

Detection and Identification of Subcutaneous Adipose Tissue Protein Related to Obesity in New Zealand Obese Mouse

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Abstract. New Zealand obese (NZO) mouse, a genetic model of obesity, shows hyperphagia, hyperinsulinemia and leptin resistance. We analyzed subcutaneous adipose tissue proteins in NZO mice with a two-dimensional gel electrophoresis technique followed by protein sequence analysis. NZO mice showed hyperinsulinemia and hyperleptinemia. Abdominal subcutaneous adipose tissue was inspected in NZO and C57BL/6J lean mice. Two-dimensional gel electrophoresis detected 4 spots which were obviously reduced in NZO mice. Those spots were p26, p19, p18 and p15. Internal sequences of the p26 and p15 protein were homologous with those of carbonic anhydrase III, p19 was cytochrome b5, p18 was superoxide dismutase. Serum arachidonic acid level in NZO mice was lower by 80% of C57BL/6J mice. The present study demonstrated the reduction of several enzymes related to lipid metabolism in NZO mice. These data raises the hypothesis that the supposed changes of membrane fluidity caused by altered membrane lipid content may involve central leptin resistance of this model of obesity.

Key Words: NZO mouse, Cytochrome b₅, Superoxide dismutase, Carbonic anhydrase

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GENETICALLY obese (*ob/ob*) and diabetic (*db/db*) mice show hyperphagia and hyperinsulinemia, but only genetically diabetic (*db/db*) mice shows hyperleptinemia [1, 2]. Genetically obese (*ob/ob*) mouse has a genetic defect in leptin production of adipose tissue, while peripheral administration of recombinant mouse leptin inhibits food intake and reduces excessive body weight gain [3, 4]. In contrast, genetically diabetic (*db/db*) mouse has a mutation in leptin receptor, resulting in no response to peripherally administered leptin [2]. In those models of obesity, lipid metabolism is modulated in adipose tissue [5–7]. But since adipose tissue expresses short-form leptin receptor (Ob-Ra) [8], defects in leptin signaling to adipose tissues may affect lipid metabolism in both

obese (*ob/ob*) and diabetic (*db/db*) mice.

Similarly with genetically obese (*ob/ob*) and diabetic (*db/db*) mice, New Zealand obese (NZO) mice, another genetic model of obesity [9], show hyperphagia, hyperinsulinemia, and leptin resistance. It is known that NZO mice have no genetic defects in adipose tissue leptin production and leptin receptor. However, NZO mice may show leptin resistance in the brain, since intracerebroventricular administration of recombinant mouse leptin inhibits food intake, in spite of no anorexigenic response to peripherally administered leptin [10]. It is supposed that leptin signaling is normally functioning in this model. To determine changes in lipid metabolism by obesity, we analyzed adipose tissue protein in NZO mice by using a two-dimensional electrophoresis technique 2-DE [11].

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Materials and Methods

Animals

Male New Zealand Obese (NZO) mice and C57BL/6J mice as lean controls of NZO mice were purchased from M&B A/S (Denmark). As the genotype of NZO mice is fixed by continuous inbreeding [12], metabolically normal controls with an identical genetic background are not available. Therefore we compared the obese NZO mice with lean C57BL/6J mice. All animals were fed standard diet and they had free access to food and water. They were housed in a temperature controlled room ($24 \pm 1^\circ\text{C}$) with a 14: 10 light/dark cycle (illumination from 0500 h to 1900 h).

Two-dimensional gel electrophoresis (2-DE)

All mice were decapitated at age of 20 weeks and, abdominal subcutaneous adipose tissue was immediately excised from 1000 h to 1200 h in a day. Excised adipose tissues were cut into the small pieces and kept frozen at -80°C until analysis. A piece of frozen tissue about 100 mg was homogenized with a Teflon glass homogenizer in a 10-fold volume of extraction medium comprised of 5M urea, 1M thiourea solution containing 0.5% 2-mercaptoethanol and 0.1mM N^α -tosyl-L-lysylchloromethane hydrochloride. The homogenate was centrifuged with a TOMY TMA-6 rotor at 15,000 rpm for 20 min, and the clear supernatant was subjected to the first-dimension isoelectric focusing of 2-DE. We performed the 2-DE according to our procedure [11]. The isoelectric focusing agarose gel for the first dimension electrophoresis was 260 mm in length and 3 mm in diameter in a glass tube. The slab gel for the second dimension electrophoresis was 15% polyacrylamide gel and was 195 mm in width, 120 mm in height, and 1.5 mm in thickness. The isoelectric focusing was conducted at 600V for 18 hours at 4°C , and the second dimension SDS electrophoresis was carried out according to the stacking system of Laemmli [13]. Five hundred μg of the protein extract was applied for the first dimension isoelectric focusing. The slab gels after the second dimension electrophoresis were stained with Phast-Gel Blue R (Coomassie brilliant blue R 350; Pharmacia Biotech AB, Uppsala, Sweden).

Protein content determination from electrophoretic patterns

A Coomassie-stained 2-DE gel was interposed between two wet cellophane sheets and stretched with two styrene plastic frames to be dried in a draft chamber at 60°C for 2 hours. To precisely compare protein constituents of the NZO and C57BL6J tissues, we repeated 2-DE three times; the first was the C57BL6J tissue extract, the second the NZO one, and the third a 1:1 mixture of the two. The third 2-DE pattern was quite important, since without it we were unable to discriminate whether a pair of C57BL6J and NZO spots located very close to each other in the first two 2-DE patterns were identical or not. It also worked for our identifying proteins in the NZO mouse, which are normal in 2-DE position but abnormal in protein content. When we look carefully at either of the first two 2-DE patterns, we can discern which protein is more and which is less. When a protein spot in the 2-DE pattern of C57BL6J is denser than a nearby protein spot, but less dense in the NZO pattern, that spot would be a candidate for an abnormal protein. We then look for a corresponding spot in the third 2-DE patterns and compare the spot density with nearby spot densities. If the comparison comes up to our expectation that the 1:1 mixture 2-DE patterns is between the first two, the candidate protein in the NZO tissue would likely be abnormal in protein content.

In-gel digestion of proteins for internal amino acid sequencing

A protein spot that contained a target protein was cut out from a 2-DE gel and subjected to NH_2 -terminal amino acid sequence analysis (HPG1005A Protein Sequencing Systems; Hewlett-Packard Co., Palo Alto, CA). Amino acid sequence was performed by the in-gel digestion method described by Rosenfeld *et al.* [14].

Assay

NZO and C57BL/6J mice were decapitated and blood samples were collected. Serum was obtained after centrifugation and stored at -30°C . Two samples were combined as a sample. Serum immunoreactive insulin (IRI) concentrations were as-

sayed by a radioimmunoassay using Phadeceph Insulin Kit (Pharmacia Japan, Tokyo, Japan). Serum immunoreactive leptin (IRL) concentrations were assayed by a radioimmunoassay using Mouse Leptin RIA Kit (Linco Research, Inc., St. Charles, MO, U.S.A.). Serum glucose concentrations were determined by automatic analyzer using glucose oxidase method. In addition, we examined changes in serum fatty acid composition of these animals by gas-liquid chromatography method.

Statistical analysis

All data are expressed as mean \pm SE. Statistical analysis was performed by analysis of variance (ANOVA), followed by Student's t-test for the individual comparisons of the means.

Results

Circulating glucose, insulin and leptin levels in NZO and C57BL/6J

Circulating glucose, insulin and leptin levels are summarized in Table 1. There was no significant difference in serum glucose concentrations. Serum IRI concentrations were significantly higher in NZO mice than in C57BL/6J mice. Serum IRL concentrations were also increased in NZO mice.

Protein content disparity and amino-acid sequences in the NZO and C57BL/6J abdominal subcutaneous adipose tissue

Fig. 1 shows 2-DE patterns of abdominal subcutaneous adipose tissue extracts of the C57BL/6J (A), NZO (B) mice and a 1:1 mixture of both mice (C). A part of each panel of Fig. 1 is expanded and

shown in Fig. 2. Each protein spot in Fig. 1 is named by the molecular weight in the 2-DE pattern, *i.e.*, the protein spot in Fig. 1 denoted as p26 is 26 KDa in apparent molecular weight. The C57BL/6J and NZO patterns reveal general similarities, but we can still identify the differences in several spots. Four dense spots named as p26, p19, p18 and p15 are faint in the NZO tissue. Since these proteins were supposed to decrease in NZO mice, they were analyzed for their amino acid sequences.

We analyzed ten amino acid sequences from N-terminal of four selected protein obtained from the spots mentioned above by 2-DE analysis. Table 2 shows the amino acid sequences of the four spots together with the names of homologous proteins identified in the protein identification resources database. Internal sequences of the p26 and p15 protein were homologous with those carbonic anhydrase III, p19 was cytochrome b_5 , and p18 was superoxide dismutase.

Serum fatty acid composition

Table 3 demonstrated serum fatty acid composition of C57BL/6J and NZO mice. The ratio of unsaturated fatty acids tended to be higher in the sera of NZO mice than in C57BL/6J mice. Serum arachidonic acid level of NZO mice was reduced by 80% of C57BL/6J mice.

Discussion

The present study reconfirmed that NZO mice show hyperinsulinemia and hyperleptinemia. We analyzed abdominal subcutaneous adipose tissue protein constituents in C57BL/6J and NZO mice. Four spots were obviously decreased in NZO mice. The protein analysis of N-terminal ten amino acid sequences showed that those proteins are carbonic anhydrase III, cytochrome b_5 and superoxide dismutase.

First, we found that cytochrome b_5 content was reduced in adipose tissue of NZO mice. Cytochrome b_5 in rat liver microsomes acts as an intermediate electron carrier which passes reducing equivalents from NADH, NADPH and ascorbate to the cyanide-sensitive factor where fatty acid desaturation takes place, and plays a similar role in fatty acid

Table 1. Circulating glucose, insulin and leptin levels in C57BL/6J and NZO mice.

	Glucose (mg/dl)	IRI (μ U/ml)	IRL (ng/ml)
C57BL/6J	179.8 \pm 3.7	13.0 \pm 1.7	3.08 \pm 0.25
NZO	184.6 \pm 3.4	37.0 \pm 3.6 ^a	9.53 \pm 0.79 ^a

^a $p < 0.01$ vs. C57BL/6J mice $n = 5$ each

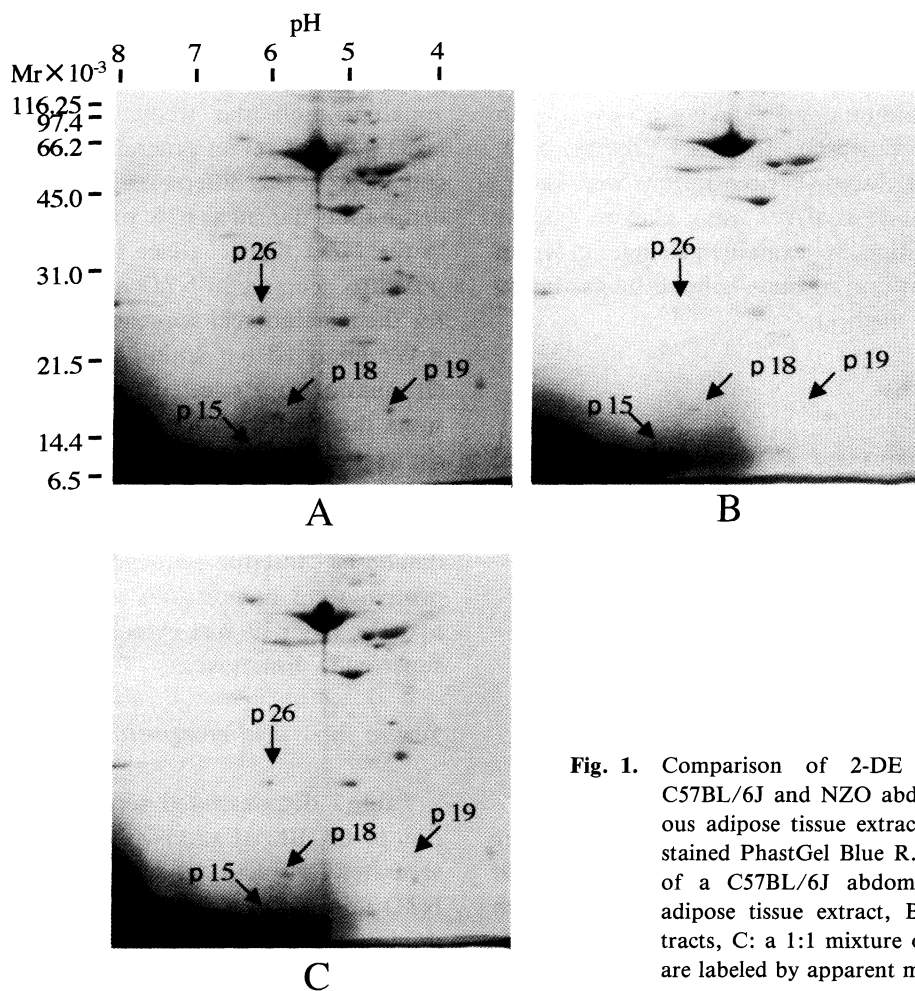


Fig. 1. Comparison of 2-DE patterns of the C57BL/6J and NZO abdominal subcutaneous adipose tissue extracts. The gels were stained PhastGel Blue R. A: 2-DE patterns of a C57BL/6J abdominal subcutaneous adipose tissue extract, B: NZO tissue extracts, C: a 1:1 mixture of the two. Spots are labeled by apparent molecular weight.

desaturation in epididymal adipose tissue [15]. In streptozotocin-induced diabetes rat, cytochrome b_5 level of liver were elevated and returned to normal after insulin treatment [16, 17], suggesting that hyperinsulinemia is related to the decrease of liver cytochrome b_5 content in NZO mice. In mice, feeding of fat-free diet significantly reduced cytochrome b_5 in liver, but increased it in lung [18]. It is supposed that cytochrome b_5 is related to fat intake [19].

However, there have been few reports on the changes of adipose tissue cytochrome b_5 contents in models of obesity. No significant effect on cytochrome b_5 content and P450 reductase activity was seen in obese rats induced by overfeeding had [20], nor were there any significant differences in the cytochrome b_5 contents of ventromedial hypothalamus lesioned rats [21]. Therefore, it is possible that the observed reduction of cytochrome b_5 content can't be

explained by obesity alone and may be specific for NZO mice.

Cytochrome b_5 reductase is detected not only in liver, but also in adipose tissue microsomes [22]. In a case of generalized deficiency of cytochrome b_5 reductase in congenital methemoglobinemia, there was a decrease in total unsaturated fatty acids and an increase in palmitic acid, indicating an undeveloped pattern of fatty acid composition in adipose tissue, and the proportions of arachidonic acids (AA) were decreased to less than half of normal levels [23]. Mammalian membrane polyunsaturated fatty acid composition modifies membrane fluidity and its function [24]. Exposure of cultured cerebrovascular endothelial cells to AA increases membrane fluidity, while addition of AA and H_2O_2 leads to persistent alteration of endothelial cell permeability [25]. Arachidonic acid composition was reduced in

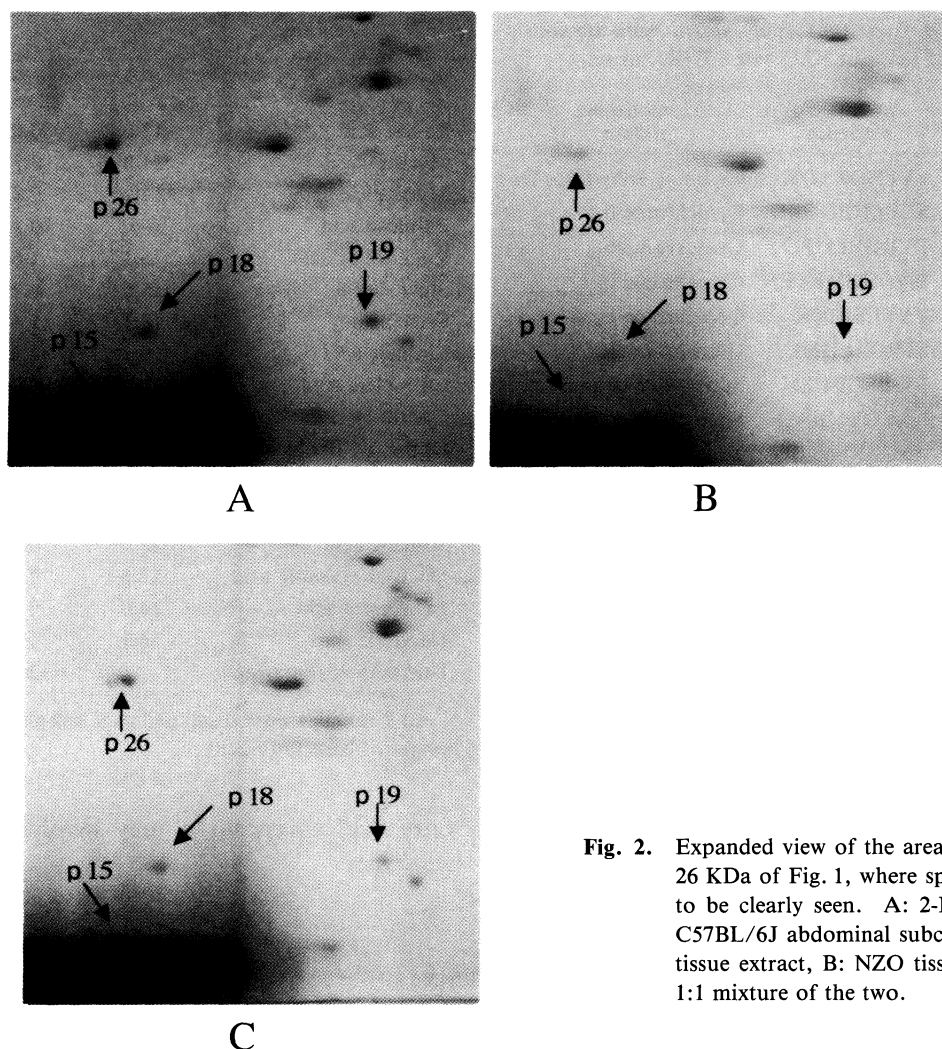


Fig. 2. Expanded view of the area from 15 KDa to 26 KDa of Fig. 1, where spots are too small to be clearly seen. A: 2-DE patterns of a C57BL/6J abdominal subcutaneous adipose tissue extract, B: NZO tissue extracts, C: a 1:1 mixture of the two.

the serum of NZO mice. The reduction of cytochrome b_5 in NZO mice may modify the fatty acid composition of body lipids as well as brain lipids. The changes of brain lipid contents, such as reduction of AA content, may modulate membrane composition and membrane fluidity of brain microvessels, possibly involving central leptin resistance of this animal [10].

In addition, we found the reduction of two more enzymes in NZO mice, carbonic anhydrase III (CAIII) and superoxide dismutase. CAIII is a major constituent of murine adipose tissue and located in the perinuclear and peripheral cytoplasm bordering fat droplets [26]. While CAIII is highly expressed in red skeletal muscle, it has been reported that CAIII is low in *ob/ob* and MSG-obese mice. This decrease in

CAIII expression was unique to adipose tissue [27]. It is suggested that the reduction of CAIII levels may be correlated with the degree of obesity. Since CAIII is low in insulin-treated 3T3 adipocytes [28], the obesity-related decrease in CAIII may be associated with hyperinsulinemia in obesity. Since NZO mice also show marked hyperinsulinemia as shown in Table 1, the observed reduction of CAIII should be attributable to hyperinsulinemia accompanied with obesity.

Regarding the other enzyme, superoxide dismutase (SOD), manganese (Mn) SOD activities in brown adipose tissue of *ob/ob* mice are lower and adrenalectomy failed to restore MnSOD activities, suggesting that glucocorticoid is not related to the reduction of SOD activities in *ob/ob* mice [29]. Lower SOD

Table 2. N-terminal amino-acid sequences from the proteins obtained from four spots which were obviously different between NZO and C57BL/6J mice.

Source	Fraction	Amino-acid sequence	Homologous protein
p26	1	VVFDDTYDR	Carbonic anhydrase III
p19	1	FLEEHPGGEE	Cytochrome b ₅
	2	TYIIGELHPD	Cytochrome b ₅
	3	EQAGGDATEN	Cytochrome b ₅
	4	YYTLEEIQK	Cytochrome b ₅
		STWVILHHK	Cytochrome b ₅
p18	1	VISLSGEHSI	Superoxide dismutase
		LACGVIGIAQ	Superoxide dismutase
	2	ASGEPVVLSG	Superoxide dismutase
p15	1	QFHLHWGSSD	Carbonic anhydrase III
	2	HDPSLQPWSA	Carbonic anhydrase III

activities in liver was eliminated by food restriction, but not in kidney [30]. The observed reduction of SOD content may be related to hyperphagia associated with obesity.

The present study demonstrated the reduction of several enzymes related to lipid metabolism in NZO mice. The reduction of cytochrome b₅ may be specific for NZO mice and the subsequent changes of

Table 3. Serum fatty acid composition in NZO and C57BL/6J mice.

Fatty acid		C57BL/6J	NZO
Lauric acid	12:0	0.02	0.06
Myristic acid	14:0	0.31	0.35
Myristoleic acid	14:1	0.41	0.23
Palmitic acid	16:0	20.16	21.45
Palmitoleic acid	16:1	3.66	3.66
Stearic acid	18:0	6.77	6.68
Oleic acid	18:1	15.49	18.26
Linoleic acid	18:2	32.66	31.08
α -Linoleic acid	18:3	0.92	0.92
Gondoic acid	20:1	0.85	0.93
Dihomo- γ linolenic acid	20:3	1.38	1.09
Arachidonic acid	20:4	7.25	5.84
Eicosapentaenoic acid	20:5	1.97	1.98
Behenic acid	22:0	0.28	0.27
Docosahexaenoic acid	22:6	7.32	6.55
Lignoceric acid	24:0	0.18	0.14
Nervonic acid	24:1	0.40	0.24
Unsaturated/Saturated		2.609	2.454

All 9 samples were combined as a sample. Values were % weight of each fatty acid.

fatty acid composition may involve central leptin resistance.

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