

## **PPARgamma induces the insulin-dependent glucose transporter GLUT4 in the absence of C/EBPalpha during the conversion of 3T3 fibroblasts into adipocytes.**

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*J Clin Invest.* 1998;101(1):22-32. <https://doi.org/10.1172/JCI1244>.

### Research Article

To define the molecular mechanisms that control GLUT4 expression during adipogenesis, NIH-3T3 fibroblasts ectopically expressing different adipogenic transcription factors (C/EBPbeta, C/EBPdelta, C/EBPalpha, and PPARgamma) under the control of a tetracycline-responsive inducible (C/EBPs) or a constitutive retroviral (PPARgamma) expression system were used. Enhanced production of C/EBPbeta (beta2 cell line), C/EBPbeta together with C/EBPdelta (beta/delta39 cell line), C/EBPalpha (alpha1 cell line), or PPARgamma (Pgamma2 cell line) in cells exposed to dexamethasone and the PPARgamma ligand ciglitazone (a thiazolidinedione) resulted in expression of GLUT4 mRNA as well as other members of the adipogenic gene program, including aP2 and adipsin. Focusing our studies on the beta/delta39 cells, we have demonstrated that C/EBPbeta along with C/EBPdelta in the presence of dexamethasone induces PPARgamma, adipsin, and aP2 mRNA production; however, GLUT4 mRNA is only expressed in cells exposed to ciglitazone. In addition, enhanced expression of a ligand-activated form of PPARgamma in the beta/delta39 fibroblasts stimulates synthesis of GLUT4 protein and gives rise to a population of adipocytic cells that take up glucose in direct response to insulin. C/EBPalpha is not expressed in the beta/delta39 cells under conditions that stimulate the adipogenic program. This observation suggests that PPARgamma alone or in combination with C/EBPbeta and C/EBPdelta is capable of activating GLUT4 gene expression.

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# PPAR $\gamma$ Induces the Insulin-dependent Glucose Transporter GLUT4 in the Absence of C/EBP $\alpha$ During the Conversion of 3T3 Fibroblasts Into Adipocytes

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## Abstract

To define the molecular mechanisms that control GLUT4 expression during adipogenesis, NIH-3T3 fibroblasts ectopically expressing different adipogenic transcription factors (C/EBP $\beta$ , C/EBP $\delta$ , C/EBP $\alpha$ , and PPAR $\gamma$ ) under the control of a tetracycline-responsive inducible (C/EBPs) or a constitutive retroviral (PPAR $\gamma$ ) expression system were used. Enhanced production of C/EBP $\beta$  ( $\beta$ 2 cell line), C/EBP $\beta$  together with C/EBP $\delta$  ( $\beta/\delta$ 39 cell line), C/EBP $\alpha$  ( $\alpha$ 1 cell line), or PPAR $\gamma$  (P $\gamma$ 2 cell line) in cells exposed to dexamethasone and the PPAR $\gamma$  ligand ciglitazone (a thiazolidinedione) resulted in expression of GLUT4 mRNA as well as other members of the adipogenic gene program, including aP2 and adipsin. Focusing our studies on the  $\beta/\delta$ 39 cells, we have demonstrated that C/EBP $\beta$  along with C/EBP $\delta$  in the presence of dexamethasone induces PPAR $\gamma$ , adipsin, and aP2 mRNA production; however, GLUT4 mRNA is only expressed in cells exposed to ciglitazone. In addition, enhanced expression of a ligand-activated form of PPAR $\gamma$  in the  $\beta/\delta$ 39 fibroblasts stimulates synthesis of GLUT4 protein and gives rise to a population of adipocytic cells that take up glucose in direct response to insulin. C/EBP $\alpha$  is not expressed in the  $\beta/\delta$ 39 cells under conditions that stimulate the adipogenic program. This observation suggests that PPAR $\gamma$  alone or in combination with C/EBP $\beta$  and C/EBP $\delta$  is capable of activating GLUT4 gene expression. (*J. Clin. Invest.* 1998. 101:22–32.) Key words: adipogenesis • transcription factors • insulin action • glucose transporter 4 • antidiabetic drugs

## Introduction

Transport of glucose across an impermeable cell membrane is facilitated by a family of glucose transporters (GLUT1-5 and GLUT7) that are expressed in a tissue-restricted manner (1, 2). The insulin-dependent glucose transporter, GLUT4, is expressed exclusively in adipose tissue, cardiac muscle, and skeletal muscle (3–7), where it functions to regulate glucose up-

take into these tissues in response to elevated levels of insulin in the circulation. GLUT1 is also involved in transporting glucose into adipose tissue and muscle, but its expression is not limited to these sites since it has been identified in nearly all cell types where it is thought to account for basal uptake of glucose (2). The molecular mechanisms regulating the tissue-restricted expression of GLUT4 are essentially unknown.

Both GLUT4 and GLUT1 have been shown to be differentially expressed during development of striated muscle and brown adipose tissue (8). In the fetal and early postnatal stages of mouse development, GLUT1 is the predominant transporter. After birth, there is an extensive increase in GLUT4 expression in striated muscle and brown adipose tissue with a corresponding decrease in GLUT1 expression. This developmental pattern of glucose transporter gene expression is mimicked to some extent in various mouse cell lines that give rise to either adipocytes or myocytes in culture. GLUT4 is not produced in preadipocytes or myoblasts, but its expression is enhanced manyfold during differentiation of each of these cell types into adipocytes and myocytes, respectively (7, 9, 10). The observation that a different set of transcription factors regulates the differentiation of these two cell types raises the following question: is the expression of the GLUT4 gene in adipocytes and myocytes regulated by a corresponding set of tissue-restricted transcription factors, or is it regulated by other factors that are not involved in determining the phenotype of these specific tissues? In the case of muscle-specific expression of GLUT4, it has been suggested that myocyte enhancer factor 2 (MEF2) and thyroid hormone receptor  $\alpha$ 1 (TR $\alpha$ 1) play a direct role in its regulation (10, 11). The promoter of the GLUT4 gene contains several putative binding sites for many regulatory proteins, including an MEF2 and TR $\alpha$ 1 site. There are also several E box elements that have the potential of binding the MyoD family of transcription factors; however, there is no data to suggest that these myogenic factors are involved in regulating GLUT4 expression in muscle.

There is significantly less information on the mechanisms responsible for the extensive induction of GLUT4 during adipogenesis. Differentiation of preadipocytes into adipocytes is regulated by at least two families of transcription factors: the PPARs<sup>1</sup> (peroxisome proliferator-activated receptors) and the C/EBPs (CCAAT/enhancer binding proteins). The PPARs (PPAR $\alpha$ , PPAR $\gamma$ , and PPAR $\delta$ /NUC1) are members of the nuclear hormone receptor superfamily that includes receptors for the retinoid, thyroid, and steroid hormones (12–14). There are varying levels of these PPARs in many tissues where their function is to regulate the metabolism of lipids by activating expression of key enzymes (15). Of the known members of the

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Received for publication 18 July 1997 and accepted in revised form 3 November 1997.

*J. Clin. Invest.*

© The American Society for Clinical Investigation, Inc.  
0021-9738/98/01/0022/11 \$2.00

Volume 101, Number 1, January 1998, 22–32  
<http://www.jci.org>

1. Abbreviations used in this paper: C/EBP, CCAAT/enhancer binding protein; DEX, dexamethasone; GPD, glycerol phosphate dehydrogenase; MIX, methylisobutyl xanthine; PPAR, peroxisome proliferator-activated receptors; TZD, thiazolidinediones.

PPAR family, PPAR $\gamma$  appears to be primarily involved in adipogenesis (16). Expression of PPAR $\gamma$  is high in adipose tissue where it is induced quite early during differentiation of preadipocytes into adipocytes (17, 18). In this regard, ectopic expression of PPAR $\gamma$  in nonadipogenic fibroblasts promotes their conversion into fat-laden adipocyte-like cells after their exposure to a PPAR activator or ligand (18). As with other nuclear hormone receptors, the ability of PPAR $\gamma$  to function as a transcription factor is dependent on its binding to a ligand. Although the biological ligand for PPAR $\gamma$  has not yet been identified, recent studies have demonstrated that 15-deoxy- $\Delta^{12,14}$  prostaglandin J<sub>2</sub> (15d-J<sub>2</sub>) and the thiazolidinediones can act as direct ligands (19–21). The thiazolidinediones that include ciglitazone, pioglitazone, and troglitazone among others are a synthetic class of insulin-sensitizing drugs that can lower blood glucose when given to diabetic animals (22–24).

The C/EBP family consists of several members, the most notable being  $\alpha$ ,  $\beta$ , and  $\delta$ , which are expressed at specific times during adipogenesis in a manner that is consistent with a regulatory role for each protein during the differentiation process (25). In contrast to PPAR $\gamma$ , however, none of the C/EBPs is expressed in an exclusively tissue-restricted fashion. C/EBP $\alpha$  is expressed in high abundance in adipose tissue and liver (26). Its expression is induced during adipogenesis in culture after the induction of PPAR $\gamma$ , but preceding the synthesis of many of the enzymes and proteins characteristic of the fully differentiated adipogenic phenotype. In fact, C/EBP $\alpha$  may play a direct role in establishing and maintaining the terminally differentiated state of adipocytes, since constitutive expression of an antisense C/EBP $\alpha$  RNA in 3T3-L1 preadipocytes blocks the expression of several adipogenic genes, including GLUT4, and prevents accumulation of cytoplasmic fat droplets (27). The relatively late induction of C/EBP $\alpha$  during adipogenesis, however, suggests that it is not a master regulator of adipogenesis. Nevertheless, forced overexpression of C/EBP $\alpha$  in some fibroblastic cell lines can induce their conversion into fat-laden adipocytic cells (28). Recently, McKnight and coworkers suggested that C/EBP $\beta$  and C/EBP $\delta$  may play an early catalytic role in differentiation of 3T3-L1 preadipocytes, relaying the effects of dexamethasone (DEX) and methylisobutylxanthine (MIX), respectively, in a cascade-like fashion that ultimately leads to induction of C/EBP $\alpha$  (29). Our recent studies also demonstrate that conditional ectopic expression of C/EBP $\beta$  and C/EBP $\delta$  in NIH-3T3 fibroblasts ( $\beta/\delta$ 39 cell line) induces expression of PPAR $\gamma$  in the presence of glucocorticoids, and their subsequent exposure to a PPAR activator, 5, 8, 11, 14-icosatetraynoic acid (ETYA), stimulates their conversion into fat-laden adipocytic cells (30).

Since GLUT4 is abundantly expressed in fully mature adipocytes, it is quite likely that PPAR $\gamma$  and/or the C/EBPs play a principal role in controlling its expression during the differentiation of preadipocytes into adipocytes. The circumstantial evidence mentioned previously, where the expression of an antisense C/EBP $\alpha$  RNA in preadipocytes blocked GLUT4 expression, suggests that C/EBP $\alpha$  is involved in regulating this gene (27). In addition, earlier studies on the GLUT4 gene promoter have identified a C/EBP binding site that may serve to facilitate C/EBP-dependent activation of the GLUT4 promoter/CAT gene construct in *in vitro* transient transfection assays (31). Other investigations have shown that the PPAR $\gamma$  ligand pioglitazone enhances expression of several adipogenic genes including GLUT4 during the differentiation of 3T3-L1

and 3T3-F442A preadipocytes into adipocytes (32, 33). Despite these observations, however, there is no direct evidence indicating whether any of the C/EBPs or PPAR $\gamma$  are responsible for inducing expression of GLUT4 during adipogenesis.

To define the molecular mechanisms that control GLUT4 gene expression during conversion of mesenchymal stem cells into adipocytes, NIH-3T3 fibroblasts ectopically expressing different combinations of the adipogenic transcription factors C/EBP $\beta$ , C/EBP $\delta$ , C/EBP $\alpha$ , and PPAR $\gamma$  using either a tetracycline-responsive inducible (C/EBPs) or a constitutive retroviral (PPAR $\gamma$ ) expression system (18) were used. The cell lines were induced to differentiate, and expression of GLUT4 mRNA and protein were analyzed. The results demonstrate that conditional ectopic expression of C/EBP $\beta$  and C/EBP $\delta$  together in NIH-3T3 cells exposed to glucocorticoids induces expression of PPAR $\gamma$ . Subsequent treatment of these cells with the PPAR $\gamma$  ligand ciglitazone results in their extensive conversion into fat-laden adipocytes and induction of GLUT4 mRNA and protein, as well as an increase in insulin-sensitive glucose uptake. There appears to be no direct involvement of C/EBP $\alpha$  in inducing GLUT4 mRNA or protein expression in these cells.

## Methods

**Plasmids and cell lines.** The tetracycline-responsive expression system that comprises two plasmids—pUHD15-1 (tTA) and pUHD10-3—was obtained from H. Bujard (Zentrum für Molekulare Biologie, University of Heidelberg, Germany; 34). To construct a tetracycline-dependent C/EBP $\alpha$  expression vector, the 3.5 kb of KpnI-Xba restriction fragment of the rat C/EBP $\alpha$  gene (35), which corresponds to 125 bp 5'-upstream from the AUG start codon to 1.0 kb of the 3'-downstream untranscribed region of the C/EBP $\alpha$  gene, was subcloned into the pUHD 10-3 vector. The resultant plasmid, Tet-O-C/EBP $\alpha$ , is driven by the CMV promoter containing the tet operator upstream of the C/EBP $\alpha$  gene in response to coexpression of tTA from the pUHD15-1 plasmid.

The stable NIH-3T3 cell lines—tA,  $\beta$ 2,  $\beta/\delta$ 39, and  $\delta$ 23—were created as described previously (30, 36). The P $\gamma$ 2 cell line that overexpresses PPAR $\gamma$ 2 by viral infection was kindly provided by Dr. Bruce Spiegelman (Dana Farber Institute, Harvard Medical School; 18). The NIH-3T3  $\alpha$ 1 cell line was generated by transfecting Tet-O-C/EBP $\alpha$  expression vector along with a pBabe-puromycin plasmid into the tA cell line. Transfection was performed using lipofectAMINE following the procedure outlined by the supplier (GIBCO BRL, Gaithersburg, MD). The transfected cells were selected in DMEM containing 10% FBS (GIBCO BRL), 0.4 mg/ml G418 (GIBCO BRL), 1.5  $\mu$ g/ml puromycin (Sigma Chemical Co, St. Louis, MO) and 1  $\mu$ g/ml of tetracycline for 10–14 d. The resistant clones were subsequently isolated and propagated into cell lines.

**Cell culture.** 3T3-L1 preadipocytes were grown to confluence in DMEM with 10% normal calf serum (Intergen Co., Purchase, NY) and then induced to differentiate as described previously (37). The NIH-3T3 stable cell lines were passaged in DMEM with 10% FBS in the presence of tetracycline (1  $\mu$ g/ml). Tetracycline was withdrawn from the medium to induce expression of the transfected genes. The cells were allowed to grow for an additional 48 h in the absence of tetracycline, during which time they reached confluence. At this stage, designated as day 0, differentiation was initiated by exposure of the cells to a cocktail containing 0.5 mM MIX, 1  $\mu$ M DEX, 5  $\mu$ g/ml insulin, and 10% FBS in DMEM for 48 h. The cells were then maintained in DMEM containing 10% FBS, 5  $\mu$ g/ml insulin, and 10  $\mu$ M ciglitazone (Upjohn Co., Kalamazoo, MI) unless otherwise indicated. Cells were refed every 2 d.

**RNA analysis.** Total RNA was extracted from the NIH-3T3 cell lines and the 3T3-L1 cells following the procedure of Chomczynski

and Sacchi (38). In brief, cells were lysed with guanidine thiocyanate and extracted with acidic phenol/chloroform, followed by isopropanol precipitation overnight at  $-20^{\circ}\text{C}$ . Total RNA (20–25  $\mu\text{g}$ ) from each sample was subjected to Northern blot analysis as described previously (39). Probes were labeled by random priming using the Klenow fragment of DNA polymerase I (New England Biolabs Inc., Beverly, MA) and [ $\alpha$ - $^{32}\text{P}$ ]dCTP (DuPont-NEN, Boston, MA). cDNAs used as probes were as follows: C/EBP $\alpha$ , C/EBP $\beta$ , and C/EBP $\delta$  (25); 422/aP2 (40, 41); PPAR $\gamma$  (17); adipsin (42); glycerol phosphate dehydrogenase (GPD; 43); and GLUT4 and GLUT1 (glucose transporter 4 and 1; 7).

**Western blot (immunoblot analysis).** Total membrane proteins were isolated from NIH-3T3  $\beta$ /839 and 3T3-L1 adipocytes (44, 45). In brief, cells were lysed in ice-cold buffer A (250 mM sucrose, 20 mM Hepes, 1 mM EDTA, and 1 mM PMSF). Cell lysates were placed in a homogenization vessel and immediately homogenized with a motor-driven Teflon pestle on ice. Total membrane proteins were recovered by centrifugation of the homogenates at 55,000 rpm in a 60Ti rotor for 90 min at  $4^{\circ}\text{C}$ . The total membrane pellets were dissolved in buffer B (20 mM Hepes, 1 mM EDTA, and 1 mM PMSF) and quantified using a BCA protein assay kit (Pierce, Rockford, IL). Total membrane proteins from  $\beta$ /839 cells (300  $\mu\text{g}$ ) and 3T3-L1 adipocytes (150  $\mu\text{g}$ ) were fractionated by 10% SDS-PAGE and electrophoretically transferred to a nitrocellulose membrane (Schleicher & Schuell, Inc., Keene, NH), which was then subjected to Western blot analysis as described previously (46). The primary antibody for GLUT4 protein was obtained from Dr. Paul Pilch at Boston University School of Medicine (46). The secondary antibody for GLUT4 was a goat anti-mouse polyvalent consisting of the immunoglobulins IgA, IgM, IgG (1:1,000 dilution; Sigma Chemical Co., St. Louis, MO).

**2-Deoxy-D-glucose uptake.** Glucose uptake was performed following the protocol described previously (47). In brief, cells were stimulated with 100 nM insulin at  $37^{\circ}\text{C}$  for 8 min before the assay. The glucose transport assay was then carried out in a cocktail containing Krebs-Ringer Hepes (KRH) buffer (pH 7.4) with 90  $\mu\text{M}$  of D-glucose and 1  $\mu\text{Ci/ml}$  of [ $^3\text{H}$ ]2-deoxyglucose (1 ml per 35-mm dish; DuPont-NEN, Boston, MA) for 3 min at room temperature. The assay was terminated by two washes with KRH buffer. The cells were then lysed by incubation in digitonin release buffer (0.25 M mannitol, 17 mM potassium Mops, 2.5 mM EDTA, and 8 mg/ml of digitonin, pH 7.4; 1 ml/well). An aliquot (0.3 ml) from each lysate was used to determine the amount of radioactivity by liquid scintillation counting. Nonspecific diffusion was determined in the presence of 5  $\mu\text{M}$  cytochalasin B (Sigma Chemical Co.). Measurements were performed in triplicate and normalized by protein concentrations in the lysates. They were corrected by subtracting the nonspecific diffusion. The final results were presented as pmol/min/mg protein.

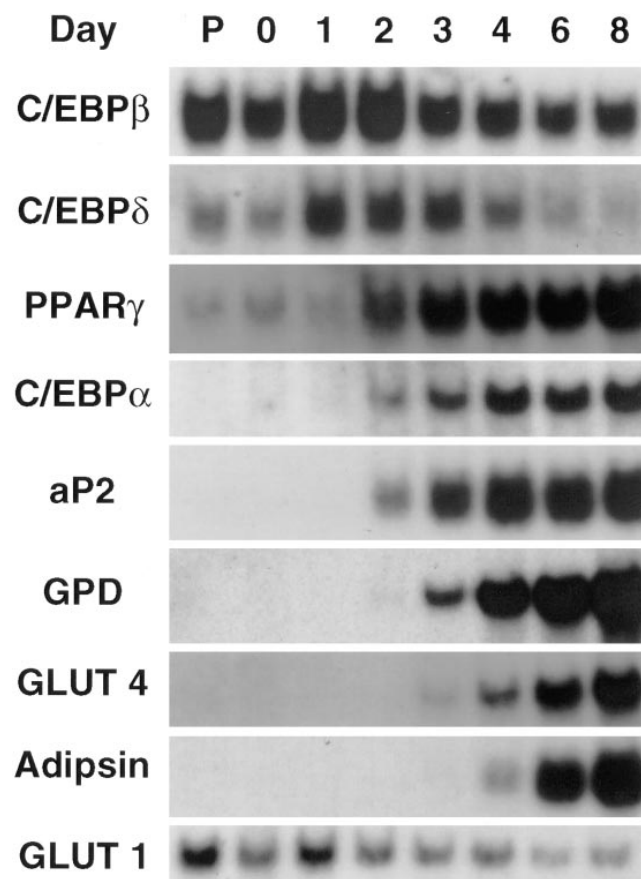
**Oil Red O staining.** Oil Red O staining was performed following the procedure described by Green and Kehinde (48) with minor modifications. In brief, cells were washed twice with PBS and fixed with 10% formalin in PBS for 15 min. After two washes in PBS, cells were stained for at least 1 h in freshly diluted Oil Red O solution (six parts Oil Red O stock solution and four parts  $\text{H}_2\text{O}$ ; Oil Red O stock solution is 0.5% Oil Red O in isopropanol). The stain was then removed and the cells were washed twice with water, with or without counterstain (0.25% giemsa for 15 min) and then photographed.

## Results

**Temporal pattern of expression of adipogenic genes during the differentiation of 3T3-L1 preadipocytes.** To determine the temporal pattern of expression of the adipogenic transcription factors and other adipocyte-specific genes relative to each other, we analyzed adipogenic gene expression during the conversion of 3T3-L1 fibroblasts into adipocytes by Northern blot hybridization. Fig. 1 shows that C/EBP $\beta$  and C/EBP $\delta$  are expressed in proliferating preadipocytes (P). Exposure of a con-

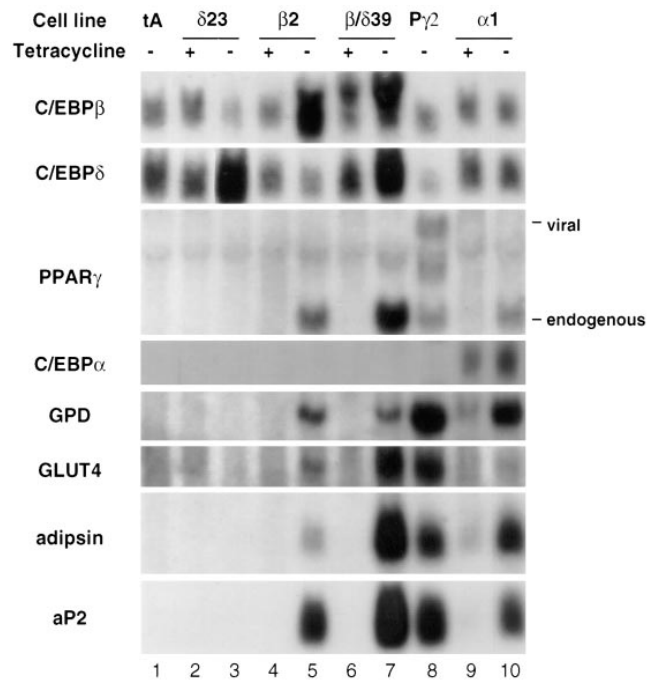
fluent population of these cells to the adipogenic inducers (DEX, MIX, insulin, and FBS) results in a transient increase in both C/EBP $\beta$  and C/EBP $\delta$  within the first 48 h. The levels of these mRNAs decrease to  $\sim 30$ –50% of the original prestimulatory amounts between 6 and 8 d. This peak of C/EBP $\beta$  and C/EBP $\delta$  mRNA expression precedes the induction of both PPAR $\gamma$  and C/EBP $\alpha$  which are activated at 2 d, reaching their maximum levels of expression by days 3 and 4, respectively. The downstream adipogenic genes are activated in a sequential manner after induction of both the C/EBP $\alpha$  and PPAR $\gamma$  transcription factors. The fatty acid-binding protein, aP2, is induced early in the differentiation process, immediately after PPAR $\gamma$  and C/EBP $\alpha$  expression. GPD is induced at day 3, the insulin-dependent glucose transporter (GLUT4) at day 4, and adipsin at day 5. The ubiquitous glucose transporter, GLUT1, is expressed in proliferating preadipocytes and is gradually downregulated during the differentiation process.

*Ectopic expression of C/EBPs and PPAR $\gamma$  in NIH-3T3 fibroblasts induces the terminal phase of adipogenesis as indi-*



**Figure 1.** Sequential activation of gene expression during the differentiation of 3T3-L1 preadipocytes into adipocytes. Subconfluent 3T3-L1 preadipocytes were grown and passaged in DMEM with 10% calf serum. Confluent 3T3-L1 preadipocytes (day 0) were exposed to a differentiation cocktail containing 1  $\mu\text{M}$  DEX, 0.5 mM MIX, 10  $\mu\text{g/ml}$  insulin, and 10% FBS in DMEM for 48 h. The cells were then maintained in DMEM with 2.5  $\mu\text{g/ml}$  insulin and 10% FBS and replenished with this medium every 2 d. Total RNA (20  $\mu\text{g}$ ) extracted at various times as indicated during the differentiation process was analyzed by Northern blot hybridization using the following  $^{32}\text{P}$ -labeled cDNA probes: C/EBP $\beta$ , C/EBP $\delta$ , PPAR $\gamma$ , C/EBP $\alpha$ , aP2, GPD, GLUT4, adipsin, and GLUT1.

cated by expression of the insulin-responsive glucose transporter (*GLUT4*). As shown in Fig. 1, the C/EBPs and PPAR $\gamma$  are expressed before other adipogenic genes during differentiation of 3T3-L1 preadipocytes. It is conceivable, therefore, that these transcription factors are directly responsible for activating the adipocyte genes (i.e., *GLUT4*) that are indicative of the mature adipocyte phenotype. Previous investigations have shown that a number of adipose-specific gene promoters and/or enhancers [*GLUT4* (31), *aP2*, *SCD1* (steroyl CoA desaturase 1; 49), and *PEPCK* (phosphoenol pyruvate carboxykinase; 50–52)] contain binding sites for C/EBP and PPARs, and in some cases these factors are capable of transactivating the corresponding genes in *in vitro* assays. In addition, overexpression of each of these transcription factors—C/EBP $\beta$ , C/EBP $\alpha$ , or PPAR $\gamma$ —in nonadipogenic cells induces their conversion into fat-laden cells that express some of the markers of the terminally differentiated phenotype, i.e., *aP2*, *adipsin*, and *GPD* (18, 28, 29, 36, 53). Although these cells accumulate fat droplets and turn on part of the adipogenic gene program, it is not known whether they can function as mature adipocytes. In these studies, we chose to define the transcriptional events that induce expression of genes that correlate with the terminal stages of adipogenesis (as illustrated in Fig. 1) with an emphasis on the insulin-responsive glucose transporter *GLUT4*. To achieve this goal, we conditionally expressed C/EBPs in NIH-3T3 fibroblasts using the tetracycline-responsive system as previously described by us (36). The resulting stable cell lines,  $\delta 23$ ,  $\beta 2$ ,  $\beta/\delta 39$ , and  $\alpha 1$ , can be induced to ectopically express C/EBP $\delta$ , C/EBP $\beta$ , C/EBP $\beta$  in combination with C/EBP $\delta$ , and C/EBP $\alpha$ , respectively. The stable cell line P $\gamma 2$ , shown in Fig. 2, constitutively overexpresses PPAR $\gamma 2$  by retroviral infection (18). To determine which adipogenic genes are expressed in each of these cell lines, differentiation was induced by culturing the cells in tetracycline-free medium (when appropriate) followed by exposure of the cells to a cocktail of the adipogenic inducers DEX, MIX, insulin, FBS, and a PPAR ligand, ciglitazone. Northern blot analysis of total RNA extracted from the various cell lines at day 8 after differentiation is presented in Fig. 2. The tA cells that ectopically produce only the tetracycline activator protein from the pUHD15-1 plasmid express low levels of both C/EBP $\beta$  and C/EBP $\delta$ , equivalent to the levels observed in the parent NIH-3T3 cell line (data not shown). Furthermore, these control cells show no sign of adipocyte-specific gene expression. The  $\delta 23$  cells respond to depletion of tetracycline from the culture medium by enhancing C/EBP $\delta$  mRNA expression, but they do not express the adipocyte-specific mRNAs. In contrast, induction of C/EBP $\beta$  in the  $\beta 2$  cells results in expression of PPAR $\gamma$ , *GPD*, *aP2*, and *adipsin*, as observed previously (36), and these  $\beta 2$  cells express *GLUT4* mRNA. Ectopic expression of C/EBP $\beta$  and C/EBP $\delta$  together in the  $\beta/\delta 39$  cells results in a similar pattern of adipogenic gene expression as the  $\beta 2$  cells, but to a significantly greater extent. Retroviral-mediated expression of PPAR $\gamma$  in NIH-3T3 cells has no effect on C/EBP $\beta$  or C/EBP $\delta$  mRNA synthesis; however, it is capable of transactivating the endogenous PPAR $\gamma$  gene and stimulating terminal differentiation of these cells as illustrated by the production of *GPD*, *aP2*, *adipsin*, and *GLUT4* mRNAs. The level of *GLUT4* expression is as high in this cell line as it is in the  $\beta/\delta 39$  cells, even though expression of PPAR $\gamma$  mRNA, including both the exogenous and endogenous forms, is several times lower in the P $\gamma 2$  cells compared with its level in the  $\beta/\delta 39$  cells.



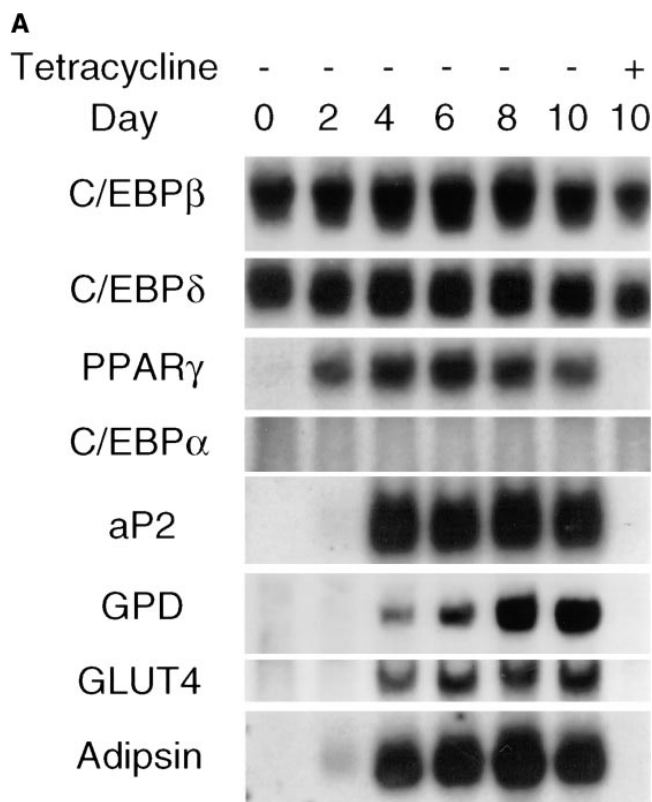
**Figure 2.** Induction of the adipogenic genes in various NIH-3T3 stable cell lines expressing C/EBPs or PPAR $\gamma$ . NIH-3T3 fibroblasts were cultured as described in Methods. 3 d before differentiation, half the cultures of the  $\delta 23$ ,  $\beta 2$ ,  $\beta/\delta 39$ , and  $\alpha 1$  were maintained in medium containing tetracycline, while the remaining cells were cultured in tetracycline-free medium. Upon reaching confluence, the cells were induced to differentiate by exposure to 1  $\mu$ M DEX, 0.5 mM MIX, 5  $\mu$ g/ml insulin, and 10% FBS in DMEM for 48 h. They were subsequently maintained in DMEM containing 5  $\mu$ g/ml insulin and 10% FBS, as well as a synthetic PPAR $\gamma$  ligand, ciglitazone (10  $\mu$ M), for an additional 6 d. Total RNA was extracted, and 25  $\mu$ g of each RNA was subjected to Northern blot analysis. The following cDNAs were used as probes: C/EBP $\beta$ , C/EBP $\delta$ , PPAR $\gamma$ , C/EBP $\alpha$ , *GPD*, *GLUT4*, *adipsin*, and *aP2*. tA, tetracycline activator cell line;  $\delta 23$ , cell line expressing C/EBP $\delta$ ;  $\beta 2$ , cell line expressing C/EBP $\beta$ ;  $\beta/\delta 39$ , cell line expressing both C/EBP $\beta$  and C/EBP $\delta$ ; P $\gamma 2$ , cell line expressing PPAR $\gamma 2$ ;  $\alpha 1$ , cell line expressing C/EBP $\alpha$ .

It is of interest that none of these cell lines ( $\beta 2$ ,  $\beta/\delta 39$ , and P $\gamma 2$ ) expresses C/EBP $\alpha$  mRNA, suggesting that one aspect of adipogenesis is not induced in NIH-3T3 cells at least in response to PPAR $\gamma$ , C/EBP $\beta$ , and/or C/EBP $\delta$ . To determine whether C/EBP $\alpha$  is also capable of stimulating terminal differentiation in NIH-3T3 cells (i.e., *GLUT4* expression), we constructed an additional cell line that ectopically produces C/EBP $\alpha$  in response to culture in tetracycline-depleted medium. Unlike the other cell lines, ( $\delta 23$ ,  $\beta 2$ , and  $\beta/\delta 39$ ), the  $\alpha 1$  cells express a low level of C/EBP $\alpha$  mRNA, even in the presence of a dose of tetracycline (1  $\mu$ g/ml) that completely suppresses transcription of the exogenous genes in the other engineered cells. Despite this low level of leakiness, the  $\alpha 1$  cells respond to the withdrawal of tetracycline by inducing a level of PPAR $\gamma$  expression equivalent to that of the endogenous PPAR $\gamma$  mRNA observed in the P $\gamma 2$  cells. This event results in activation of *GPD*, *adipsin*, and *aP2* mRNA expression, but is only modestly capable of enhancing *GLUT4* expression. It appears, therefore, that the level of *GLUT4* expression correlates with the total

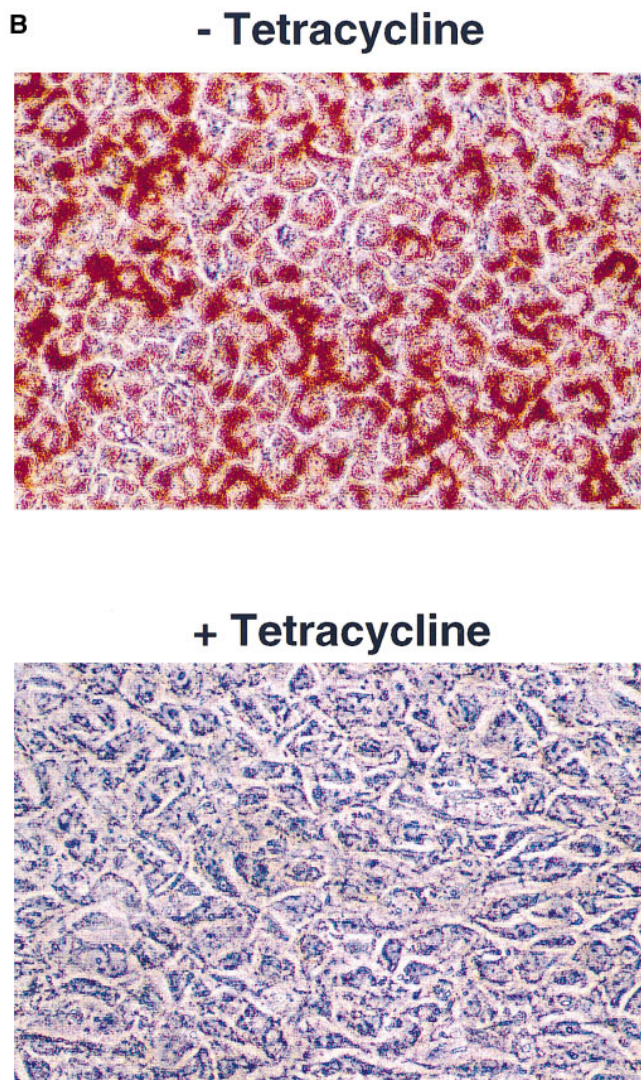
amount of PPAR $\gamma$  mRNA (endogenous and retroviral in the case of the P $\gamma$ 2 cells) expressed in each cell line, suggesting that PPAR $\gamma$  plays an important role in activating the GLUT4 gene. To further dissect the role of PPAR $\gamma$  in regulating GLUT4, we chose to study the  $\beta/\delta$ 39 cells since the level of PPAR $\gamma$  and GLUT4 expression in these cells is relatively high, and the adipogenic gene program can be readily switched on and off by the presence or absence of tetracycline in the culture medium.

*Sequential expression of the adipogenic genes during the conversion of the  $\beta/\delta$ 39 cells into adipocytes.* As observed in Fig. 1, there is a sequential activation of gene expression during 3T3-L1 preadipocyte differentiation. To determine whether the pattern of gene expression in the  $\beta/\delta$ 39 cells resembles that of the 3T3-L1 preadipocytes during normal adipogenesis, we analyzed the expression of select adipocyte mRNAs in these engineered cells after stimulating them to differentiate (Fig. 3 A). Proliferating  $\beta/\delta$ 39 cells were switched to tetracycline-free medium for 48 h, during which time they reached confluence and expressed maximum amounts of C/EBP $\beta$  and C/EBP $\delta$

mRNAs. At confluence (day 0) when they express C/EBP $\beta$  and C/EBP $\delta$  but negligible amounts of PPAR $\gamma$  and the other adipogenic mRNAs, they were exposed to the differentiation cocktail containing DEX, MIX, and insulin for 48 h. During this period the only gene that was induced was PPAR $\gamma$ . After the initial 2-d exposure to these inducers, the cells were switched to maintenance medium containing FBS, insulin, and the PPAR $\gamma$  ligand ciglitazone, which resulted in sequential activation of the adipogenic mRNAs. aP2 and adipsin mRNAs reached maximum levels of expression by day 4 of the differentiation process, whereas GPD and GLUT4 continued to accumulate and finally reached a plateau between 8 and 10 d. As observed in Fig. 2, C/EBP $\alpha$  mRNA was not activated at any time during the conversion of the  $\beta/\delta$ 39 cells into adipocytes. The presence of tetracycline in the differentiation medium for the entire 10-d period completely inhibited expression of the adipocyte mRNAs. To assess the extent of conversion of the  $\beta/\delta$ 39 fibroblasts into fat-laden adipocytes, cells were induced to differentiate for 8 d, and were then stained with Oil Red O. Approximately 100% of the cells contained fat droplets when

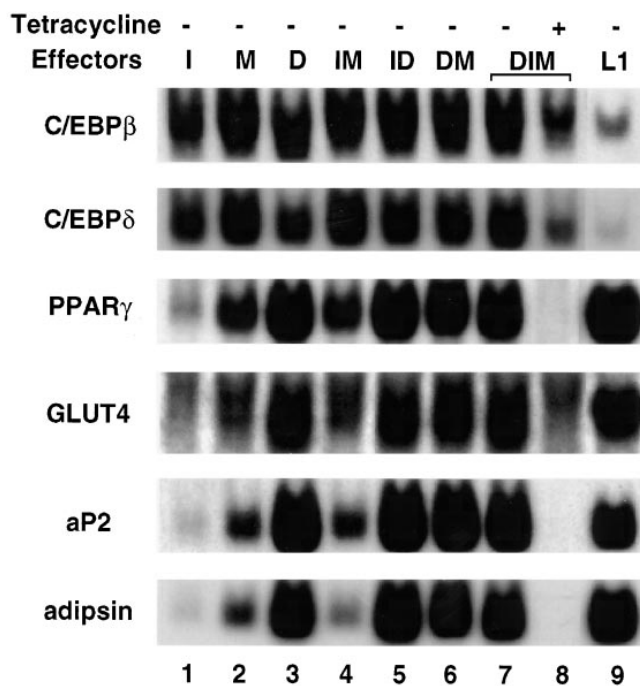


**Figure 3.** Sequential activation of adipogenic gene expression during the conversion of NIH-3T3  $\beta/\delta$ 39 cells into adipocytes.  $\beta/\delta$ 39 cells were grown in the presence or absence of tetracycline to confluence (day 0) and then exposed to DEX, MIX, and insulin for 48 h. After this initial stimulation, the cultures were maintained for 8 d in medium containing insulin, ciglitazone, and FBS, in the presence or absence of tetracycline as indicated. (A) Total RNA was extracted at the indicated times, and 25  $\mu$ g of each RNA was subjected to Northern blot analysis. (B)  $\beta/\delta$ 39 cells were grown and induced to differentiate in the absence or presence of tetracycline as described in A. At day 10 after differentiation, the cells were stained with Oil Red O, and then counterstained with giemsa before being photographed.



cultured in the absence of tetracycline, whereas cells exposed to the antibiotic for the entire differentiation period exhibited a typical 3T3 fibroblast morphology (Fig. 3B). One of the similarities of the sequential gene activation during differentiation of both 3T3-L1 and the  $\beta/\delta 39$  cells is the activation of PPAR $\gamma$  before the induction of other adipogenic genes.

*Induction of GLUT4 gene expression in the  $\beta/\delta 39$  cells requires exposure to the adipogenic inducers that also stimulate PPAR $\gamma$  production.* To identify the effectors responsible for activating GLUT4 expression and to correlate this process with the expression of PPAR $\gamma$ , we cultured the  $\beta/\delta 39$  cells in tetracycline-free medium, thereby enhancing C/EBP $\beta$  and C/EBP $\delta$  expression, and then exposed them to various combinations of insulin, MIX, and DEX in the presence of the PPAR $\gamma$  ligand ciglitazone. The Northern blot in Fig. 4 shows that culture of these cells in medium containing only insulin activates PPAR $\gamma$  to a minor extent, and is incapable of inducing GLUT4 expression (lane 1). Exposure of the cells to MIX in the absence or presence of insulin (lanes 2 and 4) stimulates PPAR $\gamma$  expression somewhat further than insulin, but only modestly enhances GLUT4 expression. As observed previously (30), the most potent inducer of PPAR $\gamma$  mRNA production is DEX, which also activates GLUT4 as well as aP2 and adipsin mRNAs, whether the cells are cultured in DEX alone (lane 3) or DEX in combination with the other effectors (lanes 5, 6, and 7). The level of expression of these adipogenic genes (PPAR $\gamma$ , GLUT4, aP2, and adipsin) in these fibroblasts ( $\beta/\delta 39$  cells) is

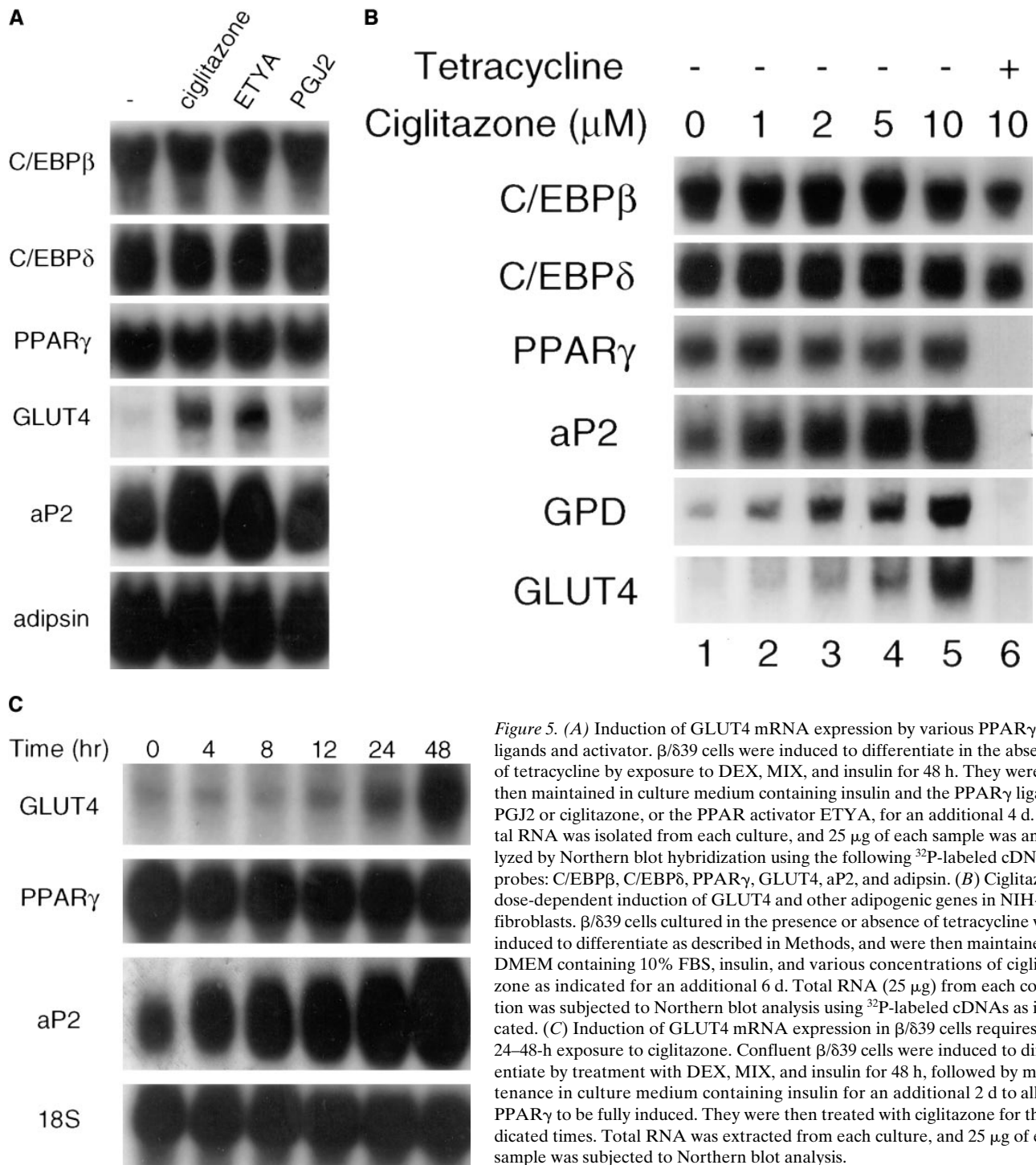


**Figure 4.** Effects of the adipogenic inducers on activation of PPAR $\gamma$  and GLUT4 mRNA in the  $\beta/\delta 39$  cells.  $\beta/\delta 39$  cells were grown to confluence in the absence or presence of tetracycline. They were then exposed to various combinations of the effectors DEX, MIX, and insulin for 48 h. They were subsequently maintained in medium containing FBS, insulin, and ciglitazone for an additional 4 d. Tetracycline (1  $\mu\text{g}/\text{ml}$ ) was present in the control culture as indicated. Total RNA was extracted at day 6 from each culture, and 20  $\mu\text{g}$  of each was subjected to Northern blot analysis. I, insulin (5  $\mu\text{g}/\text{ml}$ ); D, DEX (1  $\mu\text{M}$ ); M, MIX (0.5 mM). L1, total RNA isolated from 3T3-L1 adipocytes cultured for 8 d as described in Fig. 1.

almost equivalent to that expressed in fully differentiated 3T3-L1 adipocytes (lane 9). The  $\beta/\delta 39$  cells maintained in tetracycline throughout the culture period exhibit normal fibroblast levels of C/EBP $\beta$  and C/EBP $\delta$ , and do not express either PPAR $\gamma$  or GLUT4 mRNAs, even though they have been exposed to DEX, MIX, and insulin (lane 8).

*Induction of GLUT4 expression is dependent on exposure of  $\beta/\delta 39$  cells to a PPAR $\gamma$  ligand.* In order for PPAR $\gamma$  to act as a transcription factor it needs to associate with an appropriate ligand such as the thiazolidine ciglitazone, or the prostaglandin PGJ2. Thus, to assess the role of PPAR $\gamma$  in regulating GLUT 4 gene expression, we analyzed the effect of PPAR ligands on GLUT4 mRNA production during the conversion of  $\beta/\delta 39$  cells into adipocytes. In the experiment shown in Fig. 5,  $\beta/\delta 39$  cells were primed to differentiate by culture in tetracycline-free medium containing DEX, MIX, insulin, and 10% FBS for 48 h, which activated PPAR $\gamma$  expression. The cells were then exposed to fresh medium containing insulin, 10% FBS, and the PPAR $\gamma$  ligands ciglitazone or PGJ2, as well as ETYA (an activator of PPAR) for an additional 4 d, at which time total RNA was isolated and subjected to Northern blot analysis. Fig. 5A shows that the adipogenic inducers DEX, MIX, insulin, and FBS are potent inducers of PPAR $\gamma$ , aP2, and adipsin mRNAs, but they are incapable of activating GLUT4 mRNA production in the  $\beta/\delta 39$  cells (lane 1). In contrast, exposure of these cells to ciglitazone, ETYA, or PGJ2 after stimulation with the adipogenic inducers results in activation of GLUT4 mRNA expression to varying extents (lanes 2–4). Fig. 5B shows that the dose of ciglitazone required to induce GLUT4 mRNA expression in the presence of elevated levels of C/EBP $\beta$ , C/EBP $\delta$ , and PPAR $\gamma$  is 10  $\mu\text{M}$ . As seen in Fig. 5A, production of aP2 mRNA occurs in the absence of ciglitazone, although its level of expression is enhanced severalfold with increasing concentrations of the thiazolidinedione. To determine the kinetics of induction of GLUT4 gene expression,  $\beta/\delta 39$  cells were treated with FBS, DEX, MIX, and insulin for 48 h, followed by maintenance in medium containing FBS and insulin for an additional 2 d to allow PPAR $\gamma$  expression to be fully induced (“primed cells”; Fig. 5C, lane 1). The abundance of GLUT4 mRNA was measured by Northern blot analysis at different times after exposure of these cells to 10  $\mu\text{M}$  of ciglitazone. Fig. 5C shows that expression of GLUT4 mRNA is not detectable until 12–24 h after addition of ciglitazone. Furthermore, it takes 48 h for its expression to reach a maximum level. This is in contrast to the rapid activation of aP2 mRNA production, which occurs during the initial 4 h of drug treatment.

*The ciglitazone-dependent induction of GLUT4 mRNA expression in the  $\beta/\delta 39$  cells is accompanied by synthesis of GLUT4 protein and an increase in glucose uptake in response to insulin.* One of the major functions of fully mature adipocytes is to increase glucose uptake in response to elevated levels of insulin, which is facilitated by a transport system that involves GLUT4 protein. The results shown above demonstrate that enhanced expression of an activated form of PPAR $\gamma$  induces the expression of abundant amounts of GLUT4 mRNA in NIH-3T3 fibroblasts. Previous investigations have shown, however, that overexpression of GLUT4 mRNA in nonadipogenic cells that have insulin receptors and normal intracellular organelles does not recapitulate the insulin-regulatable glucose transport system (54–56). To assess the extent to which the  $\beta/\delta 39$  cells express the mature adipogenic phenotype, we



**Figure 5.** (A) Induction of GLUT4 mRNA expression by various PPAR $\gamma$  ligands and activator.  $\beta$ /839 cells were induced to differentiate in the absence of tetracycline by exposure to DEX, MIX, and insulin for 48 h. They were then maintained in culture medium containing insulin and the PPAR $\gamma$  ligands PGJ2 or ciglitazone, or the PPAR activator ETYA, for an additional 4 d. Total RNA was isolated from each culture, and 25  $\mu$ g of each sample was analyzed by Northern blot hybridization using the following  $^{32}$ P-labeled cDNA probes: C/EBP $\beta$ , C/EBP $\delta$ , PPAR $\gamma$ , GLUT4, aP2, and adipsin. (B) Ciglitazone dose-dependent induction of GLUT4 and other adipogenic genes in NIH-3T3 fibroblasts.  $\beta$ /839 cells cultured in the presence or absence of tetracycline were induced to differentiate as described in Methods, and were then maintained in DMEM containing 10% FBS, insulin, and various concentrations of ciglitazone as indicated for an additional 6 d. Total RNA (25  $\mu$ g) from each condition was subjected to Northern blot analysis using  $^{32}$ P-labeled cDNAs as indicated. (C) Induction of GLUT4 mRNA expression in  $\beta$ /839 cells requires a 24–48-h exposure to ciglitazone. Confluent  $\beta$ /839 cells were induced to differentiate by treatment with DEX, MIX, and insulin for 48 h, followed by maintenance in culture medium containing insulin for an additional 2 d to allow PPAR $\gamma$  to be fully induced. They were then treated with ciglitazone for the indicated times. Total RNA was extracted from each culture, and 25  $\mu$ g of each sample was subjected to Northern blot analysis.

analyzed whether expression of GLUT4 mRNA in these fibroblasts gives rise to the corresponding protein, and whether induction of PPAR $\gamma$  can also turn on the insulin-responsive glucose transporter system. In the experiment shown in Fig. 6 and Table I, the  $\beta$ /839 cells were cultured in the presence of different extracellular inducers, resulting in varying levels of PPAR $\gamma$  and GLUT4 mRNA expression. The Western blot analysis shown in Fig. 6 demonstrates that abundant quantities of GLUT4 protein are synthesized only in the  $\beta$ /8 cells that also express an activated form of PPAR $\gamma$ . In other words, these cells

are cultured in tetracycline-free medium to enhance C/EBP $\beta$  and C/EBP $\delta$ , and are then exposed to DEX and ciglitazone, which effectively induces PPAR $\gamma$  and ensures the presence of a potent ligand. In fact, if cells are cultured in medium either containing tetracycline or in the absence of ciglitazone where differentiation either does not occur or progresses poorly, the amount of GLUT4 protein is negligible. The data showing the results of the glucose uptake studies are presented in Table I. In 3T3-L1 adipocytes, glucose uptake is increased about five-fold in response to insulin stimulation. In the  $\beta$ /839 cells, glu-



**Table I. Insulin-dependent Glucose Uptake 2-Deoxyglucose Uptake (pmol/mg/min)**

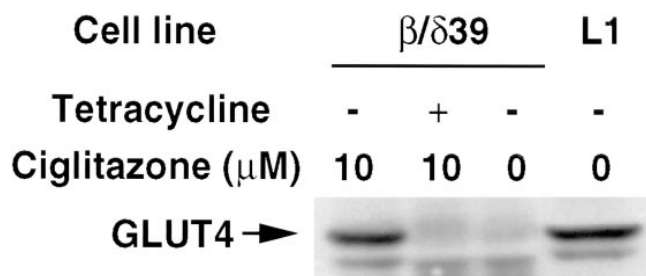
Cell line	$\beta/\delta 39$			L1
	-	+	-	-
Tetracycline	-	+	-	-
Ciglitazone	+	-	-	-
+ Insulin	726±53	593±41	582±31	735±67
- Insulin	353±27	607±36	539±23	145±25
Fold	2.1	1.0	1.1	5.1

$\beta/\delta 39$  cells were grown and induced to differentiate under the conditions as described in Fig. 6. Cells were subjected to [ $^3$ H]2-deoxyglucose uptake assay as described in Methods at day 8 after the initiation of differentiation. 3T3-L1 adipocytes were included in the assay as a control.

glucose uptake is increased about twofold under optimal differentiation conditions. In the control cells, however, where the cells are cultured either in the presence of tetracycline or in the absence of ciglitazone, not only is GLUT4 protein minimally expressed, correlating with the expression of the mRNA, but the cells are not responsive to stimulation with insulin measured by glucose uptake. These data demonstrate that PPAR $\gamma$  activates the fully differentiated adipogenic program that includes both the induction of GLUT4 gene expression and insulin-responsive glucose uptake.

## Discussion

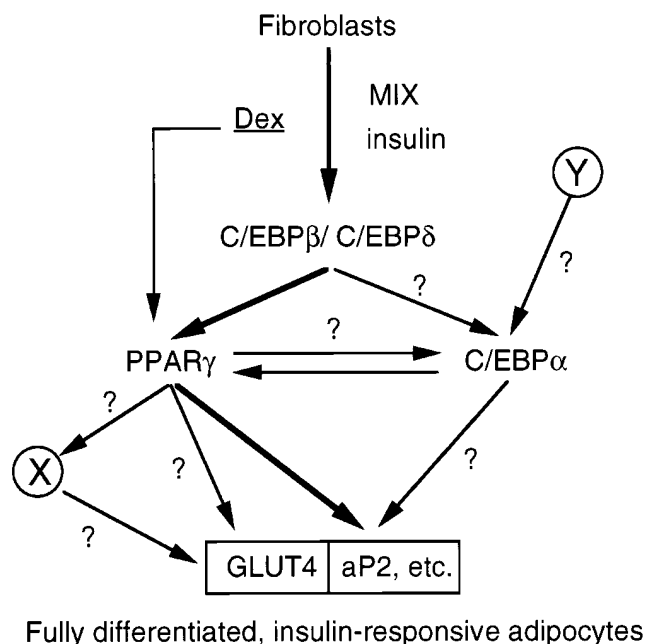
Adipocytes are highly specialized cells that play a major role in energy homeostasis in the organism. Their primary function is to synthesize and store triglycerides at times of caloric excess and to mobilize these stores when caloric intake is low. Insulin plays an important role in regulating lipid metabolism in adipose tissue by stimulating glucose uptake and lipogenesis, as well as inhibiting lipolysis. To facilitate the response to insulin, adipocytes express a host of proteins and enzymes that function in many different metabolic processes to maintain the balance of energy. Transcription of several of the genes that code



**Figure 6.** Induction of GLUT4 protein during adipogenic conversion of the  $\beta/\delta 39$  cells.  $\beta/\delta 39$  cells were grown to confluence and then induced to differentiate by exposure to DEX, MIX, and insulin for 48 h in the presence or absence of tetracycline. After initiation of differentiation, the cells were maintained in DMEM and 10% FBS in the presence or absence of tetracycline, with or without ciglitazone as indicated for an additional 6 d. Total membrane protein was isolated from each culture at day 8, and 300  $\mu$ g of each was subjected to Western blot analysis using anti-GLUT4 and anti-mouse polyvalent immunoglobulins (IgA, IgM, IgG) as primary and secondary antibodies, respectively. Total membrane protein (150  $\mu$ g) from 3T3-L1 adipocytes at day 10 of differentiation was included as a positive control.

for these proteins is activated during the differentiation of preadipocytes into adipocytes (57). The present study provides evidence demonstrating that induction of the insulin-dependent glucose transport system during conversion of mesenchymal stem cells into adipocytes is regulated in part by PPAR $\gamma$ . Specifically, the data show that ectopic expression of C/EBP $\beta$  and C/EBP $\delta$  in NIH-3T3 cells exposed to glucocorticoids induces PPAR $\gamma$  expression, and in the presence of a PPAR $\gamma$  ligand (ciglitazone) these cells are stimulated to convert into fat-laden adipocytes that express both GLUT4 mRNA and protein (Figs. 3 and 6). In addition, expression of a ligand-activated form of PPAR $\gamma$  in NIH-3T3 fibroblasts also activates the insulin-responsive glucose transport system since exposure of the  $\beta/\delta 39$  adipocytes to insulin stimulates 2-deoxyglucose uptake (Table I). Activation of the adipogenic program in these fibroblasts occurs in the absence of C/EBP $\alpha$ . We can conclude, therefore, that the induction of PPAR $\gamma$  in nonadipogenic fibroblasts exposed to a PPAR $\gamma$  ligand is sufficient to promote their differentiation into mature adipocytes that express the insulin-dependent glucose transporter GLUT4. Based on the results acquired in this investigation and our previous studies (30, 36), we outline a potential network of regulatory pathways involving PPAR $\gamma$  and C/EBPs that regulate adipogenesis (Fig. 7).

Although the molecular mechanisms that regulate expression of the GLUT4 gene during adipogenesis are unknown,



**Figure 7.** Schematic model of the pathways controlling differentiation of fibroblasts into adipocytes. Overexpression of C/EBP $\beta$  and C/EBP $\delta$  in NIH 3T3 fibroblasts activates PPAR $\gamma$  expression in the presence of adipogenic inducers DEX or MIX and insulin. PPAR $\gamma$  induces the expression of aP2, GLUT4, and other adipocyte differentiation-dependent genes, and converts these fibroblasts into fully differentiated insulin-dependent adipocytes. Expression of GLUT4 in these fibroblasts is activated by PPAR $\gamma$ , which likely involves other unknown factor(s) (X). C/EBP $\alpha$ , however, is absent in these cells despite the fact that C/EBP $\beta$  and C/EBP $\delta$  as well as PPAR $\gamma$  are expressed. This fact suggests that regulation of C/EBP $\alpha$  requires additional unknown factor(s) (Y).

the observations presented in this study allow us to speculate on the role of at least two families of transcription factors: the C/EBPs and the PPARs. These data strongly suggest that PPAR $\gamma$  plays a significant role in activating GLUT4 transcription during the terminal stages of adipogenesis in NIH-3T3 cells. In addition, induction of GLUT4 expression by PPAR $\gamma$  requires 24–48 h of exposure to ciglitazone, and appears to be dependent on protein synthesis (data not shown). These data suggest that PPAR $\gamma$  activates the expression of additional transcription factors (*X*, see Fig. 7) that may cooperate with PPAR $\gamma$  to initiate GLUT4 transcription. The genes encoding aP2 and PEPCK have a similar temporal pattern of expression during adipogenesis as the GLUT4 gene; the promoters for these genes have been shown to contain PPAR binding sites that can facilitate their respective activation by PPAR $\gamma$  in *in vitro* transfection assays (17, 52). Thus, it is also possible that there is a direct interaction between PPAR $\gamma$  and the corresponding nuclear hormone response elements in the promoter/enhancer of the GLUT4 gene. This possibility needs to be further investigated in the future when more sequences of the GLUT4 gene become available.

The role of the C/EBPs in activating GLUT4 gene expression is unclear. A previous study identified a C/EBP binding site in the promoter of the mouse GLUT4 gene (31). The data presented in our study, however, demonstrate that overexpression of C/EBP $\beta$  and C/EBP $\delta$  are not sufficient to induce GLUT4 transcription (Fig. 3 A, lane I; and Fig. 4, lane I). It appears that the major role of C/EBP $\beta$  and C/EBP $\delta$  along with glucocorticoids is to activate PPAR $\gamma$  expression, which is responsible for the induction of GLUT4 transcription. In addition, C/EBP $\alpha$  is not required for activation of GLUT4 and the other adipocyte genes since it is absent in the fully differentiated cell lines (including  $\beta$ 2,  $\beta$ / $\delta$ 39, and P $\gamma$ 2) that express GLUT4 as well as other major markers of the mature adipocyte phenotype. It is possible, however, that the artificially high level of C/EBP $\beta$  in some NIH-3T3 cell lines ( $\beta$ 2 and  $\beta$ / $\delta$ 39) may be capable of substituting for C/EBP $\alpha$  by synergizing with PPAR $\gamma$  to activate GLUT4 expression during the terminal stages of the differentiation process.

The absence of C/EBP $\alpha$  in the differentiated NIH-3T3 cell lines ( $\beta$ 2,  $\beta$ / $\delta$ 39, and P $\gamma$ 2) suggests that PPAR $\gamma$  alone or in combination with C/EBP $\beta$  and C/EBP $\delta$  is not sufficient to activate C/EBP $\alpha$  expression in nonadipogenic fibroblasts. One possibility is that the C/EBP $\alpha$  gene is maintained in a repressed state by suppressor proteins, which may need to be inactivated before the required transcription factors can induce its expression.

GLUT4 plays an important role in maintaining glucose homeostasis in mammals. Down regulation of its expression in adipocytes is a universal feature of insulin-resistant states. A number of transgenic studies show that overexpression of GLUT4 in either muscle (58, 59) or adipose tissue (60) alone or together (61, 62) enhances glucose tolerance and insulin-dependent glucose uptake *in vivo*. Specifically, elevating the level of GLUT4 expression in these tissues prevents insulin resistance in normal mice (62) and ameliorates diabetes in mice with metabolic perturbations (58, 60). The molecular mechanisms regulating this important transporter, however, are essentially unknown. The results presented here shed light on the transcriptional regulation of GLUT4 during adipocyte differentiation.

As mentioned at the outset, the thiazolidinediones (TZDs)

were originally developed as synthetic drugs that are capable of sensitizing individuals who suffer from non-insulin-dependent diabetes mellitus to insulin and effectively lower blood glucose (63). More recently, investigations have demonstrated that TZDs are synthetic PPAR $\gamma$  ligands and as such are capable of promoting the conversion of some PPAR $\gamma$ -expressing cell lines into adipocytic cells (19–21). It is not known, however, whether the PPAR $\gamma$  ligand activity of the TZDs is involved in processes that lower blood glucose in animals with diabetes. The results presented here not only demonstrate that PPAR $\gamma$  induces GLUT4 expression, they also suggest a mechanism by which the TZDs increase the sensitivity of adipose tissue to insulin. Such a mechanism may include induction of genes that encode other proteins involved in insulin-dependent glucose uptake, since overexpression of the GLUT4 protein in nonadipogenic cells does not recapitulate the insulin-regulatable glucose transport system (54–56). The decrease in blood glucose levels in response to elevated levels of insulin is facilitated by muscle and liver as well as adipose tissue. The mechanisms by which TZDs improve insulin sensitivity in these tissues are also unknown. Studies have shown that pioglitazone can increase insulin sensitivity by activating insulin receptor kinase activity in muscles of obese or high fat-fed rats (64, 65). This TZD was also demonstrated to increase P-I-3-kinase activity upon insulin stimulation in cultured myotubes (66). In addition, it was found to increase insulin sensitivity in diabetic rat liver by regulating the transcription of two key enzymes—glucokinase and PEPCK—in gluconeogenic/glycolytic pathways (23). One possibility is that TZDs function in all insulin-responsive tissues by activating PPAR $\gamma$ , which induces the appropriate genes involved in glucose metabolism. In the case of liver, TZDs may activate PPAR $\gamma$ 1, the hepatic isoform of PPAR $\gamma$ , and in doing so may regulate gluconeogenesis/glycolysis. In muscle tissue, PPAR $\gamma$  is expressed at very low levels, but it is possible that its level of expression may be enhanced by TZDs via an autoregulatory mechanism. In this regard, it will be important to determine whether expression of the GLUT4 gene in muscle tissue is similarly regulated by PPAR $\gamma$ . It is also possible that the action of TZDs through PPAR $\gamma$  in adipose tissue might result in production and secretion of molecules that in turn regulate the insulin-signaling pathway in liver and muscle. Further analysis of other targets of PPAR $\gamma$  and their possible involvement in insulin signaling may provide important information to help combat obesity and its related disorders.

## Acknowledgments

We are grateful to Deepanwita Prusty for critical reading of the manuscript and valuable suggestions. We thank Dr. Jacqueline Stephens for advice on the glucose uptake assay. We acknowledge Dr. Bruce Spiegelman for the P $\gamma$ 2 cell line and Dr. Paul Pilch for the GLUT4 antibody.

This work was funded by National Institutes of Health grants CA39099 and DK51586.

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