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# Obesity: molecular bases of a multifactorial problem

Received: 15 September 1999 Accepted: 10 June 2000 **Summary** Obesity could well become the most common health problem of the 21<sup>st</sup> century. There are more opportunities to consume large quantities of food: big portions of tasty, varied food, at reasonable prices, are available everywhere. Moreover, our bodies are better adapted to combat weight loss than to combat weight gain, since for thousands of years our species evolved in circumstances where nutrients were in short supply.

The response of each individual to diet and other environmental factors varies considerably, depending on the characteristics of his/her body weight control mechanisms. The differentiating element in the future, especially as regards the dietary and pharmacological control of obesity, will be knowledge of an individual's possible response depending on his/her genetic background.

Obesity can occur as a result of genetic or acquired changes in three main types of biochemical processes, which are the main focus of this review: a) *feeding control*, which determines the sensations of satiety and hunger through processes that depend

on an interplay between internal signals (notably leptin) and environmental factors; b) *energy efficiency*, in particular the activation of thermogenesis mediated by uncoupling proteins (UCPs) that makes it possible to dissipate part of the energy contained in food as heat instead of accumulating it as fat, and c) *adipogenesis*, the process by which cells specialised in fat storage (adipocytes) are formed, which is controlled by an interplay of transcription factors, including members of the C/EBP, PPARγ and ADD families.

The knowledge of a growing number of genes and molecules implicated in these three types of processes and of their metabolic relationships is leading toward a molecular understanding of the body weight regulatory system, and is paving the way for new methods of obesity control, especially pharmacological but also nutritional and possibly involving genetic intervention.

**Key words** Obesity – feeding control – adipogenesis – thermogenesis – obesity genes

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## The genetic-molecular bases of obesity

Obesity occurs when energy intake exceeds energy expenditure as a result of genetic or acquired changes in feeding control, energy efficiency or adipogenesis. The genes as-

sociated with these three types of biochemical processes and the metabolic location and links between their protein products are the main focus of this review:

• Feeding control [1, 2]: i.e. the biochemical processes that determine the sensations of satiety and hunger, in respect of both quantity and quality, including prefer-

ence for certain types of food, appetite, frequency of food intake etc. These processes depend in turn on internal and environmental factors, including social habits. The state and activity of energy reserves, mainly in adipose tissue, are communicated to the CNS by leptin and other signals.

- Control of energy efficiency [3]: i. e. the biochemical processes that control the degree to which energy from food is used. Of particular interest is the control of energy efficiency through changes in thermogenesis mediated by uncoupling proteins (UCPs) [4]. Activation of thermogenesis makes it possible to dissipate part of the energy contained in food as heat instead of accumulating it as fat.
- Adipogenesis [5, 6]: i. e. the process by which cells specialised in fat storage (adipocytes) are formed. The adipose tissue is at the centre of a key regulatory system exerting a pivotal influence on hormone-regulated fuel partitioning in peripheral tissues, and it relates to many metabolic complications of obesity.

## **Feeding control**

There are various aspects to be considered in the regulation of feeding behaviour [1, 2]. There is the time aspect of appetite control mechanisms: short-term control, by physical signals and release of digestive peptides in response to food, and chronic or medium-long term control, effected by signals (such as leptin) that indicate the levels of the energy reserves in the body. There are also qualitative aspects of appetite control, i. e. mechanisms underlying the selection of certain specific nutrients or groups of nutrients. Finally, it must be remembered that these processes are coordinated by integrating mechanisms.

Signals indicating the availability of energy resources

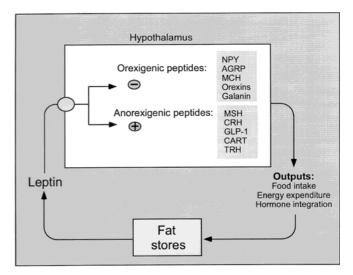
There may be various types of biomolecules linking all the information regarding the external energy situation (food available) with the internal energy situation (energy-nutritional reserves). Various possibilities were first suggested for several metabolites and hormones (glucose, ketone bodies, amino acids, insulin, glucocorticoids etc.), and more recently for oleoyl-estrone and related compounds [7, 8]. Nevertheless, although other possible signals should be kept in mind, only for leptin – and linked with it, insulin – is a sufficient body of knowledge available to enable us to interpret physiologically the processes involved in the control of energy balance and to explain them, at least partly, in genetic-molecular terms.

Leptin as indicator of internal energy reserves and regulator of energy balance

The ob gene, expressed by adipocytes, encodes the hormone leptin, which is released by the adipose tissue to the circulatory system and which, in the brain, acts on the leptin receptors and provides information about the level of fat reserves. Leptin determines changes in feeding behaviour, with suppression of appetite, and an increase in metabolic activity and energy expenditure (thermogenesis). It also affects different aspects of hormonal action which regulate the break up of nutrients and their metabolism in different tissues [9].

When the ob gene was cloned in December 1994 [10] and its protein product – later named leptin, from the Greek leptos, meaning thin – was described, the complex molecular mechanisms integrating the regulation of food intake, energy expenditure and fat reserves began to be understood. A year later, the db (or lepR) gene, which encodes the leptin receptors (expressed in the hypothalamus, in other parts of the CNS and also in peripheral tissues), was also identified [11] and characterised [12, 13]. Subsequently, several orexigenic and anorexigenic neuropeptides were described in the CNS, whose function is interlinked and connected with that of leptin [1, 2, 14–16; Fig. 1].

The data deriving from the leptin mechanism fit in with the lipostatic theory [17], which stated that the size of the body fat depots was regulated by a product of these depots which, via the circulatory system, acted on the CNS to con-



**Fig. 1** Orexigenic and anorexigenic neuropeptides involved in the control of food intake and energy expenditure. *NPY* neuropeptide Y; *AGRP* agouti related protein; *MCH* melanine-concentrating hormone; *MSH* melanocyte-stimulating hormone; *CRH* corticotropin-releasing hormone; *GLP-1* glucagon-like peptide-1; *CART* cocaine-and amphetamine-regulated transcript; *TRH* thyrotropin-releasing hormone.

trol food intake. The hypothesis of Coleman [18] that ob/ob genetically obese mice lacked this hormone while db/db genetically obese mice were insensitive to it, with both types of the mutant having identical obese phenotypes, has been now confirmed with the discovery that the ob mutation is located in the gene encoding leptin, and the db mutation is located in the gene encoding the leptin receptor [12, 13, 19].

Effectiveness of administered leptin in normalising the metabolic parameters and reducing the body weight of ob/ob genetically obese mice was confirmed in three studies published simultaneously [20–22], which used either biologically active forms of recombinant leptin expressed in bacteria, or leptin purified from blood plasma. These studies also showed that there was no slimming effect of leptin on db/db mice [22, 23], confirming Coleman's idea [18] that in these mice the receptor for the lipostatic signal had mutated. Mice obese because of hypothalamic damage and mutants on the db locus showed increased ob-mRNA expression in adipose tissues [24], such as could be expected from secondary overexpression to compensate lack of sensitivity to leptin. It was finally concluded that leptin is a hormone generated in adipose tissue, present in the blood of the normal mouse and in human blood and able (at doses of 0.1 mg to 1 g/kg of body weight) to correct obesity in the ob/ob mouse, thus normalising its main metabolic parameters (glycemia, insulinemia) through effects on the CNS.

Based on anatomical and functional data, it appears that leptin exerts its effects on energy balance mainly by acting in the brain. Thus, intravenous leptin injection activates neurons in the arcuate, ventromedial and dorsomedial hypothalamic nuclei and in brainstem neuronal circuits implicated in the regulation of feeding behaviour and energy balance [25, 26]. Intracerebroventricular leptin injection inhibits food intake and decreases adiposity more potently than peripheral leptin administration [22]. However, there are several variants of the leptin receptor, resulting from differential db mRNA processing, distributed in many tissues outside the CNS [12, 13, 19], including adipose tissue, which could mediate direct effects of leptin in these tissues. For example, leptin stimulates lipolysis and the expression of fatty acid oxidation enzymes in isolated adipocytes, an effect that depends on the expression of functionally active leptin receptors in the cell membrane of these cells [27].

Besides its effects on food intake, leptin increases energy expenditure by activating thermogenesis; in particular, it increases norepinephrine turnover in thermogenic tissues [28] and favours the expression of uncoupling proteins [29–34]. Moreover, leptin also stimulates the rate of lipolysis and the expression of enzymes of fatty acid oxidation in adipose [27, 35] and pancreatic cells [29], causing a reduction of the triglyceride content of these cells which is not accompanied by a parallel release of fatty acids [27]. Taken together, these results suggest that leptin favours the internal consumption of fatty acids as thermogenic fuels.

Some of these effects of leptin appear to be direct (extraneural) effects, since they are seen in isolated cells or cells in culture [27, 29, 35] and depend on the expression of functionally active leptin receptors in the cell membrane [27]. The effect of leptin to stimulate thermogenesis is the basis of perhaps one of the most potentially interesting aspects of the exogenous administration of leptin, since it allows the maintenance of a high metabolic rate and a gradual and extensive elimination of fat reserves even under conditions of low energy intake (dieting) [36].

Initial data showed that leptin production reflects the size of fat depots, but more recently leptin production in non-adipose tissues such as murine [37] and human stomach [38], placenta [39, 40], skeletal muscle [41], and mammary epithelium [42] was reported. Brain was also suggested to be a source of leptin, based on arteriovenous differences in human studies [43], although actual expression of leptin has not been detected in human brain.

Leptin has diverse effects in addition to long-term regulation of body weight [9, 44]. In particular, leptin plays significant physiological roles in various aspects of reproduction in humans, and appears to be necessary for the maturation of the reproductive axis [45]. Leptin also exerts acute effects on glucose and lipid metabolism [27, 35]. Local leptin expression in the stomach could regulate satiety [37, see below], and leptin signalling in the intestine could be involved in the regulation of nutrient absorption and intestinal motility [46]. Leptin has also been implicated in the regulation of the cardiovascular and renal function and in the functioning of the immune system [47]. It may also play an important role in development, as suggested by the formation of leptin in placenta, widespread expression of leptin and its receptors in fetal tissues and stimulation of hematopoiesis and angiogenesis by leptin [39, 40, 48, 49].

In summary, the initial view of leptin as an anti-obesity hormone has changed to a more complex view: leptin is produced in a variety of tissues, it is targeted to a variety of tissues, and it is involved in the regulation of a variety of functions, including energy balance, metabolism, neuroendocrine and immune function, and development.

Satiety signals from the digestive system as indicators of external energy resources

The living organisms can accommodate to a wide variety of foods and eating habits – with meals varying in size, number and composition, taken at different times – and nonetheless maintain the right energy balance. This points to the existence of acute, finely tuned food intake control mechanisms, which are activated once food intake has begun. These control mechanisms are based on satiety signals triggered by food, which contribute to ending the meal [1].

Cholecystokinin (CCK) is the best known and the most representative of the peptides secreted by the digestive tract during meals. Over 25 years ago it was shown that, when administered to rats before meals, CCK causes a dose-dependent reduction of food intake [50]. Since then, the role of this intestinal peptide has been extensively studied, but there are others with similar effects, such as gastrin and the peptides of the bombesin family (bombesin, gastrin-releasing peptide, neuromedin B) and the glucagon family. Satiety peptides combine with other signals, e. g. physical signals such as gastric distension, to synergistically reduce meal size. With regard to their therapeutic use in obesity treatment, pharmacological studies have shown that satiety peptides are generally well tolerated in humans [1, 51], although repeated administration does not seem to alter body weight, since their action is offset by more frequent meals [52].

Satiety peptides carry their signal to the CNS via peripheral nerves such as the afferent vagal fibres, or via the circulatory system, which allow these peptides to reach specific receptors in the brain.

# Leptin as a potential link between internal and external energy resources

Besides indicating the size of the body fat stores, leptin may help indicate that food is available. Thus, recently it was reported that the stomach of rats can produce and store leptin and release it into the blood in response to food intake, leading (in a few minutes) to an increase in plasma leptin levels [37]. Two satiety signals, CCK and gastrin, were found to stimulate the secretion of the leptin stored in the rat stomach [37]. More recently, we reported the presence of significant leptin levels in the stomach glands of the human [38]. Ultrastructural immunocitochemistry showed leptin immunoreactivity both in the pepsinogen granules of chief cells and in the granules of a specific endocrine cell type, suggesting the use of leptin in both endocrine and exocrine ways. Interestingly, in one of the patients studied (who did not follow the medical request before endoscopia and was not under food deprivation conditions) gastric glands appeared depleted of leptin. All together these findings suggest a role for gastric leptin and that leptin may mediate, at least in part, the satiety response produced by gastrointestinal peptides. Thus, leptin may somehow be linking acute and chronic regulation of feeding behaviour, connecting information from both external (food intake) and internal (fat stores) energy resources and the CNS (Fig. 2).

#### Resistance to the action of leptin in obese humans

If leptin plays a central role in regulating energy balance and body weight, its function is expected altered in the obese. By homology with the mouse, deficiencies in leptin production or leptin reception might cause energy imbalances and obesity in humans. However, leptin production

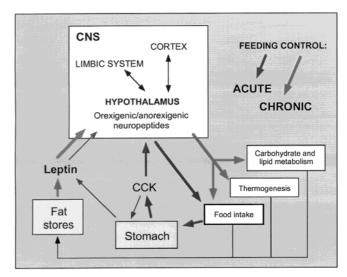


Fig. 2 General system of acute and chronic feeding control. Chronic feeding control depends on leptin released from fat stores, while acute control is based on gastric satiety peptides such as cholecystokinin (CCK). Leptin released from stomach in response to food intake may represent a link between acute and chronic control systems.

is not deficient in most obese humans, neither do frequent mutations of the leptin gene or the leptin receptor gene occur in humans (see below), so the alterations must be either in the transport of leptin to the CNS or in post-receptor events. These alterations will lead to a failure in leptin action that could be responsible for the hyperleptinemia, which is a general feature of obesity [53–58].

The first data reported from extremely obese humans indicated high levels of ob-mRNA expression in their fat depots, and that both the levels of leptin expression in adipocytes and the circulating leptin levels correlated positively with the degree of obesity [53–58]. Since the expected response to increased leptin levels is a reduction of energy intake and an increase of energy expenditure, it follows that obese people are insensitive to their endogenous leptin.

In the majority of obese humans, the leptin (ob) gene is not mutated; actually, only two of the several thousand families studied were shown to have mutations that stop leptin production and are responsible for their familiar obesity [59, 60]. Changes in the leptin receptor (db) gene do not appear either to be a common factor in human obesity, except in the isolated case of a Kabyle family [61] in which this gene has mutated at a splicing site, so that the receptor lacks transmembrane and intracellular domains essential for signal transduction and is therefore not functional.

The transport of leptin into the CNS is a regulatory element to consider. Leptin is transported into the CNS by a saturable system located in the endothelial cells of the brain [62], which is encoded by one of the mRNA splicing variants (the smallest one) of the leptin receptor (db) gene

[63, 64]. In obese humans, high serum leptin levels are not matched by proportionally high levels of leptin in the cerebrospinal fluid, suggesting a causal relationship between a deficit in the transport system bringing leptin to the CNS and obesity [65], although this has not yet been fully established at the molecular level.

#### Regulation of leptin synthesis

Leptin expression is influenced by the status of fat stores, as evidenced by increased adipose *ob* mRNA and serum leptin levels in obese humans and other mammals [9] and by the existence of a correlation, at the adipocyte level, between fat content and leptin expression [55]. However, leptin production is not equal in the different adipose tissue depots, since each has a distinct ontogenic pattern of leptin expression [66].

Plasma leptin levels are higher in women than in men [67], are subjected to daily rhythms in both sexes [68], and they drop with fasting and increase with food intake [36].

Insulin plays a key although indirect role in the leptin system. The administration of insulin stimulates leptin expression [69], but it takes several hours for this increase to be reflected in the circulating leptin levels [70]. Leptin and insulin have marked similarities as signals since the concentration of both of them is proportional to the degree of obesity, both reach the brain via saturable systems located in the endothelial cells, and both act on hypothalamic receptors, triggering similar responses [1]. Moreover, secretion of both insulin and leptin depends on the level of energy reserves of the organism and immediate changes in the energy balance [1], including food intake [37]. However, several observations suggest that leptin has a more important role than insulin in the central control of energy homeostasis [2]. For example, leptin deficiency causes severe obesity, with hyperphagia that persists despite high insulin levels. In contrast, obesity is not induced by insulin deficiency. In addition, in rats with pharmacologically induced insulin-deficient diabetes (that have low levels of both insulin and leptin), the administration of leptin at basal plasma concentrations prevents the development of diabetic hyperphagia, indicating that the latter is due to deficiency of leptin, rather than of insulin [71].

Leptin production in adipocytes is stimulated by certain cytokines in anorexia associated with infection [72] and by corticosteroids [73], whereas it appears to be suppressed by activation of the sympathetic nervous system (SNS), with intervention of the ß3-adrenergic receptors [74]. Secretion of stomach leptin, on the other hand, is stimulated by two satiety signals related to food intake, CCK and gastrin [37]; the latter was also found to activate leptin expression and secretion in rat adipose tissues, through activation of an adipocyte gastrin/CCK-B receptor [75].

UDP-N-acetylglucosamine (UDP-GlcNAc), the end product of the hexosamine biosynthetic pathway, may be

the metabolic intermediary responsible for stimulating the expression, synthesis and secretion of leptin in adipocytes and muscle cells [41]. The effect could be mediated by the n-acetylglycosylation of proteins that positively regulate leptin gene expression. UDP-GlcNAc accumulates in conditions in which flow through the hexosamine biosynthetic pathway increases, as for example after blockage of glycolysis due to an increase of intracellular fatty acid levels. Thus, UDP-GlcNAc could link the specific energy status of each cell with its leptin production [41].

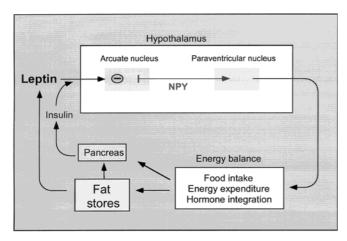
Organisation of feeding control in the central nervous system

Neuronal circuits organised in the arcuate nucleus (ARC) of the hypothalamus have highly specialised roles in energy homeostasis [2]. The ARC is a collection of neuronal cell bodies occupying approximately one-half of the length of the hypothalamus, to the floor of the third ventricle. Two orexigenic neuropeptides, NPY (neuropeptide Y) and AGRP (Agouti-related peptide) are co-localised in ARC neurons [76, 77]. The anorexigenic peptides POMC (proopiomelanocortin) and CART (cocaine-amphetamine related transcript) are co-localised in a distinct, but adjacent, subset of ARC neurons [78]. A majority of both NPY/AGRP and POMC/CART neurons coexpress leptin receptors [79, 80] and both types of neurons are regulated by leptin, but in an opposing manner. Conditions characterised by reduced insulin or leptin levels activate NPY/AGRP neurons [76, 77, 81-83] and inhibit POMC/CART neurons [78, 84-86]. Taken together, these findings indicate that the ARC is a major site for transduction of adiposity signals into a neuronal response [2]. Other hypothalamic areas which are richly supplied by axons from ARC neurons such as the paraventricular nucleus (PVN), zona incerta, perifornical area and lateral hypothalamus (LH) may also participate in the energy homeostasis circuit [87, 88]. The link between the LH and the higher centres of the brain which regulate hunger and satiety is an important aspect of the regulatory system, and two types of neuropeptides associated with neurons apparently exclusive to the LH have been characterised: the MCH (melanin-concentrating hormone) [89] and the orexins [90, 91].

#### *The neuropeptide Y pathway*

Leptin, acting through its hypothalamic receptor, determines a suppression of NPY expression and release, leading to a decrease in food intake and an increase in metabolic activity (Fig. 3). This was the first hypothalamic pathway for leptin action that was suggested after the leptin gene was cloned [82].

NPY is a well-known potent stimulator of food intake



**Fig. 3** The NPY pathway. Feedback regulation of body fat stores integrating the action of leptin, secreted by the adipocytes, and insulin, secreted by the endocrine pancreas, both acting in the brain controlling energy balance via a mechanism that likely involves inhibition of NPY.

when injected directly into the brain [92]. The action of NPY is channelled via the parasympathetic nervous system, producing hyperinsulinemia and an increase in glucocorticoid production, leading to an accumulation of fat in the adipose tissue, and reduced thermogenesis and muscular uptake of glucose. In conditions associated with weight loss or with a negative balance, such as caloric restriction, lactation and intense exercise, the NPY pathway becomes activated, causing increased appetite. This is a response mediated, at least in part, by a reduction of the negative feedback from leptin, with possible intervention of changes in insulin sensitivity [1, 93].

Central injection of NPY virtually evokes all features of leptin deficiency, including hyperphagia, hyperinsulinemia with insulin resistance, and decreased thermogenesis [1], and repeated NPY central injection produces obesity within a matter of days [92]. In ob/ob mice (which lack functional leptin and have high levels of NPY), the knockout of the NPY gene attenuates the degree of obesity [94], demonstrating the importance of the pathway; however, these mice display nonetheless a severe obesity and they respond normally to the satiety effects of leptin, indicating that, in addition to NPY, other downstream components must be involved in the leptin pathway.

NPY acts via Y1, Y2 and Y5 G-protein coupled receptors expressed in hypothalamic neurons. The Y5, and also the Y1, receptors mediate the stimulatory effects of NPY on food intake [95]. The Y2 receptor, on the other hand, appears to mediate an inhibitory effect of NPY at low concentrations that could be important for basal control of body weight, in view that Y2 null mutant mice developed both increased food intake and body weight [96]. The action of NPY on its receptors can be affected by other neurotransmitters, such as GLP–1 (glucagon-like peptide–1),

which inhibits food intake and diminishes the orexigenic effect of NPY, probably by antagonising NPY receptors Y5 and Y1 [97]. NPY receptors are a main focus of research in the development of new drugs for controlling appetite.

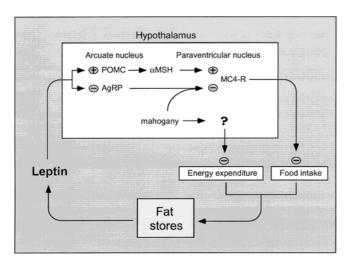
The glucocorticoids produced in the adrenal cortex participate in energy regulation potentiating the NPY orexigenic pathway, probably as endogenous antagonists of leptin and insulin [1]. Thus, adrenalectomy attenuates the effect of fasting to increase both appetite and NPY expression, and potentiates the anorexigenic and slimming effects of insulin and leptin, and these effects are offset by administration of glucocorticoids [1].

The agouti gene and the MC4 melanocortin receptor pathway

Several dominant mutations in the agouti (Ay) gene cause obesity, yellow colouring and a non-insulin dependent form of diabetes mellitus in mice. All these mutations give rise to generalised expression of the agouti protein in tissues in which it is not normally expressed (it is normally found only in the hair follicles of the skin) [98]. The agouti protein antagonises various melanocortin receptors, and it normally functions as an antagonist of the cutaneous MC1 melanocortin receptor (MC1-R), thus inhibiting pigment synthesis (hence the yellow coat colour of the agouti mutants) [99]. The agouti protein is also a specific antagonist of the MC4 melanocortin receptor (MC4-R), which is expressed primarily in the hypothalamus and other areas of the brain, and this antagonistic action could cause obesity, since melanocortinergic neurons have been shown to exert a tonic inhibition on food intake [100]. Thus, chronic blockage of this inhibitory (anorexigenic) signal – owing to ectopic agouti production within the brain – seems to be the most logical explanation of the agouti obesity syndrome (Fig. 4).

At the MC4-R a regulatory system would therefore be established, with two types of opposing binders: agonists (melanocortins, in particular the melanocyte-stimulating hormone, αMSH), with anorexigenic action, and antagonists (proteins similar to that encoded by the agouti gene but normally expressed in the brain, like the Agouti Related Peptide, AGRP [101]), with orexigenic action. This hypothesis is supported by sound experimental evidence, such as the fact that genetic knock-out of the MC4-R causes obesity similar to that of the Ay mouse but without affecting pigmentation [102], and the observation that food intake is reduced after central administration of a MC4-R agonist (\alpha MSH) and increased after administration of a synthetic antagonist of this receptor [100]. In addition, mutations in the MC4-R gene have been shown to cause obesity in humans [103].

 $\alpha$ MSH is formed from pro-opiomelanocortin (POMC) in arcuate nucleus (ARC) neurons that express the leptin receptor and project their axons (containing  $\alpha$ MSH) to



**Fig. 4** The MC4-R pathway. A model of leptin action in the hypothalamus throughout the MC4-R melanocortin receptor pathway. Leptin positively regulates POMC (the precursor of  $\alpha$ MSH), and negatively regulates AGRP. Neuronal release of  $\alpha$ MSH activates MC4-R and thereby reduces food intake. Conversely, reduced MC4-R signalling induced by AGRP causes hyperphagia and obesity. *POMC* pro-opiomelanocortin.

MC4 post-synaptic neurons in other areas of the hypothalamus. Production of  $\alpha$ MSH is potentiated by leptin, which stimulates the expression of POMC in the ARC neurons [84, 2]. AGRP is also characteristically expressed in the ARC and also appears to be regulated by leptin, but in an opposing manner, since its expression is stimulated by leptin deficiency, as in ob/ob mice [104, 2]. It is significant that overexpression of AGRP causes obesity similar to that of MC4 receptor knock-out mice [101].

The latter results establish a prominent role of the MC4-R pathway in leptin action. However, not all leptin action seems to be mediated through this pathway, since knockout or blockage of the MC4-R does not produce hypercortisolemia, or have any effects on the reproductive system such as those produced by leptin deficiency.

Another gene involved in energy homeostasis that appears to be related to melanocortin signalling is the mahogany gene. This gene is mainly expressed in neurons of the ventromedial hypothalamus, encodes a single-transmembrane-domain receptor-like protein, and its mutation can suppress diet-induced obesity [105] as well as the obesity and yellow-coat colour of the agouti mutant mice [106]. The mahogany protein normally functions to potentiate signalling from antagonists (like agouti protein and AGRP) on MC4-R [105]. Thus, the loss-of-function of the mahogany protein favours signalling from anorexigenic agonists (α-MSH) and can compensate for antagonist over-expression.

MCH and the orexins of the lateral hypothalamus (LH) participate in integrated appetite control

Two types of orexigenic neuropeptides located primarily in the LH have been described: the melanin-concentrating hormone (MCH) [89] and the A and B orexins [90, 91].

MCH neurons project from the LH to the nucleus of the solitary tract and the parabrachial nucleus, but they also have monosynaptic projections to the medial prefrontal cortex, which suggests that MCH may be involved in complex integrative behaviours. Renewed interest in MCH came from the observation that its mRNA is overexpressed in the hypothalamus of obese ob/ob mice compared with controls [89], and that MCH-knockout mice have reduced food intake and are excessively lean [107]. A G-protein-coupled receptor previously known as SLC-1 has been identified as the natural receptor of MCH [108]. This receptor is expressed in several brain regions, in particular those involved in olfactory learning and reinforcement mechanisms, further suggesting the involvement of MCH in the neuronal regulation of food consumption.

Two additional neuropeptides involved in the regulation of food intake were discovered simultaneously by two groups, the so-called A and B orexins [90], also known as hypocretins 1 and 2 [91]. Orexins are derived (by proteolysis) from a common precursor, and function through G-protein coupled receptors. Their expression seems to be limited to the neurons of the LH and nearby region, although there is also some expression in the testicles. Central administration of orexins stimulates food intake, and orexin production increases with fasting [90].

# Control of energy efficiency by adaptive thermogenesis

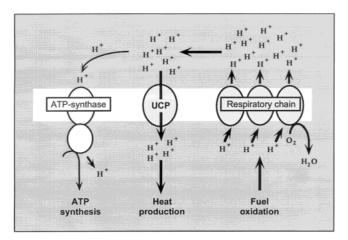
Although some energy is released as heat (thermogenesis) in all bioenergetic transformations, here we will refer only to adaptive or facultative thermogenesis mechanisms, which specifically function to produce heat in a physiologically regulatable manner. It is easy to see why the regulation of thermogenesis and the degree of efficiency in the utilisation of nutrients has become one of the main focuses of obesity research.

Almost everyone who is trying or has tried to lose weight envies those who seem able to eat whatever they like and stay slim. Higher or lower metabolic efficiency, with a substantial inherited component according to Bouchard's studies [109], may be the key. We have been familiar with the thermogenin or UCP of the brown adipose tissue (today UCP1) [110, 111] in small mammals for twenty years, and with UCP2 [112, 113] and UCP3 [114–116] in different tissues of rodents and humans since autumn 1997 [4]. This family of genes governs energy use during the mitochondrial oxidation of nutrients.

# The adaptive thermogenesis mechanism

The adaptive thermogenesis mechanism is well understood only in a particular type of adipose tissue, the brown adipose tissue (BAT), which, unlike the white, contains many nerve endings of the SNS, and it is very vascularised [3, 111, 117]. Also, brown adipocytes contain several vacuoles of fat instead of just one, are rich in mitochondria and contain a unique protein, the thermogenin or uncoupling protein (UCP1) [3, 111, 117]. The production of heat in BAT is stimulated by cold (CIT or cold-induced thermogenesis) and diet (DIT or diet-induced thermogenesis) [118, 119] and driving the mechanism is the UCP1, which is located at the inner mitochondrial membrane of brown adipocyte mitochondria, and whose function is to short-circuit the proton gradient generated by the oxidation of nutrients (mainly fatty acids) in the respiratory chain [111]. Finally, the energy obtained from nutrients is dissipated, in an adjustable way, as heat via the UCP1, instead of the proton gradient being channelled through the ATP-synthase and used in ATP synthesis (Fig. 5).

Up to now it has been possible to characterise this type of mechanism only in the BAT of mammals. However, results obtained by the group of Nagase [120] and in our laboratory [121, 122] have shown that the basic gene in this process, the one encoding UCP1, and thus probably adaptive thermogenesis, can appear in other tissues (white adipose tissue and muscle) with appropriate stimulus. Even more important, it has been shown that proteins similar to thermogenin, such as UCP2 [112, 113] and UCP3 [114–116], are expressed in a variety of non-BAT tissues (white adipose tissue, muscle and others). Several studies indicate that these UCPs also have proton transport activity [112, 113, 116, 123, 124]. This has opened up new possibilities and encouraged interest in adaptive thermogenesis, especially because these new UCPs are widely



**Fig. 5** The three conceptual elements involved in the function of the uncoupling proteins: fuel oxidation, energy dissipation and energy conversion. (Modified from [111]).

expressed in human tissues. However, the *in vivo* function of these UCP homologues, with respect to thermogenesis and regulation of mitochondrial energy metabolism, is presently uncertain [125], and it is an active area of investigation (see appendix). A so-called UCP4 has also been described [126, 127]; it is present in the brain but its homology with UCP1 is poor and its function unknown.

# Regulation of adaptive thermogenesis

Adaptive thermogenesis is deficient in almost all the animal models of obesity studied [117, 128]. In addition, when an animal model with low BAT content was developed (using the UCP1 promoter to direct expression of the A chain of the diphtheria toxin) transgenic mice with less BAT, marked obesity and increased susceptibility to develop diet-induced obesity were obtained [129].

The regulation of adaptive thermogenesis by exogenous factors depends primarily on stimulation of SNS, which densely innervates BAT [130]. In general, BAT thermogenesis can be regulated through changes in the intrinsic activity of UCP1 (seconds), the quantity of UCP1 (hours), the number of mitochondria and adipocytes (days) or by generalised hyperplasia of the BAT (days/weeks) [130, 131]. Norepinephrine (NE) released by the SNS has a major role on brown adipocytes, stimulating UCP1 activity and synthesis, and also cell division [111, 131]. NE increases UCP1 and UCP1-mRNA levels mainly by affecting transcription of the UCP1 gene [132, 133]; this effect is mediated mainly through  $\beta 3$  adrenergic receptor ( $\beta 3$ -AR) and an increase of the intracellular cAMP levels [132, 134, 135] and, to a lesser degree, through the al adrenergic receptor [132]. A putative role for a recently described atypical β-AR, named β4-AR, has also been suggested [136]. In addition NE has an effect in potentiating the stability of UCP1-mRNA [137], and increasing UCP1 protein half-life [138]. Besides NE, triiodothyronine (T3) also stimulates UCP1 transcription, depending on the function of type II tyroxine 5'-desiodase in the brown adipocytes, the activity of which is increased by NE [139].

Actual activation of thermogenesis basically depends on the presence of fatty acids, which directly act on UCP1 stimulating its proton transport activity and also serve as the main thermogenic fuel. The availability of fatty acids depends in turn on cAMP levels and adrenergic regulation [111].

In laboratory animals, long-term overfeeding with the so-called cafeteria diet – a variety of energy-rich, palatable foods, offered in excess quantities [composition and other details in 140, 141] – is accompanied by hyperplasia of BAT and increased UCP1 levels [142–144], and also of UCP2 mRNA expression [144], a response that confers a relative protection against the development of obesity (hypothesis first put forward by Rothwell and Stock [118]). In fact, an impairment of this DIT response was seen in fe-

male rats, which gained more weight than male rats after cafeteria diet feeding [144]. Although cafeteria diet-induced overweight is usually lost when the animals are put back on a normal diet, we have observed that under certain conditions (prolonged feeding of a cafeteria diet during the period of development) a persistent dietary obesity can develop, with changes in the thermogenic mechanism and other biochemical parameters [141, 142, 145, 146].

Studies carried out in our laboratory show that different mitochondrial subpopulations, which likely represent different stages of mitochondriogenesis, display different thermogenic capacity [147–150] and point to the importance of the regulation of mitochondrial biogenesis in obesity. Changes in the control of mitochondrial turnover may be an important factor in the modulation of energy balance, although to gain a better understanding of these aspects more has to be learned about the genesis and recycling of mitochondria in BAT and other tissues.

In summary, adaptive thermogenesis represents a chapter of energy expenditure of critical importance in the overall energy balance, and considerable interest has been raised on uncoupling proteins as the target of antiobesity drugs or treatments aimed at enhancing thermogenesis. Several questions are still waiting for answers, in particular, what are the physiological roles of UCP2 and UCP3, and also whether other mechanisms independent of BAT and of the uncoupling protein systems are dominant components in human thermogenesis. The knowledge of such mechanisms and their integration in the complex apparatus controlling body weight should help in designing new strategies against obesity and its complications.

#### **Adipogenesis**

When considering the possible causes of obesity (and increased fat deposition in localised zones) the factors that regulate the number of adipocytes and their maturity and differentiation should be taken into account. Moderate obesity results mainly from an increase in the size of the adipocytes due to increased triglyceride content (hypertrophic obesity), while more extreme obesity, or obesity which occurs at an earlier age, also implies an increase in the number of adipose cells (hyperplastic obesity) [151, 152]. The capacity to make new adipocytes continues throughout life, and can be activated by the size, frequency and composition of meals, and by other environmental factors.

The adipocyte cell line derives from a multipotent embryonic precursor, which can differentiate into various types of mesodermic cells [151]. In recent years, a great deal has been learned about the bases of differentiation and gene expression in adipocytes; in particular transcription factors which promote adipogenesis have been identified. These factors belong to three families: C/EBP, PPAR and ADD (or SREBP) [reviewed in 5, 6, 151].

The C/EBPs are a family of basic leucine zipper transcription factors; two members of this family, C/EBPβ and C/EBP $\delta$ , are induced early in the adipogenesis program, in response to hormonal stimulation, and they cooperate to induce the expression of another transcription factor PPARy, which is a key activator of the entire adipogenesis program [5, 6], capable of promoting not only the conversion of fibroblasts into adipocytes [153], but also the transdifferentiation of committed myoblasts into adipocytes [154]. PPARs (peroxisome proliferator-activated receptors  $\alpha$ ,  $\beta$ and  $\gamma$ ) are a subfamily of the nuclear hormone receptor superfamily that form heterodimers with retinoid X receptors (RXRs); the heterodimeric complexes recognise and bind to particular sequences in target genes and activate transcription upon ligand binding [155]. One of the two isoforms of PPARy, PPARy2, is characteristically expressed in fat cells and, after ligand activation, functions as a direct regulator of many fat-specific genes such as the adipocyte fatty acid-binding protein (aP2) and phosphoenolpyruvate carboxykinase genes [152]. Given the central role of PPARy in adipocyte development (and also in glucose homeostasis), PPARy is seen as a target for new drugs to control obesity-related metabolic disorders.

PPARγ can be activated by a variety of synthetic ligands including clofibrate, ETYA, Wy 14643 and antidiabetic drugs of the tiazolidinedione group [5], and by natural metabolites such as one prostaglandin of the J series (15-deoxy-Δ 12, 14- prostaglandin J2) [156, 157] and certain eicosanoids and polyunsaturated fatty acids [158]. It appears that the endogenous ligand must be a fatty acid derivative, and that a member of the ADD/SREBP (adipocyte determination differentiation, also known as sterol regulatory element binding protein) family of transcription factors, ADD1/SREBP1, which specifically regulates aspects of cholesterol and fatty acid metabolism, plays a key role in the generation of the endogenous ligand of PPARγ[159].

A recently described co-activator of PPARy, named PGC-1 [160], could be important in the developmental bifurcation between white and brown fat cells [3, 5]. PGC-1 is highly expressed in brown but not white fat, and also expressed in other tissues such as heart, kidney, brain and skeletal muscle. This factor was initially connected to adaptive thermogenesis because of its marked and rapid induction in BAT and in muscle upon cold exposure of mice. In addition to PPARy, PGC-1 also binds to a variety of other nuclear receptors including the retinoic acid and thyroid hormone receptors, both of which positively regulate expression of UCP1 [111]. Ectopic expression of PGC-1 in cultured cells activates and co-ordinates multiple aspects of the adaptive thermogenesis programme. Mitochondrial biogenesis is induced, and also many genes of the electron transport system and the expression of UCPs, in a cell-selective manner [161]. UCP1 but not UCP2 or UCP3 is induced when PGC-1 is introduced into white fat cells, whereas UCP2 but not UCP1 or UCP3 is induced when PGC-1 is expressed in muscle cells. In both fat and muscle cells, these changes in gene expression are reflected in increased respiration, both coupled and uncoupled [161].

A third member of the C/EBP family, C/EBPα, is also involved in adipogenesis. Ectopic expression of C/EPBα at high concentrations can stimulate adipogenesis in many types of fibroblastic cell lines [162]. However, C/EBPα is unlikely to be a primary signal in adipogenesis, since it is induced late during this process, following PPARy induction. C/EBP\alpha does play a role, however, in maintaining terminal differentiation, probably through its interaction with the tumour suppressor retinoblastoma protein (pRB), according to a hypothesis put forward in 1994 by our group [163]. Thus, we have shown that the expression of pRB increases during differentiation of adipose cells and have demonstrated a physical and functional interaction between pRB and C/EBPα that is linked to the expression of adipocyte marker genes, such as UCP1 in brown adipocytes [163–165].

In summary, the conversion of pre-adipocytes into mature adipose cells follows a series of linked steps:

- Stimulation of C/EBPβ and C/EBPδ expression by hormonal stimulation.
- Activation of PPARγ expression mediated by C/EBPβ and C/EBPδ, and production of the PPARγ endogenous ligand, stimulated by ADD1/SREBP1.
- Increase in insulin sensitivity and progress in differentiation, stimulated by activated PPARγ.
- Induction of C/EBPα and pRB expression, required for terminal differentiation and for maintenance of the differentiated phenotype.

### A further look at the obesity genes

Obesity represents the archetype of phenotypic complexity [166]: body weight can be affected by very diverse factors that affect the size and composition of any tissue, organ or individual system in our organism.

Several simple mutations of individual genes that cause obesity have been identified in laboratory animals (see monogenic obesity in Table 1). The situation in humans is much more complex. The most common forms of human obesity depend on the interaction of many genes (Table 1 and Fig. 1), environmental factors, behavioural habits and lifestyle.

Only a small set of concrete mutations causing human obesity are known, each one representing a tiny percentage of obesity cases, but could be the object of a very specific therapeutic treatment. However, more than 200 genes and other markers associated or linked with human obesity phenotypes have been identified [167, 168]. A future goal will be to look at the roles they play, together with other genes not yet discovered.

Study of candidate genes

One of the strategies of current research is to identify and characterise candidate genes. These are genes identified on the basis of the obesity that their alteration causes in animals, or genes suspected to be linked with some physiological process on which obesity depends.

Simple mutations that cause obesity have only been found in a few human families. These include two families with defects in the ob (leptin) gene [59, 60], and one family with a mutation in the db (leptin receptor) gene [61]. A mutation in the prohormone convertase 1 gene was found associated with obesity in a single female [169]; this abnormality is related to that caused in the rat by the fat (carboxypeptidase E) mutation, which leads to defective processing of several neuropeptides and prohormones [169]. Mutations in the MC4-R gene [103] and the POMC gene [170] also cause obesity in humans, reflecting the importance of the melanocortin system in the control of human body weight. The individuals with loss-of-function POMC mutations are not only obese but they also display altered pigmentation and adrenal insufficiency because of the absence of aMSH and ACTH, melanocortin agonists for MC1-R and MC2-R, respectively [168, 170]. Taking into account the low incidence of these mutations in humans, their study does not directly address genetic causes in the population as a whole, but it provides important insight into the underlying physiological pathways.

In addition, some interesting associations have been described between obesity and/or obesity-related traits and the presence of polymorphic markers in or around certain genes. In Mexican-Americans, for example, the sum of skinfolds was statistically associated with a fragment close to the leptin gene on chromosome 7 [171]; also, body mass index (BMI) was associated with markers of the leptin chromosomal region [172]. A recent study has shown the linkage of serum leptin levels with chromosome 2 at band 21 in a population of African-Americans [173]. Interestingly, this region of chromosome 2 includes the POMC gene, the loss-of-function of which results in monogenic obesity in mice and humans [170].

Certain mutations of the \$\beta\$-adrenergic receptors also appear to be related to obesity. Thus, the Trp64Arg \$\beta 3-AR\$ mutation that occurs frequently in the Pima Indian population [174] – a group with high incidence of obesity – and in other human populations [174–176] is significantly associated with a certain predisposition to obesity and its complications. Specifically, this mutation is associated with a lower metabolic rate and various characteristics of the insulin resistance syndrome: increased BMI, abdominal adiposity, hyperinsulinemia, increased blood pressure and earlier appearance of diabetes. However, these results do not hold for all the populations studied [e. g. 177] and it is accepted that this \$\beta 3-AR\$ mutation cannot be a major determining factor in the predisposition to obesity. In addition, a clear association has been established between poly-

**Table 1** The main gene products and other mediators involved in obesity

1. Monogenic obesity		MCH	Melanin-concentrating hormone
Ob, Lep	Leptin or OB protein	Anorexigenic peptides:	
Db, LepR	Leptin receptor	Lep, Ob	Leptin, OB protein
Ay, ASIP	Agouti protein and related proteins	POMC	Pro-opiomelanocortin
Tub	Tubby hypothalamic protein	αMSH	α Melanocyte-stimulating hormone
Fat, CPE	Carboxypeptidase E	CART	Cocaine-amphetamine related transcript
PC1	Prohormone convertase 1	IGF-I and II	Insulin-like growth factors
POMC	Pro-opiomelanocortin	MOT	Motilin
MC4-R	Melanocortin-4 receptor	BOM	Bombesin
		OXT	Oxytocin
2. Adipocytes and peripheral thermogenesis		NTS	Neurotensin
ß3AR	ß3-adrenergic receptor	TRH	Tyrotropine releasing hormone
ß2AR	β2-adrenergic receptor	CRH	Corticotropine releasing hormone
UCP1	Uncoupling protein 1	SOM	Somatostatin
UCP2	Uncoupling protein 2	CCK	Colecistokinin
UCP3	Uncoupling protein 3	NPK	Neuropeptide K
PKA	Protein kinase A	GLP-1	Glucagon-like peptide-1
LPL	Lipoprotein lipase	Neurotransmitters in the CNS:	
PPARγ2	Peroxisome proliferation activated receptor γ 2	5HT	Serotonin
PRB	Retinoblastoma protein	NE, NA	Norepinephrine
C/EBPs	CCAAT/enhancer binding proteins	DPM	Dopamine
$TNF\alpha$	Tumor necrosis factor α	Trp	Tryptophan
		5HTP	5-hydroxytryptophan
3. Feeding control		3.2. Short-term feeding control (satiety digestive peptides)	
3.1. Chronic feeding control		CCK	Colecistokinin
Orexigenic peptides:		GAST	Gastrin
NPY	Neuropeptide Y	GLP	Glucagon
GAL	Galanin	NMD	Neuromedin
ßEND	ß-Endorphin	BOM	Bombesin
DNF	Dinorphine	LEP	Leptin, OB protein
GH-RH	Growth hormone releasing hormone	3.3. Main receptors linked with feeding control	
OREX	A and B orexins, hypocretins 1, 2	MCH-R, MC4-R, Y5, Y1, CRH-R, GAL-R, OREX-R, GH-R,	
ART, AGRP	Agouti-related peptides	CCK-A-R, GLP-1-R, LepR, Mahogany.	

morphic variants of the \( \beta 2-AR \) gene and a predisposition to obesity, the level of energy expenditure and the lipolytic rate [178–181].

A linkage between obesity and polymorphic markers in the genes encoding uncoupling proteins has also been described. A greater tendency to gain weight and to have a lower metabolic rate associated with the presence of one of the two main alleles of the UCP1 gene in humans was first reported in 1994 [182]. This genetic variant of UCP1 was also associated with weight loss resistance [183]. More recently, it has been shown that UCP1 polymorphisms of the UCP1 gene, and also of the LPL and \( \beta \)-AR genes, are more closely linked with the medical complications of obesity than with obesity per se, with variants of individual genes or combinations of these being associated with the incidence of risk factors [184]. Also, in French Canadians, an area around the UCP2 gene on the D11S911 chromosome was found to be linked with the basal metabolic rate, BMI and the percentage of body fat [185]. In any case,

variants of thermogenic genes do not appear to be the main cause of widespread obesity, although they may be partly responsible for it and for related medical complications.

# Prospecting or unspecific genomic scanning

This means investigating the genotypical association between obesity and a series of polymorphisms, located at regular intervals on the genome, e. g. using some 300 markers, with no prior indication that they could be linked with obesity [166]. The results allow the identification of chromosomal regions or, in some cases, candidate positional genes. Inter alia, an association has been described between obesity and two interesting regions of chromosomes 2 and 8, which are very significant: a region of chromosome 2 that includes the gene encoding POMC [186] – which is the precursor of various hormones some directly related with feeding behaviour, such as αMSH – and a re-

gion of chromosome 8 which contains the gene for the  $\beta$ 3-AR [187].

# Future trends and therapeutic implications

The extraordinary progress made in the molecular understanding of the mechanisms regulating body weight is paving the way for new methods of obesity treatment, especially pharmacological but also nutritional and possibly involving genetic intervention.

Some drug-based strategies to combat obesity are foreseen. Table 2 lists the basic pharmacological agents that are now or will shortly be available. It also lists possible genes and basic compounds that are the subject of extensive research and pharmacological development. However, given the complexity of the metabolic network controlling energy balance, the idea of having just one drug to control weight in the majority of obese people looks unrealistic. At any case, some strategies can be outlined [188]: 1) inhibi-

 Table 2 Potential types of anti-obesity drugs (and their specific targets)

#### 1. Inhibitors of food intake:

Up-regulators of neurotransmitter levels (serotonin, norepinephrine, dopamine) in the CNS.

Agonists of receptors such as LepR, MC4-R, CRH-R, CCK-A-R, GLP-1-R, Bombesin R.

Antagonists of receptors such as Y5, Y1, MCH-R, Gal-R, Orexin-R.

*Products developed:* Phenfluramine (withdrawn), Dexfenfluramine (withdrawn), Phentermine, Fen/Phen (withdrawn), Sibutramine.

# 2. Stimulators of energy expenditure (thermogenesis)

Activators of the expression or activity of UCPs and PKA. B3-AR agonists.

Products developed: none

#### 3. Activators of fat mobilisation

Agonists of LepR, ß3-AR, GH-R. Activators of PKA.

Products developed: Leptin

#### 4. Inhibitors of fat absorption

Products developed: Orlistat

tion of food intake, by blocking orexigenic signals or enhancing anorexigenic signals; 2) stimulation of energy expenditure, by enhancing the levels and activity of UCPs; 3) activation of fat mobilisation, while maintaining the body protein; 4) blocking nutrient absorption, particularly fat, as does the recently developed Orlistat [189–191], whose action inhibits pancreatic and digestive lipases, reducing the intestinal digestion of fats and, consequently, their absorption and use. In any case, these pharmacological approaches should be complemented with exercising, nutritional advice and behavioural advice for full success.

The nutritional approach to obesity should take into account not only the energy and/or plastic properties of foods, but also their selective effects on the expression of specific genes. Phenotypic expression – both the degree of obesity and various pathological manifestations – must depend to a great extent on the regulation of the obesity genes by exogenous factors, mainly diet. In our laboratory, we have described the positive effect of retinoic acid, an active form of vitamin A, on the thermogenic capacity of rodents [192, 193], and a similar effect of \( \beta\)-carotene and several other carotenoids [194], and certain fatty acids [195]. Knowledge of nutrients with greater thermogenic properties could be useful in designing diets to help control body weight.

The differentiating element in the future, especially as regards the dietary and pharmacological control of obesity, will be the knowledge of an individual's possible response depending on his/her genetic characteristics. It is paradoxical that as a rule excess weight in an obese person is not yet regarded as a specific, individual medical problem, except in cases where it has led to other pathological conditions. This may change considerably, to a more individual approach, on the basis of more direct knowledge of the mechanisms responsible for obesity, the genetic variants involved in each case and the different obesity types and possible complications associated to them.

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**Appendix** A direct evidence for a role of UCP3 in thermogenesis has been provided by Clapham et al. [125b]. They showed that male mice overexpressing human UCP3 in skeletal muscle are hyperphagic but they weigh less than their wild type littermates.

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