

The Molecular Control of Adipogenesis, with Special Reference to Lymphatic Pathology

EVAN D. ROSEN

Beth Israel Deaconess Medical Center, Boston, Massachusetts 02215, USA

ABSTRACT: Adipogenesis is the process by which mature fat cells are formed from pre-adipocytes. Adipogenesis has come under increasing scrutiny not only because the availability of reliable *in vitro* models makes it an attractive choice for developmental studies, but also because adipocytes are increasingly recognized as major players in a variety of physiological and pathophysiological states, such as obesity and type 2 diabetes. Adipocytes develop from mesenchymal stem cell precursors that are characterized by multipotency. Under the influence of various cues, these cells become committed to the adipocyte lineage. Further hormonal stimulation recruits these pre-adipocytes to accumulate lipid, express fat-specific markers, and become sensitive to the metabolic effects of insulin. A complex transcriptional cascade regulates this process, involving several distinct classes of transcription factor. In particular, the role of the nuclear hormone receptor PPAR γ will be discussed, along with bZip family members C/EBP α , C/EBP β , and C/EBP δ . The relationship of adipose depots to the lymphatic system will also be discussed.

KEYWORDS: adipogenesis; PPAR γ ; C/EBP; lymphedema; lymph nodes

WHY STUDY ADIPOGENESIS?

In the not-so-distant past, few tissues were felt to be as unworthy of study as adipose tissue. Fat has been routinely ignored and discarded by anatomists and physiologists, while the general public has invested adipocytes with more emotional baggage than any other non-neoplastic cell type. In the last decade or so, the tide has begun to turn in favor of adipose tissue as a subject of scientific inquiry. The reasons for this are threefold. First, the development of immortal preadipocyte cell lines by Green and colleagues in the 1970s has

Address for correspondence: Evan D. Rosen, M.D., Ph.D., Beth Israel Deaconess Medical Center, 99 Brookline Ave., Boston, MA 02215. Voice: 617-667-3221; fax: 617-667-2927. erosen@caregroup.harvard.edu

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made tractable the study of adipocyte development and physiology.^{1,2} There are few other developmental processes that can be reliably studied in a nearly synchronous population of cells *in vitro*. Compared to many other cellular lineages, fat cell differentiation *in vitro* is rather authentic, recapitulating most of the key features of adipogenesis *in vivo*. This includes morphological changes associated with lipid accumulation, cessation of cell growth, expression of many lipogenic enzymes, and establishment of sensitivity to most or all of the key hormones that impact on this cell type. The second reason for the recent surge in popularity of adipocytes is the recognition that these cells are far more than passive depots for energy storage. Fat is now known to secrete a wide variety of proteins that influence energy homeostasis (such as leptin and adiponectin),^{3–5} coagulation (such as PAI-1),^{6,7} blood pressure (such as angiotensinogen),⁸ and immune function (such as TNF- α , IL-6, adipon).^{9,10} These findings firmly establish fat as an endocrine organ to be reckoned with. Finally, the dramatic rise in the incidence of obesity and type 2 diabetes worldwide has also focused attention on the biology of the adipocyte.¹¹

HOW DO ADIPOCYTES DEVELOP?

Adipose development is unusual in that it occurs *de novo* in multiple, anatomically distinct sites. Generally speaking, most adipose tissues form at sites rich in loose connective tissues, such as the subcutaneous layers between the muscle and dermis. However, fat deposits form in many locations, such as around the heart, kidneys, and other internal organs. Older studies have described subcutaneous fat development in some morphological detail. In the absence of a clear molecular marker for pre-adipocytes, the earliest event associated with adipogenesis is a proliferating network of capillaries in an otherwise undistinguished region of loose connective tissue. These “primitive organs,” as they have been called, develop into *bona fide* adipose tissue.¹² These observations also point out a potentially important relationship between blood vessel development and adipogenesis. It is not clear, however, whether adipogenesis can induce angiogenesis, vice versa, or both.

Adipocytes develop from multipotent mesenchymal stem cells that can also give rise to muscle, bone, or cartilage^{13,14} (FIG. 1). In the developing fat pad, these cells become committed to the adipocytic lineage under the influence of “cues” that remain undiscovered. These cues might be hormonal interactions, or the result of cell–cell or cell–matrix interactions, for example. This process, called determination, results in a cell with fibroblastic morphology called a pre-adipocyte. Unfortunately, there are no known expression markers that absolutely identify a cell as a pre-adipocyte. Because of the complexity inherent in these systems, almost all work on adipogenesis has

utilized predetermined clonal cell lines, such as 3T3-L1 and 3T3-F442A. Upon reaching confluence, exposure to a regimen including dexamethasone, methylisobutylxanthine (a phosphodiesterase inhibitor), and insulin (DMI) leads to differentiation of these cells.

Adipogenesis occurs in both the prenatal and postnatal states in humans; in rodents, most fat cell development occurs postnatally. While older literature suggested that people are born with all the adipocytes they will possess in life, there is now convincing evidence that adipogenesis occurs throughout the lifetime of an organism. This adipogenesis occurs both as a consequence of normal cell turnover, and as a consequence of the requirement for additional fat mass that arises with significant calorie storage and weight gain.¹⁵ Indeed, while fat cell size can vary with the amount of lipid stored, there is a physical limit to how large these cells can become. On the other hand, humans and other animals will continue to gain fat as long as energy intake exceeds nutritional requirements, demonstrating a theoretical requirement for *de novo* differentiation of adipocytes. More convincing evidence has come from studies of rats fed a high-calorie diet, where [³H]thymidine incorporation into new fat cells occurs throughout adulthood.¹⁶ Whether this is true for humans is unknown, but it is clear that pre-adipocytes purified from the fat pads of even elderly people can be induced to differentiate *in vitro*.¹⁷⁻¹⁹ This observation argues for a role for both adipocyte hypertrophy and hyperplasia in human obesity.

HORMONAL AND ENVIRONMENTAL ASPECTS OF ADIPOGENESIS

The literature is rife with papers identifying extracellular and intracellular signals that control pre-adipocyte growth and terminal differentiation. The first agent noted to affect this process was insulin, the classic hormone of the fed state. Insulin increases the percentage of cells that differentiate and also increases the amount of lipid that each fat cell contains.²⁰ Recent data have shown that neutralization of insulin *in vivo* stimulates the apoptosis of fat cells,²¹ dramatically confirming the importance of this hormone in adipocyte biology. Glucocorticoids have also been used for many years to induce optimal differentiation of cultured pre-adipose cell lines and primary adipocytes. It is not as clear, however, if glucocorticoids are required for efficient adipogenesis *in vivo*; since patients with Cushing's syndrome (elevated circulating glucocorticoids, usually from a pituitary or adrenal source) show visceral obesity but wasting of subcutaneous fat.²² The effects of other hormones are also not completely understood. Growth hormone, for example, can clearly induce adipogenesis in a variety of cultured pre-adipose cell lines, but primary pre-adipocytes do not show this effect.²³⁻²⁵ In fact, differentiation of

these cells appears to be inhibited by growth hormone. This is consistent with the observation that humans with growth hormone deficiency have normal fat stores, and can, in fact, be obese. Thyroid hormone,²⁶ retinoic acid,²⁷ and various prostaglandins²⁸ are some of the wide variety of other hormones that have been shown to affect adipogenesis *in vitro*, but for which there is scant evidence to support such a role *in vivo*.

A variety of cytokines have been found to suppress fat cell differentiation. TNF- α , IL-1, and many other pro-inflammatory cytokines have this effect on most cultured pre-adipocyte lines, and in fact can “de-differentiate” already mature fat cells.^{29,30} Indeed, the suppression of adipocyte lipoprotein lipase was used to purify “cachectin,” which was then found to be identical to TNF- α .³¹ The precise molecular basis for these cytokine effects is still not known, though suppression of expression of several key transcriptional regulators of adipogenesis has been observed. In addition, several growth factors are rather potent inhibitors of adipogenesis, including epidermal growth factor (EGF), platelet-derived growth factor (PDGF), and fibroblast growth factor (FGF).³² Much of this inhibition is likely to be through activation of mitogen-activated protein (MAP) kinases (see below).

As might be expected from the wide array of hormones, cytokines, and growth factors that can affect adipogenesis, several different signal transduction pathways have been implicated in the process as well. There has been quite a bit of interest in the MAP kinase family of intracellular protein kinases. As just described, many growth factors that exert their influence through tyrosine kinase receptors inhibit fat cell differentiation. It is now clear that much of this inhibition occurs through activation of the “classic” MAP kinases, Erk 1 and 2. These kinases directly phosphorylate PPAR γ (see subsequent text), and inhibit its adipogenic activity.³³ The JNK MAP kinase can also phosphorylate PPAR γ at this inhibitory site.³⁴ In contrast, p38 MAP kinase has been associated with an activation of adipogenesis. Chemical p38 inhibitors and a dominant negative allele of p38 decrease fat cell differentiation, and overexpression of constitutively active MKK6, an activator of p38, enhance the process.^{35,36} The relevant targets of p38 are unknown at this time, but speculation centers on C/EBP β , an early actor in the adipogenic transcriptional cascade. Another kinase, Akt (also known as PKB) has been shown to be a downstream effector of certain of the metabolic effects of insulin. Interestingly, expression of a constitutively active form of Akt causes spontaneous differentiation of 3T3-L1 cells.³⁷ The experimental manipulation of cAMP, various G proteins, and protein kinase C isoforms have also been shown to affect adipogenesis *in vitro*.³⁸ A more thorough knowledge of the critical extracellular signals involved in fat cell development would better enable us to place these findings in their appropriate context.

Another environmental condition that affects adipogenesis is hypoxia, which inhibits the process. This effect seems to be mediated through

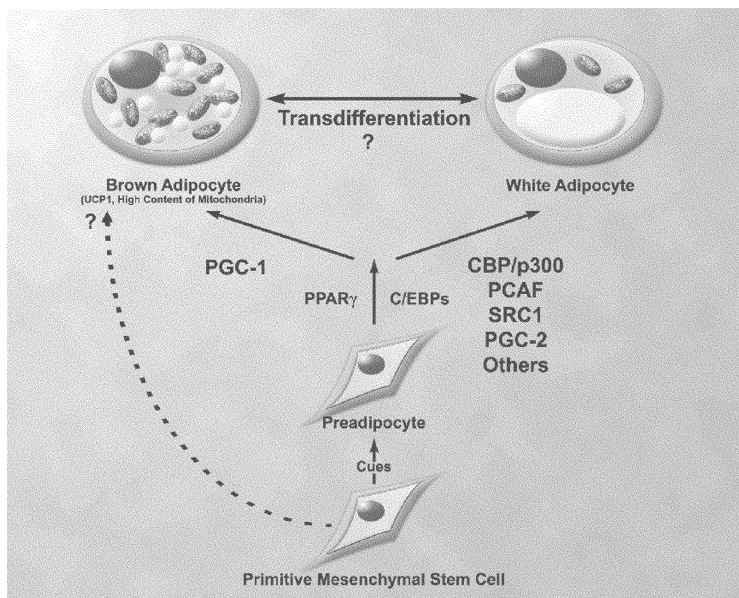


FIGURE 1. Adipogenesis proceeds from mesenchymal stem cells in two major steps. First, the multipotent stem cells become committed to the adipocytic lineage in a process called determination. Next, the committed pre-adipocytes fully differentiate through the concerted actions of a host of transcriptional regulators (see text for details). It is not known whether brown and white adipocytes use similar pathways for adipogenesis. There is some evidence that these two cell types can “*trans*-differentiate” into one another. Alternatively, brown adipocytes may develop along an independent pathway.

hypoxia-inducible factor 1 α (HIF-1 α), which represses transcriptional induction of PPAR γ via an intermediate factor, called DEC1/Stra13.³⁹

TRANSCRIPTIONAL CONTROL OF ADIPOSE DIFFERENTIATION

Studies in the pre-adipose cell lines 3T3-L1 and 3T3-F442A have yielded enormous insight into the transcriptional cascade that operates during adipose conversion (FIG. 2). Several groups have published data on a handful of transcription factors that are intimately involved in the transition from pre-adipocyte to adipocyte. We know, for example, that members of the CCAAT/enhancer binding protein (C/EBP) family are important in this process. C/EBP β and C/EBP δ are expressed early in adipogenesis *in vitro*, reaching maximum levels within the first 2 days after differentiation is induced.^{40, 41}

These factors in turn induce C/EBP α and the nuclear hormone receptor peroxisome proliferator-activated receptor γ (PPAR γ), whose levels peak after a few days of differentiation and remain elevated throughout the life of the adipocyte. The ectopic addition of either C/EBP α or C/EBP β is sufficient to drive the complete program of adipogenesis in pre-adipocyte cell culture models; C/EBP δ is not sufficient per se, but does accelerate differentiation induced by C/EBP β .⁴² *In vivo*, the total loss of C/EBP α is associated with neonatal lethality resulting from hepatic and other defects⁴³; until recently, this has hampered a careful study of the effect of loss of C/EBP α on postnatal events such as fat cell development. New studies have now been performed with alternative strategies that rescue the hepatic phenotype; a strong case has been made that C/EBP α is required for the normal development of white adipose tissue (WAT), but not for brown adipose tissue (BAT).^{44,45} Interestingly, combined loss of C/EBP β and C/EBP δ has the converse effect—modest reductions in WAT with more dramatic defects in BAT.⁴⁶

A role for PPAR γ in adipogenesis was first suggested by analysis of the aP2 (the adipocyte-specific fatty-acid-binding protein) 5'-flanking region. Elements were identified in this promoter region that were shown to be both necessary and sufficient to direct gene expression from a minimal promoter specifically to fat cells in culture and in transgenic mice.^{47,48} Cloning of the cognate *trans*-acting factor identified it as a heterodimer consisting of two nuclear receptors, PPAR γ and RXR α (retinoid X receptor- α).⁴⁹ PPAR γ exists as two isoforms created by alternative splicing at the 5' end of a single gene; PPAR γ 2 contains 30 amino acids more at the N-terminus than does PPAR γ 1. While many tissues express a low level of the PPAR γ 1 protein, fat expresses high levels of PPAR γ 2 (and also PPAR γ 1).

As a member of the nuclear hormone receptor superfamily, PPAR γ is activated through the binding of ligands to a distinct carboxyl-terminal ligand-binding domain. It is now appreciated that the synthetic thiazolidinedione (TZD) class of anti-diabetic drugs function as ligands for PPAR γ .⁵⁰ These molecules, which have affinity (K_D) in the 50–700 nM range, were originally developed through medicinal chemistry approaches, with no insight into their mechanism of action. While these compounds are very effective at promoting adipogenesis in culture and *in vivo*, it is not known whether this effect is related to the anti-diabetic actions of these drugs. The endogenous PPAR γ ligand is not known. Certain fatty acids can bind PPAR γ with low affinity, but most investigators feel that these compounds are not present at physiological concentrations in nuclei *in vivo*. An unusual prostanoid, 15-deoxy- $\Delta^{12,14}$ -PGJ2 (prostaglandin J2), has also been identified as a ligand for PPAR γ .^{51, 52} but it is not known if this compound even exists in nature. This prostanoid has also been shown to activate other, unrelated signal transduction pathways in cells (such as NF- κ B), making it difficult to ascribe its effects as belonging to PPAR γ .⁵³

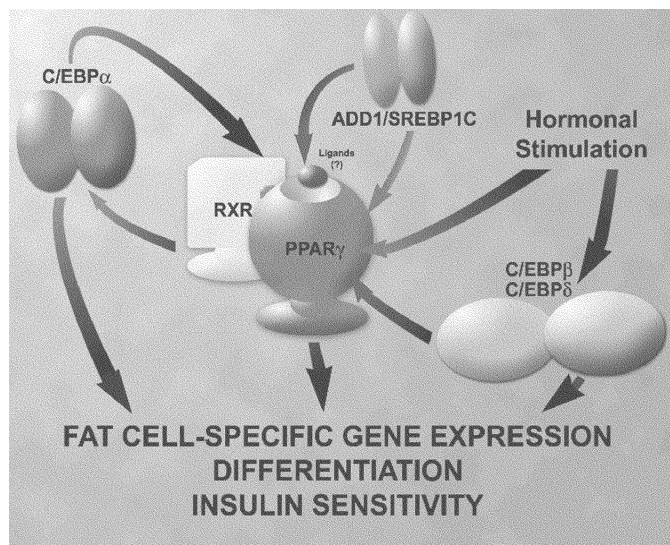


FIGURE 2. Transcriptional cascade in adipogenesis. Under the influence of unknown cues, C/EBP β and C/EBP δ rise early during the conversion of pre-adipocytes to adipocytes. These factors induce the expression of C/EBP α and PPAR γ , each of which maintains the expression of the other. Together these factors (and ADD1/SREBP1c) induce terminal gene expression and the final differentiated phenotype.

PPAR γ plays a crucial role in the function of many fat-cell selective genes. PPAR γ binding is absolutely required for the function of the fat-selective enhancers for the *FABP4* (aP2) and *PEPCK* genes in cultured fat cells.⁵⁴ This analysis of PEPCK has recently been extended *in vivo*, where the expression of the gene in fat was shown to be dependent on PPAR γ binding, while expression in other tissues was not.⁵⁵ In addition to directly binding to and regulating fat cell-selective genes, PPAR γ plays a dominant role in the regulation of differentiation per se. This was shown first in “gain of function” experiments that expressed PPAR γ in non-adipogenic, fibroblastic cells (NIH-3T3) using retroviral vectors.⁵⁶ While ligands selective for PPAR γ were not known at this time, application of the pan-PPAR ligand ETYA (5,8,11,14-eicosatetraynoic acid) activated PPAR γ and caused a powerful differentiation response. The use of high-affinity TZD ligands has greatly improved these experiments. PPAR γ -mediated differentiation included lipid accumulation and the expression of many endogenous genes characteristic of this cell type. The ability of PPAR γ to promote adipogenesis is not limited to fibroblastic cells. Myoblastic cell lines can also be converted to adipocytes, particularly when the cells co-express both C/EBP α and PPAR.⁵⁷

Loss-of-function studies with PPAR γ have been more difficult to perform, because mice with targeted ablation of PPAR γ die *in utero* at embryonic day 9.5–10.^{58,59} This occurs because of a failure of placentation, precluding useful analysis of the role played by this factor in adipogenesis, most of which occurs postnatally in rodents. Our group has circumvented this problem by using chimeric lineage analysis to demonstrate that PPAR is required for adipogenesis *in vivo*.⁶⁰ Another group reported the same results using tetraploid rescue of the placental defect in PPAR γ knockout mice.⁵⁹ These findings were extended by demonstrating that PPAR γ null ES cells or primary embryonic fibroblasts were incapable of undergoing adipogenesis *in vitro*.^{58,60}

The synthesis of these and other studies has led to the following model: C/EBP β and C/EBP δ are activated by unknown cues in the committed pre-adipocyte to induce PPAR γ and C/EBP α . These two factors then induce each other's expression in a positive feedback loop that maintains the differentiated state. We and others have shown that cells lacking C/EBP α can in fact be differentiated to adipocytes as long as PPAR γ is added ectopically (although they lack normal insulin sensitivity).^{61,62} This raises the question of whether C/EBP α and PPAR γ represent redundant pathways in adipogenesis or whether the role of C/EBP α is primarily directed at inducing and maintaining PPAR γ levels. We now have data from PPAR γ null fibroblasts that shows that C/EBP α *cannot* rescue the adipogenic phenotype in these cells.⁶³ The role of C/EBP α in adipogenesis may in fact be more ancillary than had been previously thought; at least one major function of C/EBP α is to induce and maintain appropriate levels of PPAR γ .

In addition to this cross-regulation, it is clear that these proteins can act synergistically to activate differentiation and differentiation-linked gene expression. The molecular basis for this synergy is not known, but is worth noting that many fat cell genes have binding sites for both C/EBP and PPAR γ /RXR. Possibilities for this synergy include regulation of co-activators involved in adipogenesis, and/or the possibility that C/EBP α is involved in regulatory genes that produce PPAR γ ligands.

Another transcription factor that promotes adipogenesis is adipocyte determination and differentiation factor-1 (ADD1), also known as sterol regulatory element binding protein-1c (SREBP1c). ADD1/SREBP1c is induced in differentiating 3T3-L1 cells at around the same time as PPAR γ and C/EBP α .⁶⁴ A constitutively active form of ADD1/SREBP1c enhances 3T3-L1 adipogenesis, while a dominant negative form represses this process.⁶⁵ There is evidence that ADD1/SREBP1c activates the PPAR γ promoter,⁶⁶ and may also contribute to the generation of a PPAR γ ligand.⁶⁷ Beyond these effects, ADD1/SREBP1c mediates some of the transcriptional effects of insulin in adipose tissue, particularly on lipogenic genes such as fatty acid synthase, acetyl-CoA carboxylase, and stearoyl-CoA desaturase.⁶⁸

There have been reports of several other transcription factors that are linked to adipogenesis. Though none of these have been shown to affect adipogenesis as profoundly as PPAR γ and the C/EBPs, it is quite possible that some of these will be important modulators of fat cell development and function. PPAR δ in particular has been studied in this light, with conflicting results. Some workers have shown that NIH-3T3 fibroblasts stably expressing PPAR δ are unable to undergo differentiation,⁶⁹ while others have shown that they can as long as a cAMP-inducing agent is added to the differentiation cocktail.⁷⁰ Similarly, claims have been made that some pre-adipocyte lines (such as Ob1771 and 3T3-F442A) can be induced to differentiate more completely if PPAR δ is forcibly expressed or if a PPAR δ ligand like 2-bromopalmitate is added.^{71,72} Another group showed that 3T3-L1 pre-adipocytes, on the other hand, were only modestly affected by the addition of a more specific PPAR δ ligand.⁷⁰ Loss-of-function studies with PPAR δ have not shed as much light as might be hoped. Two different groups have generated PPAR δ null mice; most PPAR δ $-/-$ embryos die mid-gestation, but a few survive to term and show reduced adiposity.^{73,74} Of note, mice with PPAR δ targeted only in adipocytes show no decrease in adiposity, indicating that an extra-adipose site must be involved in the decreased body mass seen in the global knockout.⁷³ Other factors have also been discovered, including the forkhead factor *foxc2* which is expressed in an adipose-selective manner and which promotes adipocyte-specific (especially BAT-specific) gene expression in a transgenic model.⁷⁵

Finally, a few transcription factors have been shown to inhibit adipogenesis. These include GATA2 and GATA3, which are expressed in pre-adipocytes.⁷⁶ These factors work at least in part by repressing the PPAR γ 2 promoter. Reductions in GATA2 and GATA3 levels are required for adipogenesis to proceed *in vitro*. DFosB is a naturally occurring variant of FosB that appears to repress adipogenesis in marrow stromal cells while promoting the formation of osteoblasts.⁷⁷

WHAT IS THE RELATIONSHIP OF ADIPOGENESIS TO LYMPHATIC PATHOLOGY?

Adipose tissue is found in discrete depots scattered through the body. Some of these depots are more metabolically active than others, and tend to expand or shrink in proportion to nutritional status. Other depots, such as the structural fat found in the heel and fingerpads, are quite metabolically inert, and barely change in size even in the leanest animals. Another place where fat can always be found, regardless of nutritional status, is around lymph nodes. These perinodal adipocytes typically do not respond to fasting, but are fully capable of activating lipolysis when stimulated by local lymph nodes or

co-cultured lymphoid cells.^{78,79} There are interesting studies to demonstrate that adipocytes that are physically juxtaposed to lymphatic tissue are exquisitely sensitive to the lipolytic effects of lymphoid-derived cytokines like TNF- α and interleukin-6, while other adipocytes from distal sites within the same depot do not respond to these stimuli to the same magnitude.⁸⁰ There also appear to be qualitative differences in the fatty acid composition of resident triglycerides in perinodal adipocytes relative to fat cells elsewhere.⁸¹ These observations have led to the hypothesis that adipose tissue forms an important energy depot for local lymphoid metabolism, and that these stores are important enough that they are spared by more mundane stimuli, such as fasting. Consistent with this notion is the fact that chronic inflammatory states such as Crohn's disease can lead to redistribution of fat.⁸²

Another pathological state involving the lymphatic system is lymphedema, characterized by the accumulation of interstitial lymph in a defined region of the body, often as a result of interruption of lymphatic drainage. Chronic lymphedema leads to a variety of pathological changes in the affected region, including overgrowth of connective tissue and adipose tissue.⁸³ This exuberant growth of adipose tissue has led some to question whether lymph possesses an adipogenic activity, although there has been remarkably little work done to address this possibility. One study showed that cultured rabbit pre-adipocytes could be induced to differentiate more completely if lymph was included in the medium.⁸⁴ The stimulatory effect could be fully replicated by adding chylomicrons to the medium in place of whole lymph. On the one hand, this observation might suggest that the phenomenon is created by pre-existing, small adipocytes that take up and incorporate the triglycerides in the chylomicrons. The effect would thus be on lipogenesis rather than on adipogenesis *per se*. One should not, however, discount the possibility that a *bona fide* adipogenic stimulus is present in the chylomicron fraction of lymph. An example of this might be a lipophilic ligand for PPAR γ , which could be enriched in the very low-density lipoprotein (VLDL).

CONCLUSIONS

Despite its complexity, adipogenesis has proven to be a developmental system tractable to study, because of the availability of cultured cell lines that faithfully mimic fat cell development *in vivo*. Such studies have allowed the identification of several critical transcription factors that promote the differentiated state. These factors include PPAR γ , ADD1/SREBP1c, and members of the C/EBP family. Despite these advances, many aspects of adipogenesis remain mysterious, including the steps that lead to commitment of the multipotent mesenchymal stem cell to the adipocytic lineage, as well as the control of terminal gene expression in mature fat cells. Additionally, several obser-

vations indicate the presence of cross-talk between adipocytes and the lymphatic system. Unraveling these mysteries will certainly lead to insights that could have benefits in conditions ranging from obesity and type 2 diabetes to lymphedema.

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