Glycemic index differences of high-fat diets modulate primarily lipid metabolism in murine adipose tissue.

Physiol Genomics 43: 942–949, 2011.
First published June 14, 2011; doi:10.1152/physiolgenomics.00042.2011.

Glycemic index differences of high-fat diets modulate primarily lipid metabolism in murine adipose tissue

Evert M. van Schothorst,[1,2] Annelies Bunschoten,[1,2] Eline Verlinde,[2] Patrick Schrauwen,[1,3] and Jaap Keijer[1,2]

[1]*Top Institute Food and Nutrition;* [2]*Human and Animal Physiology, Wageningen University, Wageningen; and* [3]*Department of Human Biology, Maastricht University, Maastricht, The Netherlands*

Submitted 14 March 2011; accepted in final form 7 June 2011

van Schothorst EM, Bunschoten A, Verlinde E, Schrauwen P, Keijer J. Glycemic index differences of high-fat diets modulate primarily lipid metabolism in murine adipose tissue. *Physiol Genomics* 43: 942–949, 2011. First published June 14, 2011; doi:10.1152/physiolgenomics.00042.2011.—A low vs. high glycemic index of a high-fat (HF) diet (LGI and HGI, respectively) significantly retarded adverse health effects in adult male C57BL/6J mice, as shown recently (Van Schothorst EM, Bunschoten A, Schrauwen P, Mensink RP, Keijer J. *FASEB J* 23: 1092–1101, 2009). The LGI diet enhanced whole body insulin sensitivity and repressed HF diet-induced body and white adipose tissue (WAT) weight gain, resulting in significantly reduced serum leptin and resistin levels and increased adiponectin levels. We questioned how WAT is modulated and characterized the molecular mechanisms underlying the glycemic index-mediated effects using whole genome microarrays. This showed that the LGI diet mainly exerts its beneficial effects via substrate metabolism, especially fatty acid metabolism. In addition, cell adhesion and cytoskeleton remodeling showed reduced expression, in line with lower WAT mass. An important transcription factor showing enhanced expression is PPAR-γ. Furthermore, serum levels of triglycerides, total cholesterol, and HDL- and LDL-cholesterol were all significantly reduced by LGI diet, and simultaneously muscle insulin sensitivity was significantly increased as analyzed by protein kinase B/Akt phosphorylation. Cumulatively, even though these mice were fed an HF diet, the LGI diet induced significantly favorable changes in metabolism in WAT. These effects suggest a partial overlap with pharmacological approaches by thiazolidinediones to treat insulin resistance and statins for hypercholesterolemia. It is therefore tempting to speculate that such a dietary approach might beneficially support pharmacological treatment of insulin resistance or hypercholesterolemia in humans.

dietary starch; transcriptomics; insulin sensitivity; humanized diet

LOW VS. HIGH GLYCEMIC INDEX (LGI and HGI, respectively) diets have previously been shown to result in beneficial effects on health, as expressed by fat mass and measures of insulin resistance, including glucose tolerance tests (GTT), in rodents as well as in humans (3, 16, 22, 23, 30, 31). Although rodents consume the same experimental diet throughout the intervention period, the results obtained in humans indicate major effects, even when only part of the daily consumed diets fulfills the glycemic index (GI) criteria of experimental design. However, some human studies reported a lack of effects (e.g., Ref. 47) or confounding factors (20). The rodent studies have been performed using low-fat (~10% kcal fat) diets, which are healthier than diets with a high-fat (HF) content (11). In contrast to low-fat diets, HF diets induce obesity and insulin resistance in mouse strains sensitive to development of diet-induced obesity, such as C57BL/6J (9).Therefore, we previously studied the effects of differences in GI (LGI vs. HGI) in the context of an HF (30% kcal fat) diet, rather than a low-fat diet, in obesity-prone C57BL/6J adult male mice (43). The dietary HF content of 30 kcal% can be considered as moderate and more human relevant fat content compared with rodent studies using 60 kcal% HF diets (i.e., Refs. 12, 15). We showed that an LGI diet significantly delays the HF-induced increase in fat mass and progression of insulin resistance, while simultaneously levels of white adipose tissue (WAT) secreted peptide hormones (adipokines) were beneficially affected compared with an HGI diet.

While this outcome is clear cut, it is not clear what the underlying mechanisms are. WAT is essential for maintaining a healthy glucose and lipid homeostasis, and dysfunctional WAT results in insulin resistance and dyslipidemia. The primary function of adipose tissue is the storage of lipids. Its capacity to expand is essential to maintain healthy levels of circulating lipids in times of abundant food supply and provides a source of energy in times of need. WAT is an active organ communicating with other tissues by receiving signals and secreting a variety of adipokines and metabolites (48). Daily intake of HF diets results in general in a constant energy overload and will result in metabolic dysfunction, leading to diseases associated with obesity, in particular insulin resistance, which progresses into Type II diabetes. Dysfunctional WAT is considered as one of the initial steps in the progression of diet-induced obesity-related metabolic disturbances (reviewed by e.g., Refs. 18, 46).

In studies using low-fat diets, impaired hepatic fatty acid oxidation was identified as potential cause of effects induced by an HGI vs. LGI diet (14, 37). Another mechanism may involve a direct effect on insulin signaling. Insulin signals are transferred through the insulin receptor via a cascade of protein phosphorylations to either phosphorylation and activation of proteins including protein kinase B (PKB)/Akt or to transcription factors regulating target gene expression involved in fatty acid metabolism (1, 24). PKB activation is crucial for glucose transporter Slc2a4/Glut4 translocation to the cell membrane mediating glucose uptake in many tissues and, as such, for insulin sensitivity (49). For effective translation to humans not only the beneficial effects, but also elucidation of underlying molecular mechanisms, are needed.

Therefore, we analyzed here gene expression profiles in white adipose tissue of mice fed an HF diet, LGI vs. HGI, to elucidate pathways underlying the changes in WAT by GI differences.

Address for reprint requests and other correspondence: E. M. van Schothorst, Dept. of Human and Animal Physiology, Wageningen Univ., Marijkeweg 40, 6709 GP Wageningen, PO Box 338, 6700 AH Wageningen, The Netherlands (e-mail: Evert.vanschothorst@wur.nl).

MATERIALS AND METHODS

Animals and diets. The study has been reported previously and was approved by the Animal Welfare Committee of Wageningen University, Wageningen, The Netherlands (43). In brief, 110 wild-type C57BL/6J male mice aged 9 wk were fed a semipurified HF (30% kcal fat) LGI diet for 3 wk, followed by placing them into three groups matched in body weight at the start of the experimental intervention: $t = 0$ group ($n = 10$; 25.6 ± 0.6 g, mean ± SE), an HF HGI dietary group ($n = 50$, 25.7 ± 0.2 g), and an HF LGI dietary group ($n = 50$, 25.6 ± 0.2 g). The LGI and HGI diets differ solely in starch type (HGI: 100% amylopectin, LGI: ~60% amylose and ~40% amylopectin, both from Cerestar Benelux, Bergen op Zoom, The Netherlands), not in the amount of starch in the diets, and both diets contain, per kg, 534.5 g starch, 220.0 g casein, and 3.0 g L-cysteine as protein source, 50.0 g cellulose, 101.5 g lard, and 43.5 g corn oil as fat, 35 g mineral premix, 10.0 g vitamin premix, and 2.5 g choline bitartrate as described previously in detail (see Table 1 in Ref. 43) and as such closely resembles the Western human dietary fat intake. The mice were individually housed in macrolon type II cages at 20–22°C and 45% humidity, with lights switched on from 6 AM to 6 PM. Food and water were supplied weekly ad libitum. At the start of the intervention, the $t = 0$ group was killed, while the remaining mice were killed after 13–14 wk intervention. In each dietary group, at a 3-wk interval, blood was sampled via the tail ($n = 10$), or GTT ($n = 10$) or insulin tolerance tests (ITT, $n = 30$) were performed in 5 h-fasted mice. All mice remained in their subgroup from the start of the intervention onward. At the end of the intervention, 2 h fasted mice were anesthetized, blood was drawn by orbital puncture, they were killed by cervical dislocation, and organs were isolated, weighed, and snap-frozen in liquid nitrogen and stored at −80°C. Ten mice of the ITT subgroup received an insulin injection (0.75 IU/kg body wt) 30 min prior to section. Here, only the subset of mice used for longitudinal blood collection ($n = 10$) was used for analysis of serum lipid markers together with $t = 0$ group, while 10 mice undergoing ITT and those receiving an insulin injection before section ($n = 10$) were used for analysis of PKB/Akt phosphorylation status in muscle (see below).

RNA isolation and microarray analysis. Total RNA was isolated from epididymal WAT (epiWAT) as described (43) from the subset of mice undergoing longitudinal blood collection ($n = 10$ each dietary group), quantified using Nanodrop, and qualified using Experion Automated Electrophoresis System (Bio-Rad, Veenendaal, The Netherlands), which resulted in the exclusion of one LGI sample because of low RNA amount (9 LGI vs. 10 HGI samples were used for microarray hybridization). Whole mouse genome gene expression microarray analysis (G4122A, 44K; Agilent Technologies, Santa Clara, CA) was performed as described previously using the Agilent low RNA input fluorescent linear amplification protocol version 3.1 (27). In brief, 500 ng of purified individual total RNA was used for cDNA synthesis and subsequent cRNA labeling and synthesis with Cy5 and Cy3 dyes. Cy3 samples were pooled on a equimolar basis and served as a reference pool, and individual Cy5-labeled samples were hybridized against the reference pool. After being washed, arrays were scanned on an Agilent scanner, and spot intensities were quantified using Feature Extraction (Agilent). Quality control was performed based on raw fluorescence data by MA-plot and M-box plot using R (http://www.R-project.org). As a result, we excluded two arrays, and eight LGI vs. nine HGI arrays were finally used for downstream analysis. Data normalization was performed as published using GeneMaths XT (Applied Maths, Sint-Martens-Latem, Belgium), including identification of transcripts being expressed using a mean signal threshold of two times above local background level (32); LOWESS normalization was included in the normalization scheme. Student's *t*-test and random forest (RF) were used to identify differentially expressed transcripts as published (17, 35). Fold change (FC) is expressed as mean LGI/HGI. Pathway analysis was performed using Metacore (version 4.3; GeneGo, St. Joseph, MI) on the basis of significantly regulated genes ($P < 0.05$) and RF criterion and ranked according to their significance value as obtained from MetaCore (7). All arrays are deposited in the National Center for Biotechnology Information's Gene Expression Omnibus database (http://www.ncbi.nlm.nih.gov/geo/) under accession number GSE26930.

Protein phosphorylation detection by Western blot analysis. Gastrocnemius muscle homogenates for Western blot analysis of (phosphorylated) PKB/Akt were performed as described before (36). Equal amounts of protein were loaded on SDS-PAGE and, after Western blotting, incubated with p-Akt (Ser273) and Akt antibodies (#9271 and #9272, respectively; Cell Signaling Technology, Bioké, Leiden, The Netherlands). After incubation with the appropriate secondary antibodies, specific protein bands were visualized by chemiluminescence and analyzed by Chemidoc XRS system (Bio-Rad).

Serum metabolism parameters. Serum levels of triglycerides (TG), total and HDL-cholesterol, and glycerol were analyzed in individual samples in duplicate using commercial kits (Human, Instruchemie, Delfzijl, The Netherlands) with slight modifications to reduce sample amount needed. Furthermore, TG levels were corrected for serum glycerol levels due to the feature of the TG kit and the significant differences we observed in serum glycerol levels. LDL-cholesterol was determined using the modified Friedewald formula (6, 8). Only samples with coefficient of variation <15% between duplicates were included for data analysis.

Statistical analysis. Statistical analyses were performed using GraphPad Prism 5 (GraphPad software, San Diego, CA) and SPSS 15.0 (IBM, Chicago, IL). The data were checked for normality using the Shapiro-Wilk test. If data were not normally distributed, data were log2 transformed and tested again. This was done for serum glycerol and HDL-cholesterol levels. Statistically significant differences were analyzed by 1-way analysis of variance and post hoc Tukey tests, or Student's *t*-test if mean of two groups were compared. $P < 0.05$ was considered significant. Data are shown as means ± SE unless otherwise stated.

RESULTS

Physiological data. Wild-type C57BL/6J male mice fed a semipurified HF, low LGI vs. an HF, HGI diet showed a significant lower body weight, lower serum levels of WAT secreted adipokines like leptin and resistin, as well as significant lower basal and insulin-stimulated serum levels of free fatty acids (FFA), as previously reported (43). Glucose tolerance was significantly increased and insulin resistance decreased in the LGI-fed mice, while food and energy intake were not significantly different. Furthermore, hepatic TG accumulation was significantly reduced (43). Together, this indicated a more insulin-sensitive phenotype for the LGI vs. HGI group at the whole body level (43). In agreement with significant lower body weight (LGI: 29.9 ± 1.2 g vs. HGI: 34.0 ± 1.2 g, $P < 0.05$) and lower serum leptin levels (LGI: 3.53 ± 0.74 ng/ml vs. HGI: 10.45 ± 1.37 ng/ml, $P < 0.0001$), also a lower WAT weight [LGI: 579 ± 78 mg epiWAT corresponding to 1.9 ± 0.2% epiWAT (wt/wt%) vs. HGI: 997 ± 96 mg epiWAT corresponding to 2.9 ± 0.2% epiWAT, all $P < 0.01$] was observed in the subset of mice analyzed here (Fig. 1). To further support the dietary effects on insulin sensitivity, we investigated the phosphorylation status of PKB/Akt in skeletal muscle. Phosphorylated Akt is significantly induced upon insulin stimulation only in the LGI group (Fig. 2), while total Akt levels remained similar. This strengthens the higher insulin sensitivity in the LGI-fed mice not only for WAT, but also for muscle.

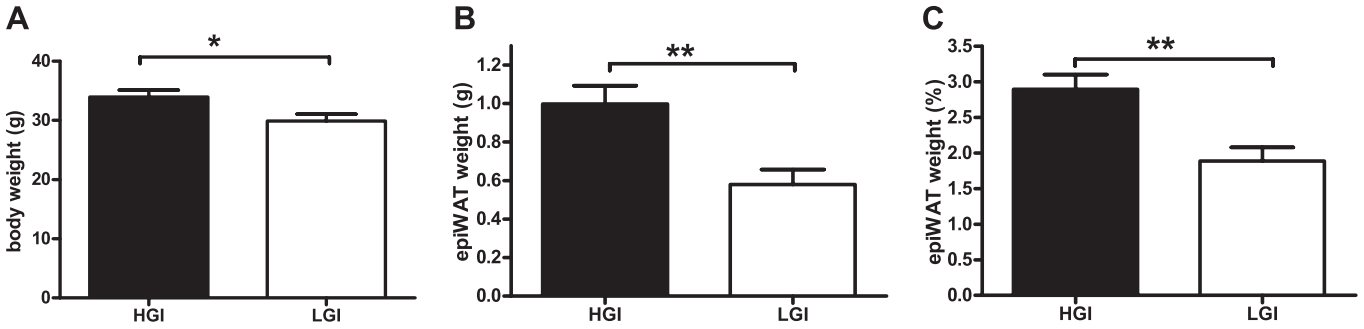

Fig. 1. Body weight and adipose tissue weight modulation by high fat (HF) glycemic index (GI) diets. Body weight (*A*), absolute (*B*), and relative (*C*) epididymal white adipose tissue (epiWAT) weights are shown as means ± SE for HF, high glycemic index (HGI; black bars, $n = 10$) and low glycemic index (LGI; white bars, $n = 10$) fed mice used for gene expression profiling. *$P < 0.05$, **$P < 0.01$.

Transcriptome analysis. The role of WAT in the development of insulin resistance and the reduced WAT weights led us to speculate that retardation of whole body insulin insensitivity may be caused by differences in WAT, which, due to the endocrine and metabolic function of WAT, affects other organs like liver and muscle. To strengthen this hypothesis and obtain mechanistic insights in effects imposed by the dietary GI differences, we performed whole genome transcriptomics analysis of epididymal WAT. After normalization, 20,134 transcripts were found to be expressed (48%), of which 1,649 were differentially expressed between LGI and HGI; these comprise 1,390 transcripts based on significance supplemented with 259 based on RF criterion. The majority of significant differentially expressed genes showed an FC of LGI over HGI between 1.2 and 1.5 (Fig. 3), that is, upregulation of gene expression. Remarkably, although these relative small FC are in line with other nutritional studies using wild-type animals (17, 29), they appeared lower than expected based on the physiological effects seen in these mice. We then analyzed differential regulated pathways to assess orchestrated regulation at the pathway level. This revealed insulin regulated fatty acid metabolism as highest ranked pathway based on significance (Table 1). Other pathways that appeared in the top 15 were associated with substrate metabolism, such as TCA cycle and carbohydrate metabolism and regulation, but also cell adhesion and cytoskeleton remodeling appeared (Table 1). Pathway analysis using the subset of genes identified by significance and not by RF criterion revealed an identical ranking order of pathways (data not shown). Detailed examination of the genes constituting the top 15 pathways showed that cytoskeleton remodeling and cell adhesion constitute the same pathway. Likewise, the propionate and butyrate pathways overlap for seven out of nine upregulated transcripts, which in turn overlap with two genes of the TCA cycle and largely overlaps with the pathway containing metabolism of amino acids leucine, valine, and isoleucine. Thus, an LGI modifies WAT gene expression encoding proteins mainly involved in cellular glycolysis, TCA cycle, and fatty acid synthesis on the one hand and cell adhesion and cytoskeleton remodeling on the other.

Changes in expression of cell adhesion and cytoskeleton remodeling are in agreement with the significant differences in the epididymal WAT weight between the LGI and HGI groups, most likely resulting from differences in adipocyte hypertrophy. As expected, this process was downregulated in the LGI-fed mice. Beta-actin and alpha-2 actin (Fig. 4), exemplifying this process, were significantly lower expressed in the LGI-fed mice. In contrast, peroxisome proliferator-activated receptor-gamma (Ppar-γ) showed an increase upon LGI (FC 1.20).

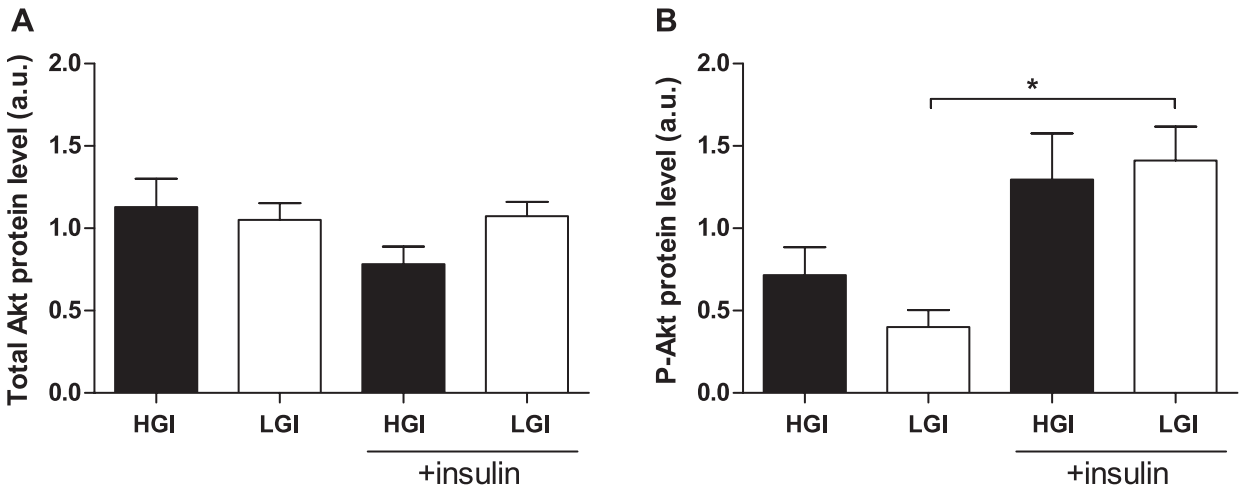

Fig. 2. Protein kinase B/Akt phosphorylation in gastrocnemius muscle. Levels of total Akt (*A*) and phosphorylated Akt (*B*) are shown at basal, 2 h fasting level, and after a 30 min challenge to insulin (as analyzed by Western blotting, see MATERIALS AND METHODS; shown by + insulin). Data are shown as means ± SE for HGI (black bars, $n = 10$) and LGI (white bars, $n = 10$). *Significant difference (1-way ANOVA, Tukey post hoc test, $P < 0.05$).

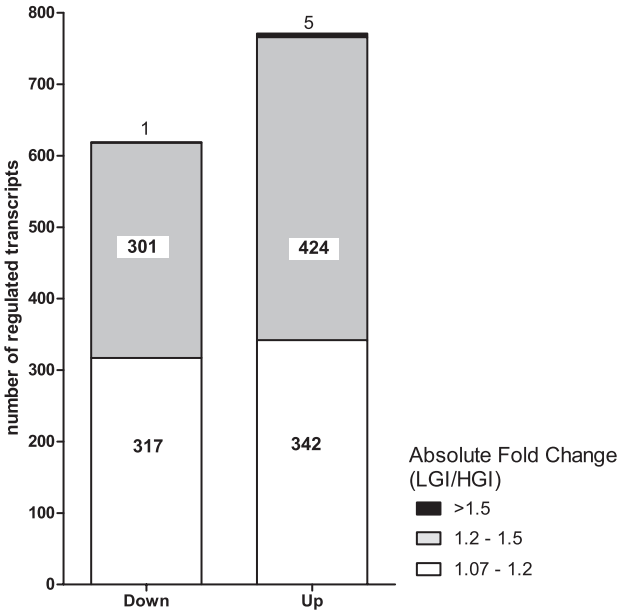

Fig. 3. Numbers of significant differentially regulated genes in murine WAT by an HF, LGI vs. HGI diet. Significant differential expression is shown for downregulation and upregulation by LGI vs. HGI. Observed absolute fold changes are subdivided into 3 groups: $1.07 \leq |FC| \leq 1.2$ (white), $1.2 < |FC| < 1.5$ (gray), and $|FC| \geq 1.5$ (black), and the number of transcripts per group is shown.

A large number of the target genes encoding the enzymes involved in cellular glycolysis, TCA cycle, and fatty acid synthesis are under the control of the nuclear transcription factor SREBF/SREBP1, which is upregulated by LGI at gene expression level (FC 1.24, Fig. 4). Furthermore, SREBP1 target genes involved in TG synthesis like Scd-1 and Gpam are significantly upregulated, while Fasn shows a tendency to upregulation (Fig. 4). Genes encoding key enzymes involved in fatty acid oxidation like subunits Acaca and Acacb encoding acetyl-coA carboxylase and carnitine palmitoyl transferases present (Cpt1a, Cpt1b, and Cpt2) are nonsignificantly upregulated but are included in the subset on the basis of RF criterion. Cumulatively, this might be indicative for an increased storage of TG in WAT. However, we observed significantly lower epiWAT weights after an LGI vs. HGI intervention (Fig. 1, Ref. 43). Therefore, we focused on a "pathway" not included in the software program, namely differentially expressed genes between classical adipocytes containing a single large lipid droplet and adipocytes containing multiple mitochondria and lipid droplets, the so-called brownish phenotype (38, 45). Several genes are regulated in such a way that the LGI diet favors a more brownish phenotype, including Cidea and Ppargc1alpha (Fig. 4), and TCA genes. The delicate balance between synthesis, deposition, and usage of energy in the form of TG and theoretically the size of adipocytes and its lipid droplets seems therefore marginally changed favoring TG usage and smaller adipocytes containing more but smaller lipid droplets upon LGI vs. HGI intervention.

A selected subset of genes, from different significantly regulated pathways, was analyzed by real-time quantitative PCR (Q-PCR), confirming fold changes observed by microarray data analysis (data not shown).

Lipid metabolism. Based upon the observations that several WAT lipid metabolism pathways were differentially altered,

Table 1. *Top 15 differentially regulated pathways by LGI vs. HGI dietary intervention*

Map/Process	General Function	Cell Process	*P* Value	Objects	
Insulin regulation of fatty acid metabolism	regulation of lipid metabolism	response to hormone stimulus	3.15E-06	15 (10/5)	46
Regulation of lipid metabolism via LXR, NF-Y, and SREBP	regulation of lipid metabolism	transcription	9.32E-06	13 (8/2)	31
Propionate metabolism	carbohydrates metabolism		1.67E-05	11 (9/0)	24
Ligand-dependent transcription of retinoid-target genes	transcription factors	transcription	7.80E-05	17 (7/10)	32
Regulation of fatty acid synthase activity in hepatocytes	regulation of lipid metabolism		1.17E-04	8 (3/0)	16
Integrin-mediated cell adhesion and migration	regulatory processes/cell adhesion	cell adhesion	2.07E-04	15 (5/10)	45
RXR-dependent regulation of lipid metabolism via PPAR, RAR, and VDR	regulation of lipid metabolism	transcription	2.45E-04	10 (5/0)	26
Cytoskeleton remodeling	cytoskeleton remodeling		5.39E-04	23 (10/13)	96
Butanoate metabolism	carbohydrates metabolism		6.28E-04	10 (9/1)	24
TCA	aminoacid metabolism		7.68E-04	8 (6/0)	20
ChREBP regulation pathway	transcription factors	transcription, G protein-signaling pathway	1.50E-03	8 (3/5)	13
Kappa-type opioid receptor activation of ERK	protein function/G proteins/GPCR	response to extracellular stimulus, G protein-signaling pathway	1.60E-03	8 (0/8)	22
Apoptosis and survival, HTR1A signaling	protein function/G proteins/GPCR	apoptosis, G protein-signaling pathway	1.92E-03	12 (5/8)	38
Dopamine D2 receptor transactivation of PDGFR in CNS	G proteins/GPCR regulatory processes	G protein-signaling pathway	2.01E-03	11 (4/7)	18
Leucine, isoleucine, and valine metabolism	amino acid metabolism	cell process	2.22E-03	9 (7/0)	28

The top 15 pathways obtained using MetaCore (GeneGO) are sorted based on significance. For each pathway, the function, process, its *P* value, and the number of unique regulated genes/objects (within parentheses the number of significantly up- and downregulated genes) and total number of genes are shown. LGI, low glycemic index; HGI, high glycemic index.

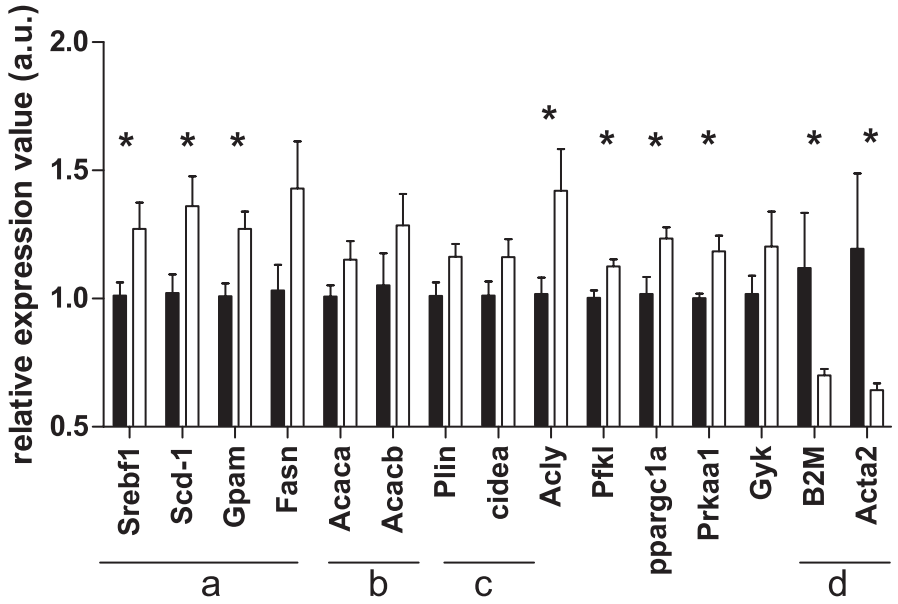

Fig. 4. WAT gene expression levels of genes involved in significantly regulated metabolic pathways. Data were obtained using Agilent microarrays. *Significant difference ($P < 0.05$, *t*-test; Benjamini-Hochberg false discovery rate-adjusted *P* values > 0.64). Per gene, mean level of relative expression is set to 1.0 for HGI (black bars) and shows relative changes in LGI (white bars). Data are expressed as means ± SE ($n = 8–9$). Lipid metabolism related processes are shown by the following symbols: a (fatty acid synthesis), b (inhibition of beta-oxidation), c (markers of lipid droplets and lipolysis), and d (cellular matrix proteins). Srebf1, sterol regulatory element binding transcription factor 1 ($P = 0.041$); Scd-1, stearoyl-Coenzyme A desaturase 1 ($P = 0.018$); Gpam, mitochondrial glycerol-3-phosphate acyltransferase ($P = 0.0045$); Fasn, fatty acid synthase ($P = 0.068$); Acaca, acetyl-Coenzyme A carboxylase-α ($P = 0.12$); acacb, acetyl-Coenzyme A carboxylase-β ($P = 0.16$); Plin, perilipin ($P = 0.056$); Cidea, cell death-inducing DNA fragmentation factor, α-subunit-like effector A ($P = 0.13$); Acly, ATP citrate lyase ($P = 0.027$); Pfkl, phosphofructokinase, liver, B-type ($P = 0.0073$); Ppargc1a, peroxisome proliferative activated receptor-γ, coactivator 1α ($P = 0.021$); Prkaa1, protein kinase, AMP-activated, α-1 catalytic subunit ($P = 0.0099$); Gyk, glycerol kinase ($P = 0.22$); B2M, β-2 microglobulin ($P = 0.050$); Acta2, α-2 actin ($P = 0.049$).

we analyzed a subset of serum lipid metabolites. Previously, we showed that basal fasting serum FFA levels were significantly lower in the LGI-fed mice supportive for a more insulin-sensitive phenotype in WAT at the tissue level (43). Basal fasting serum TG and glycerol levels were decreased in these mice, although nonsignificantly (Fig. 5, *A* and *B*). Total cholesterol and LDL- and HDL-cholesterol levels were all significantly lower in the LGI mice (Fig. 5, *C–E*), suggesting hepatic differences between LGI- and HGI-fed mice and supportive for a more insulin-sensitive phenotype at the whole body level. Moreover, the serum cholesterol levels in the LGI-fed mice are nonsignificantly different from $t = 0$ group, thus abolishing the HF diet-induced increase in serum cholesterol.

DISCUSSION

Physiological changes following a LGI vs. HGI HF dietary intervention in mice, as performed here, shows that WAT gene expression is significantly changed in pathways relating to insulin sensitivity and its regulation of fatty acid metabolism. Furthermore, the PKB/Akt phosphorylation status of muscle supports a more insulin-sensitive phenotype in LGI-fed mice. Previously, we showed a decreased level of intrahepatic fat, suggesting beneficial effects in liver as well (43). This was accompanied with significantly decreased lipid serum levels of total cholesterol and HDL- and LDL-cholesterol in LGI mice. This suggests that besides WAT, muscle and liver also play an important role in the differential whole body responses to diets of different GI. It is tempting to speculate that previous findings with respect to differential effects of GI diets on substrate use (higher fat oxidation in low fat, low vs. high GI mice) and hepatic gene expression patterns (14, 37) are due to accelerated WAT dysfunction on an HGI compared with LGI and that the reduced WAT insulin sensitivity in HGI vs. LGI fed mice might be a first step in the cascade of development of insulin resistance (14). As shown, epiWAT weight was significantly lower in LGI vs. HGI-fed mice. Based on earlier observations using HF diets with 30% fat, it can be expected that other WAT depots are similarly affected (44), This suggests that body weight gain is mainly caused by an increase in WAT, especially given the fact that increased WAT weight, but not lean mass, was observed after HF feeding (e.g., Ref. 5), or a GI-based intervention (14).

Recently, a significant positive correlation was shown between omental adipocyte cell size and fatty liver in metabolically healthy, severely obese (26), suggesting, but not proving, that insulin sensitivity and insulin regulation in the omental adipocytes are of major impact. This is supported by the notion that treatment of insulin resistance with TZD ligands of PPAR-γ results in smaller adipocytes and hence results in increased insulin sensitivity (10, 33, 34), partly due to a shift in adipokine secretion (39). Furthermore, PPAR-γ activation induces multilocularization of adipocytes, and it is suggested that this leads to favorable conditions for mobilization of lipids from adipocytes with enhanced lipolytic and lipogenic activities (19). In fact, our gene expression patterns support this view, and although the gene expression changes are quite small, the long-term increase of expression of these genes might be underlying the biological effects observed after 13 wk. Moreover,

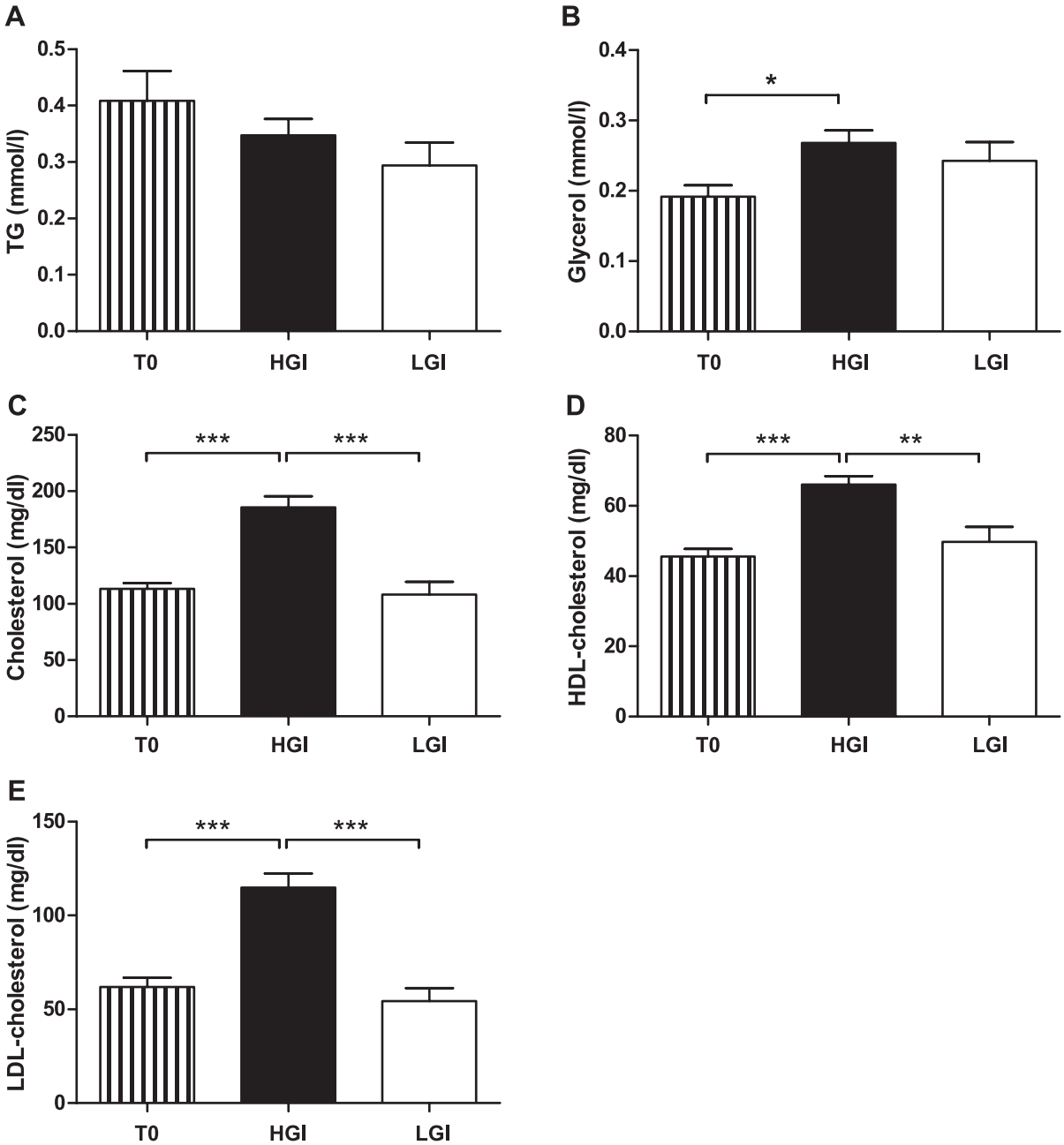

Fig. 5. Serum lipid metabolites. Serum metabolite levels after 2 h fast at $t = 0$ (striped bar) and after 13 wk intervention of LGI (white bar) or HGI (black bar) are shown as means ± SE ($n = 10$). *A*: triglycerides (TG), *B*: glycerol, *C*: total cholesterol, *D*: HDL-cholesterol, *E*: LDL-cholesterol. *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$ (ANOVA, Tukey post hoc tests).

changes in adipocyte size directly correlate with alterations in cytoskeletal proteins.

The role of cytoskeleton alterations is known to play an important role in adipocyte differentiation. It involves drastic cell shape alterations that are accompanied by changes in expression of cytoskeletal and extracellular matrix proteins, including decreases in actin and tubulin levels (reviewed by Ref. 41). Alternatively, upon a decrease in WAT mass in overweight/obese subjects following a weight loss program, proteomics analysis of WAT showed also differential effects of the cytoskeletal protein tubulin 5 as well (2). Moreover, microtubule disruption substantially inhibited insulin-stimulated GLUT4 translocation, suggesting that transport of GLUT4 storage vesicles to the plasma membrane takes place along microtubules and that this transport is obligatory for insulin-stimulated GLUT4 translocation in adipocytes (4). Insulin increases actin polymerization near the plasma membrane and disruption of this process inhibited GLUT4 exocytosis, linking alterations in the cytoskeleton to insulin sensitivity (21). Indeed, we see decreased actin and beta2-microglobulin gene expression levels in WAT and simultaneously increased WAT and whole body insulin sensitivity in LGI-fed mice. This is further supported by the gene expression profile for genes involved in classification of type of adipocytes: classical adi-

pocytes containing one lipid droplet versus a brownish phenotype in which adipocytes contain multiple smaller lipid droplets. Therefore, we hypothesize that alterations in mitochondrial content and/or lipid droplets may be underlying the phenotypic differences observed, but this needs to be elaborated on in future studies.

Of notice, the dietary intervention is comprised solely of a difference in the type, and not the amount, of dietary starch as carbohydrate, while the biological pathways differentially regulated are mainly linked to fatty acid metabolism. The latter is not completely unexpected, as we analyze here the effects in WAT, the main organ for lipid accumulation in times of surplus energy provided by the HF diets. However, while Isken et al. (14) reported a lack of changes in serum FFA and cholesterol levels in low fat low vs. high GI-fed mice, we observed significant reduced serum levels of FFA (43) in line with findings in impaired glucose tolerance subjects consuming LGI food (50). Furthermore, we observed significant lower serum levels of total, HDL-, and LDL-cholesterol in LGI vs. HGI mice, showing a similar, although reduced, effect compared with dietary treatment with phytosterols/stanols (25). Besides genetic differences between mice and human linked to lipid metabolism, e.g., a functional CETP gene has not yet been identified in mice (13), the differences in serum levels of cholesterol might partly be explained by the higher animal fat content, and thus the cholesterol content, of our diets, with beneficial effects of the LGI diet. Indeed, in humans consuming an average dietary fat content of 30–40%, significant lower LDL-cholesterol levels were observed accompanied with a tendency for lower total cholesterol levels in the LGI vs. HGI group after 10 wk (40), while a single LGI meal/day for 3 wk showed no effects on serum cholesterol levels (28). Similarly, the GI of diets did not result in serum cholesterol differences in obese men when analyzed during 1 wk integrated with an exercise protocol (42). Reduction of serum cholesterol levels is a major aim in treatment of obesity, diabetes Type II, metabolic syndrome, and cardiovascular disease, and it is therefore tempting to speculate that a pharmacological approach using statins or a dietary approach using phytosterols/stanols might be enhanced by dietary treatment using low GI diets, even on an HF diet.

In conclusion, we show that on an HF diet background, an LGI vs. HGI diet mainly exerts its beneficial effects in WAT on substrate metabolism, especially insulin signaling of fatty acid metabolism. In addition, cell adhesion and cytoskeleton remodeling showed reduced expression in line with lower WAT mass and lower serum lipid markers, which cumulatively indicate beneficial health effects of LGI.

ACKNOWLEDGMENTS

We thank Matthijs Hesselink from Maastricht University for help with muscle biopsies and analysis.

Jaap Keijer and Evert M. van Schothorst are members of NuGO, the European Nutrigenomics consortium; Jaap Keijer is member of MITOFOOD (COST Action FA0602): Bioactive food components, mitochondrial function and health.

DISCLOSURES

No conflicts of interest, financial or otherwise, are declared by the author(s).

REFERENCES

1. **Attie AD, Scherer PE.** Adipocyte metabolism and obesity. *J Lipid Res* 50, *Suppl*: S395–399, 2009.
2. **Bouwman FG, Claessens M, van Baak MA, Noben JP, Wang P, Saris WH, Mariman EC.** The physiologic effects of caloric restriction are reflected in the in vivo adipocyte-enriched proteome of overweight/obese subjects. *J Proteome Res* 8: 5532–5540, 2009.
3. **Byrnes SE, Miller JC, Denyer GS.** Amylopectin starch promotes the development of insulin resistance in rats. *J Nutr* 125: 1430–1437, 1995.
4. **Chen Y, Wang Y, Ji W, Xu P, Xu T.** A pre-docking role for microtubules in insulin-stimulated glucose transporter 4 translocation. *FEBS J* 275: 705–712, 2008.
5. **de Wilde J, Smit E, Mohren R, Boekschoten MV, de Groot P, van den Berg SA, Bijland S, Voshol PJ, van Dijk KW, de Wit NW, Bunschoten A, Schaart G, Hulshof MF, Mariman EC.** An 8-week high-fat diet induces obesity and insulin resistance with small changes in the muscle transcriptome of C57BL/6J mice. *J Nutrigenet Nutrigenomics* 2: 280–291, 2009.
6. **DeLong DM, DeLong ER, Wood PD, Lippel K, Rifkind BM.** A comparison of methods for the estimation of plasma low- and very low-density lipoprotein cholesterol. The Lipid Research Clinics Prevalence Study. *JAMA* 256: 2372–2377, 1986.
7. **Ekins S, Nikolsky Y, Bugrim A, Kirillov E, Nikolskaya T.** Pathway mapping tools for analysis of high content data. *Methods Mol Biol* 356: 319–350, 2007.
8. **Friedewald WT, Levy RI, Fredrickson DS.** Estimation of the concentration of low-density lipoprotein cholesterol in plasma, without use of the preparative ultracentrifuge. *Clin Chem* 18: 499–502, 1972.
9. **Gallou-Kabani C, Vige A, Gross MS, Rabes JP, Boileau C, Larue-Achagiotis C, Tome D, Jais JP, Junien C.** C57BL/6J and A/J mice fed a high-fat diet delineate components of metabolic syndrome. *Obesity (Silver Spring)* 15: 1996–2005, 2007.
10. **Gray SL, Vidal-Puig AJ.** Adipose tissue expandability in the maintenance of metabolic homeostasis. *Nutr Rev* 65: S7–12, 2007.
11. **Hartline-Grafton HL, Rose D, Johnson CC, Rice JC, Webber LS.** Energy density of foods, but not beverages, is positively associated with body mass index in adult women. *Eur J Clin Nutr* 63: 1411–1418, 2009.
12. **Hoffler U, Hobbie K, Wilson R, Bai R, Rahman A, Malarkey D, Travlos G, Ghanayem BI.** Diet-induced obesity is associated with hyperleptinemia, hyperinsulinemia, hepatic steatosis, and glomerulopathy in C57Bl/6J mice. *Endocrine* 36: 311–325, 2009.
13. **Hogarth CA, Roy A, Ebert DL.** Genomic evidence for the absence of a functional cholesteryl ester transfer protein gene in mice and rats. *Comp Biochem Physiol B Biochem Mol Biol* 135: 219–229, 2003.
14. **Isken F, Klaus S, Petzke KJ, Loddenkemper C, Pfeiffer AF, Weickert MO.** Impairment of fat oxidation under high- vs. low-glycemic index diet occurs before the development of an obese phenotype. *Am J Physiol Endocrinol Metab* 298: E287–E295, 2010.
15. **Johnston SL, Souter DM, Tolkamp BJ, Gordon IJ, Illius AW, Kyriazakis I, Speakman JR.** Intake compensates for resting metabolic rate variation in female C57BL/6J mice fed high-fat diets. *Obesity (Silver Spring)* 15: 600–606, 2007.
16. **Kabir M, Rizkalla SW, Champ M, Luo J, Boillot J, Bruzzo F, Slama G.** Dietary amylose-amylopectin starch content affects glucose and lipid metabolism in adipocytes of normal and diabetic rats. *J Nutr* 128: 35–43, 1998.
17. **Keijer J, van Helden YG, Bunschoten A, van Schothorst EM.** Transcriptome analysis in benefit-risk assessment of micronutrients and bioactive food components. *Mol Nutr Food Res* 54: 240–248, 2010.
18. **Keijer J, van Schothorst EM.** Adipose tissue failure and mitochondria as a possible target for improvement by bioactive food components. *Curr Opin Lipidol* 19: 4–10, 2008.
19. **Koh YJ, Park BH, Park JH, Han J, Lee IK, Park JW, Koh GY.** Activation of PPAR gamma induces profound multilocularization of adipocytes in adult mouse white adipose tissues. *Exp Mol Med* 41: 880–895, 2009.
20. **Livesey G, Taylor R, Hulshof T, Howlett J.** Glycemic response and health–a systematic review and meta-analysis: the database, study characteristics, and macronutrient intakes. *Am J Clin Nutr* 87: 223S–236S, 2008.
21. **Lopez JA, Burchfield JG, Blair DH, Mele K, Ng Y, Vallotton P, James DE, Hughes WE.** Identification of a distal GLUT4 trafficking event controlled by actin polymerization. *Mol Biol Cell* 20: 3918–3929, 2009.

22. **Ludwig DS.** The glycemic index: physiological mechanisms relating to obesity, diabetes, and cardiovascular disease. *JAMA* 287: 2414–2423, 2002.
23. **Maki KC, Rains TM, Kaden VN, Raneri KR, Davidson MH.** Effects of a reduced-glycemic-load diet on body weight, body composition, and cardiovascular disease risk markers in overweight and obese adults. *Am J Clin Nutr* 85: 724–734, 2007.
24. **Mora S, Pessin JE.** An adipocentric view of signaling and intracellular trafficking. *Diabetes Metab Res Rev* 18: 345–356, 2002.
25. **Moruisi KG, Oosthuizen W, Opperman AM.** Phytosterols/stanols lower cholesterol concentrations in familial hypercholesterolemic subjects: a systematic review with meta-analysis. *J Am Coll Nutr* 25: 41–48, 2006.
26. **O'Connell J, Lynch L, Cawood TJ, Kwasnik A, Nolan N, Geoghegan J, McCormick A, O'Farrelly C, O'Shea D.** The relationship of omental and subcutaneous adipocyte size to metabolic disease in severe obesity. *PLoS One* 5: e9997, 2010.
27. **Pagmantidis V, Meplan C, van Schothorst EM, Keijer J, Hesketh JE.** Supplementation of healthy volunteers with nutritionally relevant amounts of selenium increases the expression of lymphocyte protein biosynthesis genes. *Am J Clin Nutr* 87: 181–189, 2008.
28. **Pal S, Lim S, Egger G.** The effect of a low glycaemic index breakfast on blood glucose, insulin, lipid profiles, blood pressure, body weight, body composition and satiety in obese and overweight individuals: a pilot study. *J Am Coll Nutr* 27: 387–393, 2008.
29. **Patsouris D, Reddy JK, Muller M, Kersten S.** Peroxisome proliferator-activated receptor alpha mediates the effects of high-fat diet on hepatic gene expression. *Endocrinology* 147: 1508–1516, 2006.
30. **Pawlak DB, Bryson JM, Denyer GS, Brand-Miller JC.** High glycemic index starch promotes hypersecretion of insulin and higher body fat in rats without affecting insulin sensitivity. *J Nutr* 131: 99–104, 2001.
31. **Pawlak DB, Kushner JA, Ludwig DS.** Effects of dietary glycaemic index on adiposity, glucose homoeostasis, and plasma lipids in animals. *Lancet* 364: 778–785, 2004.
32. **Pellis L, Franssen-van Hal NL, Burema J, Keijer J.** The intraclass correlation coefficient applied for evaluation of data correction, labeling methods, and rectal biopsy sampling in DNA microarray experiments. *Physiol Genomics* 16: 99–106, 2003.
33. **Puri V, Ranjit S, Konda S, Nicoloro SM, Straubhaar J, Chawla A, Chouinard M, Lin C, Burkart A, Corvera S, Perugini RA, Czech MP.** Cidea is associated with lipid droplets and insulin sensitivity in humans. *Proc Natl Acad Sci USA* 105: 7833–7838, 2008.
34. **Roberts R, Hodson L, Dennis AL, Neville MJ, Humphreys SM, Harnden KE, Micklem KJ, Frayn KN.** Markers of de novo lipogenesis in adipose tissue: associations with small adipocytes and insulin sensitivity in humans. *Diabetologia* 52: 882–890, 2009.
35. **Rodenburg W, Heidema AG, Boer JM, Bovee-Oudenhoven IM, Feskens EJ, Mariman EC, Keijer J.** A framework to identify physiological responses in microarray-based gene expression studies: selection and interpretation of biologically relevant genes. *Physiol Genomics* 33: 78–90, 2008.
36. **Schrauwen P, Hoeks J, Schaart G, Kornips E, Binas B, Van De Vusse GJ, Van Bilsen M, Luiken JJ, Coort SL, Glatz JF, Saris WH, Hesselink MK.** Uncoupling protein 3 as a mitochondrial fatty acid anion exporter. *FASEB J* 17: 2272–2274, 2003.
37. **Scribner KB, Pawlak DB, Ludwig DS.** Hepatic steatosis and increased adiposity in mice consuming rapidly vs. slowly absorbed carbohydrate. *Obesity* 15: 2190–2199, 2007.
38. **Seale P, Conroe HM, Estall J, Kajimura S, Frontini A, Ishibashi J, Cohen P, Cinti S, Spiegelman BM.** Prdm16 determines the thermogenic program of subcutaneous white adipose tissue in mice. *J Clin Invest* 121: 96–105, 2011.
39. **Skurk T, Alberti-Huber C, Hauner H.** Effect of conditioned media from mature human adipocytes on insulin-stimulated Akt/PKB phosphorylation in human skeletal muscle cells: role of BMI and fat cell size. *Horm Metab Res* 41: 190–196, 2009.
40. **Sloth B, Krog-Mikkelsen I, Flint A, Tetens I, Bjorck I, Vinoy S, Elmstahl H, Astrup A, Lang V, Raben A.** No difference in body weight decrease between a low-glycemic-index and a high-glycemic-index diet but reduced LDL cholesterol after 10-wk ad libitum intake of the low-glycemic-index diet. *Am J Clin Nutr* 80: 337–347, 2004.
41. **Smas CM, Sul HS.** Molecular mechanisms of adipocyte differentiation and inhibitory action of pref-1. *Crit Rev Eukaryot Gene Expr* 7: 281–298, 1997.
42. **Solomon TP, Haus JM, Kelly KR, Cook MD, Riccardi M, Rocco M, Kashyap SR, Barkoukis H, Kirwan JP.** Randomized trial on the effects of a 7-d low-glycemic diet and exercise intervention on insulin resistance in older obese humans. *Am J Clin Nutr* 90: 1222–1229, 2009.
43. **van Schothorst EM, Bunschoten A, Schrauwen P, Mensink RP, Keijer J.** Effects of a high-fat, low- versus high-glycemic index diet: retardation of insulin resistance involves adipose tissue modulation. *FASEB J* 23: 1092–1101, 2009.
44. **Van Schothorst EM, Franssen-van Hal N, Schaap MM, Pennings J, Hoebee B, Keijer J.** Adipose gene expression patterns of weight gain suggest counteracting steroid hormone synthesis. *Obes Res* 13: 1031–1041, 2005.
45. **Vernochet C, Peres SB, Farmer SR.** Mechanisms of obesity and related pathologies: transcriptional control of adipose tissue development. *FEBS J* 276: 5729–5737, 2009.
46. **Virtue S, Vidal-Puig A.** Adipose tissue expandability, lipotoxicity and the Metabolic Syndrome–an allostatic perspective. *Biochim Biophys Acta* 1801: 338–349, 2010.
47. **Vrolix R, van Meijl LE, Mensink RP.** The metabolic syndrome in relation with the glycemic index and the glycemic load. *Physiol Behav* 94: 293–299, 2008.
48. **Wang P, Mariman E, Renes J, Keijer J.** The secretory function of adipocytes in the physiology of white adipose tissue. *J Cell Physiol* 216: 3–13, 2008.
49. **Wang Q, Somwar R, Bilan PJ, Liu Z, Jin J, Woodgett JR, Klip A.** Protein kinase B/Akt participates in GLUT4 translocation by insulin in L6 myoblasts. *Mol Cell Biol* 19: 4008–4018, 1999.
50. **Wolever TM, Mehling C.** Long-term effect of varying the source or amount of dietary carbohydrate on postprandial plasma glucose, insulin, triacylglycerol, and free fatty acid concentrations in subjects with impaired glucose tolerance. *Am J Clin Nutr* 77: 612–621, 2003.