

*For debates***New insights into obesity genes****M. Guerre-Millo¹, B. Staels², J. Auwerx²**¹ U 177 INSERM, Institut Biomédical des Cordeliers, Paris, France² U 325 INSERM, Institut Pasteur de Lille, Lille, France

Obesity is a major health problem in industrialized societies and the prevalence is increasing. Most human obesities appear to have a significant genetic component, but the multifactorial nature of the disease has confounded efforts to identify the genetic factors involved. In the last few years, however, major progress has been made toward the identification of the genes contributing to obesity.

Mouse models of obesity

Mouse models of polygenic obesity: Using a statistical approach known as quantitative trait locus analysis in two mouse models of polygenic obesity, seven separate chromosomal loci linked to body fat have been mapped [1–3]. To our knowledge, none of the genes present at these loci has yet been identified, but it is expected that this approach will yield interesting results in the near future.

Genetic analysis of mouse models of monogenic obesity has been more successful, leading to the identification of five “obesity genes”: *agouti*, *fat*, *tub*, *ob* and *db*. This significant progress has been achieved by using the method of positional cloning.

Mutations at the agouti locus result in ectopic expression of the protein: At least two mutations at the mouse *agouti* locus (A^y and A^{vy}) are associated with adult-onset obesity. The mouse *agouti* gene was identified independently by two groups in 1992 [4, 5].

Agouti transcripts are normally expressed exclusively in the skin of neonatal mice, whereas they are detected in virtually all tissues in adult obese A^y mutants. This results from a large deletion which brings the coding region of the *agouti* gene under the control of a ubiquitous promoter [6]. Recent experiments with transgenic mice expressing the *agouti* cDNA under the control of the β -actin promoter confirmed that ubiquitous expression of the protein induces the obese phenotype [7, 8]. *Agouti* is a secreted protein, which shares homologies with toxins known to interact with ion channels. Indeed, it has been recently shown that intracellular free calcium concentrations are increased in cells incubated in the presence of the recombinant protein [9, 10]. *Agouti* is also known to antagonize the binding of the α -melanocyte stimulating hormone to its receptors, preventing the rise in cAMP normally induced by this hormone in melanocytes [11]. In humans, at variance with mice, the *agouti* gene is expressed in several tissues including adipose tissue [12, 13]. It is tempting to speculate that *agouti* has a direct effect on adipose cells. Excessive secretion could induce a decrease in cAMP levels, reducing lipolysis and favouring fat storage. Alternatively or concomitantly, by increasing calcium concentration, *agouti* has the potential to alter the signalling pathways of hormones involved in the regulation of fat storage. Such mechanisms could promote obesity if higher levels than normal of the *agouti* protein are secreted by the adipose cells.

The fat mutation results in the loss of carboxypeptidase-E activity: In 1995 a single base mutation was found to occur in the gene of the enzyme carboxypeptidase-E (CPE), in obese fat/fat mice [14]. This is associated with loss of CPE activity, leading to hyperproinsulinaemia which is one of the earliest phenotypic characteristics caused by the *fat* mutation. The relationship between this hormonal defect and the

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Abbreviations: CPE, Carboxypeptidase-E; PPAR, peroxisome proliferator activated receptor; PPRE, peroxisome proliferator response element; C/EBP, CCAAT enhancer binding protein; HMG, high mobility group.

later appearance of obesity remains unclear. To our knowledge, such a mutation in the CPE gene has not been reported in humans.

The tub mutation disrupts a gene of unknown function: The mutated gene responsible for the tubby obesity was identified in 1996 by two independent groups [15, 16]. A single base mutation in the gene abolishes a splice donor site, resulting in the replacement of 44-carboxy-terminal amino acids of the tub protein with 24 intron-encoded amino acids. Whether this induces a loss of function remains to be determined. The carboxy-half terminal of tub is similar to sequences previously cloned in various organisms, but nothing is known about their biochemical roles. Since *tub* mRNA is abundantly expressed in the hypothalamus, it is possible that the protein plays a role in the regulation of feeding behaviour and energy balance. A well-conserved human *tub* gene has been cloned [16], but it is not known whether mutations in this gene occur in obese humans.

The ob mutations result in the lack of leptin, whose receptor is encoded by the db gene: The mouse and human *ob* cDNA was cloned in 1994 and two mutations were discovered in *ob/ob* mice [17]. In the original strain, a single base mutation creates a premature stop codon resulting in the absence of the *ob* protein. The molecular basis for the second *ob* mutation is not known; however, it results in the absence of *ob* transcript, suggesting a promoter alteration. The *ob* gene, expressed exclusively in adipose tissue, encodes a new secreted protein, called leptin. Soon after the cloning of the gene it was demonstrated that daily injections of recombinant leptin induce a marked decrease in body weight and adipose tissue mass in *ob/ob* mice, diet-induced obese mice or wild type lean controls [18–20]. These observations conclusively demonstrate that leptin is an adipose-specific hormone, which plays a major role in the regulation of body weight.

The molecular mechanisms of leptin action are still poorly understood. Based on the data from previous parabiotic experiments [21], the effects of leptin were thought to be mediated by specific receptors encoded by the *db* gene. The cloning of the leptin receptor gene by virtue of leptin binding [22], followed by the demonstration that this gene is mutated in *db/db* mice [23, 24] brought clear evidence that *db* is the leptin receptor gene (*OB-R*). The *db* mutation causes an abnormal splicing of *OB-R*, which results in a receptor lacking a cytoplasmic tail. Two recent reports show that this short form of *OB-R* is unable to activate the signal transducers and activators of transcription involved in leptin signalling through the full-length *OB-R* [25, 26]. Although the tissue sites at which leptin exerts its action remain to be determined, the presence of full-length *OB-R* in the

hypothalamus [25] shows that this tissue is a target of the hormone. It is conceivable that leptin alters the expression of specific genes involved in energy homeostasis, like the hypothalamic neuropeptide-*Y*, which is a potent stimulator of food intake and whose synthesis is inhibited by leptin [27].

No evidence for a lack of leptin in obese people has been reported so far, although there are indications for linkage of the *ob* gene region with extreme obesity [28, 29]. In contrast, a positive correlation between body mass index and plasma leptin has been consistently observed, suggesting some kind of leptin resistance in obese humans. This potential syndrome does not appear to be due to defects in hypothalamic *OB-R* [30]. Thus, further detailed studies are needed to demonstrate the importance of leptin in the pathogenesis of human obesity.

Genes involved in adipose cell differentiation

In addition to the study of genes identified by the analysis of mouse models of obesity, significant progress has been made in research aimed at determining the factors involved in differentiation of adipose cells.

Transcription factors of the peroxisome proliferator activated receptor (PPAR) family: PPARs are members of the superfamily of nuclear hormone receptors which regulate the expression of genes possessing the specific response elements (peroxisome proliferator response element [PPREs]) in their regulatory sequences (reviewed in [31]). The pivotal role of PPAR γ in adipose differentiation has been demonstrated by the induction of an adipocyte phenotype in fibroblasts and myoblasts infected with a retroviral vector overexpressing the gene [32, 33]. This effect is likely to be due to an activation of several key adipocyte genes containing functional PPREs in their regulatory sequence [31]. Finally, several natural or synthetic PPAR γ activators, including fatty acids, prostaglandins and thiazolidinediones [34–37], have the potential to induce adipose differentiation through this transcription factor.

Transcription factors of the (C/EBP) family: C/EBP, which belong to the basic-leucine zipper superfamily of transcription factors, are also implicated in adipose differentiation. Arguments in support of a role of C/EBP α in adipose differentiation come from the temporal activation of C/EBP α expression before adipocyte specific genes [38], the capacity of antisense C/EBP α mRNA to inhibit differentiation [39] and the fact that premature induction or overexpression of C/EBP α triggers adipocyte differentiation [40, 41]. The important role of this factor in adipogenesis was confirmed in C/EBP α -null mice,

which failed to accumulate lipids in adipose tissue [42].

(HMG) DNA-binding proteins: HMGI-C is a member of the HMG family of DNA-binding proteins which are thought to play a role in chromatin conformation and hence, influence transcription. It was recently discovered that in benign tumours of adipose tissue, mutations in the HMGI-C gene result in the generation of fusion proteins with the HMGI-C DNA-binding domain linked to a transactivation domain, turning HMGI-C into a transcriptional activator [43, 44]. Furthermore, this gene is deleted in the mouse mutant *pygmy*, which is characterized by small size and disproportionately reduced body fat content [45]. Thus, the lack or reduced expression of HMGI-C could predispose to leanness, whereas the juxtaposition of the DNA-binding motif to transcriptional regulatory domains could promote adipogenesis.

Although major progress has been made into clarifying the basic role of transcription factors in adipocyte differentiation, major challenges lie ahead before this can be extrapolated to the human situation. Future research should determine whether altered function of certain of these factors might induce obesity, and if this is the case, find ways to overcome these potential defects.

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