from ref. 490)

insulin as a mediator of exercise-induced pituitary hormone secretion. Considerations such as these set the stage for the possible involvement of additional factor(s) as mediators of exercise-induced pituitary hormone secretion. We therefore postulate that:

- *Musculin concentrations in the systemic circulation increase during physical exercise in increments that correlate directly with the exercise intensity.*
- *Musculin acts directly on the brain to mediate the anterior pituitary hormone and appetite responses to exercise.*

### GH

From the aforementioned review, we postulate that:

- *Musculin acts directly on ARC GRF neurons to increase the synthesis and release of GRF into the hypophysial-portal circulation.*

Since physical exercise also increases Prepro-GAL gene expression in the Locus Ceruleus (A6 area, 500), we postulate that:

- *Musculin binds directly to GAL neurons in the A6 area and stimulates GAL synthesis and secretion.*

Since the A6 area does not lie outside the blood-brain barrier (501), we postulate that, like insulin and leptin (455, 466-469, 502-505),

- *Musculin may gain access to the brain by a receptor-mediated active transport mechanism.*

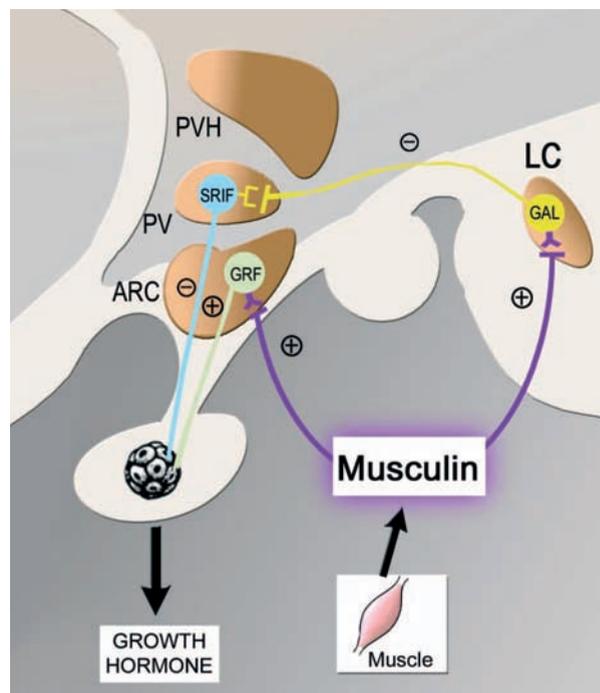
Studies in the rat and in man suggest that GAL stimulates GH secretion by both increasing GRF release and by inhibiting SRIF secretion (506-513). Since axons derived from A6 GAL-immunoreactive neurons project to the periventricular part of the PVH (377) and synapse directly with those SRIF neurons that project to the median eminence (514), we propose that:

- *Musculin also increases GH secretion by enhancing the inhibitory galaninergic regulation of hypothalamic SRIF release.*

These postulates are schematically illustrated in Figure 32.

### ACTH

As previously stated, it is currently accepted that the hypothalamus only provides a unidirectional, sti-



**Figure 32.** A hypothetical scheme depicting the mechanisms by which *Musculin* may mediate the Growth Hormone response to exercise. It is suggested that *Musculin* may bind directly to ARC GRF neurons and stimulate GRF synthesis and its release into the hypophysial-portal circulation. In addition, it is hypothesized that *Musculin* binds to galanin neurons in the locus ceruleus and increases galanin gene expression at this site. These galanin neurons give rise to axons which innervate SRIF neurons in the periventricular area. The galaninergic regulation of SRIF is inhibitory and the resultant reduction in SRIF secretion into hypophysial-portal blood would also be expected to facilitate Growth Hormone secretion. ARC, arcuate nucleus; GAL, galanin; GRF, Growth Hormone-Releasing Factor; LC, locus ceruleus; PV, periventricular area; PVH, paraventricular hypothalamic nucleus; SRIF, somatostatin

mulatory regulation of ACTH secretion and that this is predominantly mediated by the neuropeptides CRF and AVP. In turn, the hypothalamic CRF and AVP neurons that project to the median eminence receive noradrenergic and adrenergic inputs derived from the brainstem and in previous studies, we have shown that the noradrenergic input stimulates the release of both CRF and AVP into the hypophysial-portal circulation of the conscious sheep (515). Moreover, physical exercise has also been shown to increase the concentrations of NE and its metabolite 3,4-dihydroxyphenylglycol (DHPG) in the pons-medulla (516, 517). As

previously described, the noradrenergic innervation of the PVH is derived from the A1, A2, and A6 areas, but since the A1 NE neurons mainly project to the magnocellular subdivisions of the PVH which are not concerned with HPA axis regulation and since NE turnover in the A6 area is not affected by exercise (500), we postulate that:

- *Musculin binds to NE neurons in the A2 area where it stimulates NE synthesis, thereby increasing the stimulatory noradrenergic regulation of those hypothalamic CRF and AVP neurons concerned with regulation of the HPA axis.*

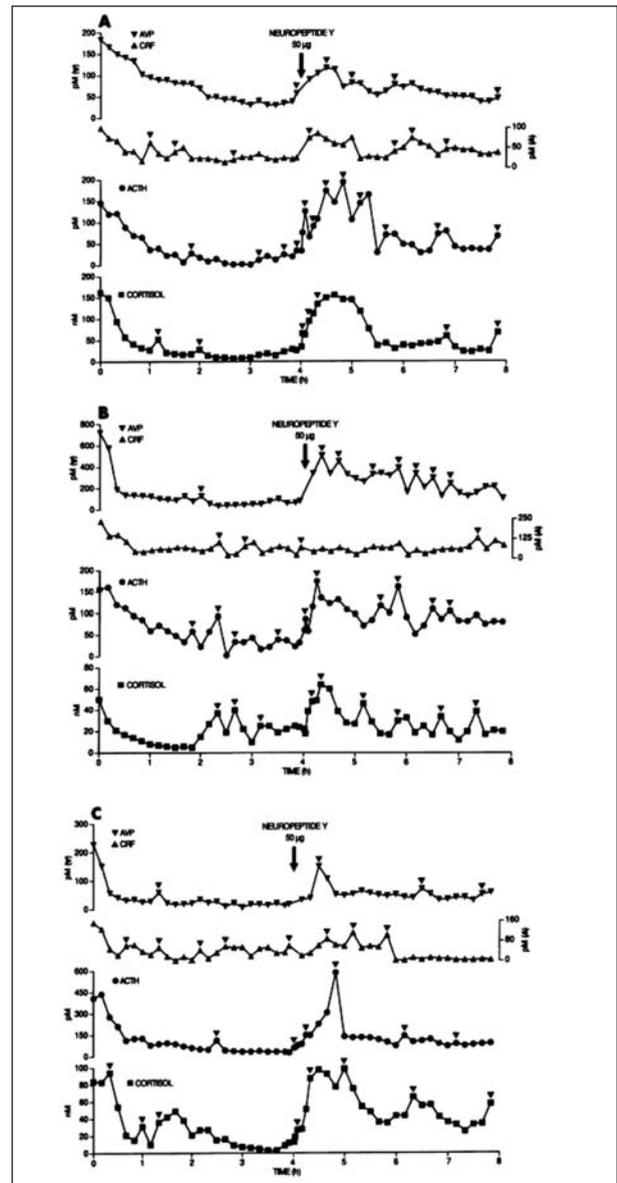
The paraventricular hypothalamic CRF and AVP neurons concerned with HPA axis regulation also receive peptidergic inputs and a prominent contribution is made by NPY axons that are mainly derived from ARC NPY neurons (370). Since physical exercise increases ARC NPY gene expression and since NPY activates the HPA axis in a number of species (515, 518, 519) by increasing CRF and AVP secretion into the hypophysial-portal circulation (Figure 33, 515), we postulate that:

- *Musculin binds to ARC NPY neurons where it increases NPY synthesis, thereby increasing the stimulatory NPYergic input to those hypothalamic CRF and AVP neurons that regulate the HPA axis.*

These postulates are illustrated schematically in Figure 34.

### PRL

As previously mentioned, prolactin secretion by the anterior pituitary is tonically inhibited by DA and stimulated by a number of hypothalamic releasing factors such as VIP, TRH, and OT. A number of studies have shown that the icv administration of GAL increases the release of VIP from periventricular structures into the cerebrospinal fluid (520, 521). Since the icv administration of GAL also increases prolactin secretion which is attenuated by the concomitant icv administration of a VIP antiserum (520-523), the findings support the hypothesis that GAL stimulates prolactin secretion by increasing the hypothalamic release of VIP. The VIP neurons that project to the median eminence are concentrated in the medial parvocellular subdivision of the PVH (345) and this area,

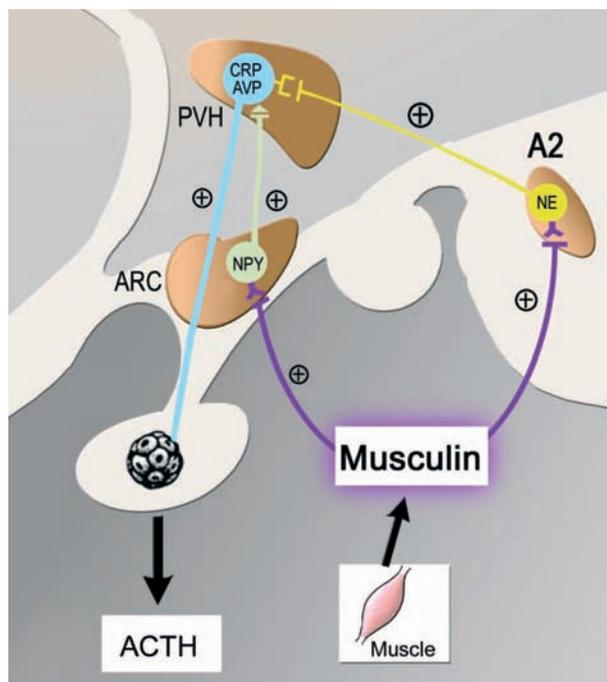


**Figure 33.** Activation of the hypothalamic-pituitary-adrenal axis by neuropeptide Y. The effect of neuropeptide Y (50 µg icv) on plasma CRF, AVP, ACTH, and cortisol levels in three ewes (reproduced with permission from ref. 515)

together with the periventricular and anterior parvocellular subdivisions of the PVH, receive a prominent input of galanergic fibers that are derived from the A6 area (377).

Since exercise increases GAL biosynthesis in the A6 area, we postulate that:

- *Musculin may bind to the GAL neurons in the A6 area and stimulate GAL synthesis and secretion.*



**Figure 34.** A hypothetical model of the mechanisms by which *Musculin* may mediate the Adrenocorticotropin response to exercise. It is suggested that *Musculin* binds to ARC neuropeptide Y neurons and increases NPY synthesis and secretion. ARC neuropeptide Y neurons project heavily to the PVH where they form synaptic contacts with CRF and AVP neurons. Neuropeptide Y stimulates CRF and AVP release into the hypophysial-portal circulation and thus increases adrenocorticotropin secretion. In addition, it is postulated that *Musculin* binds to noradrenergic (NE) neurons in the A2 area and increases NE synthesis. The A2 noradrenergic neurons give rise to axons which innervate the PVH and form synapses with CRF and AVP neurons. NE also stimulates CRF and AVP release into the portal circulation and thus increases adrenocorticotropin secretion. ACTH, adrenocorticotropin; ARC, arcuate nucleus; AVP, arginine vasopressin; A2, nucleus of the tractus solitarius; NE, norepinephrine (noradrenaline); NPY, neuropeptide Y; PVH, paraventricular hypothalamic nucleus

- *The increased galaninergic drive may stimulate the hypothalamic release of VIP from the PVH and increase the secretion of prolactin by the lactotropes of the anterior pituitary.*

As previously stated, prolactin secretion is tonically inhibited by tuberoinfundibular dopaminergic (TIDA) neuron secretion but, to our knowledge, *in vivo* microdialysis studies of the effects of physical exercise on DA secretion from ARC TIDA neurons have yet to be performed. However, it has been shown

that physical exercise acutely increases the release of DA, NE, and GLU from the rat striatum (524, 525), and although the mechanisms underlying these effects remain unclear, it is conceivable that exercise could similarly affect TIDA neuronal activity. Since activation renders TIDA neurons susceptible to the inhibitory effects of GAL (526), we postulate that:

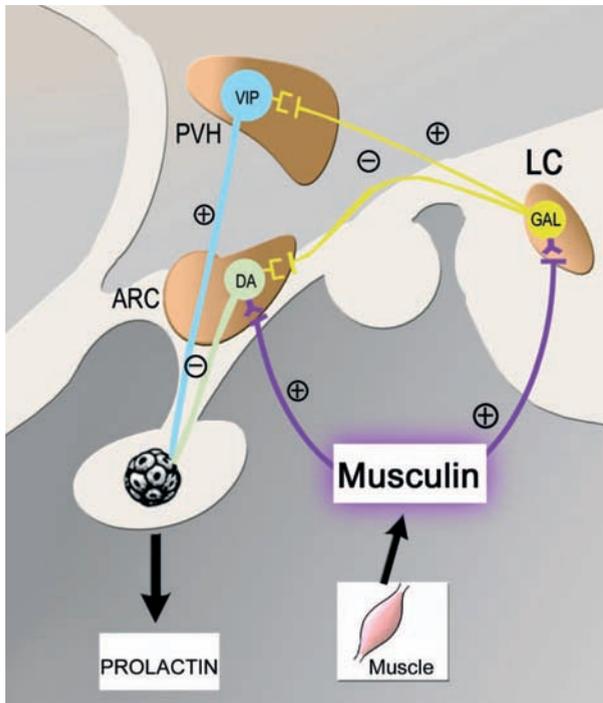
- *Musculin may bind directly to and activate ARC TIDA neurons.*
- *Musculin-induced activation may render ARC TIDA neurons susceptible to the inhibitory effects of GAL, thereby reducing the dopaminergic drive to the lactotropes and thus increasing prolactin secretion.*

These postulates are illustrated schematically in Figure 35.

#### *Postulated mediation by Musculin of exercise-induced anorexia*

To date, the earliest described change in hypothalamic neuropeptide gene expression in response to short-term (42 h) exercise is a singular 1.5-2.0-fold increase in CRF mRNA in the dorsal DMH (490), there being no discernible effects on ARC neuropeptide gene expression. However, long-term exercise causes a 5-fold induction of DMH CRF mRNA, it subsequently induces NPY gene expression in the DMH, and increases ARC NPY and POMC mRNAs (490, 527).

Several lines of evidence support the suggestion that the early induction of DMH CRF mRNA in response to short-term exercise cannot be easily ascribed to the actions of leptin or insulin. Firstly, although the DMH does contain ObRs and responds to intravenously injected leptin with an induction of neuronal Fos immunoreactivity (ir), the Fos-ir is characteristically observed in the caudal portion of the ventral subdivision, rather than in the dorsal part of the nucleus where the CRF neurons are located (528). Secondly, most studies in man suggest that short-term physical exercise appears to have no discernible effect on serum leptin concentrations, although this statement may not be applicable to rodents. Thirdly, although long-term exercise has been shown to cause



**Figure 35.** A hypothetical model of the mechanisms by which *Musculin* may mediate the Prolactin response to exercise. It is suggested that *Musculin* binds to galanin neurons in the locus ceruleus and increases galanin gene expression. The galanin neurons give rise to axons which innervate the paraventricular hypothalamus where they form synaptic contacts with vasoactive intestinal polypeptide neurons. The galaninergic regulation of vasoactive intestinal polypeptide is stimulatory in nature and since vasoactive intestinal polypeptide is a prolactin-releasing factor, this mechanism would be expected to increase prolactin secretion. In addition, it is suggested that *Musculin* binds to and activates ARC tuberoinfundibular dopamine (TIDA) neurons. Activation of TIDA neurons renders them susceptible to the inhibitory effects of galanin, and since dopamine tonically inhibits the release of prolactin, a posulated net reduction in dopaminergic tone would also be expected to increase prolactin secretion. ARC, arcuate nucleus; DA, dopamine; GAL, galanin; LC, locus ceruleus; PVH, paraventricular hypothalamic nucleus; VIP, vasoactive intestinal polypeptide

a ~20% reduction in serum insulin concentrations, the magnitude of this effect has not been found to be statistically significant (494). Moreover, the profound insulinopenia that characterizes the diabetes resulting from the administration of the islet  $\beta$ -cell toxin, streptozotocin, causes changes in ARC gene expression, but does not seem to affect neuropeptide expression in the DMH (529). From these considerations, we suggest that:

- The exercise-induced changes in DMH CRF gene expression are unlikely to be mediated by leptin or insulin.
- *Musculin* may constitute a separate non-leptin, non-insulin hormonal pathway that mediates the exercise-induced changes in DMH neuropeptide gene expression.
- *Musculin* binding and activation of DMH CRF neurons may constitute an early event in the mediation of exercise-induced anorexia.

As previously noted, long-term exercise causes a 5.0-fold induction of DMH CRF mRNA and also increases ARC POMC gene expression. A number of immunohistochemical studies have shown the presence of abundant  $\alpha$ -MSH fibers and terminals within the DMH (530, 531). Since retrograde studies have shown that the majority of inputs to the DMH arise in the hypothalamus (486), it seems reasonable to conclude that ARC POMC neurons are the major source of  $\alpha$ -MSH fiber projections to the DMH. In recent studies, Lechan and coworkers have sought to determine the DMH neuronal subpopulations that project to the PVH (531). When cholera toxin  $\beta$ -subunit was injected into the PVH, ~65% of all the DMH neurons that were retrogradely labeled were found in the medial portion of the ventral subdivision (DMHv) and ~26% were diffusely distributed in the dorsal subdivision (DMHd). Moreover, ~39% of the DMHd-labeled cells were contacted by  $\alpha$ -MSH-stained axon terminals. Since CRF-stained neurons are located in the DMHd and project to the PVH (490, 532), it is possible that some of these retrogradely labeled cells were CRF neurons. Moreover, recent studies have demonstrated a functional link between the central melanocortin system and CRF-producing neurons, albeit in the PVH (533, 534). The MC4-R is expressed in ~10-15% of the CRF neurons in the PVH and the icv administration of  $\alpha$ -MSH causes phosphorylation of the cAMP response element binding protein (CREB) in CRF (and TRH) neurons in several subdivisions of the PVH (533). Furthermore, the administration of the melanocortin agonist, MTII, rapidly increases CRF hnRNA, increases plasma corticosterone levels, and causes anorexia (534). The DMH is also known to express the MC4-R mRNA (535, 536) and although, to our knowledge, anatomical and functional stu-

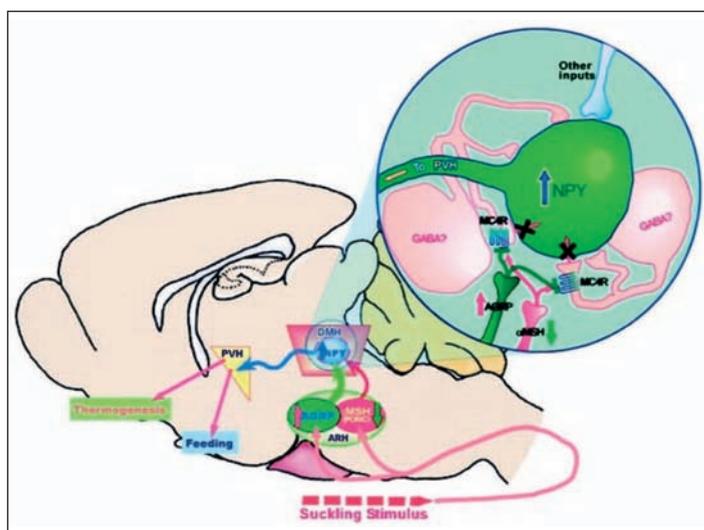
dies of a possible melanocortin-CRF interaction have yet to be performed in the DMH, we postulate that:

- *Musculin may bind to ARC POMC neurons and increase POMC gene expression.*
- *The resultant increase in ARC POMC mRNA expression may secondarily potentiate CRF gene expression in the DMH by increasing an  $\alpha$ -MSH-mediated stimulation of the DMH CRF gene.*

As previously stated, long-term exercise induces DMH NPY gene expression in the DMH (490, 527), and it is noteworthy that this phenomenon has also been demonstrated in the following pathophysiological and physiological states - firstly, it has been observed in several rodent models of obesity including obese MC4-R<sup>-/-</sup> and obese *A<sup>y</sup>* mice (537-539). Since these animals represent two examples of the melanocortinergic obesity syndrome and are respectively characterized by diminished or absent melanocortin signaling, it has been proposed that des-acetyl- $\alpha$ -MSH released at MC4-R-containing synapses in the DMH normally inhibits NPY gene expression in this nucleus (537). However, the absence of DMH NPY gene expression in nonobese *A<sup>y</sup>* animals indicates that abrogation of melanocortinergic signaling alone is not sufficient to cause the phenomenon. Secondly, DMH NPY gene expression has been found after long-term food restriction (494), after the administration of naloxone, which also causes mild anorexia and a reduction in food intake (540), and in diet-induced obesity (541).

Thirdly, DMH NPY gene induction occurs during lactation in the rat, in which 3 h of suckling is sufficient to activate DMH NPY gene expression, but 24 h of suckling is required to increase NPY mRNA in the caudal portion of the ARC (542). The studies by Smith and colleagues (542-545) also suggest that the DMH NPY gene is inhibited by melanocortin signaling since lactation also reduces ARC POMC mRNA (545), and bilateral injections of an MC4-R/3-selective agonist (melanotan II) into the DMH of the lactating rat greatly attenuates the induction of DMH NPY gene expression and the suckling-induced hyperphagia (536). A schematic diagram summarizing this postulated sequence of events is shown in Figure 36.

As noted, long-term physical exercise *increases* both ARC NPY and POMC mRNAs (490, 527). Moreover, this pattern of ARC neuropeptide gene expression seems unique, since it differs from that caused by leptin and insulin, which both increase ARC POMC mRNA and decrease ARC NPY mRNA (451-453, 457, 458, 479, 484, 546), and suckling, which increases ARC NPY mRNA and decreases ARC POMC mRNA. Therefore, although a role for melanocortin signaling in the induction of DMH NPY mRNA seems established in obese rodent models of melanocortinergic obesity and lactation as described above, the rise in ARC POMC mRNA during long-term exercise renders it difficult to invoke withdrawal of melanocortinergic signaling in the DMH as a pri-

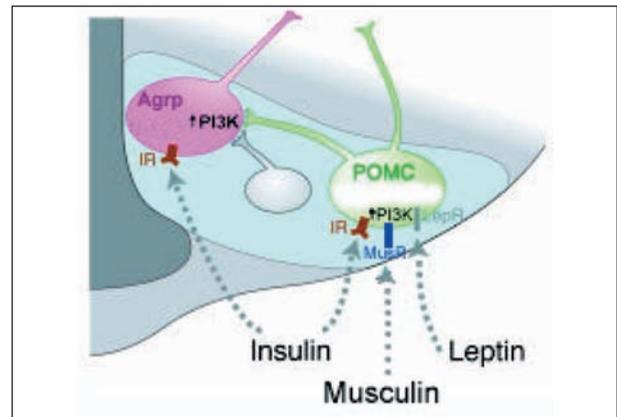


**Figure 36.** Schematic diagram summarizes the proposed hypothesis for MC4R-mediated activation of DMH NPY neurons and the hyperphagic response during lactation. During lactation, ARH AGRP/NPY input to the DMH is elevated whereas ARH POMC tone into the DMH is reduced. Most of these inputs likely terminate on inhibitory interneurons expressing MC4R (i.e. GABAergic) in the DMH. The inset depicts MC4R signaling. The increased AGRP input in combination with reduced POMC input from the ARH causes a reduction in MC4R signaling, leading to a decrease in GABAergic inhibition on the DMH NPY neurons, resulting in activation of NPY mRNA expression during lactation. The activated NPY neurons in the DMH may be involved in a number of modulations during lactation, including hyperphagia and energy expenditure, probably via projection to the PVH (reproduced with permission from ref. 536)

primary mechanism responsible for the induction of DMH NPY gene expression by exercise, and points towards mechanism(s) other than those mediated by the MC4-R.

It is possible that the induction of DMH NPY mRNA by long-term physical exercise is the result of metabolic or hormonal effects of the exercise and this suggestion is supported by studies which have examined the effects of acute food deprivation or chronic food restriction in the rat (547). These studies have demonstrated that both experimental methods of caloric deprivation elevate ARC NPY and decrease ARC POMC gene expression, but only chronic food restriction induces NPY gene expression in the DMH. Although acute food deprivation and chronic food restriction both cause weight loss and identical reductions in serum leptin, plasma glucose and insulin levels are only reduced by acute food deprivation. These data indicate that ARC and DMH NPY mRNAs are differentially regulated, and unlike ARC NPY mRNA which is responsive to short-term alterations in food intake, DMH NPY gene expression may only respond to long-term alterations in energy intake or expenditure. Moreover, the findings also suggest that DMH NPY gene expression is not regulated by leptin, a conclusion which is further strengthened by the lack of colocalization of the ObRs in DMH NPY neurons (547). Finally, studies in the lactating rat have shown that DMH NPY neurons may also be hormonally regulated by prolactin, since the suckling-mediated induction of DMH NPY gene expression is significantly attenuated when the associated hyperprolactinemia is prevented by the dopaminergic agonist, bromocriptine (548).

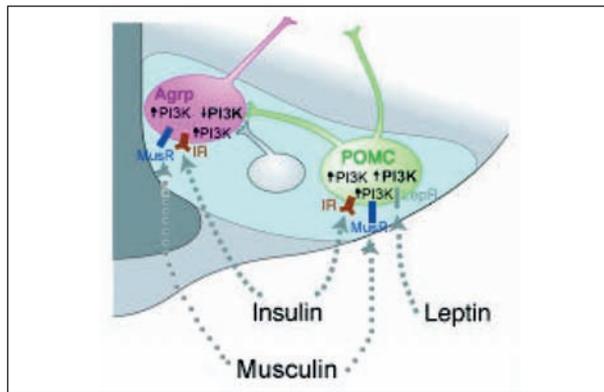
It is possible that several etiological factors could underly the exercise-induced increase in ARC NPY and POMC mRNAs. Firstly, this pattern of ARC gene expression could be entirely caused by the direct effects of *Musculin*. *Musculin* binding to ARC POMC neurons could increase PI3K, as has been demonstrated for leptin and insulin, and this would result in a model whereby the effects of leptin, insulin, and *Musculin* are integrated at the level of these anorexigenic neurons (Figure 37). If *Musculin* also activated ARC NPY/Agrp neurons by synaptic interaction with POMC neurons, as has been demonstrated for leptin



**Figure 37.** A schematic representation of the modulation of arcuate nucleus neurons by leptin and insulin, and postulated modulation by *Musculin*. This figure is a modification of Figure 29 and PI3K activity is depicted as a mediator and/or marker of neuronal activation and neuropeptide release in both Agrp (pink) and POMC (green) neurons. For the sake of clarity, the effects of insulin and leptin on PI3K activity have been omitted, but are identical to that shown in Figure 29. The figure proposes that the effects of *Musculin* on Agrp neurons are synaptically mediated from POMC or other neurons. However, in contrast to leptin which decreases PI3K activity in Agrp neurons, it is suggested that *Musculin* may increase PI3K in these neurons. IR, insulin receptor; LepR, leptin receptor; MusR, *Musculin* receptor

(485), then one would predict that PI3K activity would increase in response to *Musculin*, thereby opposing the actions of leptin. However, one could also envisage a model whereby *Musculin* bound both POMC and ARC neurons separately and increased PI3K activity in both neuronal subtypes (Figure 38).

Finally, it also remains possible that the exercise-induced increases in ARC NPY and POMC mRNAs could represent a combination of the direct effects of *Musculin* binding to POMC neurons and the indirect effects of the metabolic and hormonal responses to exercise on NPY/Agrp neurons. For example, as previously detailed, exercise in man and rodents is associated with a reduction in serum insulin concentrations. Moreover, although studies in man have generally suggested that acute exercise has little effect on serum leptin levels, exhaustive exercise in man and long-term exercise in rodents does reduce leptin concentrations (549-551). As noted, ARC NPY/Agrp neurons respond to leptin and insulin withdrawal with an upregulation of NPY mRNA expression and these mechanisms could theoretically account for the in-



**Figure 38.** An alternative schematic representation of the modulation of arcuate nucleus neurons by leptin and insulin, and postulated modulation by *Musculin*. This figure is also a modification of Figure 29 and PI3K activity is depicted as a mediator and/or marker of neuronal activation and neuropeptide release in both AgRP (pink) and POMC (green) neurons. The effects of insulin on PI3K activity are direct in both neuronal subtypes, but the effects of leptin on PI3K activity in AgRP neurons require synaptic transmission from POMC or other (gray) inhibitory synaptic neurons. This figure proposes that the effects of *Musculin* on PI3K are also direct and that PI3K is increased in both neuronal subtypes. IR, insulin receptor, LepR, leptin receptor; MusR, *Musculin* receptor

creased ARC NPY mRNA observed in long-term exercise.

### Future directions

Although much of the content of this manuscript is hypothetical, we suggest that a search for a protein with the characteristics described for *Musculin* may be worthwhile, since analogues of such a substance may be of therapeutic benefit in the management of the current global diabetes and obesity epidemic (552-560).

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