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The Pathogenesis, Complications and Therapeutic Strategy for Hepatitis C Virus-associated Insulin Resistance in the Era of Anti-viral Treatment

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Abstract: Recent experimental and clinical studies have shown that chronic hepatitis C virus (HCV) infection causes insulin resistance. Since insulin resistance decreases response to antiviral treatments, promotes inflammatory and fibrogenic reactions and increases a risk of hepatocellular carcinoma (HCC), amelioration of insulin resistance may be a novel therapeutic target, which could improve the prognosis in patients with HCV-related chronic liver disease. Despite the increased awareness of health risk of insulin resistance, there is no common therapeutic strategy for HCV-associated insulin resistance. Indeed, treatments with exogenous insulin or sulfonylureas may be rather harmful because these treatments are associated with the development of HCC in patients with HCV infection. Meanwhile, we, along with others, have found distinctive treatments which improve HCV-associated insulin resistance. Administration of branched-chain amino acids (BCAA), especially as a late evening snack, improves glucose metabolism by improving insulin-signal cascades in insulin resistance patients with HCV infection. In this paper, we discuss the pathogenesis and complications for HCV-associated insulin resistance and further review a recent clinical therapeutic strategy using these agents for the treatment of this devastating disorder. We also discuss therapeutic potentialities of incretin-based therapies, new anti-diabetic agents for HCV-associated insulin resistance and the significance of insulin resistance in the era of new anti-viral treatments.

Keywords: Hepatitis C virus, insulin resistance, hepatocellular carcinoma, branched-chain amino acids, incretin.

INTRODUCTION

Since hepatitis C virus (HCV) was identified in 1989 [1, 2], underlying pathophysiology of chronic hepatitis C has been disclosed tremendously [3-7]. Individuals infected with HCV frequently develop chronic infection, which is associated with the development of liver cirrhosis and hepatocellular carcinoma (HCC) [8-10]. In addition, epidemiological data from East-West show an association between HCV infection and insulin resistance [11-21]. Recent basic and clinical researches have revealed the mechanisms of HCV-associated insulin resistance and insulin resistance is now recognized as a sequela of chronic HCV infection [14, 22-30].

Generally, insulin resistance is associated with the development of diabetes mellitus (DM), hypertension and cardiovascular diseases [31]. Besides these complications, insulin resistance is also involved in many events in patients with chronic hepatitis C, including antiviral treatment, fibrogenic reaction and the development of HCC [25, 28, 32-35].

It is now clear that insulin resistance is a critical factor for the progression of any stage of chronic hepatitis C [36]. Despite the accumulated evidences for the risk of insulin resistance, therapeutic strategy for HCV-associated insulin resistance has not been established yet [37]. In HCV-infected patients with diabetes, cardio-vascular disease occupies only

less than 5% of cause of death and is not a significant prognostic factor [38]. Prognostic factors are HCC, liver failure, and esophageal varices even in HCV-infected patients with diabetes [38], and the therapeutic strategy should be considered based on mechanisms and life-threatening complications for HCV-associated insulin resistance.

Recently, we have found that an inactivation of incretin is a causative factor for HCV-associated insulin resistance [39]. Incretin mimetics and incretin enhancer are new anti-diabetic agents. Theoretically, it seems that replenishment and/or enhancement of incretin is proper therapeutic approach and these new anti-diabetic agents may ameliorate insulin resistance, prevent the development of HCC and improve the prognosis in patients with HCV infection.

In this review, we summarize the pathogenesis for HCV-associated insulin resistance and propose the clinical therapeutic strategy for the treatment of HCV-associated insulin resistance. In addition, therapeutic potentialities of incretin-based therapies and the significance of insulin resistance in the era of new anti-viral treatments are discussed.

MECHANISMS FOR HCV-ASSOCIATED INSULIN RESISTANCE

Indirect Effects of HCV

Various factors are reported to be associated with the development of HCV-associated insulin resistance (Table 1). Similar to the life style-associated insulin resistance, obesity with decreased serum adiponectin levels [40-42], inflammatory cytokines [41, 43, 44], oxidative stress [45-47], hepatic steatosis [48], pancreatic beta-cell function [49], and serum

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Table 1. Factors Associated with Insulin Resistance in Patients with HCV Infection

Factor	References
Obesity and decreased serum adiponectin levels	[40-42]
Inflammation and inflammatory cytokines	[41, 43, 44]
Oxidative stress	[45-47]
Decreased serum PEDF levels	[77, 187]
Portal-systemic shunt	[50]
Hepatic iron accumulation	[57, 58]
HCV core	[14, 26, 29]
Amino acid substitutions of the HCV core region (Gln70 (His70) and/or Met91)	[22]

pigment epithelium-derived factor (PEDF) levels are also involved in the development of HCV-associated insulin resistance. In addition to those common factors, liver specific factors are underlying in the development of HCV-associated insulin resistance.

Ferenci *et al.* reported that portal-systemic shunts caused not only hepatic encephalopathy, but also insulin resistance in patients with liver cirrhosis [50]. Reduced hepatic blood flow may lead liver dysfunction and subsequent insulin resistance. In fact, Tanabe *et al.* reported that occlusion of portal-systemic shunt improved glucose metabolism in patients with liver cirrhosis [51].

Hepatic iron accumulation is one of characters for HCV infection. Hcpidin is a key negative regulator of iron metabolism [52] and hepcidin levels are correlate with hepatic iron accumulation in HCV transgenic mice [53] and patients with chronic hepatitis C [54, 55]. Excessive iron induces reactive oxygen species mediated oxidative stress [56]. In patients with HCV infection, hepatic iron accumulation is associated with insulin resistance [57, 58]. Furthermore, iron depletion by phlebotomy reduces serum and hepatic levels of thioredoxin, a marker of oxidative stress, and homeostasis model assessment-insulin resistance, an index for insulin resistance in patients with chronic hepatitis C [46]. Thus, hepatic iron accumulation may cause insulin resistance through induction of inflammatory cytokines and oxidative stress.

Direct Effects of HCV on the Development of Insulin Resistance

Direct effects of HCV on the development of insulin resistance are still debatable. Tsochatzis E *et al.* reported that insulin resistance is not associated with viremia [59]. On the other hand, some previous studies reported that serum HCV RNA levels is associated with insulin resistance in a dose-dependent manner, independent of the visceral adipose tissue area [60-62] and HCV suppression by anti-viral treatment correlates with improvement in insulin resistance [63-65]. These findings suggest a possible role of HCV in the development of insulin resistance. Recently, HCV is now known to directly associate with insulin signaling molecules and cause insulin resistance. HCV core protein causes nuclear translocation of signal transducer and activation of transcription 3 and subsequent up-regulation of suppressor of cytokine signaling (SOCS) 3 proteins in various hepatoma cell

lines [26]. SOCS3 is known to block insulin signaling cascade by ubiquitin-mediated degradation of insulin receptor substrate (IRS)1/2 [66]. Down-regulation of IRS1/2 are seen in livers from HCV-core transgenic mice and in livers of patients with HCV infection [26] and therefore, HCV core-induced SOCS3 up-regulation may promote proteasomal degradation of IRS1 and IRS2 through ubiquitination, leading to insulin resistance in patients with HCV infection [26, 67] (Fig. 1).

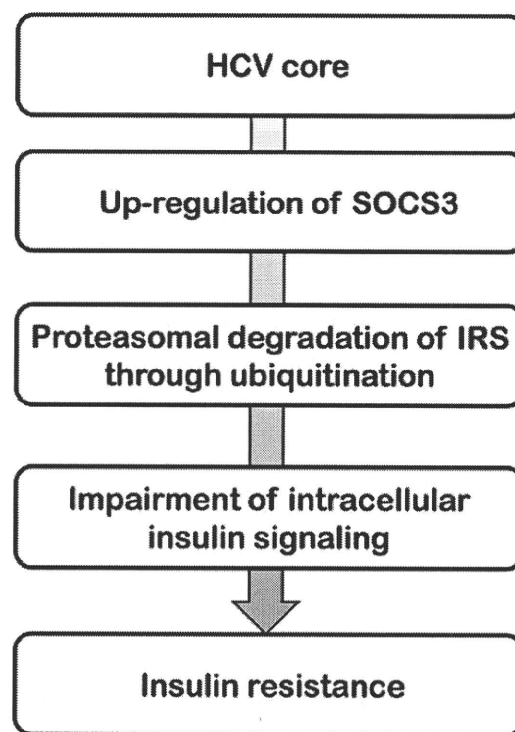


Fig. (1). Direct effects of HCV on the development of insulin resistance.

HCV core protein up-regulates suppressor of cytokine signaling (SOCS) 3 protein. SOCS3 ubiquitinates insulin receptor substrate (IRS) and causes proteasomal degradation of IRS. Since IRS is a central molecule of intracellular insulin signaling, down-regulation of IRS blocks insulin signaling cascade, leading to insulin resistance in patients with HCV infection.

In addition to down-regulation of IRS1/2, HCV core protein also up-regulates serine phosphorylation of IRS1 or down-regulate tyrosine phosphorylation of IRS1 and subsequently impairs Akt signaling pathway, a downstream signaling of IRS1 *in vitro* [68] and in HCV-core transgenic mice [29]. Possible mechanism for changes in serine or tyrosine phosphorylation of IRS1 is due to increased activation of mammalian target of rapamycin [69] or Jun-N-terminal kinase [68]. Although changes in serine phosphorylation of IRS1 have not been validated in human liver tissue, down-regulation in tyrosine phosphorylation of IRS1 and subsequent Akt signaling pathway has been reported in human liver tissue [24].

HCV Genotype and Insulin Resistance

Although associations between HCV genotypes and the development of insulin resistance are still controversial [26, 59, 70, 71], HCV genotype-specific interactions of insulin resistance are reported in patients with HCV genotype 1b, 3a, and 4 [61, 69].

HCV genotype 1b significantly suppresses IRS1 expression compared to HCV genotype 2 in HepG2 cell [67]. The suppression of IRS1 expression is due to two different pathways. HCV genotype 1b up-regulates SOCS3, which causes proteasomal degradation of IRS1 [26]. Alternatively, HCV genotype 1 activates mammalian target of rapamycin, which suppress IRS1 expression [69]. Recently, Akuta *et al.* found that amino acid substitutions in the HCV core region of genotype 1b were associated with severe insulin resistance in patients without cirrhosis [22]. Although the precise mechanisms for the development to insulin resistance by amino acid substitutions in the HCV core region are unclear, HCV core seems to impair intracellular insulin signaling through several pathways.

In *in vitro* experiments, HCV genotype 3a modulates SOCS7 expression and causes down-regulation of IRS1 [69, 72]. In fact, patients infected with HCV genotype 3 frequently associated with insulin resistance [73]. In patients infected with HCV genotype 3, a decrease in total and high molecular weight adiponectin is another causative factor for the development of insulin resistance [74].

High prevalence of insulin resistance is also seen in patients infected with HCV genotype 4 and insulin resistance is a major determinant of both rapid virologic response and sustained virologic response [61, 75]. Normal BMI and no significant fibrosis are characters for patients HCV genotype 4 infected with insulin resistance [61, 76]. Although molecular mechanisms of HCV genotype 4 associated insulin resistance is not unclear, these findings suggest the genotype specific interaction with intracellular insulin signaling.

COMPLICATIONS OF HCV-ASSOCIATED INSULIN RESISTANCE

Insulin regulates not only glucose metabolism, but also protein synthesis, lipid metabolism and cell proliferation through activation of various intracellular signaling molecules [77]. Therefore, insulin resistance is involved in not only the development of DM, but also non-response to anti-

viral treatment [25, 28] and hepatic fibrosis [32]. In addition, insulin resistance causes esophageal varices [78] and HCC [33-35], life-threatening complications. Recently, the development of lichen planus [79], multiple primary carcinomas [80], and other extrahepatic manifestations [81] are associated with insulin resistance. Thus, insulin resistance could play crucial roles in the development to variety of complications in patients with HCV infection. In this review, we focused on an association between insulin resistance and HCC, a major cause of death for patients with HCV infection.

DIABETES MELLITUS AND HCC

DM has been found as a potential risk factor for the development of HCC. Three large population based cohort studies, in Sweden [82], Denmark [83], and the United States [84], reported that the development of HCC was increased 2 to 4 fold in patients with diabetes. Moreover, in some case-control studies, the positive association between DM and HCC has been suggested [85-88]. However, in patient HCV infection, an association between DM and HCC remains unclear, because most of these study populations had not been routinely surveyed for serological marker of HCV or contained only small number patients with HCV infection.

Table 2 shows a summary of recent seven cohort studies that investigated an association between DM and the development of HCC. Three of 7 studies reported by Tazawa *et al.* [89], Chen *et al.* [90] and Wang *et al.* [91] found that DM was significantly associated with the development of HCC in patients with HCV infection, with relative risk ranging from 3.1 to 9.4. On the other hand, three studies reported by Ohota *et al.* [92], Lai *et al.* [93] and Henderson *et al.* [94] found that there was no significant association between DM and the development of HCC in patients with HCV infection. Although the reason for this discrepancy is unclear, one possible explanation is that DM is diagnosed based on fasting plasma glucose and hemoglobin A1c levels. Both plasma glucose and hemoglobin A1c levels are not adequate diagnostic markers for DM in patients with HCV infection because of depletion of hepatic glycogen content and increased turnover of erythrocytes [95]. Thus, underdiagnosis of DM is a possible reason for the discrepancy. Recently, measurement of serum insulin levels is reported as a relevant clinical marker for predicting the development of HCC [96].

INSULIN RESISTANCE/HYPERINSULINEMIA AND HCC

Insulin is known as one of the most important factors not only for a variety of metabolic pathways, but also for cell growth. Insulin stimulates, via phosphorylation of IRS, phosphatidylinositol 3-kinase and Akt cascade [97] as well as Ras and mitogen-activated protein kinase cascade [98]. Since these cascades regulate hepatocyte proliferation and apoptosis, hyperinsulinemia may stimulate growth of HCC. Saito *et al.* demonstrated that postprandial hyperinsulinemia accelerated tumor doubling time of HCC in patient with cirrhosis [99]. Moreover, several previous studies showed that insulin resistance and subsequent hyperinsulinemia contributed to progression of liver fibrosis in patients with HCV infection, regardless of the degree of steatosis [100, 101]. As

Table 2. A Summary of Seven Cohort Studies for an Association Between Diabetes Mellitus and the Development of HCC in the Population Based on HCV Infection

Year	Country	No. of Cases	No. of Cohort	No. of Cohort with HCV (%)	RR (95% CI)	Adjustment	References
2002	Japan	13	279	279 (100%)	9.4 (ND)*	age, sex, alcohol, blood transfusion, α -fetoprotein, biopsy, IFN, HCV genotype, viral road	[89]
2003	Japan	101	161	161 (100%)	1.58 (0.62-3.99)	age, sex, BMI, alcohol, ALT, triglyceride, cholesterol, IFN, HCV genotype, HCV core protein	[92]
2006	Taiwan	115	54979	2087 (3.8%)	0.62 (0.22-1.76)	age, sex, alcohol, cigarette	[93]
2008	Netherland Canada Germany Switzerland	38	541	541 (100%)	2.07 (0.95-4.47)	age, sex, BMI, bilirubin, albumin, platelet count, HCV genotype, HCV viral road, HBe-Ab	[188]
2008	Taiwan	291	23820	1095 (4.6%)	3.52 (1.29-9.24)*	age, sex, alcohol, cigarette	[90]
2009	Taiwan	111	5929	982 (16.6%)	3.1 (1.7-5.4)*	age, sex, BMI, alcohol, cigarette	[91]
2009	United State	262	32806	32806 (100%)	1.17 (0.90-1.52)	age, sex, race, duration on dialysis	[94]

Abbreviation: RR; relative risk, CI; confidence interval, ND; no description in the text, IFN; interferon, BMI; body mass index, ALT; alanine aminotransferase. * P value < 0.05

a pathogenesis of these positive associations, it has been demonstrated that hyperinsulinemia promotes fibrogenesis by stimulating the secretion of connective tissue growth factor from hepatic stellate cells [102]. Therefore, it is suggested that the insulin resistance/hyperinsulinemia causes progression of hepatic fibrosis, leading to development of HCC in patients with HCV infection.

THERAPEUTIC STRATEGY FOR HCV-ASSOCIATED INSULIN RESISTANCE

In this review, we propose the clinical therapeutic strategy for the treatment of HCV-associated insulin resistance, which can be determined by life-style and stage of the liver disease, but not by definition of metabolic syndrome (Fig. 2).

The International Diabetes Federation definition of metabolic syndrome is central adiposity plus two or more of the following factors; 1) raised concentration of triglycerides, 2) reduced concentration of HDL cholesterol, 3) raised blood pressure, and 4) raised fasting plasma glucose concentration [103]. In general, overeating and less activity induce metabolic syndrome through changes in adipocytokines. Therefore, diet therapy and exercise are recommended to patients with central adiposity [104]. However, none of the adipocytokines is associated with insulin resistance in patients with HCV infection, suggesting life-style may not be a major cause of HCV-associated insulin resistance [105]. Excessive life style modification such as fasting and over exercise could worsen liver function in patients with chronic liver

disease [106-108], diet therapy and exercise are recommended if patients are overeating or less active.

Nutritional Therapy

Treatment for the insulin resistance could be a therapeutic strategy to prevent the development of HCC and to improve the prognosis in patients with HCV infection. Nutritional therapy and exercise are fundamental for patients with metabolic syndrome, which is defined by as well as patients with HCV-associated insulin resistance. However, in patients with liver cirrhosis, glucose metabolism is characterized as postprandial hyperglycemia induced by decreased glucose uptake of the liver [109, 110] and as fasting hypoglycemia induced by decreased glycogen storage in the liver, accompanied with increased ratio of lipid combustion in fasting state [108, 111-114]. Therefore, in order to improve glucose metabolism, divided energy intake into a larger number of meals per day including a late evening snack has been recommended for cirrhotic patients [115].

Branched-chain Amino Acids (BCAA)

BCAA has been recently demonstrated to play a role in glucose metabolism [116-119], while it improves the complications and prognosis induced by liver cirrhosis, such as hyperammonemia, encephalopathy, or HCC [120-122]. Therefore, nutritional therapy containing BCAA is most essential when considering a nutritional therapy for liver cirrhosis as well as DM. The mechanism of BCAA action on glucose metabolism is suggested as follows. In a rat model

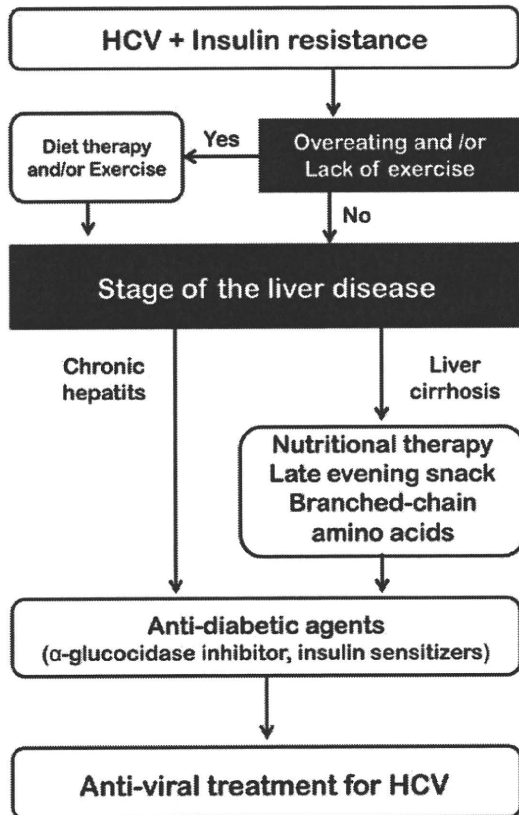


Fig. (2). Flow chart for the therapeutic strategy for HCV-associated insulin resistance. The therapeutic strategy for HCV-associated insulin resistance can be determined not only by life-style, but also by stage of the liver disease.

with liver cirrhosis, leucine and isoleucine upregulate glucose uptake on skeletal muscle [123]. Similarly, a dipeptide constituted of leucine and isoleucine also stimulates glucose uptake in myotube and skeletal muscle cells [124]. BCAA has potential to improve abnormal glucose metabolism such as insulin resistance through anti-obese effect in mice [125, 126]. In human, BCAA-enriched supplementation is also demonstrated to improve the insulin resistance or glucose tolerance of patients with chronic liver disease or liver cirrhosis [64, 127, 128]. Alternatively, intake of enteral nutrients for liver failure that are conditioned with enriched BCAA and high fisher's ratio as late evening snack would improve glucose metabolism [118].

It has been recently demonstrated that BCAA supplementation is potential to prevent the incidence of HCC [122]. Although the mechanism remains unclear, anti-diabetic and anti-obese effects might reduce the HCC incidence because both DM and obesity are shown to be risk factors for HCC. In addition, BCAA is shown to inhibit in vitro vascularization under the high concentration of glucose and/or insulin or in vivo vascularization of the liver in a diabetic rat model with liver injury [129]. Because HCC is a hypervascular tumor, the inhibitive effect of vascularization through the improvement of glucose metabolism by BCAA might reduce the incidence of HCC.

Anti-diabetic Agents

Anti-diabetic agents are generally used if nutritional and exercise therapies are not sufficient to improve hyperglycemia. When using anti-diabetic agents, the risk for adverse effects should be considered carefully because most of them are metabolized in liver. or α -glucosidase inhibitor [130] have been reported to have an adverse effect of severe liver injury that could be life-threatening complications for cirrhotic patients. In addition, use of biguanide in cirrhotic patients would be riskier for lactic acidosis than diabetic patients because lactic acid is also metabolized in liver. Thiazolidinedione is an insulin-sensitizing agent and improves virological response to peginterferon alpha-2b/ribavirin combination therapy in hepatitis C genotype 4 patients with insulin resistance [131]. However, thiazolidinedione causes overproduction of hydrogen peroxide, leading to severe hepatotoxicity [132-134]. Thus, these risks for adverse effects may limit the use of anti-diabetic agents and exogenous insulin tends to be administrated in patients with HCV infection.

An Association Between Anti-Diabetic Agents and Malignancies

Insulin therapy is generally selected for the treatment of cirrhotic patients with DM, however, insulin therapy has recently raised a question concerning to cancer incidence. In fact, use of anti-diabetic agents has been recently demonstrated to influence the tumor-free survival in diabetic patients. Currie CJ *et al.* demonstrated that overall tumor-free survival in diabetic patients receiving insulin-based therapy or sulfonylurea, but not metformin, was significantly worse than receiving no diabetes medications [135]. Although insulin or sulfonylurea does not seem to increase any tumor incidence, these agents could influence the incidence of digestive system cancers such as colorectal and pancreatic cancers. Similarly, Yang Y *et al.* demonstrated that the risk of colorectal cancer was increased by insulin therapy [136]. Li D *et al.* also demonstrated that the risk of pancreatic cancer was increased by insulin or sulfonylurea and reduced by metformin [137].

Concerning to HCC incidence, Donadon V *et al.* implied an association between HCC incidence and use of insulin or sulfonylurea [138]. Subsequently, they carried out a large-scale survey, demonstrating a direct association of HCC with use of insulin and sulfonylurea and an inverse relationship with metformin [139]. We also demonstrated that insulin or sulfonylurea was an independent risk factor for HCC incidence and hepatocarcinogenic effects of these anti-diabetic agents are evident in patients who were male or non-cirrhotic [140]. In addition, Komura T *et al.* described that insulin therapy was a significant factor contributing HCC recurrence after surgical treatment [141]. Thus, these results strongly suggest a potential risk factor of insulin for HCC incidence because either insulin administration or sulfonylurea intake increases insulin level in serum.

The mechanism between insulin and cancer incidence is little known. Since insulin has biological activities of cell proliferation, insulin may stimulate cancer cell proliferation and develop the cancer [142, 143]. In addition, it has been shown that the expression of phosphatase and tensin ho-

molog or SH2 domain-containing inositol phosphatase 2, suppressive molecules of insulin signaling in cells, is decreased in HCC tissues, indicating enhanced action of insulin in HCC [35, 144-146]. Thus, insulin therapy might worsen the prognosis of the patients with HCC because suppressors of intracellular insulin signaling are inactivated in HCC and therefore, insulin effects may be more evident in HCC than in hepatocytes.

Anti-viral Treatment for HCV

Since HCV itself plays crucial role in the development of insulin resistance, eradication of HCV by anti-viral treatment has a significant impact when patients meet the criteria. We along with others have shown that clearance of HCV improves insulin resistance, beta-cell function, and hepatic IRS1/2 expression [25, 28, 65]. Although clearance of HCV is a fundamental therapeutic strategy for patients with HCV infection, Tsochatzis *et al.* described that insulin resistance develops early in the course of the disease, and negatively affects treatment response and the development of liver cirrhosis and HCC, irrespective of genotype [147]. Thus, amelioration of insulin sensitivity may inhibit the progression of HCV-associated liver disease.

GUT HORMONES AND GLUCOSE METABOLISM

The gut has currently been recognized as an endocrine system that regulates glucose metabolism [148, 149]. Among several gut hormones called "incretin", glucagon-like peptide-1 (GLP-1) is well known to be involved in the glucose metabolism. GLP-1 is secreted from endocrine L-cells of the distal intestine and colon in response to enteric nutrient ingestion, such as carbohydrates, fatty acids, essential amino-acids and dietary fiber [150, 151]. GLP-1 exerts a direct insulinotropic effect on the pancreatic β -cell [151, 152]. In addition, GLP-1 activates adenylate cyclase and subsequently enhances insulin secretion via GLP-1 receptor on the cell-membrane of pancreatic β -cell [153], and glucose disposal [154]. GLP-1 also inhibits glucagon secretion via GLP-1 receptor on pancreatic alpha-cells [155]. Thus, GLP-1 exerts carbohydrate assimilation and inhibits gluconeogenesis, consequently, GLP-1 is considered as a therapeutic target for DM as well as insulin resistance [150, 151, 155].

Active type of GLP-1 is rapidly inactivated by dipeptidyl peptidase-IV (DPP-4, enzyme code number 3.4.14.5) [151, 152, 156, 157]. DPP-4 is a membrane-associated peptidase and is widely distributed in numerous tissues, such as intestinal brush-border, endothelial cell and hepatocytes. DPP-4 inactivates GLP-1 within a few minutes. Therefore, DPP-4 inhibitor (incretin enhancer) may be a suitable agent for the treatment of insulin resistance.

GLP-1 AND GLUCOSE METABOLISM IN LIVER

GLP-1 reduces hepatic glucose production [158]. Although direct effect of GLP-1 on hepatocytes remains unclear, GLP-1 increases glycogen synthesis in hepatocytes by stimulating glycogen synthase alpha via GLP-1 receptor in rat hepatocytes [159, 160]. In addition, GLP-1 receptor agonist improve hepatic glucose homeostasis by promoting he-

patic insulin signaling in diabetic rats [161]. In human study, GLP-1 receptor antagonist promotes hepatocyte proliferation via induced c-AMP [162] and GLP-1 inhibits glucose disposal rather than increasing glucose disposal [163]. These findings indicate that GLP-1 has a direct effect on hepatocytes in the regulation of glucose metabolism.

HCV-ASSOCIATED INSULIN RESISTANCE AND GLP-1

We have previously demonstrated that the up-regulation of DPP-4 causes a decrease in serum active GLP-1 levels, resulting in a decrease in hepatic glycogen contents and the development of insulin resistance in patients with HCV infection [39]. The mechanism of increased DPP-4 expression is unclear. However, a significant increase in DPP-4 expression is seen in a hepatoma cell line transfected with a HCV non-structural genome region [164]. In addition, eradication of HCV by treatment with interferon-alpha decreases serum DPP-4 activity [165]. These findings may indicate that HCV directly up-regulates DPP-4 expression. Although limited information is available for the effects of DPP-4 inhibitor in HCV-associated insulin resistance, this therapeutic agent could improve the initial step of the development of insulin resistance and is considered as a new therapeutic strategy for HCV-associated insulin resistance.

THE SIGNIFICANCE OF INSULIN RESISTANCE IN THE ERA OF NEW ANTI-VIRAL TREATMENTS

It is no doubt that these new anti-viral agents will markedly change the treatment for HCV infection in the near future. The most of new antiviral agents for HCV infection are currently in phase I-III [166-172] and the most studied agent is an inhibitor of the HCV non-structural 3 protease, telaprevir or boceprevir [173-183]. The addition of telaprevir or boceprevir to pegylated interferon- α and ribavirin combination therapy significantly enhance sustained virologic response rates even in HCV genotype 1 patients [168, 175, 180, 181, 184, 185]. However, the rates of sustained virologic response of triple therapy with telaprevir, pegylated interferon- α and ribavirin are still up to about 50% in patients who had previously treated by pegylated interferon- α and ribavirin [181]. In addition, the resistance profile of the HCV non-structural 3 protease inhibitor is elucidated. Thus, the triple therapy is not promising to cure all of patients with chronic HCV infection.

Recently, Akuta *et al.* examined the impact of substitution of amino acid in the core region of HCV genotype 1b in triple therapy with telaprevir, pegylated interferon- α and ribavirin and identified that substitutions of amino acid 70 and 91 as independent responsible factors associated with early virologic response [186]. Although the significance of insulin resistance in the triple therapy with telaprevir, pegylated interferon- α and ribavirin has never been investigated, insulin resistance may be a crucial factor even in the new era of anti-viral treatments because substitutions of amino acid 70 and 91 in the core region of HCV genotype 1b are closely associated with the development of insulin resistance [22].

CONCLUSION

In this review, we summarize the pathogenesis for HCV-associated insulin resistance. Similar to the life style-associated insulin resistance, obesity, inflammatory cytokines, oxidative stress, and serum PEDF levels are involved in the development of HCV-associated insulin resistance. Besides these factors, HCV itself also causes insulin resistance through down-regulation of hepatic IRS1/2. Insulin resistance is responsible for the development of cirrhotic complications including HCC, however, there is no common therapeutic strategy for HCV-associated insulin resistance.

Clearance of HCV by anti-viral treatment is a fundamental therapeutic strategy for patients with HCV infection. In addition, amelioration of insulin sensitivity may inhibit the progression of HCV-associated liver disease, and could improve the survival of these patients. Late evening snack and BCAA are nutritional therapies which could improve insulin resistance. However, use of anti-diabetic agents and exogenous insulin are not always recommended because of adverse effects and possible link to the development of HCC.

HCV also affects insulin resistance through activation of DPP-4 and subsequent inactivation of GLP-1, a key regulator of insulin secretion and hepatic glucose metabolism. Although availability of DPP-4 inhibitor in HCV-associated insulin resistance is yet unclear, this therapeutic agent could improve the early step of the development of insulin resistance and is expected to be a new therapeutic strategy for HCV-associated insulin resistance.

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LIST OF ABBREVIATIONS

BCAA	=	branched-chain amino acids
DM	=	diabetes mellitus
DPP-4	=	dipeptidyl peptidase-IV
GLP-1	=	glucagon-like peptide-1
HCC	=	hepatocellular carcinoma
HCV	=	hepatitis C virus
IRS	=	insulin receptor substrate
PEDF	=	serum pigment epithelium-derived factor
SOCS	=	suppressor of cytokine signaling

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Structure-Function Relationships of PEDF

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Abstract: Pigment epithelial-derived factor (PEDF) is a 50-kDa secreted glycoprotein that belongs to the non-inhibitory serpin. It has an α/β core serine-protease inhibitor domain, 3 major β -sheets, and 10 α -helices. Although PEDF does not inhibit either serine or cysteine proteinases, PEDF exerts diverse physiological activities including anti-angiogenesis, anti-vasopermeability, anti-tumor, and neurotrophic activities. Recent studies have shown that a variety of peptides derived from PEDF possess activities similar to those of the parent molecule through interactions with the extracellular matrix, binding to PEDF receptors, nuclear localization and phosphorylation. Thus, peptides derived from PEDF have therapeutic potential for various diseases and therefore, it is important to clarify the structure-function relationship of PEDF. In this review, we summarize structural features of PEDF that could affect various target organs such as blood vessels, tumors, and the central nervous system. In addition, since PEDF is recently identified as a regulator for glucose and lipid metabolism, we also discuss PEDF structures specially related to insulin-sensitizing and triglyceride-reducing properties.

Keywords: Pigment epithelial-derived factor, functional domain, anti-angiogenic activity, anti-vasopermeability activity, anti-tumor activity, neurotrophic activity, glucose metabolism, lipid metabolism.

Pigment epithelial-derived factor (PEDF) is widely expressed throughout the human body and has multiple biological activities. A variety of peptides derived from PEDF exerts diverse physiological activities including anti-angiogenesis, anti-vasopermeability, anti-tumor, and neurotrophic activities as shown in Table 1. In this review, we summarize structure-function relationships of PEDF.

REGULATION OF SECRETION OF PEDF

C-terminal amino-acid residues play an important role in the secretion of various proteins [1-5]. The insertion of a reactive center loop (RCL) into the β -sheet, which is called "loop-sheet polymerization" is involved in impaired secretion of various types of proteins [6, 7]. PEDF is a secretory protein, and the C-terminal of PEDF contains highly exposed typical RCL [8-10]. Truncation of the C-terminal tail of PEDF (Pro415–Pro418) inhibits the secretion of PEDF by Chinese hamster ovary cells [11]. Since Pro415 is mostly buried and interacts with Phe231 and Lue223, truncation of PEDF at Pro415 causes disruption of the hydrophobic interactions imposed by Pro415 and exposure of Asp414 to the negatively charged C-terminus, resulting in inefficient secretion of PEDF [11]. In addition, not only deletion of Pro373-Ala380, but also alanine substitution at Gly376 and Leu377 inhibits the secretion of PEDF. Gly376 and Leu377 are located within the highly exposed segment of the RCL. Therefore, these two residues are indispensable for (i)

interactions of PEDF with components of the quality control system in the endoplasmic reticulum and (ii) subsequent efficient secretion of PEDF [11].

INTERACTIONS OF PEDF WITH THE EXTRACELLULAR MATRIX

PEDF accumulates in the extracellular matrix [12]. The extracellular matrix is a complex of proteins, proteoglycans, and glycosaminoglycans, and plays a crucial role in the mechanical strength of cells and the regulation of cell proliferation and differentiation [13, 14]. It has been speculated, therefore, that PEDF exerts its diverse biological activities by interacting with different components of the extracellular matrix [15].

The crystal structure of human PEDF shows an asymmetrical charge distribution, which is one of the structural characters of PEDF [8]. A high density of basic residues exists at the center of β sheet A-strand 2 and 3, and helix F. This region is densely populated with lysines exposed to the surface (aa134, aa137, aa189, aa191, aa212, and aa124), which interact with various glycosaminoglycans [16-18].

The heparin-binding motif is XBBXB (where B represents basic amino acids; X represents residues excluding acidic amino acids) [19] and is localized at the basic surface of PEDF (aa145-148), which is in the loop region between sheet 2A and helix E [8, 16]. Studies using site-directed mutagenesis showed that three clustered basic amino acid residues, Arg145, Lys146, and Arg148, are necessary for heparin binding [18]. Binding with heparin increases the proteolytic susceptibility of PEDF by trypsin and induces a conformational change in the vicinity of Lys178 of PEDF [20]. Heparin mediates the binding of PEDF to a receptor on the cell surface of Y-79 retinoblastoma

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Table 1. Functional Sites of PEDF

Amino Acids	Function	References
16-26	Anti-angiogenic activity	[28]
24	Protein kinase CK2 phosphorylation site Neutrophic activity Anti-angiogenic activity	[59, 137]
24-57	PEDF receptor binding site Anti-angiogenic activity Apoptotic activity in endothelial cells	[28]
32-380	Neurotrophic activity	[43]
39-57	Chemotaxis activity Apoptotic activity in endothelial cells	[51]
40-64	Anti-tumor activity Osteogenic differentiation activity Collagen I-binding site	[55]
41-44	Collagen I-binding site	[22]
44-77	PEDF receptor (Laminin receptor) binding site	[31]
44-121	Neurotrophic activity	[43]
46-70	PEDF receptor (Laminin receptor) binding site Apoptotic activity in endothelial cells Anti-migration activity in endothelial cells Anti-tube-like formation activity in endothelial cells Anti-angiogenic activity	[31]
58-101	Neuroendocrine differentiation activity	[28]
64	Collagen I-binding site	[22]
78-94	PEDF receptor binding site Neuroendocrine differentiation activity Neurotrophic activity	[28]
78-102	Anti-proliferation activity Collagen I-binding site	[55]
78-121	PEDF receptor (PNPLA2) binding site Neuroendocrine differentiation activity Lipase activity Anti-vasopermeability activity	[24, 29, 73, 91]
82-121	Neutrophic activity	[93]
90-114	Collagen I-binding site Anti-VEGF expression activity	[55]
101, 103, 112	Anti-vasopermeability activity	[73]
114	Protein kinase CK2 phosphorylation site Neutrophic activity Anti-angiogenic activity	[59, 137]
115	Anti-vasopermeability activity	[73]
127, 128, 130	Heparin binding site	[20]
134, 137	Glycosaminoglycans binding site	[16]
139-147	Cytotoxic T-lymphocyte activity	[138]

(Table 1). Contd.....

Amino Acids	Function	References
141-149	HA-binding site	[23]
145-148	Heparin binding site	[18]
146-149	Nuclear localization signal motif	[35]
149, 166, 167	Heparin binding site	[139]
189, 191	Glycosaminoglycans/polyamions	[16]
189-194	HA-binding site	[23]
212, 214	Glycosaminoglycans binding site	[16]
227	Protein kinase A phosphorylation site Anti-angiogenic activity Neutrophilic activity	[69, 137]
255-258, 290, 291, 296, 299, 300	Collagen-I binding site	[17, 18, 22]
285	Secretion activity	[140]
272-279	Cytotoxic T-lymphocyte activity	[138]
354-359	Cell differentiation activity Neuroprotective activity	[94, 141, 142]
373-380, 376, 377	Secretion activity	[11]
387-411	Anti-invasion activity Anti-VEGF expression activity	[55]
389-397	Cytotoxic T-lymphocyte activity	[138]
415-418	Secretion activity	[11]

cells, and a structural change in PEDF is thought to be a mechanism for enhanced receptor binding [12].

PEDF binds to collagen type I and type III, but not collagen type II and type IV [21]. An increase in ionic strength, lower pH, or modifications of carboxylic groups of PEDF decrease the affinity of PEDF for collagen I, suggesting that acidic and /or negatively charged sites of PEDF (Glu41, Glu42, Glu43, Asp44, Asp64, Asp256, Asp258, Glu290, Glu291, Glu296, Asp300, and Glu304) are possible collagen I-binding sites [22]. Collagen I-binding sites are also localized to the side opposite the heparin-binding site. At this site, the acidic amino acid residues Asp255, Asp257, and Asp299 are critical to collagen I-binding [18]. Mutation of the collagen I-binding site (aa299) of PEDF abolishes anti-tumor activity through anti-angiogenic activity [17].

PEDF is found within hyaluronan (HA) rich tissues and contains amino acids sequence for putative HA-binding motifs, BXB2BX2B and BX3AB2XB motifs (B represents basic amino acids; X represents residues excluding acidic amino acids; A represents negatively charged amino acids). Becerra *et al.* examined the HA-binding site of PEDF by site-directed mutagenesis and identified two HA-binding motifs (aa141-149 and aa189-194) in PEDF [23]. The BXB2BX2B motif (aa189-194) was located between α -helix F and β -strand s3A and the BX3AB2XB motif (aa141-149) was localized between β -strand s2A and α -helix F. Although PEDF is a member of the serine-protease inhibitor

(serpin) superfamily, none of the other serpins have these HA-binding sites [23].

PEDF RECEPTOR-BINDING SITES

PEDF is a secreted protein with various biological effects and deposits in the cell membrane. In addition, effects of PEDF are blocked by antibodies which are cell surface-binding antagonists [24-27]. These findings suggest an interaction between PEDF and its receptor(s) [12]. Radioligand-binding assays and crystallization analysis demonstrated that cleaved PEDF (aa24-57, aa32-380, aa78-94, and aa44-121) and N-terminal regions of PEDF are possible regions that bind to PEDF receptors [8, 24, 28].

The 44-mer peptide (aa78-121) binds to the cell surface 80-kDa protein in retinoblastoma cells and some neuronal cells, and the 44-mer peptide competes with 121I-PEDF binding in retinoblastoma Y-79 cells [24]. Notari *et al.* identified an 80-kDa phospholipase A2/nutrin/patarin-like phospholipase domain-containing 2 (PNPLA2) as a putative receptor for PEDF in retinal epithelial cells and, using a cell-free system, and showed that the interaction was involved in lipase activity of PEDF [29].

We found that a protein of molecular mass of ca. 60-kDa could be one of the candidates for PEDF receptor on endothelial cells [30]; later, 67-kDa laminin receptor (67LR) was shown to be a putative receptor

for PEDF in endothelial cells [31]. The 67LR consists of two 37-kDa laminin receptor precursor (37LRP) polypeptide chains, and both yeast two hybrid and immunoprecipitation methods revealed the interaction between PEDF and 37LRP/67LR. Further, the 25-mer peptide (aa46-70) derived from a helix-loop-helix structure of PEDF co-localized with the LR on plasma membranes and caused apoptosis of endothelial cells, inhibition of endothelial cell migration, and angiogenesis *in vitro* and *ex vivo* [31].

NUCLEAR LOCALIZATION OF PEDF

Although PEDF is a secreted protein, it is localized in the nucleus of mammalian cells [32-34]. The nuclear localization signal motif, KKRK, is located in aa146-149 domain of PEDF [35]. PEDF regulates cell cycle [36] and interacts with p53 [37-40]. Moreover, a response element specific for nuclear molecules (p63 and p73) is found in the PEDF promoter region, suggesting that PEDF is a direct target of nuclear molecules [41]. Thus, PEDF may play a crucial role in cell cycle in the nucleus.

NON-INHIBITORY SERINE PROTEASE ACTIVITY OF PEDF

PEDF is a member of the serpin superfamily. Serpins are a group of proteins with the same overall tertiary structure [42]. The C-terminal region of all serpins has an RCL that is susceptible to proteolysis [43]. The serpin active site (P1) binds to the primary specificity pocket of the target protease, leading to a change in serpin conformation from the stressed form to the relaxed form by incorporation of the serpin-exposed loop into the β -sheet. This conformational change increases stability and protects against denaturation, and the protease-serpin complex inhibits proteolytic activity [43].

Inhibitory activity against serpin proteases is not found for all serpins [44]. Although PEDF has a Leu residue at P1, which is known to be specific for inhibition of chymotrypsin and chymotrypsin-like

activities, PEDF does not have typical inhibitory activities of a serpins [45]. A possible explanation for this discrepancy is that the N-terminal residues of the P1 of PEDF are unfavorable for the insertion of the serpins loop into the β -sheet of the folded serpin protein. Alternatively, alanine residues between P12 and P9 of the RCL are also known to be linked to the inhibitory property of serpins [46]. Although PEDF has an RCL like other serpins, its RCL lacks the tetrad of alanine residues between P12 and P9 [47]. In addition, the three proline residues are found in the RCL of PEDF, which could block the interaction of PEDF with target proteases [48]. Thus, changes in the RCL are likely to be responsible for non-inhibitory property of serine protease in PEDF.

ANTI-ANGIOGENIC ACTIVITY OF PEDF

PEDF exerts anti-angiogenic effects through several different mechanisms; induction of apoptosis in endothelial cells [39, 49-51], inhibition of capillary tube formation [17, 18], migration of endothelial cells [52-54], reduction of vascular endothelial growth factor (VEGF) expression [25, 55, 56] and translocation or phosphorylation of VEGF receptor 1 [57]. Although the precise underlying mechanisms for its anti-angiogenic activity are unknown, several structures in PEDF are reported to be involved in its anti-angiogenic activity. A summary of our current understanding of the structure and anti-angiogenic activity of PEDF is shown in Fig. (1).

Collagen type I is an angiogenic scaffold and promotes capillary tube formation through endothelial integrin engagement of collagen type 1 [58]. Collagen type 1-binding sites of PEDF, that is, the interaction of collagen type I and PEDF, play an important role in anti-angiogenic property of PEDF [17, 18, 22, 23]. In fact, mutation of the collagen type I-binding site of PEDF causes tumor progression with neovascularization in tumor xenograft study, while wild type PEDF and mutation of the heparin binding site suppresses both tumor progression and neovascularization [17].

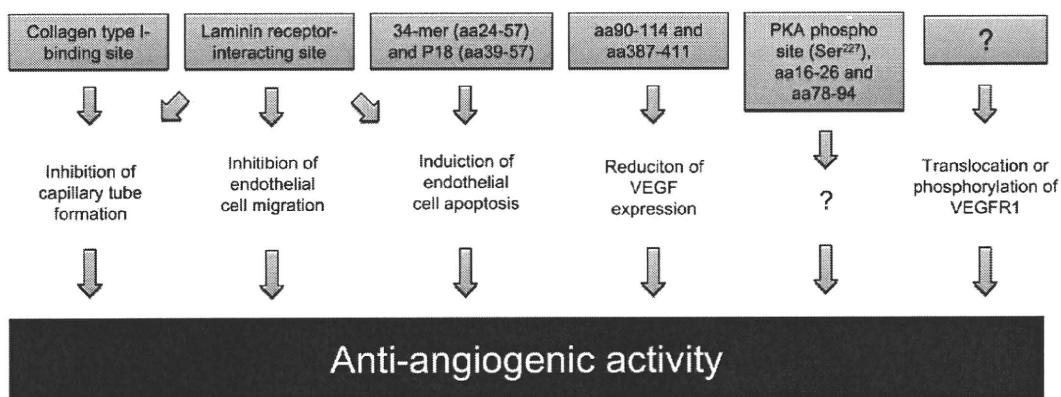


Fig. (1). Relationship between structure and anti-angiogenic activity of PEDF. VEGF, endothelial growth factor; VEGFR1, vascular endothelial growth factor receptor-1.

A ligand-receptor interaction is also important for elicitation of divergent PEDF signals. We found that PEDF exerted anti-inflammatory properties in endothelial cells *via* the interaction with a putative PEDF receptor at a molecular mass of about 60-kDa [30]. Bernard *et al.* identified a 67LR as a PEDF receptor [31], and the 25-mer peptide (aa46-70) of PEDF bound to the LR on plasma membranes and subsequently caused anti-angiogenic reactions both *in vitro* and *ex vivo* [31].

The 34-mer peptide (aa24-57) of PEDF is also reported to act on endothelial cells and cause c-jun-NH2 kinase (JNK)-dependent endothelial cell apoptosis. This effect appears to be mediated by the inhibition of nuclear factor of activated T cells c2 (NFAT), which is regulated by JNK. A NFAT target, caspase-8 inhibitor cellular Fas-associated death domain-like interleukin 1 β -converting enzyme inhibitory protein (c-FLIP) is blocked by PEDF, which was involved in the anti-angiogenic properties of PEDF [28]. Recently, Mirochnik *et al.* analyzed the function of the 34-mer of PEDF and designed 3 peptides that covered its COOH terminus: P14 (aa43-57), P18 (aa39-57), and P23 (aa34-57) [51]. Only P18, but not P14 or P23, was found to induce apoptosis in basic fibroblast growth factor-treated or VEGF-treated endothelial cells, similar to that of the parental 34-mer peptide [51].

PEDF could exert anti-angiogenic activity by reducing VEGF levels [25, 55, 56]. Ek *et al.* generated 25-mer peptides (aa90-114 and aa387-411) and found that the peptides reduced VEGF expression in human osteosarcoma cells [55]. Although the underlying mechanisms are unclear, the protein kinase A (PKA) phosphorylation site of PEDF, Ser227 [59] and peptides aa16-26 and aa78-94 could also have anti-angiogenic activity [28].

ANTI-VASOPERMEABILITY OF PEDF

Increased vascular permeability has a pathophysiologic impact on non-proliferative diabetic retinopathy [60-63], nephritic syndrome [64-66], and hypotension [67]. Moreover, increased vascular permeability accelerates cancer invasion [68, 69]. VEGF disrupts the vascular barrier by uncoupling endothelial cell-cell junctions [70].

PEDF behaves as a functional antagonist of VEGF [71, 72]. Liu *et al.* found that the 44-mer peptide of PEDF (aa78-121) counteracted the VEGF-induced increases in vascular permeability in mouse eyes [73]. The 44-mer peptide contains the exposed elements of hC, one turn of hD, and the connecting loops [8] and a study using chimeric peptides showed that Glu101, Iso103, Leu112, and Ser115 were the amino acids responsible for the anti-vasopermeability effect of PEDF [73]. Thus, the 44-mer peptide or chimeric peptides have therapeutic potential for diseases resulting from excessive vascular permeability.

ANTI-TUMOR ACTIVITY OF PEDF

Besides its anti-angiogenic effects, PEDF also has direct anti-tumor activity by inducing tumor apoptosis and by inhibiting tumor growth and invasion [47, 74-78]. A summary of our current understanding of the structure and anti-tumor activity of PEDF is shown in Fig. (2A and 2B).

Members of the family of HA-binding proteins are known to be associated with apoptosis [79-81]. PEDF contains HA-binding sites that activate caspase-8, caspase-3, and poly (ADP-ribose) polymerase, leading to apoptosis of cancer cells [2].

PEDF also acts as a tumor differentiator [9, 28, 55, 76-78, 82-87]. Alberdi *et al.* found that the 44-mer peptide (aa78-121) bound to a cell surface 80-kDa protein and induced neuronal differentiation in retinoblastoma Y-79 cells [24]. Filleur *et al.* also discovered that the 44-mer peptide (aa58-101) and its fragment (aa78-94) caused a decrease in cytokeratin K8 expression and an increase in mRNA levels of gastrin-releasing peptide/bombesin, thus suggesting the neuroendocrine differentiation of prostate adenocarcinoma cells by PEDF peptides [28]. In addition, the 25-mer peptide (aa78-102) of PEDF was also shown to suppress proliferation of osteosarcoma cells [55]. The 25-mer peptide of PEDF had similar differentiation-promoting activity in neuroblastoma [82, 86] and osteosarcoma cells [55, 83].

The extracellular matrix is deeply involved in tumor migration and invasion [88, 89]. PEDF contains an HA-binding motif and formation of PEDF-HA complexes exerts indirect anti-tumor effects by the blocking biological effects of HA, including loosening the matrix for migration and invasion [23]. Twenty five-mer peptides (aa40-64, aa78-102, and aa90-114) increased cellular adhesion to collagen type-1 [55]. Moreover, the 25-mer peptide (aa387-411) inhibits Matrigel invasion of osteosarcoma [55].

Although the precise structure has not been identified, PEDF exerts anti-tumor effects through activation of a Fas/Fas ligand pathway [25, 49] and induction of cell cycle arrest at G1 phase [87].

NEUROTROPHIC ACTIVITY OF PEDF

PEDF has neurotrophic and neuroprotective activities in the central nervous system [26, 47, 90]. The crystal structure of PEDF indicates that its neurotrophic activity is located at the exposed parts of helices C and D and at loop 90 [8]. Becerra *et al.* examined neurotrophic activity of PEDF using cleaved PEDF. Cleaved PEDF peptides (aa32-380 and aa44-121) can induce morphological differentiation and neurite outgrowth in human Y-79 retinoblastoma cells [43]. These findings suggest that the N-terminal region of PEDF is a neurotrophically active site [43]. In fact, Alberdi *et al.* generated synthetic peptides and found that the 44-mer peptide (aa78-121) derived from the N-terminal edge of PEDF had neurotrophic activity in

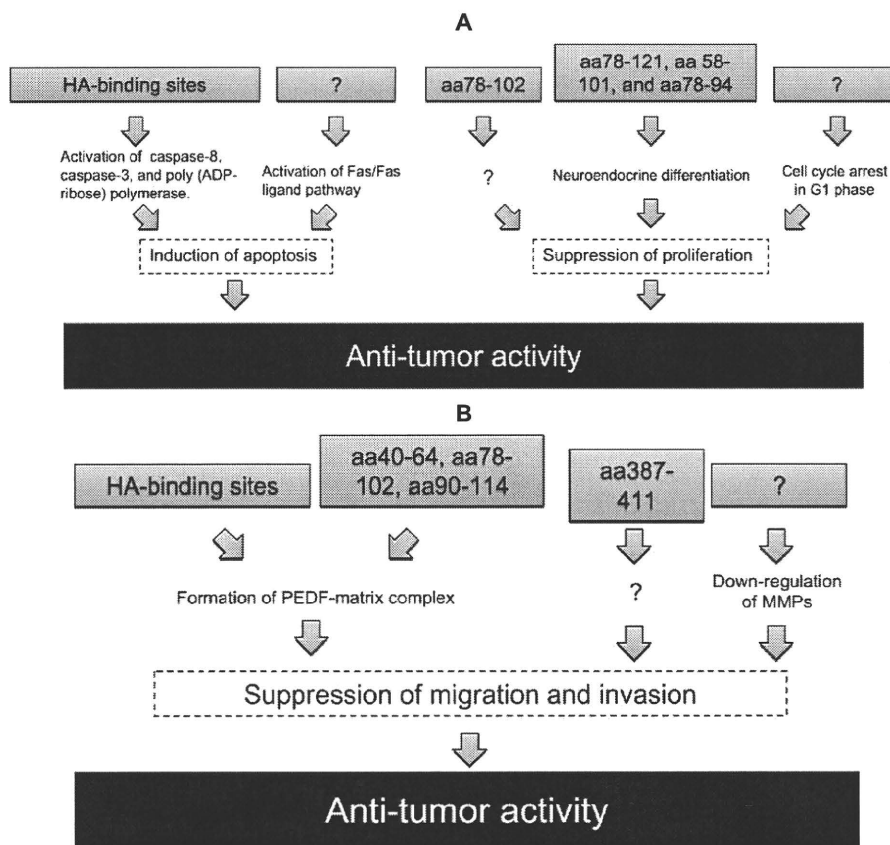


Fig. (2). Relationship between structure and anti-tumor activity of PEDF. (A) Apoptosis and growth suppression. (B) Inhibition of migration and invasion. HA, hyaluronan; MMP, matrix metalloproteinase.

retinoblastoma cells and cerebellar granule neurons [24]. The 44-mer peptide also has a neurotrophic function in motor neurons [91] and a fragment (aa78-94) within the 44-mer can induce neuroendocrine differentiation in prostate cancer cells [28].

PEDF prevents damage to retinal ganglion cells after transient ischemia reperfusion in an ischemic rat model [92]. Li *et al.* demonstrated that the 40-mer peptide (aa82-121) protected the retina from ischemic injury [93]. The thinning of the inner plexiform layer was also protected by the 40-mer peptide (aa82-121) of PEDF [93].

The crystal structure revealed the existence of protein kinase CK2 and PKA phosphorylation sites (Ser24 and Ser114, and Ser227) in PEDF [8]. Mutagenesis studies disclosed that protein kinase CK2 phosphorylated mutants (Ser24Glu and Ser114Glu) reduced the neurotrophic effect of PEDF, but enhanced its anti-angiogenic activity, while the PKA phosphorylation site mutant (Ser227Glu) reduced anti-angiogenic activity of PEDF [59]. These observations suggest that extracellular phosphorylation could completely change the nature of PEDF from a neurotrophic to an anti-angiogenic factor.

Besides the N-terminal region of PEDF, the C-terminal site also has neuroprotective properties. A fragment from the C-terminal region (aa354-359) induces both cell differentiation and neuroprotective properties in human promyelocytic leukemia cells through inhibition of phosphatidylinositol-specific phospholipase C [94]. In addition, a fragment from the C-terminal region (aa354-359) was shown to possess neuroprotective activity and counteracts the toxic effects of beta-amyloid peptides in a rat model of Alzheimer's disease [95].

EFFECTS OF PEDF ON GLUCOSE METABOLISM

PEDF is highly expressed in the liver [96], a major organ for glucose metabolism [97-104], and PEDF has a significant role in the development of insulin resistance and the pathogenesis of diabetic complications [105-120]. Although the protein structure of PEDF that is responsible for glucose metabolism has never been determined, analysis of the genomic structure of PEDF indicates an association between PEDF and glucose metabolism.

Hepatocyte nuclear factor-4 (HNF-4), CCAAT/enhancer-binding protein homologous protein

(CHOP), and upstream stimulatory factor (USF) bind to the DNA-binding sites of the PEDF gene, which are located 200 bp upstream of the transcription start site [121]. HNF-4 enhances insulin sensitivity through activation of a phosphatidylinositol 3-kinase/Akt pathway in hepatocytes [122, 123]. CHOP induces insulin stimulation and up-regulates mammalian tribbles homologs, which is associated with insulin resistance and metabolic syndromes [124]. USF also enhances hepatic insulin signaling through up-regulation of glucokinase [125]. Moreover, HNF-4, CHOP, and USF genes are responsible for the development of diabetes mellitus [126-128]. Thus, the genomic structure of PEDF suggests an association between PEDF and glucose metabolism.

EFFECTS OF PEDF ON LIPID METABOLISM

Studies have shown the existence of high affinity PEDF-binding sites and about 80-kDa proteins in plasma membranes of various cells [24, 27, 28, 91, 129, 130]. Alberdi *et al.* found that a 44-mer peptide (aa78-121) bound to a cell surface 80-kDa protein in retinoblastoma cells and some neuronal cells [24]. Using a yeast two-hybrid screening method, Notari *et al.* found that the PEDF fragments (aa35–418, aa35–266, aa35–229, and aa35–119 of the human PEDF) bound to an 80 kDa lipase-linked membrane protein, adipose triglyceride lipase (ATGL) [29]. ATGL is a member of the newly identified calcium-independent PNPLA2 family, which possesses triglyceride lipase and acylglycerol transacylase activities [131]. In fact, PEDF is highly expressed in the liver [96], a major organ for lipid metabolism [100, 101, 132-134] and reduces hepatocyte triglyceride contents *in vitro* [135]. In a mouse model of ethanol-induced hepatic steatosis, absence of PEDF is associated with triglyceride accumulation in hepatocytes, which can be reversed by administration of exogenous PEDF [136]. Thus, PEDF modulates hepatic lipid metabolism through ATGL activation and the 44-mer peptide (aa78-121) of PEDF is a potential drug target for fatty liver diseases.

CONCLUSION

PEDF is widely expressed throughout the human body and has multiple biological activities. Administration of recombinant PEDF causes anti-tumor activity, neurotrophic activity, and ameliorates glucose and lipid metabolism, thus suggesting that PEDF is a potential therapeutic target for patients with various disorders, including cancer, neurological disorders, and the metabolic syndrome. Shorter peptides have more advantages in terms of side effects and drug delivery than full-length PEDF. PEDF consists of 418 amino acids, and it has been demonstrated that peptides derived from PEDF also possess biological activities. In this review, we summarized the known structure-function relationship of PEDF. Further study of structure-function relationship of PEDF may help us to

develop peptides that can serve as new therapeutics for a broad spectrum of diseases.

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