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Selective Inactivation of c-Jun NH$_2$-Terminal Kinase in Adipose Tissue Protects Against Diet-Induced Obesity and Improves Insulin Sensitivity in Both Liver and Skeletal Muscle in Mice

Xinmei Zhang, Aimin Xu, Sookja K. Chung, Justin H.B. Cresser, Gary Sweeney, Rachel L.C. Wong, Anning Lin, and Karen S.L. Lam

OBJECTIVE—Obesity is associated with increased activation of the c-Jun NH$_2$-terminal kinase (JNK) in several metabolic organs, including adipose tissue, liver, and skeletal muscle. In this study, we aimed to define the role of JNK activation in adipose tissue in the development of obesity-related insulin resistance.

RESEARCH DESIGN AND METHODS—Transgenic mice with adipose tissue–specific overexpression of dominant-negative JNK (ap2-dn-JNK) under the transcriptional control of the aP2 gene promoter were generated and subjected to metabolic characterization together with the wild-type littermates.

RESULTS—On a high-fat diet (HFD), the ap2-dn-JNK mice displayed a marked suppression of both JNK1 and JNK2 activation in their adipose tissue, accompanied by a marked reduction in weight gain, fat mass, and size of the adipocytes. The transgenic mice were resistant to the deleterious impact of an HFD on systemic insulin sensitivity, glucose tolerance, and hepatic steatosis. Reduced hepatic gluconeogenesis was evident in in vivo and ex vivo studies and showed greater insulin-induced glucose uptake in skeletal muscles. These changes were accompanied by reduced macrophage infiltration in adipose tissue, decreased production of proinflammatory adipokines, and increased expression of adiponectin. Indirect calorimetry analysis showed that the transgenic mice had significant increases in oxygen consumption and reductions in respiration exchange rates compared with their wild-type littermates.

CONCLUSIONS—Selective suppression of JNK activation in adipose tissue alone is sufficient to counteract HFD-induced obesity and its associated metabolic dysregulations, in part through an increase in energy expenditure and a decrease in systemic inflammation. Diabetes 60:486–495, 2011

Obesity is a major risk factor of type 2 diabetes. Although the detailed molecular events linking obesity to type 2 diabetes are not well understood, mounting evidence suggests that chronic inflammation in the adipose tissue plays a major role (1,2). Systemic inflammation, characterized by elevated circulating concentrations of proinflammatory markers such as C-reactive protein, is frequently observed in obesity and predicts the development of type 2 diabetes (3). Adipose tissue is now recognized as the predominant contributor of systemic inflammation observed in obese states. Obesity is associated with macrophage infiltration in adipose tissue (4) and dysregulated production of adipokines (2,5), with increased production of proinflammatory adipokines/cytokines, which induce insulin resistance, such as tumor necrosis factor (TNF)-α, interleukin (IL)-6, monocyte chemotactic protein (MCP)-1, and adipocyte fatty acid–binding protein (A-FABP), and decreased production of adiponectin, an anti-inflammatory and insulin-sensitizing adipokine.

Recent studies (2,6) in rodents suggest that c-Jun NH$_2$-terminal kinase (JNK) is a key player in adipose tissue inflammation and provides a link between nutrient excess, inflammation, and impaired insulin signaling. The JNK group of serine/threonine kinases, JNK1, -2, and -3, belongs to the mitogen-activated protein kinase family (7); JNK1 and JNK2 are widely distributed, whereas JNK3 is restricted to the brain, heart, testis, and pancreatic islets. Through the phosphorylation of various transcription factors, including c-Jun and JunB, JNKs are involved in the regulation of development, immune response, cell survival, and apoptosis (7). Recently, it has been observed that in ob/ob rodents JNK activity is increased in liver, muscle, and, markedly, in adipose tissue (8). This is not unexpected because various stimuli that activate JNK, including fatty acids, cytokines (notably TNF-α), and endoplasmic stress (9), are increased in obesity. Activated JNK induces serine phosphorylation of insulin receptor substrate-1 at Ser307, which suppresses tyrosine phosphorylation, leading to impaired insulin action. Genetic deletion of JNK1 is associated with reduced adiposity and protection against insulin resistance and type 2 diabetes in both diet-induced and genetic obesity, as well as increased adiponectin levels and reduced expression of proinflammatory cytokines (8,10). Adenovirus-mediated delivery of dominant-negative JNK (dn-JNK) or wild-type JNK in ob/ob mice has confirmed the role of JNK activation.
in the liver in enhancing systemic insulin resistance through increasing hepatic glucose output (11). More recently, targeted deletion of JNK1 in the muscle (12) and reciprocal adoptive transfer experiments (13) show that JNK1 in muscles and macrophages also contribute to insulin resistance, but not adiposity, in mice with high-fat diet (HFD)-induced obesity. On the other hand, adipocyte-specific deletion of JNK1 improves insulin sensitivity in the liver and adipose tissue but, again, has no impact on adiposity (14).

The improvement in insulin resistance in obese mice after treatment with selective inhibitors of JNKs (6,15) suggests that the suppression of JNK activation is an attractive therapeutic approach in the management of obesity-related type 2 diabetes. In this study, using an alternative strategy of JNK inactivation, we have demonstrated for the first time, that selective suppression of both JNK1 and JNK2 activation in adipose tissue alone can protect against both increased adiposity and insulin resistance induced by an HFD.

RESEARCH DESIGN AND METHODS

Antibodies and chemicals. Rabbit polyclonal antibodies against total JNK1/2 and phospho-JNK1/2 and total Akt and phospho-Akt (Thr308) were from Cell Signaling Technology, and antibodies against hemagglutinin (HA) tag and β-actin were from Sigma. Murine monoclonal antibody against F4/80 was from Serotec. The JNK Activity Assay Kit was purchased from Abcam. Glucose, insulin, and sodium pyruvate were from Sigma. [3H]Oleic acid, [3H]mannotol, and 2-deoxy-o-[3H]glucose were purchased from Amersham.

Generation of transgenic mice. A 3.3-kb cDNA fragment encoding HA-tagged JNKK2 (KM)-JNK1 fusion protein, in which lysine 149 in the ATP domain of the JNKK2 moiety was replaced by Met to create the HA-JNKK2(K149M)-JNK1, was subcloned downstream of the 5.4-kb ap2 promoter/enhancer and upstream of the IGH polyadenylation signals. B: Detection of the dn-JNK transgene by PCR analysis in mice. Specific fragments of 653 bp spanning from the ap2 promoter to the JNK2 gene was amplified. +/+, transgene negative; +/−, transgene positive; L, 1-kb DNA ladder; PC, plasmid DNA positive control; WT, wild-type littermates.

FIG. 1. Generation and characterization of aP2-dn-JNK transgenic (Tg) mice. A: Schematic representation of the aP2-dn-JNK transgenic construct. The dn-JNK cDNA, in which lysine 149 in the ATP domain of the JNKK2 moiety was replaced by Met to create the HA-JNKK2(K149M)-JNK1, was subcloned downstream of the 5.4-kb ap2 promoter/enhancer and upstream of the IGH polyadenylation signals. B: Detection of the dn-JNK transgene by PCR analysis in mice. Specific fragments of 653 bp spanning from the ap2 promoter to the JNK2 gene was amplified. +/+, transgene negative; +/−, transgene positive; L, 1-kb DNA ladder; PC, plasmid DNA positive control; WT, wild-type littermates. C: Expression of the aP2-dn-JNK transgene by RT-PCR. The presence of the aP2-dn-JNK mRNA was analyzed in various tissues of aP2-dn-JNK transgenic mice (10 weeks old) by RT-PCR using specific primers for the dn-JNK transgene (n = 5). EPI, epididymal adipose fat; PRF, perirenal fat; SU, subcutaneous adipose fat. D: Confirmation of the dn-JNK protein expression by immunoblotting (n = 4). Protein extracts from various tissues were subjected to Western blotting with anti-HA antibody.
Measurement of \([3H]2\)-deoxyglucose uptake in skeletal muscle and antibody speci-
lysates harvested from peritoneal macrophages stimulated with or without LPS (100 ng/mL, 10 min) were subjected to immunoprecipitation using an
antibody specific to JNK1 or JNK2, followed by JNK activity assay using GST-c-Jun as a substrate. B: Epididymal fat from aP2-dn-JNK or wild-type
(WT) littersmates on the standard chow (SC) or the HFD for 8 weeks were homogenized and assayed for the activity of JNK1 and JNK2 as in A. The bar
charts below the blots were the quantitative analysis of JNK1 and JNK2 activity. IB, immunoblots. **P < 0.01 vs. wild-type littersmates (n = 5).

Quantitative real-time PCR. Total RNA from various organs of mice was
isolated using the TRIzol reagent (Invitrogen) and treated with RNase-free
DNase (Promega, Madison, WI) at 37°C for 30 min to remove genomic DNA
and was then subjected to reverse transcription and real-time PCR analysis on
an ABI Prism 7000 instrument (Applied Biosystems), as described (17,20).
Primers used for real-time PCR are listed in Supplemental Table 1.

RESULTS

Transgenic mice with adipose tissue–specific overexpression of dn-JNK exhibit lipopolysaccharide (LPS)
reduced JNK activity in obese adipose tissue and LPS-stimulated peritoneal macrophages. First, we
generated transgenic mice overexpressing HA-tagged dn-JNK under the transcriptional control of the A-FABP gene
(aP2) promoter, which has been routinely used to drive adipose tissue–specific expression of foreign genes in
transgenic mice (22). JNKK2 (KM), in which methionine (Met) replaces (Lys) 149 in the ATP-binding domain of
c-Jun NH2-terminal kinase kinase2 (JNKK2) that stimulates
JNK activation, has been demonstrated to result in the

Indirect calorimetry. Mice were individually housed in metabolic chambers
maintained at 20–22°C in a 12 h light/12 h dark cycle. Six-week-old mice were
fed with an HFD and tap water ad libitum using a computer-controlled open
-circuit indirect calorimetry system (Oxymax; Columbus Instruments) with an
airflow of 0.6 L/min and sample flow of 0.5 L/min. After the mice had adapted
to the environment of the metabolic chamber for 48 h, metabolic parameters
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inactivation of JNK (16). Thus, the JNKK2 (KM)-JNK1 fusion protein, dn-JNK, functions as a dominant-negative Jun kinase by competing with endogenous JNK1/2. Our transgenic construct consisted of 5.4 kb of the 5' flanking fatty-specific regulatory region of the αP2 gene and 21 bp of its first exon and the cDNA of dn-JNK (Fig. 1A). The transgenic construct was introduced into pronuclei, and four transgenic founders were identified by genotyping (Fig. 1B). Both mRNA and protein expression of dn-JNK were restricted mainly in white adipose tissue (WAT) and brown adipose tissue (BAT) (Fig. 1C and D, left panel) and in isolated peritoneal macrophages of the transgenic mice (Fig. 1D, right panel). On the contrary, neither the mRNA nor protein of the transgene was detectable in a panel of other major insulin-responsive tissues, except for a trace amount of dn-JNK expression in the spleen.

The transgenic expression of dn-JNK had no obvious effect on the activity of either JNK1 or JNK2 in unstimulated peritoneal macrophages (Fig. 2A) or on WAT in mice fed a standard chow (Fig. 2B). On the other hand, LPS-induced activation of both JNK1 and JNK2 in peritoneal macrophages of the transgenic mice was markedly attenuated.

FIG. 3. The αP2-dn-JNK mice were less obese than control mice under the HFD, displaying decreased fat mass and triglyceride contents in adipose tissue. A: Body weight changes on standard chow (SC) or HFD (HF) over 24 weeks in αP2-dn-JNK transgenic (Tg) mice and their wild-type (WT) littermates. B: Caloric intake, as calculated by food intake per mouse per week (g/mouse/week) × 3.07 kcal/g on the standard chow and × 4.73 kcal/g on the HFD. C: Fat-pad weights in αP2-dn-JNK and wild-type littermates, as measured after dissection at the age of 24 weeks and presented as percentage of total body weight. Insert: Adiposity index, calculated as the total weight of fat pads divided by total body weight. Fat pads: BAT, subcutaneous (SU), epididymal (EPI), perirenal (PRF), interscapular (Int), WAT, and gluteal fat (Glu). D: Representative images of hematoxylin and eosin-stained sections of epididymal WAT and interscapular BAT on the HFD at the age of 24 weeks. Scale bar: 50 μm. E: The size of adipocytes quantified using NIH ImageJ software. F: Triglyceride contents in epididymal fat pads and brown fat pads. *P < 0.05; **P < 0.01 vs. wild-type littermates (n = 6–8). A and B were analyzed by ANOVA; C, E, and F were analyzed by the Student t test. (A high-quality color representation of this figure is available in the online issue.)

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Likewise, HFD-induced elevation of JNK1 and JNK2 in the adipose tissue of the transgenic mice was also reduced to a level similar to that in lean mice, suggesting that transgenic expression of dn-JNK driven by the aP2 promoter is sufficient to inhibit the activation of both endogenous JNK1 and JNK2 in adipocytes and macrophages.

**Adipose tissue–selective inactivation of JNK protects against HFD-induced obesity and its related metabolic disorders.** On the standard chow, there was no obvious difference in body weight gain between the ap2-dn-JNK mice and their wild-type littermates (Fig. 3A). The ap2-dn-JNK mice had much less HFD-induced weight gain compared with age-matched littermates, with the difference in body weight being significant from the age of 10 weeks, despite similar caloric intake (Fig. 3B). The various fat depots weighed less in the ap2-dn-JNK mice, being significantly different from those of wild-type littermates in both WAT (subcutaneous and perirenal depots) and interscapular BAT (Fig. 3C). The adiposity index of ap2-dn-JNK mice was significantly reduced, compared with their wild-type littermates (P < 0.05) (Fig. 3C, insert), suggesting that ap2-dn-JNK mice were resistant to HFD-induced obesity.

Real-time PCR analysis demonstrated that the expression of several genes involved in adipogenesis, including neddin, preadipocyte factor, peroxisome proliferator–activated receptor-γ, CCAAT/enhancer-binding protein-α, and A-FABP, was not significantly different between ap2-dn-JNK mice and their wild-type littermates on an HFD in several types of adipose tissue (Supplementary Fig. 1), suggesting that JNK inactivation in adipose tissue did not impair adipocyte differentiation. On the other hand, histological analysis revealed that the ap2-dn-JNK mice had smaller adipocytes in the epididymal fat pads, as well as in BAT (Fig. 3D and E). Furthermore, the triglyceride contents of WAT and BAT were significantly reduced in ap2-dn-JNK mice, relative to their wild-type littermates (Fig. 3F).

The ap2-dn-JNK mice are protected from HFD-induced insulin resistance and glucose intolerance. An intraperitoneal glucose test was performed to compare the glucose tolerance of ap2-dn-JNK and wild-type mice. When fed with a standard chow, there was no obvious difference between the two groups of mice (Fig. 4A). In contrast, the ap2-dn-JNK transgenic mice were protected from HFD-induced glucose intolerance (Fig. 4B and C). The intraperitoneal insulin tolerance test also showed no significant difference in insulin sensitivity in the two groups of mice on the standard chow (Fig. 4D) but significantly better insulin sensitivity in the ap2-dn-JNK mice on HFD (Fig. 4E and F). The beneficial metabolic effects observed in the ap2-dn-JNK transgenic mice also included lower fasting glucose and insulin levels and homeostasis disorders.
model assessment of insulin resistance index on the HFD (Supplementary Table 2).

**Inactivation of JNK increases insulin-stimulated glucose uptake in skeletal muscles.** We next investigated whether the improvement in insulin-mediated glucose uptake in skeletal muscle contributed to the phenotypic changes in the transgenic mice. This analysis showed that there were no significant differences in the basal rates of Akt phosphorylation (Thr308) and glucose uptake between the ap2-dn-JNK and wild-type mice in either soleus (Fig. 5A and B) or extensor digitorum longus muscles (data not shown) when fed either a standard chow or HFD. In wild-type ob/ob mice on an HFD, insulin-evoked Akt phosphorylation and glucose uptake were decreased by approximately 55 and 61%, respectively, compared with lean controls (Fig. 5A and B). In contrast, the levels of insulin-stimulated Akt phosphorylation and glucose uptake in the transgenic mice on the HFD were comparable to those in lean mice fed a standard chow, suggesting that the protection against HFD-induced glucose tolerance in the transgenic mice was attributed, at least in part, to an increase in insulin-evoked glucose uptake in skeletal muscle. Likewise, HFD-induced phosphorylation of JNK1/2 in skeletal muscle of the transgenic mice was significantly attenuated compared with wild-type littersates (Fig. 5C). HFD-induced impairment in insulin-stimulated glucose uptake in epididymal WAT was also reversed in the transgenic mice (Supplementary Fig. 2).

**Inactivation of JNK attenuates HFD-induced hepatic steatosis and glucose production.** In the ap2-dn-JNK transgenic mice on HFD, the livers were smaller and reddish in color, in contrast to the livers from their wild-type littersates, which were bigger and had a yellowish-white color. The ratio of the liver to body weight was significantly lower in the transgenic mice (Fig. 6A). To further investigate the effects of overexpression of dn-JNK on HFD-induced hepatic steatosis, we performed a hematoxylin and eosin and oil red o staining analysis. As shown in Fig. 6B, HFD induced a marked accumulation of lipid droplets in hepatic cells accompanied by a loss of normal cell morphology. Liver sections from ap2-dn-JNK transgenic mice, in contrast, displayed a normal morphology and an obvious reduction in the number of lipid-engorged hepatic cells, similar to those in lean controls (Fig. 6B).

Compared with the wild-type mice, the ap2-dn-JNK transgenic mice on the HFD had a significantly lower glucose production in response to pyruvate challenge (Fig. 6C). The mRNA levels of the two key hepatic gluconeogenic genes, including PEPCK and G6Pase, were significantly decreased in ap2-dn-JNK mice (Fig. 6D). Furthermore, transgenic expression of dn-JNK in adipose tissue also reversed HFD-induced impairment in phosphorylation of Akt (Thr308) and elevation in phosphorylation of JNK1/2 (Supplementary Fig. 3A and B).

**Suppression of JNK reduces systemic and adipose tissue-specific inflammation.** To investigate the role of JNK in HFD-induced macrophage infiltration and aberrant production of adipokines in the adipose tissue, we examined the expression of inflammatory markers in adipose tissue and adipokines in blood from HFD-fed ap2-dn-JNK and wild-type mice. The mRNA expression of F4/80, a macrophage marker, and several proinflammatory cytokines including IL-6, TNF-α, and MCP-1, were decreased in the transgenic mice, compared with the wild-type mice (Fig. 7A). This was further confirmed by immunohistochemistry using an anti-F4/80 antibody, showing that ap2-dn-JNK mice had a markedly decreased macrophage infiltration in adipose tissue (Fig. 7B). Furthermore, the transgenic mice with dn-JNK expression in adipose tissue on HFD feeding had significantly lower serum levels of leptin and A-FABP but higher levels of adiponectin, compared with their wild-type littersates (Fig. 7C).

**Adipose tissue inactivation of JNK increases energy expenditure and lipid oxidation.** To explore whether increased energy expenditure contributed to the reduced adiposity in ap2-dn-JNK mice, indirect calorimetry measurements were performed in mice that had been on the HFD for 2 weeks before the onset of obesity. The rate of oxygen consumption (Vo2) was higher in ap2-dn-JNK mice over a 24-h period throughout the entire light/dark

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**FIG. 5. Effect of adipose tissue–selective JNK activation on HFD-induced impairment in insulin signaling in skeletal muscle.** A: The soleus muscle isolated from ap2-dn-JNK transgenic (Tg) mice and wild-type (WT) littersates at 16 weeks after the HFD (HF) or standard chow (SC) were treated with insulin (60 μU/mL) for 10 min, followed by Western blot analysis for phosphorylated Akt (Thr308) and total Akt. B: Glucose uptake in soleus muscle expressed as nmol/g wet weight/min. C: Western blot analysis for total and phosphorylated JNK1/2 in soleus muscle. The bar chart below represents the quantitative analysis for fold changes in JNK1/2 phosphorylation relative to lean controls. *P < 0.05; **P < 0.01; ***P < 0.001 (n = 5–6).
cycle, reflecting an increase in energy expenditure during the whole day (Fig. 8A). The respiration exchange rate \( \frac{V_{CO2}}{V_{O2}} \) was significantly reduced in aP2-\( \text{dn-JNK} \) mice, indicating an increase in lipid utilization (Fig. 8B). These data revealed a significant change at the level of energy expenditure, together with an overall higher rate of lipid oxidation and the preferential use of fat as a fuel source, both of which might contribute to the reduced adiposity in the transgenic mice.

**DISCUSSION**

The central role of JNK in the pathogenesis of obesity, insulin resistance, and type 2 diabetes was first suggested by the demonstration that deletion of the \( JNK1 \) gene (\( JNK1^{+/+} \)) leads to decreased adiposity and significant improvements in insulin sensitivity in both dietary and genetic (\( ob/ob \)) mouse models of obesity (8). Subsequent studies using targeted gene deletion (12,14) or reciprocal adoptive transfer (13) approaches had provided evidence for the contribution of \( JNK1 \) inactivation in the adipocytes (14), skeletal muscles (12), and myeloid cells, such as macrophages (14), to the protection against HFD-induced insulin resistance seen in the \( JNK1^{-/-} \) mice. However, none of these subsequent studies with these approaches for selective \( JNK1 \) deletion could reproduce the protection from obesity evident in the conventional \( JNK1^{-/-} \) mice. Similarly, the adenovirus-mediated hepatic overexpression of a dominant-negative (dn) form of JNK (11) also led to the improvement in whole-body insulin resistance, largely secondary to a reduction in hepatic glucose production. Again, this model of JNK inactivation in the liver, albeit only for 2 weeks, had no effect on weight gain in the treated animals. The identity of the cell type responsible for the resistance to obesity in the \( JNK1^{-/-} \) mice remains unknown. In this study, we have demonstrated that in the aP2-\( \text{dn-JNK} \) transgenic mice, selective inactivation of both JNK1 and JNK2 in the adipose tissue and macrophages can reproduce all the beneficial metabolic effects observed in the \( JNK1^{-/-} \) mice, including protection from HFD-induced adiposity.

It should be noted that the resistance to obesity, together with enhanced insulin signaling, was also demonstrated in the mice with heterozygous \( JNK1 \) deletion together with complete \( JNK2 \) deletion (\( JNK1^{+/+} JNK2^{-/-} \)) (10). The authors concluded that the most critical determinant of insulin sensitivity, inflammation, and overall weight gain in the mice on HFD is likely to be total JNK kinase activity. The findings of our study suggest that the selective suppression of total JNK kinase activity, including inactivation of both \( JNK1 \) and \( JNK2 \), in adipose tissue, resulting from the combined downregulation of JNK in adipocytes and macrophages, is sufficient to...
reproduce the beneficial effects observed in the \( JNK1^{-/-} \) or \( JNK2^{-/-} \) mice. Previous studies have demonstrated considerable overlap in the biology and functions of the macrophages and adipocytes in obesity, which appear to be important for the high level of coordination between the inflammatory and metabolic pathways (2). Our study would support the importance of a cross-talk between the macrophages and adipocytes in mediating the effect of the JNK activation in diet-induced obesity. This information is of potential importance in drug development programs using JNK as a therapeutic target for obesity and type 2 diabetes.

In this study, the \( \text{ap2-dn-JNK} \) transgenic mice had decreased adipocyte size, which was also seen in the \( JNK1^{-/-} \) mice (8). These transgenic mice had similar caloric intake as their wild-type littermates but had an increased rate of oxygen consumption and energy expenditure, findings that were also proposed to explain for the resistance to obesity in the \( JNK1^{-/-} \) mice (13). A reduction in the respiration exchange rate in the \( \text{ap2-dn-JNK} \) transgenic mice, suggesting a preferential use of fat as a fuel source, provided another possible mechanism for their reduction in adiposity and triglyceride content in adipocytes. On the other hand, an impairment in adipocyte differentiation did not appear to play a significant role in the reduced fat mass in these transgenic animals.

The mechanism whereby inactivation of JNK in adipose tissue leads to increased energy expenditure remains unknown at this stage. In rodents, BAT is the primary site for energy dissipation (23). In diet-induced obesity, inflammation also occurs in BAT (24), which might impair its thermogenic functions by inducing mitochondria dysfunction. In our transgenic mice, the dn JNK is also expressed in high abundance in BAT. Therefore, it is possible that inactivation of JNK in BAT can restore the thermogenic activities impaired by the HFD. This hypothesis is currently under investigation in our laboratory.

On the HFD, the \( \text{ap2-dn-JNK} \) transgenic mice in this study had improved glucose tolerance and insulin sensitivity compared with their wild-type littermates. Their improvement in insulin sensitivity was accompanied by enhanced insulin-stimulated glucose uptake in the skeletal muscles, as well as reduced glucose production in response by the liver to pyruvate challenge. They were also protected against HFD-induced hepatosteatosis and hepatic insulin resistance but had no improvement in skeletal muscle insulin action. Furthermore, in the adipocyte-specific \( JNK1^{-/-} \) mice, the degree
of macrophage infiltration in the adipose tissue was similar to wild-type mice and only the production of IL-6, but not TNF-α, was reduced relative to the wild-type mice. It is obvious that the ap2-dn-JNK transgenic mice in our study exhibited a much more marked protection against the inflammatory changes induced by the HFD. Not only was there a marked reduction in macrophage infiltration in the adipose tissue, there was also evidence of reduced expression of various proinflammatory cytokines and hormones, including TNF-α, MCP-1, A-FABP, and leptin in addition to IL-6. On the other hand, the circulating level of the anti-inflammatory adipokine, adiponectin, was increased. JNK activation on the HFD was also reduced in the liver and skeletal muscle, probably secondary to the reduced circulating levels of JNK-activating adipokines, such as TNF-α (9) and A-FABP (20), or to the decreased lipid contents in these tissues. These data suggest that the suppression of JNK activation in both the adipocytes and macrophages is required for the protection against HFD-induced insulin resistance in the skeletal muscles, probably consequent to the amelioration of adipose tissue inflammation and adipokine dysregulation.

In conclusion, this study has provided the first evidence that selective suppression of both JNK1 and JNK2 activation in adipose tissue and macrophages can protect against diet-induced obesity, through an increase in energy expenditure and fat utilization. Our data also support the importance of the cross-talk between the inflammatory and metabolic pathways mediated by macrophages and adipocytes in the development of obesity, insulin resistance, and type 2 diabetes.

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X.Z. researched data and wrote the manuscript. A.X. contributed to discussion and reviewed and edited the manuscript. S.K.C., G.S., and A.L. reviewed and edited the manuscript. J.H.B.C. and R.L.C.W. researched data. K.S.L.L. wrote, reviewed, and edited the manuscript.

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