

# Using Gene Knockout and Transgenic Techniques to Study the Physiology and Pharmacology of $\beta_3$ -Adrenergic Receptors

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**MANY** factors contribute to the regulation of energy balance: energy expenditure, food intake, brain, fat cells, hormones, etc. Because these various components are all interconnected, it has been difficult to determine the relative contribution of each to the pathogenesis of obesity. Mouse genetics offer two major tools useful for identifying the molecular mechanisms which regulate body fat content (Fig. 1). One general approach, positional cloning, involves going from an obese mouse to the responsible genetic defect. Over the past few years this approach has yielded much valuable information. The second general approach, gene targeting and transgenics, involves creating genetic mutations in mice, and then determining the effects of these mutations on regulation of total body fat content. This approach has also yielded significant advances.

During the past few years, all of the mouse single gene mutations which produce obesity have been identified (Table 1, reviewed in ref. [1]). The *ob* mutation causes deficiency of leptin, an adipocyte secreted hormone which communicates the status of fat stores to the brain, the *db* mutation disrupts the receptor responsible for transducing the leptin signal in the brain, the *fat* mutation abolishes carboxypeptidase E activity, the *tub* mutation

disrupts a hypothalamic protein of unknown function and the *A<sup>y</sup>* mutation leads to overexpression of *agouti*, an inhibitor of melanocortin receptors.

The mouse genome can be manipulated in two ways [2]. Transgenics involves the injection of DNA constructs into mouse zygotes to create gain-of-function mutations. Gene targeting, on the other hand, typically involves the creation of loss-of-function mutations in which genes are deleted, or “knockout out” from the genome. We have used both of these approaches to explore the regulation of energy expenditure in mice. One experiment involved the transgenic ablation of brown adipose tissue to create mice with diminished brown fat [3]. The other experiment involved knockout of the  $\beta_3$ -adrenergic receptor gene to create mice which completely lack  $\beta_3$ -ARs [4].

## Overview of Energy Balance, White Adipocytes and Brown Adipocytes

Shown in Fig. 2 is a simplified view regarding the regulation of body fat content, and the role of leptin [5]. Naturally, this is an oversimplification. Triglyceride is stored in white fat. Leptin is secreted from white fat in a manner that is proportional to the size of fat stores. Secreted leptin then communicates the status of fat stores to the brain. The brain then adjusts food intake and energy expenditure in order to maintain normal body fat stores. The brain controls energy expenditure, at least in part, via the sympathetic nervous system

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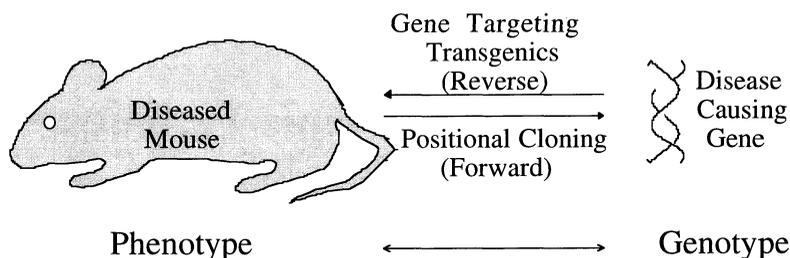


Fig. 1. Using mouse genetics to study obesity. For explanation, please see text.

Table 1. Cloning of mouse obesity genes

Mutation	Defect
<i>ob</i>	Leptin deficiency
<i>db</i>	Leptin receptor defect
<i>fat</i>	Carboxypeptidase E mutation (hormone processing defect)
<i>tub</i>	Hypothalamic protein of unknown function
<i>A<sup>y</sup></i>	Overexpression of agouti (Inhibition of melanocortin-4 receptor)

which innervates brown adipose tissue. Sympathetic stimulation of brown at markedly increase energy expenditure [6].

White and brown fat are similar in that they both contain triglyceride and express many genes which are involved in the handling of triglyceride. However, white and brown fat are completely different in function [6]. White fat stores calories while brown fat expends calories. Histologically, brown fat cells are smaller, and they tend to store lipid in a multilocular fashion. Also, brown adipose tissue is highly vascular while white adipose tissue is not. Brown adipocytes are also unique in that they have abundant mitochondria, a feature which is important for the expenditure of calories. Perhaps the most distinguishing feature of brown adipocytes, is that they uniquely express the mitochondrial protein called uncoupling protein or UCP [7, 8] (see Fig. 3).

Fuels are oxidized by means of the electron transport chain, creating a proton electrochemical potential gradient. Normally, protons descend this gradient via ATP synthase, coupling synthesis of ATP to fuel oxidation. However, if no work has been done, little ADP exists and protons cannot re-enter via ATP synthase. The proton gradient

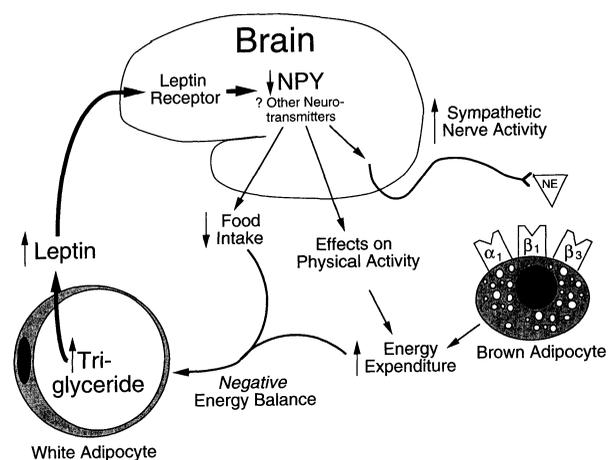


Fig. 2. Feedback loop controlling body fat stores. For explanation, please see text.

increases, electron transport slows and fuel oxidation decreases. Thus, in the absence of performing work, cells do not oxidize fuels. Fuel oxidation is "coupled" to the performance of work. Uncoupling protein, or UCP-1, causes the proton gradient to collapse by exporting free fatty acid anions which then function as cycling proton carriers [9, 10]. In essence, UCP allows FFAs to function like dinitrophenol, a classic mitochondrial uncoupler. In the uncoupled state, brown adipocytes oxidize fuels unrelated to the performance of work, the by-product being the generation of heat. Thus, stimulated brown adipocytes can expend enormous amounts of calories.

Recently, a new molecule has been identified, UCP-2 (Ricquier *et al.* GenBank Accession number U69135). It is a homologue of UCP-1 that is likely to function like UCP-1, given its amino acids similarity to UCP-1 (56% identity). However, unlike

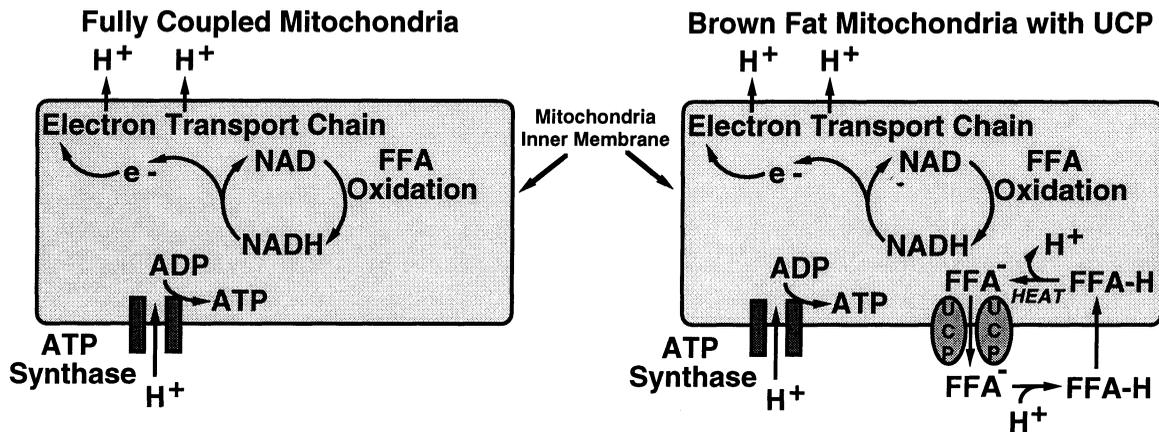


Fig. 3. Fully coupled mitochondria (left panel) and brown fat mitochondria uncoupled by UCP (right panel). For explanation, please see text.

UCP-1 it is widely expressed in mice and humans. Therefore, UCP-2 is likely to be an important determinant of total body energy expenditure. The role of UCP-2 in physiology and disease is presently under intense investigation.

### Transgenic Ablation of Brown Adipose Tissue

Some time ago we set out to assess the physiologic significance of brown fat by generating transgenic mice which have decreased brown fat [3]. To do this, the UCP-1 promoter, which is only expressed in brown fat, was used to drive expression of diphtheria toxin A-chain. Diphtheria toxin A-chain then kills brown adipocytes, thus creating mice with decreased brown fat. Of significance, mice with decreased brown fat develop obesity, strongly supporting the view that brown fat plays an important role in resisting the development of obesity in mice. More recently, we have demonstrated that transgenic mice with decreased brown fat have increased susceptibility to diet-induced obesity [11], thus supporting the hypothesis that brown fat protects against obesity caused by calorically dense diets.

### Knockout of the $\beta_3$ -AR Gene

$\beta_3$ -ARs are found predominately on brown and white adipocytes in rodents. Brown adipocyte activity is controlled by the brain via the

sympathetic nervous system. It is possible that mutations in the human  $\beta_3$ -AR could contribute to the development of obesity and there have been recent publications on this topic [12–14]. Finally, pharmaceutical companies have generated agonists which selectively stimulate  $\beta_3$ -ARs, and these  $\beta_3$ -agonists are potent anti-obesity drugs in rodents [15–17].

In order to address a number of issues, we have made gene knockout mice lacking  $\beta_3$ -ARs. To do this we have used the homologous recombination approach [4]. A targeting construct was generated in which the  $\beta_3$ -AR gene was rendered nonfunctional. This construct was then used to create  $\beta_3$ -AR gene knockout mice which lack intact  $\beta_3$ -AR mRNA and functional  $\beta_3$ -ARs. In general, these mice are phenotypically normal except for a small increase in total body fat content. If it is true that  $\beta_3$ -ARs play an important role in controlling brown fat activity, then one might have expected  $\beta_3$ -AR knockout mice to be markedly obese, which was not the case. Alternatively, other gene products might have compensated for the absence of  $\beta_3$ -ARs. Since  $\beta_1$  and  $\beta_2$ -ARs respond to the same endogenous ligands and utilize the same signaling pathway as  $\beta_3$ -ARs, it is conceivable that  $\beta_1$ - and/or  $\beta_2$ -ARs might have compensated for the absence of  $\beta_3$ -ARs. Indeed, we noted that  $\beta_1$ -AR mRNA was significantly upregulated in brown adipose tissue of  $\beta_3$ -AR gene knockout mice. Upregulation of a related family member, the  $\beta_1$ -AR, in response to knockout of the  $\beta_3$ -AR, strongly implies that  $\beta_3$ -ARs play an important role in controlling brown

adipose tissue function.

Acute treatment of mice with a  $\beta_3$ -selective agonist produces the following effects: 1) a 2-fold increase in energy expenditure, 2) a 50–100 fold increase in serum insulin levels, and 3) a 45% reduction in food intake. While the effects on energy expenditure are almost certainly mediated by  $\beta_3$ -ARs, the effects on insulin levels and food intake are less certain. To determine the role of  $\beta_3$ -ARs in mediating each of these response, control (+/+) and knockout (-/-) mice were treated with CL, a  $\beta_3$ -selective agonist. If the response to CL disappears in knockout mice, then it is assumed that that response is mediated by  $\beta_3$ -ARs.

#### *Effect of CL on oxygen consumption*

CL increases the oxygen consumption of normal mice by about 2-fold. This is a rather dramatic increase in energy expenditure and demonstrates the marked anti-obesity action of these agents in rodents. No effect was observed in knockout mice. Thus stimulation of oxygen consumption by CL is mediated entirely by  $\beta_3$ -ARs.

#### *Effect of CL insulin levels*

In normal mice, insulin levels dramatically increase by 50–100 fold following the acute administration of CL [4, 18], or other  $\beta_3$ -AR selective agonists [19]. In knockout mice, no effect was observed. Thus, stimulation of insulin secretion by CL is mediated entirely by  $\beta_3$ -ARs. However, the mechanisms for this response is not known. Of note,  $\beta_3$ -ARs are not thought to be present in pancreatic islets. Thus, it is possible that  $\beta_3$ -ARs on adipocytes somehow mediates this response.

#### *Effect of CL on food intake*

In normal mice, acute CL treatment suppresses

food intake by about 45%. No effect was observed in knockout mice. Thus, inhibition of food intake by CL is mediated exclusively by  $\beta_3$ -ARs. However, the mechanism for this effect is also unknown.

To summarize, acute treatment with  $\beta_3$ -selective agonists produces the following responses: 1) a 2-fold increase in oxygen consumption, 2) a 50–100 fold increase in insulin levels, and 3) a 45% inhibition of food intake. We have shown that each of these responses are mediated exclusively by  $\beta_3$ -ARs. Questions to be addressed include: 1) What is the role of *adipocyte* versus *non-adipocyte*  $\beta_3$ -ARs in mediating each of these responses?, and 2) What is the role of *white* versus *brown* adipocyte  $\beta_3$ -ARs in mediating each of these responses? To answer these questions, we have created mice which express  $\beta_3$ -ARs selectively in white and brown adipose tissue, or in brown adipose tissue only. These animals will be used in the future to delineate the precise the role of  $\beta_3$ -ARs in these sites in mediating each of these responses.

In a related series of experiments, we have also created mice that express human but not murine  $\beta_3$ -ARs. Prior studies have documented that rodent and human  $\beta_3$ -ARs respond differently to a number of  $\beta_3$ -selective agonists. Therefore, convenient animal models suitable for *in vivo* testing of  $\beta_3$ -selective agonists do not exist. To address this issue, we have transgenically introduced 74 kb of the human  $\beta_3$ -AR genomic locus into  $\beta_3$ -AR knockout mice. These animals express human but not murine  $\beta_3$ -ARs selectively in brown adipose tissue. "Humanized"  $\beta_3$ -AR mice should assist in the evaluation of effective  $\beta_3$ -selective agonists. In addition, these animals will provide a basis for investigating promoter/enhancer elements which confer tissue specificity on human  $\beta_3$ -AR gene expression.

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