Polymerase I and Transcript Release Factor Regulates Lipolysis via a Phosphorylation-Dependent Mechanism

Nabila Aboulaich,1 Patricia C. Chui,1 John M. Asara,1,2 Jeffrey S. Flier,1 and Eleftheria Maratos-Flier1

OBJECTIVE—Polymerase I and transcript release factor (PTRF) is a protein highly expressed in adipose tissue and is an integral structural component of caveolae. Here, we report on a novel role of PTRF in lipid mobilization.

RESEARCH DESIGN AND METHODS—PTRF expression was examined in different adipose depots of mice during fasting, refeeding, and after administration of catecholamines and insulin. Involvement of PTRF during lipolysis was studied upon PTRF knockdown and overexpression and mutation of PTRF phosphorylation sites in 3T3-L1 adipocytes.

RESULTS—PTRF expression in mouse white adipose tissue (WAT) is regulated by nutritional status, increasing during fasting and decreasing to baseline after refeeding. Expression of PTRF is hormonally regulated because treatment of mice with insulin leads to a decrease in expression, whereas isoproterenol increases expression in WAT. Manipulation of PTRF levels revealed a role of PTRF in lipolysis. Lentiviral-mediated knockdown of PTRF resulted in a marked attenuation of glycerol release in response to isoproterenol. Conversely, overexpressing PTRF enhanced isoproterenol-stimulated glycerol release. Mass-spectrometric analysis revealed that PTRF is phosphorylated at multiple sites in WAT. Mutation of serine 42, threonine 304, or serine 368 to alanine reduced isoproterenol-stimulated glycerol release in 3T3-L1 adipocytes.

CONCLUSIONS—Our study is the first direct demonstration for a novel adipose tissue–specific function of PTRF as a mediator of lipolysis and also shows that phosphorylation of PTRF is required for efficient fat mobilization. Diabetes 60:757–765, 2011

White adipose tissue (WAT) plays a critical role in energy homeostasis. Adipocytes store energy in the form of triacylglycerides (TAG) during feeding and breakdown TAG during fasting to release fatty acids and glycerol. TAG breakdown (lipolysis) is regulated by lipolytic hormones, such as catecholamines, whereas lipogenic hormones, such as insulin, stimulate the synthesis of TAG and inhibit lipolysis (1). Catecholamines stimulate lipolysis through increasing cAMP levels and activating protein kinase A (PKA) (2), whereas insulin inhibits lipolysis through activating phosphodiesterase 3B, which causes degradation of cAMP and loss of PKA activation (3). PKA phosphorylates target proteins, including lipolytic enzymes, and lipid droplet–associated proteins, including hormone-sensitive lipase (HSL) and perilipin (4–6). Phosphorylated HSL translocates from the cytosol to the surface of the lipid droplets where it catalyses the hydrolysis of TAG together with adipose triglyceride lipase (ATGL) (7).

Polymerase I and transcript release factor (PTRF), also called cav-p60 and cavin, is a 50-kDa protein that is highly expressed in smooth muscle, lung, and adipose tissue. PTRF originally was identified in the nucleus of a mouse embryonic fibroblast cell line, where it plays a role in enhancing the transcriptional activity of polymerase I and polymerase II (8,9). In addition to its nuclear localization, PTRF is found at the cytoplasmic face of caveolae and is the major caveola-associated protein in primary human adipocytes (10). Recently, PTRF was found to be required for caveolae formation and may serve as a caveolae coat protein together with caveolin-1 (11–13). Of note, it also has been demonstrated that PTRF localizes specifically to a caveolae subclass that metabolizes TAG (14,15), suggesting a potential role of PTRF in TAG metabolism. Moreover, PTRF interacts with HSL in primary human adipocytes and translocates from the plasma membrane to the cytosol in response to insulin treatment, suggesting that PTRF may function in concert with HSL in the regulation of lipolysis (16). Deletion of PTRF causes loss of caveolae and dyslipidemia in mice (17). In humans, mutations in the PTRF gene are associated with muscular dystrophy and lipodystrophy (18). These findings point to a potential role of PTRF in regulating lipid metabolism in adipose tissue.

PTRF is phosphorylated at multiple sites (19–23). In primary human adipocytes, phosphorylation of PTRF at multiple serine and threonine residues has been reported (10,14). Insulin induces phosphorylation of PTRF on a tyrosine residue in adipocytes (24,25). However, the functional significance of PTRF phosphorylation has not previously been characterized.

Here, we report that PTRF expression is under nutritional and hormonal control in the WAT of mice. Fasting and catecholamine treatment induce PTRF expression, whereas refeeding and insulin administration reduce its expression in WAT. Lentiviral-mediated reduction of PTRF expression in 3T3-L1 adipocytes significantly decreases isoproterenol-stimulated glycerol release. Conversely, overexpression of PTRF leads to increased isoproterenol-stimulated glycerol release. Changes in PTRF expression are accompanied by phosphorylation because PTRF is phosphorylated during fasting and upon isoproterenol treatment in adipocytes, and this phosphorylation is PKA dependent. Mutation of serine 42, threonine 304, or serine 368 to alanine of PTRF leads to reduced isoproterenol-stimulated...
gycerol release. Taken together, these data suggest that PTFR plays a crucial role in lipolysis and that this function is dependent on phosphorylation.

**RESEARCH DESIGN AND METHODS**

All procedures were approved by the Beth Israel Deaconess Medical Center Institutional Animal Care and Use Committee. Male C57BL/6, mice, aged 18–20 weeks, were maintained in a temperature-controlled environment at 24 °C under a 12-h light/12-h dark cycle (0600–1800 h) with ad libitum access to a standard diet (P6 rodent diet; Harlan Teklad, Madison, WI) and water or water alone when fasted. Mice were killed between 0000 and 1100 h and rapidly dissected. Tissues were flash-frozen for further analysis.

**Cell culture and differentiation.** 3T3-L1 cells were cultured in Dulbecco’s modified Eagle’s medium (DMEM) (Invitrogen, Carlsbad, CA) with 10% bovine calf serum at 5% CO2. Two days after confluence was reached, cells were differentiated in DMEM containing 1% dexamethasone (Sigma-Aldrich, St. Louis, MO), 10 μg/mL insulin (Invitrogen), and 0.5 mmol/L isobutylmethylxanthine (Sigma-Aldrich) in DMEM with 10% FBS and then maintained in medium containing insulin for another 2 days. Cells were then transferred to DMEM with 10% FBS until they were ready to be harvested. For insulin and isoproterenol experiments, adipocytes were incubated in serum-free DMEM containing 2% BSA (Sigma-Aldrich) for 16 h then treated with insulin or isoproterenol at the concentrations indicated.

**Overexpression, site-directed mutagenesis, and short-hairpin RNA-mediated knockdown of PTFR.** For overexpression of PTFR, full-length PTFR cDNA were subcloned into a lentiviral expression vector pCDH-CMV-EF1-Puro as a template according to the manufacturer’s instruction. For PTFR knockdown, five PTFR short-hairpin RNA (shRNA) constructs in lentiviral vector pLKO.1 were obtained from Open Biosystems (Huntsville, AL). The construct chosen for the knockdown experiments was TRCN0001035755. All lentiviral constructs were transfected into 293T cells using Lipofectamine 2000 (Invitrogen), along with packaging and envelope plasmids expressing gag, pol, rev, and packaging plasmid expressing VSV-G. The constructs expressing PTFR shRNA were selected using puromycin. Site-directed mutagenesis was performed with a self-packaging 75-fl virus that was then transduced into a hybrid LTQ-Orbitrap XL mass spectrometer (Thermo Scientific, Waltham, MA) in the data-dependent acquisition and positive-ion mode at 300 nL/min. MS/MS spectra collected via collision-induced dissociation in the ion trap were searched against the concatenated target and decoy (reversed) single-entry PTFR and full Swiss-Prot protein databases using Sequest (ProteomeX Broker Software, Thermo Scientific) with differential modifications for serine/threonine/tyrosine phosphorylation (+79.97). Phosphopeptide sequences were identified if they initially passed the following Sequest scoring thresholds against the target database: 1 + ions, Xcorr ≥2.0, S+ ≥0.4; 2 + ions, Xcorr ≥2.0, S+ ≥0.4; 3 + ions, Xcorr ≥2.60, S+ ≥0.4, P ≥ 5 against the target protein database. Passing MS/MS spectra were manually inspected to be sure that all b- and y-fragment ions aligned with the assigned sequence and modification sites. Determination of the exact sites of phosphorylation was aided using ProteinScape software (ProteomeX Broker Software Suite, Thermo Scientific). False-discovery rates of peptide hits were estimated below 1.25% based on reversed database hits.

**Lipolysis assays.** For basal and stimulated lipolysis, adipocytes were serum starved for 24 h and incubated in the presence or absence of isoproterenol for the indicated time. Glyceral release was measured using the free glyceral reagent kit (Sigma). Adipocytes were harvested in radioimmunoprecipitation assay buffer containing protease inhibitors, and the protein content of cell lysates was determined using the bicinchoninic acid protein assay kit (Pierce, Rockford, IL). Glyceral levels were normalized with total cellular protein.

**RESULTS**

**PTFR expression in adipose tissue is regulated by nutritional status in mice in a depot-specific manner.** PTFR is highly expressed in adipose tissue (10). We examined its expression levels in different adipose depots in mice. PTFR expression was depot specific, with the highest expression levels in gonadal adipose tissue compared with subcutaneous, retroperitoneal, and brown adipose tissue depots (Fig. 1A). Of note, no significant difference in PTFR protein expression was seen in any of the adipose tissue depots of ob/ob mice compared with wild-type mice (Supplementary Fig. 2). We next examined nutritional influences on PTFR expression. In gonadal fat, expression of PTFR was regulated by fasting and refeeding. Fasting for 48 h leads to a twofold induction in mRNA levels and a ninefold increase in protein levels compared with fed mice (Fig. 1B). The magnitude of PTFR mRNA changes was lower than that seen in protein, suggesting that PTFR expression is also modulated on the posttranscriptional level. Fasting resulted in a rapid reduction of PTFR expression to fed levels within 1 h and remained at the same levels throughout the refeeding time course (Fig. 1C). The observed increase in PTFR expression in gonadal adipose tissue was time dependent (Fig. 1C). Furthermore, PTFR expression responds to nutritional manipulation in all three WAT depots examined but not in brown adipose tissue. Although PTFR expression levels increased after a 24-h fast in WAT depots, including gonadal, subcutaneous, and retroperitoneal, expression in brown adipose tissue did not change upon fasting (Fig. 1D). A faster-migrating PTFR band was observed (Fig. 1D), which is a result of well-characterized proteolytic cleavages of PTFR in adipocytes (10). We also observed a slower-migrating PTFR band on SDS-PAGE in WAT upon fasting (Fig. 1C and D), suggesting a posttranslational modification of PTFR, such as phosphorylation.

**PTFR expression is regulated by insulin and catecholamines in WAT.** Insulin and catecholamines play a role in the response of adipocyte tissue to fasting and refeeding. We therefore evaluated the direct effects of
these hormones on PTRF expression in vivo. Mice were injected intraperitoneally with insulin (0.75 units/kg) or isoproterenol (10 mg/kg), and the expression levels of PTRF were measured 1-h postinjection. Insulin treatment resulted in a twofold reduction of PTRF protein levels compared with that in the WAT of saline-treated control mice (Fig. 2A). Conversely, treatment with isoproterenol resulted in a twofold increase in PTRF protein levels in adipose tissue compared with controls (Fig. 2A). Isoproterenol treatment also induced a slower-migrating PTRF band on SDS-PAGE (Fig. 2A) similar to that seen in response to fasting (Fig. 1C and D), suggesting that PTRF might undergo phosphorylation. The magnitude of PTRF mRNA changes in response to hormonal treatment was lower than changes in protein expression (Fig. 2B), again suggesting a posttranscriptional regulation of PTRF. Taken together, these results indicate that PTRF expression in WAT is under nutritional regulation and that this tight regulation might be mediated directly by insulin and catecholamine, suggesting a role of PTRF in lipolysis.

**FIG. 1.** PTRF expression is upregulated in WAT but not in brown adipose tissue upon fasting in mice. A: PTRF mRNA expression in gonadal (Gonad), subcutaneous (Subc), retroperitoneal (Retro), and brown adipose tissue (Bat). B: PTRF mRNA (upper panel) and protein (bottom panel) expression in gonadal adipose tissue from ad libitum-fed or fasted mice for 48 h or refed mice for the indicated time. C: PTRF expression levels were determined by immunoblot in gonadal adipose tissue of ad libitum-fed or fasted mice for 12, 24, and 48 h. D: PTRF protein expression in gonadal (Gonad), subcutaneous (Subc), retroperitoneal (Retro), and brown adipose tissue (Bat) of ad libitum-fed or fasted mice for 24 h. Gene expression and protein expression were normalized to 36B4 and to actin, respectively (n = 4–8). Data are expressed as means ± SE. *P < 0.05.
PTRF expression and phosphorylation is hormonally regulated in 3T3-L1 adipocytes. Because 3T3-L1 adipocytes provide a cell culture model system for studies of lipolysis regulation, we used these cells to assess the role of PTRF and its phosphorylation in lipolysis. We first confirmed the in vivo data on PTRF regulation and phosphorylation. Consistent with the nutritional and hormonal regulation of PTRF expression in vivo in WAT, PTRF expression in vitro in 3T3-L1 adipocytes also is regulated by serum depletion, insulin, and catecholamine. Serum depletion of 3T3-L1 adipocytes for 16 h resulted in a twofold upregulation of PTRF protein levels (Fig. 3A, left panel). The addition of insulin to serum-free media resulted in a decrease of PTRF protein levels (Fig. 3A, right panel) in a dose-dependent manner (Fig. 3B). PTRF expression decreased by 50% compared with control levels (Fig. 3B). At a concentration of 100 nmol/L insulin, reduction of PTRF levels was first seen after 2 h and persisted throughout the 24-h time course (Fig. 3C).

In contrast to insulin, isoproterenol treatment increased PTRF protein levels with a peak at 1–2 h after treatment of 3T3-L1 adipocytes (Fig. 3D). PTRF levels remained elevated from baseline up to 8 h after isoproterenol treatment and decreased to basal levels between 8 and 24 h (data not shown). PTRF also was phosphorylated in 3T3-L1 adipocytes in response to isoproterenol treatment, as indicated by the appearance of a slower-migrating PTRF band, which first appears at 0.1 μmol/L isoproterenol (Fig. 3E) and within 30 min after the incubation of 3T3-L1 adipocytes with 1 μmol/L isoproterenol (Fig. 3D). This slower-migrating band disappeared almost completely 240 min after isoproterenol incubation (Fig. 3D). This is in agreement with the phosphorylation of PTRF in WAT in response to fasting and isoproterenol treatment (Figs. 1 and 2).

Because isoproterenol induces lipolysis through activating PKA-dependent phosphorylation of lipolytic proteins, including HSL and perilipin (1), we examined the role of PKA on PTRF phosphorylation. Incubation of 3T3-L1 adipocytes with isoproterenol in the presence and absence of H89, a PKA inhibitor, substantially inhibited isoproterenol-induced phosphorylation of PTRF (Fig. 3F). Perilipin also migrates more slowly during SDS-PAGE upon isoproterenol treatment as a result of phosphorylation by PKA on multiple sites (6). As expected, treatment with H89 also reduced the PKA-induced phosphorylation of perilipin (Fig. 3F). This indicates that PTRF undergoes PKA-dependent phosphorylation upon isoproterenol treatment of 3T3-L1 adipocytes, in agreement with our mass spectrometric identification of PKA-phosphorylation sites in PTRF in WAT during fasting (Table 1).

Taken together, these in vitro results confirm the hormonally-regulated expression and phosphorylation of PTRF seen in WAT.

Loss and gain of function of PTRF have opposite effects on lipolytic activity in 3T3-L1 adipocytes. The regulation of PTRF expression by insulin and catecholamines in adipocytes suggested a possible role for PTRF in lipolysis. To assess such a potential role for PTRF, we suppressed its expression by using lentiviral-driven shRNA targeting PTRF in 3T3-L1 adipocytes. PTRF protein levels were decreased by 45% compared with adipocytes infected with the nontargeting control shRNA lentivirus (Shcont) (Fig. 4A). Although basal rates of lipolysis were not affected by PTRF knockdown, isoproterenol-stimulated lipolysis, assayed by glycerol release, revealed a 30–40% reduction following PTRF knockdown (Fig. 4B).
TABLE 1
Identification of PTRF phosphorylation sites in WAT by LC/MS/MS experimental and actual peptide sequence

<table>
<thead>
<tr>
<th>Peptide sequence</th>
<th>Site</th>
<th>Sequest final score</th>
<th>MH+</th>
<th>Difference in mass (ppm)</th>
<th>Sequest cross-correlation score</th>
<th>△Cn</th>
<th>Sequest preliminary score</th>
</tr>
</thead>
<tbody>
<tr>
<td>PYSGFPDASgRSgEPTQGEAR</td>
<td>Ser21</td>
<td>0.67</td>
<td>2258.9</td>
<td>-0.3</td>
<td>4.5</td>
<td>0.05</td>
<td>404</td>
</tr>
<tr>
<td>ATEEPSTGtsDELIK</td>
<td>Ser42</td>
<td>0.87</td>
<td>1613.7</td>
<td>-3.1</td>
<td>4.03</td>
<td>0.07</td>
<td>1131</td>
</tr>
<tr>
<td>LPALKsVSK</td>
<td>Ser169</td>
<td>0.88</td>
<td>1022.6</td>
<td>0.4</td>
<td>3.34</td>
<td>0.22</td>
<td>390</td>
</tr>
<tr>
<td>VMtYQDEVKLPALKsVsk</td>
<td>Ser171</td>
<td>0.40</td>
<td>2128.1</td>
<td>-7.1</td>
<td>3.48</td>
<td>0.08</td>
<td>151</td>
</tr>
<tr>
<td>SFPtDHyVYAR</td>
<td>Thr304</td>
<td>0.59</td>
<td>1389.2</td>
<td>1.1</td>
<td>2.34</td>
<td>0.19</td>
<td>684</td>
</tr>
<tr>
<td>GsSpVHtIILETEESDAVLVDK</td>
<td>Ser368</td>
<td>0.73</td>
<td>2534.2</td>
<td>2.6</td>
<td>4.69</td>
<td>0.17</td>
<td>486</td>
</tr>
</tbody>
</table>

PTRF was immunoprecipitated from the gonadal adipose tissue of mice fasted for 24 h. Peptides obtained from in-gel tryptic digestion of the PTRF band were subjected to LC/MS/MS. Identified PTRF phosphopeptide sequences are listed below, along with the position of the phosphorylation site in the PTRF sequence and relevant database search scores. Lowercase boldface s and t indicate phosphorylation at serine and threonine, respectively. Phosphorylation at Ser42, Ser169, and Ser368 were previously identified, whereas Ser21, Ser171, and Thr304 are novel PTRF phosphorylation sites. △Cn, Sequest cross-correlation score difference between the top-ranked and next-best peptide sequence.

Next, we overexpressed PTRF in 3T3-L1 adipocytes by infecting cells with lentivirus containing full-length PTRF cDNA. PTRF protein levels increased twofold compared with adipocytes infected with green fluorescent protein (GFP) control lentivirus (Fig. 4C). This was associated with a 25–35% increase in isoproterenol-stimulated glycerol release (Fig. 4D). PTRF overexpression had no effects on the basal rate of lipolysis (Fig. 4D). These results are consistent with a role for PTRF during lipolysis.

**Mutation of specific PTRF phosphorylation sites reduces lipolysis in 3T3-L1 adipocytes.** We next examined the effects of PTRF phosphorylation on lipolysis. We generated lentiviral constructs containing GFP as control, wild-type PTRF, or PTRF mutants in which PTRF phosphorylation sites (Table 1) were mutated to alanine. 3T3-L1 adipocytes were infected with lentivirus, and the effects of PTRF mutations were examined 5 days after infection. Isoproterenol-stimulated lipolytic activity, as assayed by glycerol release, was lower in adipocytes expressing PTRF mutants S42A, T304A, and, S368A, when compared with wild-type PTRF (Fig. 5A). On the other hand, no effect was seen in the PTRF mutants S21A, S169A, and S171A, because they all showed similar lipolytic activity as wild-type PTRF (Fig. 5A and data not shown). There was no significant effect of PTRF phosphorylation-site mutations on basal lipolysis (Fig. 5A and Supplementary Table 1). These results suggest that PTRF regulation of isoproterenol-stimulated lipolysis is dependent on serine and threonine phosphorylation of PTRF at Ser42, Thr304, or Ser368 residues.

It is known that HSL, the key enzyme responsible for lipolysis in WAT, interacts with PTRF (16) and that its function during lipolysis also is dependent on PKA phosphorylation (28). To gain insight into the mechanisms by which the mutation of PTRF phosphorylation sites suppresses lipolysis, we examined the phosphorylation status of HSL in these cells. Notably, we found that the suppressed lipolytic activity in adipocytes expressing the PTRF mutations S42A, T304A, or S368A (Fig. 5A) was accompanied by a reduction of HSL phosphorylation at serine 563 and serine 660 (Fig. 5D). PKA-mediated phosphorylation of perilipin, on the other hand, was not affected in cells expressing mutated phosphorylation sites of PTRF (data not shown). In addition, there was no effect in the PTRF mutants on HSL phosphorylation at serine 565 (data not shown), which has been shown to be a target for AMP kinase but not PKA (28). Taken together, these data indicate that phosphorylation of PTRF at serine 42, threonine 304, or serine 368 is essential for the activation of HSL by PKA during lipolysis.

**DISCUSSION**

Adipose tissue lipolysis is an important process in which TAG are mobilized, releasing fatty acids and glycerol and thus providing the body with substrates during fasting. The dysregulation of lipolysis, which can occur in obesity or lipodystrophic states, can lead to elevated levels of fatty acids in the circulation, which is associated with an increased risk for developing cardiovascular diseases and diabetes. The lipolytic machinery is complex and includes as central components perilipin, HSL, and ATGL, in addition to several factors and interacting proteins. Here, we present data suggesting PTRF as a novel physiologically regulated and critical component of the lipolytic machinery.

We found that levels of PTRF expression vary in different adipose tissue depots. Moreover, PTRF expression is under strict hormonal and nutritional control in WAT but not in brown adipose tissue. Although catecholamines and fasting increase PTRF expression, insulin and refeeding decrease its expression. This differential regional expression and regulation of PTRF might contribute to the metabolic heterogeneity observed among different adipose tissue depots (29,30). The induction of PTRF expression by fasting and catecholamines in WAT supports with a role of PTRF during lipid mobilization. Of note, PTRF also is expressed in skeletal muscle, another tissue depot that exhibits lipolytic activity. Future experiments will determine whether skeletal muscle PTRF also could be regulated in a similar manner.

Consistent with nutritional and hormonal regulation, manipulation of PTRF expression in cultured cells also changed lipid homeostasis. PTRF overexpression and knockdown resulted in enhancement and suppression of lipolysis, respectively. This is in line with PTRF subcellular location at the lipid droplets and TAG-synthesizing caveolae subclass.

Lipolysis is an important process in which TAG are mobilized, releasing fatty acids and glycerol and thus providing the body with substrates during fasting. The lipolytic machinery is complex and includes as central components...
perilipin, HSL, and ATGL in addition to several factors and interacting proteins. Recently, both HSL and perilipin were localized to TAG-synthesizing caveolae subclass (31). Other lipolytic components, such as the β-adrenergic receptors, as well as PKA also were found to associate with caveolar membranes (32). It is therefore possible that PTRF, together with other lipolytic proteins, facilitates lipolysis of TAG in lipid droplets as well as in caveolae. This is consistent with the finding that the localization of both PTRF and HSL in caveolae is under insulin control, where insulin, which inhibits lipolysis, induced translocation of both PTRF and HSL from caveolae to the cytosol (16).

During fasting, hormones including catecholamines induce lipolysis through binding to β-adrenergic receptors, activating PKA, which phosphorylates perilipin and HSL at multiple sites (5,28,33,34). PKA-dependent phosphorylation of HSL is necessary for docking of HSL at the surface of lipid droplets and for activation of lipolysis (28). However, localization of PTRF to caveolae in the plasma membrane is not influenced by β-adrenergic stimulation (16). Insulin, on the other hand, inhibits lipolysis through activating phosphodiesterase 3B, which causes degradation of cAMP and loss of PKA activation (3). Our data show that during lipolysis, PTRF also is phosphorylated by PKA at multiple sites and that this PKA-dependent phosphorylation of PTRF plays an essential role during lipolysis. A number of phosphorylation sites in the mouse and human PTRF sequences have been previously identified. However, the functional significance of PTRF phosphorylation has not previously been characterized. Here, we...
provide evidence for an adipocyte-specific functional role of PTRF phosphorylation, as mutation of PTRF at serine 42, threonine 304, or serine 368 to alanine signifi-
cantly abrogated the lipolytic response in 3T3-L1 adipocytes.

In addition to phosphorylation, the action of HSL is de-
pendent on its interaction with other proteins such as
perilipin. This interaction is necessary for translocation of
HSL from the cytosol to the lipid droplets during lipolysis
(35). Furthermore, HSL interacts with the protein lipo-
transin, which docks HSL at the surface of the lipid
droplets (36). Because PTRF has been shown to interact
with HSL (16), it is possible that PTRF also serves as a
bridge between HSL and PKA to mediate phosphoryla-
tion and activation of HSL during lipolysis. Indeed, the
decrease in lipolysis in cells expressing the PTRF mutants
S42A, T304A, and S368A was accompanied by a reduction
in serine phosphorylation of HSL. Thus, phosphoryla-
tion of PTRF is required for the subsequent phosphoryla-
tion of HSL and initiation of lipolysis. It remains to be deter-
mined whether the interaction between PTRF and HSL is phos-
phorylation dependent and whether PKA-phosphorylated
PTRF interacts with other lipolytic proteins. It also would
be of interest to determine whether PTRF itself had TAG
hydrolase activity or if it serves specifically to modulate
the activity of other hydrolases such as HSL.

Recent studies (11,12,17) have demonstrated that PTRF
is required for the formation of caveolae because knock-
down of PTRF leads to loss of caveolae. Loss of caveolae
was accompanied with rapid degradation of caveolin-1
protein (11). It is unlikely that caveolae biogenesis is af-
ected in cells expressing mutated phosphorylation sites of
PTRF because no effects were seen on caveolin-1 protein
expression in these cells (data not shown). However, it
would be interesting to determine whether PTRF phosphor-
ylation has an effect on caveolae morphology and dynamics.

Our study represents the first direct demonstration of
nutritional and hormonal control of PTRF expression and
phosphorylation in adipose tissue in mouse. We provide
evidence for a novel adipose tissue-specific function of
PTRF as a critical mediator of lipolysis, which is a central
function of the adipocytes.

ACKNOWLEDGMENTS
This work was supported by research grants from the
National Institutes of Health (R01-DK-069983, to E.M.-F.,
and R37-DK-28082, to J.S.F.) and from the Wenner-Gren
Foundations (to N.A.).

No potential conflicts of interest relevant to this article
were reported.
The authors thank Dr. H.A. Jouihan (Department of Medicine, Stanford University School of Medicine) for critical review of the manuscript; Drs. F.M. Fisher and A.C. Adams (Department of Medicine, Beth Israel Deaconess Medical Center, Harvard Medical School) for scientific feedback; and X. Yang (Department of Signal Transduction, Beth Israel Deaconess Medical Center, Harvard Medical School) for assistance with mass-spectrometry analysis.

REFERENCES
protease elastase for large-scale phosphoproteome analysis. Anal Chem
2008;80:9526–9533
phosphorylation revealing new sites in human mammary epithelial cells.
J Proteome Res 2009;8:3852–3861
for specific identification of tyrosine kinase substrates using \(^{13}\text{C}\)tyrosine.
25. Schmelzle K, Kane S, Gridley S, Lienhard GE, White FM. Temporal dy-
namics of tyrosine phosphorylation in insulin signaling. Diabetes 2006;55:
2171–2179
of post-translational glycosylation and phosphorylation of proteins from
the amino acid sequence. Proteomics 2004;4:1633–1649
27. Jaworski K, Sarkadi-Nagy E, Duncan RE, Ahmadian M, Sul HS. Regu-
lation of triglyceride metabolism. IV. Hormonal regulation of lipolysis
in adipose tissue. Am J Physiol Gastrointest Liver Physiol 2007;293:
G1–G4
28. Su CL, Sztalryd C, Contreras JA, Holm C, Kimmel AR, Londos C. Muta-
tional analysis of the hormone-sensitive lipase translocation reaction in
29. Martin ML, Jensen MD. Effects of body fat distribution on regional lipolysis
30. Wahrenberg H, Lönneqvist F, Amer P. Mechanisms underlying regional dif-
and characterization of caveolae subclasses in the plasma membrane of
primary adipocytes: segregation of specific proteins and functions. FEBS J
2006;273:3381–3392
32. Razani B, Woodman SE, Lisanti MP. Caveolae: from cell biology to animal
Isolation of cDNAs for perilipins A and B: sequence and expression of lipid
droplet-associated proteins of adipocytes. Proc Natl Acad Sci USA 1993;90:
12035–12039
34. Belfrage P, Fredrikson G, Nilsson NO, Strålfors P. Regulation of adipose-
tissue lipolysis by phosphorylation of hormone-sensitive lipase. Int J Obes
1981;5:635–641
35. Sztalryd C, Xu G, Dorward H, et al. Perilipin A is essential for the trans-
location of hormone-sensitive lipase during lipolytic activation. J Cell Biol
2003;161:1103–1103
36. Syu LJ, Saltiel AR. Lipotransin: a novel docking protein for hormone-sen-