

Fig. 3. Current hypothesis regarding the association between adipocytokines and liver diseases. Arrows, stimulatory effects

accumulation, a state of chronic low-grade inflammation. The inflammatory changes in obese adipose tissue induce adipocytokine dysregulation: an increase in offensive adipocytokines, TNF- α , IL-6, and resistin, and a decrease in the defensive adipocytokine adiponectin. Increased serum levels of TNF- α , resistin, and leptin, which are usually observed in obese subjects, may enhance steatosis, inflammation, fibrogenesis, or hepatocarcinogenesis in the liver. In addition, hypo-adiponectinemia seems to enhance hepatic steatosis, inflammation, and fibrosis, as well as hepatocarcinogenesis (Fig. 3). Attenuation of proinflammatory adipocytokines or augmentation of the function of adiponectin might be an effective therapy for metabolic syndrome. Further clinical and experimental research should elucidate the relationship between adipocytokines and liver diseases.

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MUTATION IN BRIEF

Mutations in the Small Heterodimer Partner Gene Increase Morbidity Risk in Japanese Type 2 Diabetes Patients

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Mutations in the small heterodimer partner gene (NR0B2; alias SHP) are associated with high birth weight and mild obesity in Japanese children. SHP mutations may also be associated with later obesity and insulin resistance syndrome that induces diabetes. To investigate this possibility, the prevalence of SHP mutations in Japanese with and without type 2 diabetes mellitus and the functional properties of the mutant proteins were evaluated. Direct sequencing of two exons and flanking sequences of SHP in 805 diabetic patients and 752 non-diabetic controls identified 15 different mutations in 44 subjects, including 6 novel mutations. Functional analyses of the mutant proteins revealed significantly reduced activity of nine of the mutations. Mutations with reduced activity were found in 19 patients (2.4%) in the diabetic group and in 6 subjects (0.8%) in the control group. The frequency difference between DM and control subjects adjusted for sex and age was statistically significant ($P=0.029$, odds ratio 2.67, 95% CI 1.05 – 6.81, $1-\beta=0.91$). We conclude that SHP mutations associated with mild obesity in childhood increase susceptibility to type 2 diabetes in later life in Japanese. © 2008 Wiley-Liss, Inc.

KEY WORDS: SHP, type 2 diabetes, obesity, fatty liver, NASH

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INTRODUCTION

Type 2 diabetes mellitus is characterized by defects of insulin secretion in pancreatic β -cells and insulin action in peripheral tissues. Failure of pancreatic β -cells to compensate for insulin resistance by increasing insulin secretion is thought to underlie the development of type 2 diabetes (Reaven, 1988, Polonsky, 2000).

We have previously shown that mutations in the gene encoding small heterodimer partner (*NROB2*, alias *SHP*; MIM# 604630), an orphan nuclear receptor that interacts with a number of other receptors (Seol et al., 1996, Masuda et al., 1997, Seol et al., 1998, Johansson et al., 1999), are associated with high birth weight and mild obesity in Japanese children, although the molecular mechanisms by which the *SHP* mutations cause these disorders are unknown (Nishigori et al., 2001).

Nuclear receptors such as SHP and peroxisome proliferator-activated receptor (PPAR) α that regulate lipid metabolism in liver are potential contributors to fatty liver. It should be noted that the storage of lipids in liver can trigger inter-organ crosstalk systems that affect insulin sensitivity in muscle. Farnesoid X receptor (FXR)-null mice, with reduced levels of SHP, develop severe fatty liver and elevated circulating FFAs, which is associated with elevated serum glucose and impaired glucose and insulin tolerance resulting from attenuated inhibition of hepatic glucose production by insulin and reduced peripheral glucose disposal (Ma et al., 2006). Some patients with *SHP* mutations exhibit liver dysfunction due to fatty liver (Nishigori et al., 2001). Accordingly, mutations in *SHP* may be associated with insulin resistance due to both later obesity and also to fatty liver in Japanese subjects.

Nonalcoholic fatty liver disease (NAFLD) is a polygenic disease caused by a combination of environmental and genetic factors. Potential candidate genes contributing to NAFLD, a condition comprising a spectrum of pathological liver conditions ranging from steatosis alone to non-alcoholic steatohepatitis (NASH), include those involved in fat deposition, insulin sensitivity, and hepatic lipid oxidation, synthesis, storage, and export. NASH is believed to be a hepatic expression of metabolic syndrome (Ono and Saibara, 2006). In this regard, genetic abnormalities manifested in obesity and fatty liver might well act in concert to induce diabetes.

To evaluate the influence of *SHP* mutations on risk of later development of type 2 diabetes, we examined the frequencies of these mutations in Japanese subjects with and without type 2 diabetes mellitus as well as in patients with NASH.

MATERIALS AND METHODS

Patient populations

The ADA definitions of type 2 diabetes were used. Obesity is defined in these studies as BMI of $>25 \text{ kg/m}^2$, in accord with the criteria of the Japan Society for the Study of Obesity (Japanese Society for the Study of Obesity, 2000) and the report by WHO (Western Pacific Region) and IASO/IOTF (International Association for the Study of Obesity/International Obesity Task Force) (WHO and IASO/IOTF, 2000). We evaluated the prevalence of *SHP* mutations in 805 Japanese patients with type 2 diabetes (male/female, 432/373; age, 60.3 ± 11.8 yr.; BMI, $24.1 \pm 4.0 \text{ kg/m}^2$) and 752 non-diabetic controls (male/female, 418/334; age, 59.7 ± 13.3 yr.; BMI, $22.9 \pm 2.9 \text{ kg/m}^2$). Informed consent was obtained from all of the diabetic subjects and volunteer controls. NASH patients with nonalcoholic fatty liver disease underwent liver biopsy after signed informed consent and thorough clinical evaluation. Liver biopsy was analyzed by a pathologist (H.E.) and the diagnosis of NASH was based on Brunt's criteria (Brunt et al., 1999). Laboratory blood tests and BMI were analyzed in 93 biopsy-proved NASH patients (48 males and 45 females, age: 29.2 ± 5.4 years old, BMI: $29.2 \pm 5.4 \text{ kg/m}^2$, ALT: $102.6 \pm 66.6 \text{ IU/L}$, T Cholesterol: $5.25 \pm 1.05 \text{ mmol/L}$, TG: $1.74 \pm 0.88 \text{ mmol/L}$, HDL-C: $1.24 \pm 0.35 \text{ mmol/L}$, HbA1c: $5.6 \pm 1.0 \%$, FPG: $6.03 \pm 1.79 \text{ mmol/L}$).

Mutation analysis

The two exons and flanking regions of the SHP gene were screened for mutations by direct DNA sequencing of the amplified polymerase chain reaction (PCR) products, using specific primer pairs and an ABI PRISM BigDye Terminator Cycle Sequencing FS ready Reaction Kit (Applied Biosystems, Foster City, CA). Primer pairs and PCR conditions used for screening of the SHP gene are as follows. Exon1: 5'-CATGACTTCTGGAGTCAAGG-3' and 5'-GTCCCTTTCAGGCAGGCATA-3',

5'-CATCCTTCTGGCAGCTGCCT-3' and 5'-TTAGAAGCTACCTTCCCTGGCT

GG-3' Exon2: 5'-CAGATCTTGGGCCAGTCTTG-3' and 5'-CTCCAGGAGCATTG GGTCAC-3'. Genomic DNA extracted from diabetic and control subjects was initially denatured at 95° C for 1 min, followed by 35 cycles of denaturation at 94° C for 30 sec, annealing at 60° C or 62° C for 30 sec, extension at 72° C for 30 sec, and a final extension step of 7 min. The sequencing reactions were analyzed by automatic DNA sequencers (Applied Biosystems models 3100 and 3700).

Mutation Nomenclature

The cDNA NM_021969.1 and protein NP_068804.1 sequences were used for mutation nomenclature, with DNA +1 corresponding to the A of the ATG translation initiation codon. Descriptions of all sequence variants were checked using the Mutalyzer program (<http://www.LOVD.nl/mutalyzer/>).

Functional analysis of SHP mutant proteins

Analysis of the functional properties of mutant and wild-type proteins was performed as described previously (Nishigori et al., 2001). Briefly, the SHP mutations newly identified in this study were generated by PCR-based site-directed mutagenesis and cloned in the expression pCMV-6b vector. The sequences for wild-type and mutant SHP proteins, and HNF-4 α were cloned in pCMV-6b and pcDNA3.1 (Invitrogen, Groningen, The Netherlands), respectively. For luciferase reporter assays, the promoter region of the human HNF-1 α gene was inserted into the pGL3-Basic Reporter vector (Promega, Madison, WI).

HepG2 cells (1×10^5) were grown in 6-well plates containing Dulbecco's modified Eagle's medium (DMEM) supplemented with 15% fetal calf serum. The cells were transfected with ExGen 500 solution (6.6 ml) (Fermentas, Ontario, Canada), 333 ng of HNF-1 α -promoter/reporter construct, 100 ng of HNF-4 α -expression plasmid, 0-125 ng of test DNA, and 17 ng of pRL (Renilla luciferase)-TK. Luciferase reporter activity was measured using a Dual-Luciferase Reporter Assay System (Promega) according to the manufacturer's instructions. Renilla luciferase activity was used to normalize transfection efficiencies among experiments.

Statistical analyses

Statistical difference in frequencies of SHP mutations between the diabetic and control groups was analyzed by logistic regression analysis, using a package of STATVIEW 5.0 (SAS Institute Inc., Cary, NC). Data obtained by luciferase reporter assay were analyzed by the Student's *t*-test.

RESULTS

Eight hundred five Japanese patients with adult-onset type 2 diabetes (T2DM), 752 non-diabetic controls, and 93 patients with NASH were examined. Screening of the SHP gene (*NROB2*) by direct sequencing resulted in the identification of fifteen different mutations (c.100C>T [p.Arg34X], c.112C>T [p.Arg38Cys], c.134G>C [p.Arg45Pro], c.157_166del [p.His53AlafsX50], c.160C>T [p.Arg54Cys], c.169C>T [p.Arg57Trp], c.292_300delinsAC [p.Leu98ThyfsX6], c.314T>G [p.Val105Gly], c.512G>C [p.Gly171Ala], c.532G>A [p.Asp178Asn], c.566G>A [p.Gly189Glu], c.583G>T [p.Ala195Ser], c.618G>A [p.Trp206X], c.637C>T [p.Arg213Cys], and c.647G>A [p.Arg216His]) including six novel mutations in type 2 diabetic patients (Table 1),

eight of which were previously identified in obese children (Nishigori et al., 2001) and one of which, p.Gly171Ala, was reported as a polymorphism in a study of Caucasians (Hung et al., 2003, Echwald et al., 2004, Mitchell et al., 2003). In NASH patients, only one mutation, p.Arg45Pro, was identified. We could not find any variants in flanking sequences.

Table 1: Mutations identified in the human SHP gene (NR0B2).

Exon	Codon	Nucleotide change	Designation	Patients (n=805)	Controls (n=752)
Mutations with reduced activity					
1	34	c.100C>T	p.Arg34X ^{a)(b)(c)(d)(e)}	2	0
1	53	c.157_166del	p.His53AlafsX50 ^{a)(b)(c)(e)}	2	0
1	54	c.160C>T	p.Arg54Cys*	0	1
1	57	c.169C>T	p.Arg57Trp ^{a)}	1	0
1	98	c.292_300 delinsAC	p.Leu98ThyfsX6 ^{a)(c)(e)}	6	1
1	105	c.314T>G	p.Val105Gly*	1	0
2	189	c.566G>A	p.Gly189Glu ^{a)}	3	0
2	195	c.583G>T	p.Ala195Ser ^{a)(c)(d)(e)}	1	3
2	206	c.618G>A	p.Trp206X*	2	1
2	213	c.637C>T	p.Arg213Cys ^{a)(b)(c)(e)}	1	0
			sum	19	6
				(2.4%)	(0.8%)
Mutations with normal activity					
1	38	c.112C>T	p.Arg38Cys*	1	0
1	45	c.134G>C	p.Arg45Pro*	1	0
1	171	c.512G>C	p.Gly171Ala	0	1
1-2	178	c.532G>A	p.Asp178Asn*	1	0
2	216	c.647G>A	p.Arg216His	6	9
			sum	9	10
				(1.1%)	(1.3%)

* indicates six novel variants identified in the present study.

To determine if the mutations alter the function of the SHP protein, the effect of the wild-type and mutant proteins on HNF-4 α -mediated transactivation of HNF-1 α gene transcription in HepG2 cells was examined by luciferase reporter assay (Fig. 1 and Nishigori et al., 2001). a) early-onset obesity, b) high birth weight, c) diabetes, d) fatty liver, e) decreased insulin sensitivity (Nishigori et al., 2001) Mutations were numbered according to GenBank NM_021969.1 and NP_068804.1. Nucleotide +1 is A of the ATG initiation codon.

Functional analyses of the novel mutant proteins showed significantly reduced activity of transcriptional regulation of HNF-4 α , except in the case of p.Arg38Cys, p.Arg45Pro, and p.Asp178Asn. The results of functional analyses of the mutations newly identified in this study are shown in Fig. 1. The mutations with reduced activity were found in nineteen subjects (2.4%) in the diabetic group, six (0.8%) in the control group, and none in the NASH group (Table 1). The frequency difference between DM and control groups was statistically significant by logistic regression analysis considering gender and age ($P=0.029$; $1-\beta=0.91$) with odds ratio of 2.67 [95% CI, 1.05-6.81]. This frequency difference between DM and control groups came to be not statistically significant by logistic regression analysis when considering gender, age, and BMI ($P=0.078$), with odds ratio of 2.26 [95% CI, 0.87-5.86]. Furthermore, subjects with mutations of reduced activity showed significantly higher BMI than subjects without the mutations (25.6 ± 4.6 vs 23.5 ± 3.6 , $P=0.0039$ in combined subjects, and 24.0 ± 4.0 vs 26.5 ± 5.0 , $P=0.012$ in diabetic patients). In control subjects, those with mutations of reduced activity showed similar BMI to those without mutations (22.9 ± 2.9 vs 23.1 ± 2.7 , $P=0.87$).

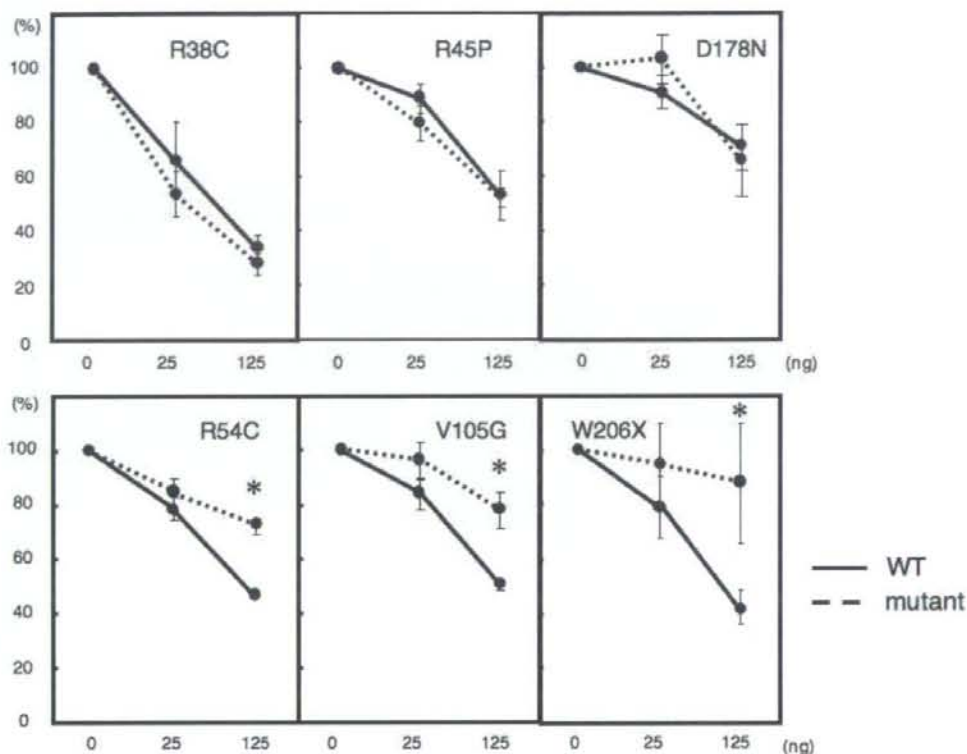


Figure 1: Inhibition of transactivation activity of HNF-4 α by wild-type and mutant SHP proteins. It has been shown previously that expression of wild-type SHP significantly decreases HNF-4 α transactivation of the HNF-1 α gene promoter in HepG2 cells, indicating that SHP is a negative regulator of HNF-4 α (Nishigori et al., 2001, Lee et al., 2000). Transcriptional regulation of the novel six mutations of p.Arg38Cys, p.Arg45Pro, p.Arg54Cys, p.Val105Gly, p.Asp178Asn and p.Trp206X was examined by luciferase reporter assay (n=3 in each experiment). Functional properties of the other mutations identified have been examined previously (Nishigori et al., 2001, Echwald et al., 2004). The relative luciferase activity (firefly/Renilla) of each construct at 0 ng, 25 ng, and 125 ng of wild-type and mutant SHP proteins was measured in HepG2 cells. Percent activity in relation to basic HNF-4 α activity is shown as mean \pm SD. * $P < 0.05$.

DISCUSSION

Mutations in the SHP gene have been shown to be associated with high birth weight and early-onset mild obesity in Japanese. Although the molecular mechanism by which these mutations increase body weight is unknown at present, one possibility is suggested by the fact that pancreatic β cells express SHP mRNAs at high levels. Since SHP inhibits HNF-4 α (MODY1 protein) (Nishigori et al., 2001, Lee et al., 2000), functional defects of SHP might well increase the activity of HNF-4 α and other downstream components of glycolytic signal transduction (Dukes et al., 1998), resulting in increased insulin secretory response to glucose (Wang et al., 2006). In addition, since insulin is a key hormone in fetal growth, high levels of fetal insulin may well be associated with high birth weight and postnatal obesity.

As adult-onset type 2 diabetes is a polygenic disorder requiring interaction of multiple genetic and environmental factors, and Japanese patients exhibit a lesser insulin secretory capacity due to pancreatic β -cell

dysfunction (Kosaka et al., 1977, Kosaka and Akanuma, 1980, Yoshinaga and Kosaka, 1999), the increased insulin secretory demand associated with *SHP* mutations might increase susceptibility to type 2 diabetes in this population. Since other nuclear receptors that interact with SHP in peripheral tissues (Seol et al., 1996, Masuda et al., 1997, Seol et al., 1998, Johansson et al., 1999) may be involved in the pathogenesis of insulin resistance due to obesity or fatty liver, the secondary demand for compensatory insulin secretion might also promote the development of overt diabetes.

FXR-null mice, which show reduced levels of SHP, exhibit elevated plasma cholesterol and triglyceride levels and excessive accumulation of fat in the liver (Ma et al., 2006). Fatty liver also was observed in some early-onset obesity patients with *SHP* mutations (Nishigori et al., 2001). In addition, increased insulin secretion derived from *SHP* mutations accelerates fat accumulation in the liver. Accordingly, we examined 93 NASH patients, and found one mutation. However, none of the mutations associated with reduced activity was found in the NASH group, suggesting that the effect of SHP on the accumulation of fat in the liver may be of little clinical importance.

While we cannot link the etiology of NASH to mutation of *SHP*, the finding that *SHP* mutations increase morbidity risk for type 2 diabetes due to mild obesity in later life in Japanese suggests a genetic link between obesity and type 2 diabetes in human. To clarify the complex relationship of type 2 diabetes with SHP deficiency, further genetic analysis and characterization of the diabetogenic factors involved is required.

According to previous epidemiological studies, low birth weight and fetal thinness are associated with insulin resistance syndrome and were therefore thought to be related to later risk of type 2 diabetes (Hales et al., 1991, Eriksson et al., 2003). In contrast, we demonstrate here an increased morbidity risk of type 2 diabetes due to *SHP* mutations associated with high birth weight and mild obesity in Japanese children. Further analysis of the functional properties of mutant SHP proteins in energy expenditure should provide new insight into the relationship between birth weight and the development of type 2 diabetes.

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臨床

NASH の治療

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要 旨

NASH は今後日本で増加することが予想されるが、NASH に対する薬物療法に関してはエビデンスレベルの高い報告は少なく、日本人を対象とした検討も少ない。NASH は内臓脂肪蓄積を基盤とするメタボリックシンドロームを背景に、インスリン抵抗性・耐糖能異常、糖尿病、脂質異常症、高血圧などを合併することが多く、その対策が NASH 治療の基本である。つまり、日常生活・生活習慣の是正や肥満の改善に加え、合併する疾患に対する治療が NASH の病態改善にも有効と考えられる。

はじめに

非アルコール性脂肪性肝炎 (NASH) は、非アルコール性脂肪性肝疾患 (NAFLD) の中で、肝細胞の変性・壊死に伴う炎症や線維化を伴う進行性の疾患である。NASH の成因機序として、Day らの提唱した“two hit theory”が広く知られている。すなわち、NASH の発生には、正常肝から単純性脂肪肝 (simple steatosis) となる“1st hit”と、単純性脂肪肝から NASH へ進行する“2nd hit”が必要と言われている¹⁾。“1st hit”には、肥満、脂質異常症、糖尿病などの生活習慣病や遺伝子多型、薬剤などが原因として考えられ、“2nd hit”には、高インスリン血症、TNF α などのサイトカイン、鉄沈着などに

起因する酸化ストレスなどが重要な因子として挙げられる。このことから、NASH の治療は肥満、糖尿病、脂質異常症、高血圧といった生活習慣病に対する食事・運動療法を主体とした生活習慣の改善が中心となる。しかし、NASH に対する薬物治療に関してはエビデンスレベルの高い報告は少なく、推奨度の高い治療法は十分確立していない²⁾。本稿では、NASH の治療に関して最近の知見を含めて紹介する。

日常生活指導

1. 食事・運動療法

NASH は、肝における生活習慣病やメタボリックシンドロームの表現型と言われており、生活習慣の改善が必須である。そのため、NASH ではメタボリックシンドロームの治療に則した食事・運動療法を行うことが重要である³⁾。食事指導の目安としては、1日当たりのエネルギーは標準体重当たり 25~35 kcal/kg 程度、タンパク質は 1.0~1.5g/kg、

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表1 NASHに対する薬物治療

治療薬	対象患者	結果 (文献 No.)
インスリン抵抗性改善薬		
ピオグリタゾン	NASH 55例	ALT 値低下, 組織学的改善 (6)
ロシグリタゾン	NASH 63例	ALT 値低下, 組織学的改善, アディポネクチン上昇 (7)
メトホルミン	NAFLD 110例	ALT 値低下, 評価可能患者の組織学的改善 (8)
糖尿病治療薬		
ナテグリニド	NASH 10例	ALT 値低下, 組織学的改善 (9)
抗酸化薬		
ビタミン E	NASH 12例	ALT 値低下, 組織学的改善 (10)
ビタミン E+C	NASH 49例	ALT 値変化なし, 組織学的線維化改善 (11)
ベタイン	NASH 10例	ALT 値低下, 組織学的改善 (12)
UDCA	NASH 166例	ALT 値低下あるもコントロール群と有意差なし (13)
UDCA+ビタミン E	NASH 48例	ALT 値低下, 組織学的改善 (14)
脂質異常症治療薬		
ゲムフィブロジル	NASH 46例	ALT 値低下 (16)
アトルバスタチン	NASH 27例	ALT 値低下 (17)
プロブコール	NASH 30例	ALT 値低下 (18)
高血圧薬		
ロサルタン	NASH 7例	ALT 値低下, 組織学的改善 (22)

略語：巻末の「今月の略語」参照

脂肪は総エネルギーの 20% 以下とする⁴⁾。また、散歩などの有酸素運動により筋肉や脂肪細胞における代謝が改善し、脂肪細胞より分泌される TNF α が減少し、インスリン抵抗性の改善やトリグリセリド (TG), VLDL の減少, HDL コレステロール (HDL-C) の増加など脂質代謝も改善する⁵⁾。この際、体重は 1 週間に 1.6kg 未満の割合で緩徐に減量することが肝要である⁶⁾。

薬物療法

NASH を含めた NAFLD に肥満, 糖尿病, 脂質異常症, 高血圧などの生活習慣病を合併する場合には, これらの合併症に対する薬物治療がまず必要である。NASH の病態進展にはインスリン抵抗性や糖代謝異常, 酸化ストレス, 脂質代謝異常, 高血圧などが重要な因子と考えられ, それぞれを分子標的とした薬物治療が行われている (表 1)。

1. インスリン抵抗性改善薬

NASH 患者の 8 割に認められるインスリン抵抗性は NASH の基本病態と考えられ, まずその治療が NASH の治療ターゲットとして挙げられる。インスリン抵抗性は, 脂肪細胞からのアディポサイトカイン分泌異常によって引き起こされると考えられており, それらの受容体や細胞内シグナル伝達に作用する薬剤が, 治療薬として用いられている。PPAR γ はインスリン感受性の作用増強にかかわる核内受容体であり, 脂肪細胞の分化, 脂質代謝調節にもかかわっている。チアゾリジン系誘導体は PPAR γ のリガンドとして作用する薬剤であり, 全身のインスリン抵抗性改善や, 肝局所において微小炎症の改善や線維化進展抑制などの作用を有することも報告されており, 最近, ピオグリタゾンとロシグリタゾンはそれぞれ二重盲検試験で NASH に対する有効性が報告されている⁶⁷⁾。本邦では, ピオグリタゾンはインスリン抵抗性改善

薬としてすでに臨床応用されており、インスリン抵抗性を呈する糖尿病を合併している NASH には試みるべき治療法である。その他、ピグアナイド系薬剤であるメトホルミンもインスリン抵抗性改善薬であり、肝での糖新生を抑制し、肝での糖取り込みを亢進させることによって血糖を調節する。腎機能障害や呼吸循環不全の患者には禁忌であるが、糖尿病患者に有効であるだけでなく NASH に対しても、トランスアミナーゼの改善、肝内脂肪化、線維化の改善作用を有することが示されている⁸⁾。また、ナテグリニドはインスリン分泌能がある程度保たれた 2 型糖尿病に用いられるが、NASH に対する有効性も報告されている⁹⁾。

2. 抗酸化療法

酸化ストレスとは、生体内の酸化還元状態を維持する機構が破綻し、種々の活性酸素種 (ROS) が過剰となった状態である。NASH では、過剰の脂肪酸負荷に対し ROS が過剰産生状態となっており、NF- κ B を活性化し、TNF α やインターロイキンの転写亢進が認められ、肝細胞死が誘導される。また酸化ストレスは肝星細胞の増殖促進、活性化作用も有しているため、肝線維化も進展させ、NASH の増悪に促進的に作用する。ビタミン E、ビタミン C、ベタイン、ウルソデオキシコール酸 (UDCA) などは抗酸化作用を有し、NASH の治療薬の候補である。ビタミン E 単独投与やビタミン C との併用により、NASH におけるトランスアミナーゼや肝線維化の改善が報告されている^{10,11)}。コリン代謝産物であるベタインはメチオニンの代謝に関与し、グルタチオンなどの抗酸化物質の供給に重要であり、小胞体のストレスを軽減する可能性があり、NASH のトランスアミナーゼや肝組織の炎症、線維化を改善する¹²⁾。

UDCA は抗酸化作用のほか、利胆作用、

肝細胞膜保護作用、免疫調節作用などさまざまな機能を有しており、NASH に対する UDCA の有効性も期待されている。しかし Lindor らが行った二重盲検試験では、UDCA 投与により肝機能検査値、肝組織所見の改善は認められたが、プラセボ投与群と有意差はなかった¹³⁾。一方 Dufour らは無作為比較試験で、UDCA とビタミン E の併用は UDCA 単独やコントロールと比較して有意に ALT の低下および組織学的改善を認めたと報告している¹⁴⁾。このような結果から、NASH に対する UDCA の効果は十分ではなく、ビタミン E などの併用がより効果的であると考えられる。また、肝内に沈着した鉄はフェントン反応を介して酸化力の強いヒドロキシルラジカルを生成し、酸化ストレスをもたらしている。NASH 患者では肝組織中の鉄沈着や血清フェリチンの上昇が高頻度に認められ、瀉血療法による生体からの適切な鉄の除去は抗酸化療法の 1 つと考えられる¹⁵⁾。

3. 脂質異常症治療薬

NAFLD、特に NASH にはメタボリックシンドロームを伴うことが多い。メタボリックシンドロームの診断基準の 1 つである高 TG 血症と低 HDL-C 血症などの脂質代謝異常に対する治療は、NASH の治療にも有用である可能性がある。PPAR α アゴニストであるフィブラート系薬剤は、肝臓や骨格筋に作用して脂肪酸燃焼を促進し、組織内脂肪量を低下させ、血中 TG は低下、HDL-C は上昇させ、インスリン抵抗性も改善するため、肝脂肪化に対して有効な薬剤と期待されている¹⁶⁾。またスタチン製剤は、コレステロール生合成の律速酵素である HMG-CoA 還元酵素を阻害することにより、肝でのコレステロール合成を抑制する。さらに、血中コレステロール、血中 TG の低下作用を有しているだけでなく、レニン・アンジオテンシン系抑制、抗炎症作

用やマトリックスメタロプロテアーゼ阻害作用など多彩な作用を有しており、NASH の治療に有用と期待されている。脂質異常症を伴った NASH 患者にスタチン製剤の1つであるアトルバスタチンを、脂質異常症のない NASH 患者には UDCA を投与した Kiyici らの前向き試験では、アトルバスタチン群において肝の脂肪化が有意に改善している¹⁷⁾。一方、プロブコールは肝でのコレステロール合成抑制作用とともに抗酸化作用を有することが知られているが、NASH に対する ALT 低下作用も報告されている¹⁸⁾。脂質異常症治療薬のトランスアミナーゼや肝脂肪化に対する作用機序は不明な点も多く、NASH に対する治療に関しては今後の検討が待たれる。

4. 高血圧治療薬

NAFLD の約 40% 近くに高血圧が認められ¹⁹⁾、血圧調整をつかさどる種々の因子が NASH の発症・増悪に関与し、特にレニン・アンジオテンシン系の活性亢進やアディポサイトカイン分泌異常の関与が重要と考えられている。脂肪組織由来のアディポサイトカインにはアディポネクチン、TNF α などが含まれ、インスリン抵抗性を介して血圧上昇に関連している。アンジオテンシン II はレニン・アンジオテンシン系の主要な因子の1つであり、昇圧反応や血管リモデリングにも重要な役割を担っている。肝星細胞の表面にはアンジオテンシン II タイプ1 受容体が発現しており、肝星細胞自体もアンジオテンシン II を産生し、オートクリンおよびパラクリンに肝星細胞自身を活性化・増殖させ、肝線維化の促進に重要な役割を果たしているが、アンジオテンシン II にはインスリン抵抗性、酸化ストレスの増強作用もある²⁰⁾²¹⁾。実際、アンジオテンシン II タイプ1 受容体拮抗薬 (ARB) には降圧効果、抗動脈硬化、インスリン抵抗性改善などの多彩な作用があり、ARB は

NASH において抗線維化作用のみならずインスリン抵抗性改善、抗炎症作用も期待できる。つまり、アンジオテンシン II をターゲットとした治療には、血圧管理、インスリン抵抗性改善、肝線維化予防の効果が期待でき、NASH の治療に有用である可能性がある²²⁾。

外科治療法

NASH の病態進行・悪化には肥満が大きく影響するが、体格指数 (BMI) が 40kg/m^2 以上の重症肥満で体重の自己コントロールが困難な場合には、外科的治療法も考慮される。外科的治療の基本的な戦略は摂取エネルギーの抑制であり、術式として消化吸収能抑制術と胃縮小手術に分けられる。消化吸収能抑制術には、小腸バイパス術、胆膵バイパス術、十二指腸転換術などが挙げられ、胃縮小手術には、胃バイパス術、胃形成術、胃バンディング術などがある²³⁾。胃バンディング術は胃上部に巻きつけたバンドにより胃の容積を減らして食事摂取量を減らす術式で、腹腔鏡下にて治療が可能である。

おわりに

本邦においてはメタボリックシンドロームの罹患者の増加が危惧されており、NASH の患者数も今後増加していくと予想される。NASH は進行性の比較的予後不良な疾患であり、EBM に基づいた治療法の早期確立が望まれる。

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1 血液検査

非アルコール性脂肪肝炎 nonalcoholic steatohepatitis (NASH) の診断のための血液検査のひとつは、NASHの基盤となる非アルコール性脂肪性肝疾患 non-alcoholic fatty liver disease (NAFLD) の診断における血液検査である。これには、脂肪肝に特徴的な血液検査に加えて、NASHへの病態の進展を評価する血液検査が含まれる。また、NASHの診断には、アルコール性脂肪肝だけでなく、各種肝炎ウイルス、自己免疫、先天的肝代謝異常など他の原因による肝疾患を除外する必要がある。したがって、除外診断のための血液検査も必要である。さらにNAFLDやNASHの確定診断には肝組織所見が不可欠であるが、NAFLDの頻度は高く、肝生検は侵襲的であるため、血液検査は、肝生検を行う患者を選択するためにも重要である。

スクリーニング検査でNAFLDが考えられる症例のうち、特に以下のような血液検査所見から、単純性脂肪肝よりNASHを疑い(表5-1)、肝生検による確定診断を行う。さらに、NASHは、Dayらが提唱したtwo hit theoryによると、肥満、高脂血症、糖尿病などの1st hitによる脂肪肝に、インスリン抵抗性や酸化ストレス、エンドトキシンなどの2nd hitが加わって発症する。したがって、このtwo hit theoryに関連する因子に関する血液検査は、NAFLDやNASHの診断にも有用であると考えられる。

表5-1 肝生検を考慮すべきNAFLD患者の血液検査所見

1. 血液・生化学検査
 - ・トランスアミナーゼの持続高値(特にALT100以上が持続)
 - ・AST/ALT比の経時的上昇
 - ・コリンエステラーゼの経時的低下
 - ・肝線維化マーカー(ヒアルロン酸、IV型コラーゲン、PIIIP)高値
 - ・血小板数の低下
 - ・血糖コントロール不良
 - ・血清フェリチン高値
 - ・HOMA-IRの上昇(2以上)
2. 特殊検査
 - ・高感度CRP高値
 - ・血清チオレドキシシン高値
 - ・TNF- α 高値
 - ・アディポネクチン低値
 - ・レプチン高値
 - ・血清CK18断片高値
 - ・DHEA-S高値

A. NAFLD および NASH 診断に有用な血液生化学検査

AST, ALT の軽度上昇が NAFLD ではみられ, さらに NASH では高い傾向にある (表 5-2)¹⁾. しかし正常の 5 倍以上になることはほとんどなく, NASH の 2/3 は正常値まで変動することがある²⁾. NASH は ALT 優位で AST/ALT 比は 1 未満であり, 1 以上となるアルコール性脂肪肝などと鑑別される. さらに, コリンエステラーゼも NAFLD や NASH で上昇する. しかし, ウイルス性慢性肝疾患と同様に NASH でも AST/ALT 比は肝線維化の進行とともに上昇し, 肝硬変では 1 以上になることから, 経過観察には有用なマーカーの一つである. コリンエステラーゼもアルブミンやプロトロンビン時間と同様に肝硬変に進展すると低下する. また, NAFLD のなかで肝線維化進展例は肝線維化非進展例と比較してトランスアミナーゼは高値であることも報告されており³⁾, トランスアミナーゼが持続高値であれば, NASH を疑う根拠となる. ALP, γ GTP は NAFLD で上昇することがあるが, 軽度であり, NASH と単純性脂肪肝の鑑別には有用ではない.

肝線維化マーカーであるヒアルロン酸, IV型コラーゲン, procollagen III polypeptide (PIIIp) は単純性脂肪肝より NASH で高値となると考えられ, 血小板数は低値となる. また, 肝合成能の指標であるアルブミン, プロトロンビン時間は NASH の病態進展とともに低下するが, 軽度の肝線維化を呈する NASH では単純性脂肪肝とほとんど変わらない.

耐糖能異常, 脂質代謝異常, 高血圧などの生活習慣病は NASH の発症や病態進展と関連することから, 血糖, HbA_{1c}, 総コレステロール, LDL コレステロール, 中性脂肪などは高値となることが多い. また, NASH は単純性脂肪肝と比較して肝組織中の鉄沈着の程度が高度であり, 血清フェリチンは NASH では高値となる. 高フェリチン血症と肝組織炎症や線維化重症度との関連もあるといわれる⁴⁾. 細胞内で過剰となった鉄がフリー鉄となり, Fenton 反応により ROS の産生を亢進させ, 肝細胞障害や肝線維化を惹起すると考えられている.

表 5-2 NASH と単純性脂肪肝患者の生化学検査値の比較*

	steatosis patients	NASH patients	P value
AST (U/ml)	33.3 ± 12.8	53.0 ± 35.5	0.01
ALT (U/ml)	57.0 ± 32.3	80.6 ± 60.0	0.08
FBS (ml/ml)	108.4 ± 16.4	123.6 ± 36.8	0.06
IRI (μ l/ml)	11.4 ± 7.8	14.1 ± 10.6	0.28
HOMA-IR	3.10 ± 2.30	4.07 ± 3.73	0.26
HDL cholesterol (mg/dl)	49.9 ± 14.4	47.9 ± 11.5	0.50
LDL cholesterol (mg/dl)	115.1 ± 31.0	129.3 ± 38.5	0.13
triglycerides (mg/dl)	170.7 ± 82.3	172.6 ± 98.5	0.94
iron (ng/ml)	116.1 ± 46.9	110.1 ± 40.2	0.59
ferritin (ng/ml)	146.6 ± 96.1	264.2 ± 245.4	0.05
hyaluronic acid (ng/dl)	27.3 ± 26.2	51.2 ± 52.2	0.05
type IV col.7s (ng/dl)	4.21 ± 0.93	4.67 ± 1.23	0.12

(* means ± SD. 文献 1 を改変)

B. 他の肝疾患除外のための血液検査

まず、ウイルス性肝炎の除外のために HBs 抗原と HCV 抗体を測定し、自己免疫性肝疾患の可能性を否定するために、抗ミトコンドリア抗体と抗核抗体を測定する。ただし、NAFLD では抗核抗体陽性者が存在することから、検査結果の解釈には注意が必要である。特徴的な臨床経過や症状などから、先天性肝代謝異常が疑われる場合には、セルロプラスミン、尿中銅、 α_1 アンチトリプシン、トランスフェリン飽和度などそれらに特異的な検査を行う (図 5-1)。

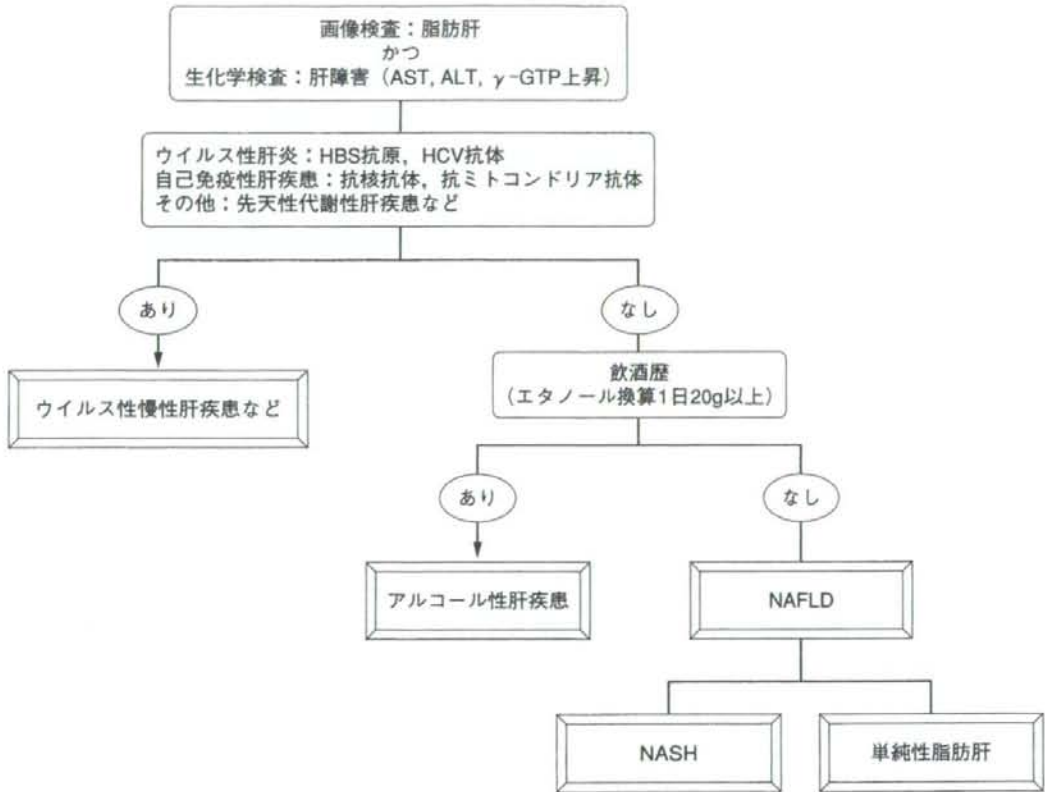


図 5-1 NASH/NAFLD の診断

C. NAFLD および NASH の病態に関連する血液検査

1. インスリン抵抗性

内臓脂肪蓄積は NAFLD の基盤として重要であり、それに伴うインスリン抵抗性は NASH の基盤となる病態である。インスリン抵抗性の評価法はいくつかあるが、現在最も応用されているのは、HOMA-IR (homeostasis model assessment insulin resistance index) で、1 回の採血で評価できることから汎用されている。HOMA-IR は空腹時血糖 (mg/dl) × 空腹時インスリン (μ U/ml) ÷ 405 の計算式で求められる。一般に、HOMA-IR が 2 未満の場合は正常、2 以上はイ