

双方)に別紙の説明文書に沿って説明を行い、十分な理解を得た上で自由意思に基づいて文書による同意を得ることとする。同意は別紙の同意書に、説明を行った医師と説明を受けた患者(未成年者の場合は親権者の双方)の署名、捺印、同意を得た日付を記載し、カルテに保管するとともに患者へも一部渡す。尚、この研究については長崎大学病院倫理委員会にて了承を得ている。

C. 研究結果

これら対象の年齢中央値は59歳、男性13例(64%)女性8例(36%)全例IL28bのSNP(rs8099917)がTTであった。これらの症例でrapid virologic response(RVR)達成例は、81%をしめた。これらでRVRに寄与する因子についてロジステック回帰分析による単変量解析で検討したが有意な因子を抽出することはできなかった。更に、導入4週以上経過観察可能な21例をテラプレビル2250mg投与群と1500mg投与群に分け検討したところ2250mg投与群と比較して、1500mg投与群では、ヘモグロビン値の低下、クレアチニン値の上昇が緩徐であり、投与4週後のRNA消失率は、2250mg投与群が75%であったのに対し、1500mg投与群は、85%と1500mg投与群においてRVRの達成率が高い傾向がみられた。

D. 考察

- ① 三剤療法によるHCVRNA消失率は、2週で37%、4週で81%であった。
- ② 2250mg投与群と比較して、1500mg投与群では、ヘモグロビン値の低下、クレアチニンの上昇が緩徐であった。
- ③ 投与4週後のRNA消失率は、2250mg投与群が75%であったのに対し、1500mg投与群は、85%であった。

E. 結論

PEG-IFN/RBV/テラプレビル三剤併用療法におけるRVR達成症率は、テラプレビル2250mg投与群と比較し1500mg投与群で高く、ヘモグロビンの低下、クレアチニンの上昇が緩徐であった。テラプレビル1500mg減量投与は、RVR達成率を維持したままクレアチニン上昇などの副作用が軽減できる可能性が示唆された。テラプレビル投与量とSVRとの関連について、今後症例の蓄積及び検討が必要である。

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2. 学会発表

なし。

G. 知的財産権の出願・登録状況

なし。

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分担研究報告書

種々の環境下の肝細胞癌におけるPIVKA-IIの分泌に関する検討

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研究要旨 PIVKA-IIは、肝細胞癌（以下肝癌）の腫瘍マーカーであるが、近年、肝癌の分子標的薬であるソラフェニブの有効症例で、治療開始後早期にPIVKA-IIの上昇が見られるという報告がある。今回、その機序解明を目的に、ソラフェニブとPIVKA-II分泌との関連性についてPIVKA-II産生性の中分化型肝癌細胞株KYN-2を用いて検討した。各種濃度（0.3125, 0.625, 1.25 μM ）のソラフェニブ添加、非添加培地で24-72時間培養し、培養上清中のPIVKA-II、prothrombin、VEGFを測定した。また、低 O_2 （1% O_2 ）環境下でも検討を行った。その結果、1.25 μM のソラフェニブを加えた場合の細胞数は24時間目より有意に低下し72時間後にはコントロールの25%まで低下した。ソラフェニブ投与によりPIVKA-IIの分泌は48時間後より著明に低下し、prothrombinの分泌とVEGFの分泌は、24時間後より有意に増加した。各種濃度のソラフェニブの投与により、0.3125 μM 以上の濃度で濃度依存性にPIVKA-IIの分泌が有意に低下し、1.25 μM では、コントロールの16%まで低下した。一方、prothrombinは、逆に0.625 μM をピークに1.4倍増加し、VEGFも最高1.8倍まで増加した。1% O_2 環境下では、通常状態に比べPIVKA-IIは約2-6倍に分泌量が増加した。また、低酸素下でもソラフェニブ投与によりPIVKA-IIの分泌は低下したが、prothrombin、VEGFの分泌は増加した。この結果に基づくとソラフェニブの治療後のPIVKA-IIの上昇の機序としては虚血による低酸素との関連性が最も考えられた。

A. 研究目的

PIVKA-IIは、1984年にLiebmanらにより肝細胞癌（以下肝癌）において発現することが初めて報告された腫瘍マーカーであるが、その後、肝癌の腫瘍径、脈管侵襲、肝内転移などと密接に関係することが報告されている。近年、肝癌の分子標的薬であるソラフェニブの有効症例で、治療開始後早期にPIVKA-IIの上昇が見られるという報告がある。このPIVKA-IIの上昇機序として、肝癌細胞の虚血（低酸素）との関連性が推察されているが、詳しい機序は不明である。今回、肝癌細胞株を使用して低酸素やソラフェニブ

のPIVKA-II産生などに及ぼす作用を検討した。

B. 研究方法

実験にはPIVKA-II産生性の中分化型肝癌細胞株KYN-2を使用した。(1) ソラフェニブ（0.3125-20 μM ）添加培地で培養し増殖抑制効果とアポトーシス誘導に関して形態的およびAnnexin V陽性細胞の有無により検討した。(2) 1.25 μM のソラフェニブ添加（S群）、非添加（C群）培地を加え経時的（24, 48, 72時間）に培養し、培養上清中のPIVKA-II、prothrombin、VEGFを測定

した。(3) 各種濃度 (0.3125, 0.625, 1.25 μM) のソラフェニブ添加 (S群)、非添加 (C群) 培地で72時間培養し、培養上清中のPIVKA-II、prothrombin、VEGFを測定した。(4) (2) と (3) の実験を1% O_2 の低酸素環境で行った。

C. 研究結果

(1) KYN-2細胞に対するソラフェニブの50%増殖抑制濃度は2.1 μM であった。ソラフェニブ投与により、形態的にアポトーシスを生じた細胞が見られ、また、Annexin V染色で有意な陽性細胞の増加を認めた。以上より、ソラフェニブによるアポトーシス誘導が確認された。

(2) 1.25 μM のソラフェニブを加えたS群の細胞数は24時間目より有意に低下し72時間後にはC群の25%まで低下した。C群のPIVKA-IIの分泌は、24, 48, 72時間後でそれぞれ、0.2, 8.4, 48.2 mAU/mL/ 10^4 cellであったが、S群では、0.2, 0.3, 0.7 mAU/mL/ 10^4 cellと著明に低下していた。prothrombinの分泌は、C群が0.32, 0.48, 0.51 ng/mL/ 10^4 cellで、S群では0.47, 1.12, 0.75 ng/mL/ 10^4 cellと有意に増加していた。VEGFの分泌は、C群では3.9, 8.9, 9.4 pg/mL/ 10^4 cellだが、S群では10.7, 31.3, 26.2 pg/mL/ 10^4 cellと有意に増加していた。

(3) 各種濃度のソラフェニブを添加したS群では、0.3125 μM 以上の濃度で濃度依存性にPIVKA-IIの分泌が有意に低下し1.25 μM では、C群の16%まで低下した。逆にprothrombinは、0.625 μM をピークに1.4倍増加した。VEGFも最高1.8倍まで増加した。

(4) 1% O_2 環境下では、通常状態に比べPIVKA-IIは約2-6倍に分泌量が増加した。また、低酸素下でもS群では、PIVKA-IIの分泌低下とprothrombin、VEGFの分泌増加を認めた。

D. 考察

PIVKA-IIは、プロトロンビンのグルタミン酸残基 (Glu基) のカルボキシ化 (Gla基化) 不全により生じる異常プロトロンビンで肝細胞癌の腫瘍マーカーとして汎用されている。PIVKA-IIの産生機序としては、 γ グルタミルカルボキシラーゼの異常、プロトロンビンの過剰産生、ビタミンKの濃度低下や取り込み低下、低酸素、そして上皮間葉転換などが報告されている。今回、ソラフェニブによる肝細胞癌の治療後、2, 3週目にPIVKA-IIが上昇する機序を解明するためPIVKA-II産生性の肝癌細胞株KYN-2を使用して、ソラフェニブの接触がPIVKA-II産生に及ぼす作用を検討した。その結果、ソラフェニブは、肝癌細胞のPIVKA-II産生を抑制し、プロトロンビンやVEGFの産生を亢進する事が明らかとなった。この結果に基づくと、ソラフェニブによる治療後にPIVKA-IIが上昇する減少は、ソラフェニブの肝癌細胞に対する直接的作用とは考えにくい。ソラフェニブは、VEGFやPDGFの受容体のリン酸化を阻害して血管新生の阻害作用を有している。低酸素によりPIVKA-IIの発現が亢進すると言う事実から推察すると、ソラフェニブ治療後のPIVKA-IIの上昇には、血管新生阻害による低酸素環境が腫瘍細胞によるPIVKA-IIの産生亢進を誘導したと推察される。今後、ソラフェニブによるPIVKA-II産生抑制機序については更に検討が必要である。

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F. 知的財産権の出願・登録状況
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難病・がん等の疾患分野の医療の実用化研究事業(肝炎関係研究分野)

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肝炎患者の病態に即した相談に対応できる相談員育成
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BACKGROUND

Worldwide, an estimated 350 million people are infected with hepatitis B virus (HBV) persistently [1,2]. HBV infection is a major global concern, because up to 40% of patients can develop grave complications, such as decompensated cirrhosis and hepatocellular carcinoma (HCC) [3]. In the natural course of chronic hepatitis B, HBeAg seroconversion, defined by the loss of HBeAg and development of the corresponding antibody (anti-HBe), is an important hallmark, because it is highly correlated with a favorable long-term outcome. Seroconversion is usually followed by sustained suppression of HBV DNA, normalization of alanine aminotransferase (ALT) levels, and clinical remission accompanied by ameliorated necro-inflammatory activities in the liver [4–6].

To date, a number of factors have been found to predispose patients to spontaneous HBeAg seroconversion [7–19]. However, few studies have evaluated pathological factors for predicting early HBeAg seroconversion. In a small series of patients from Spain, the Knodell's index of histological activity was one of the independent predictors of early HBeAg seroconversion [14]. Recently, novel markers of the replication of HBV were introduced, such as levels of HBsAg, HBeAg and HBcrAg (HBV core-related antigen), which can replace HBV DNA levels. These serological markers of HBV replication have been evaluated for sensitive and reliable prediction of early HBeAg seroconversion [20–23]. In the present study, an attempt was made to select factors predictive of early HBeAg seroconversion, from among many biochemical, virological and pathological parameters, based on the data of 234 HBeAg-positive patients with chronic hepatitis B.

MATERIAL AND METHODS

Patients and study design

This is a retrospective cohort study with use of stored sera and liver biopsy specimens from patients with chronic hepatitis B who were taken care of in the Hepatology Department, Nagasaki Medical Center, Japan, during 1991 through 2005. The clinical database was reviewed to identify consecutive patients who underwent liver biopsies and had been followed for longer than 1 year. The inclusion criteria were presence of hepatitis B surface antigen (HBsAg) for 6 months or longer, positivity for HBeAg at the time of liver biopsy, and lack of antiviral treatments before receiving liver biopsies. The exclusion criteria were co-infection with hepatitis C virus (HCV) or human immunodeficiency virus type-1, serological markers suggestive of autoimmune disease, daily intake of alcohol >50 g, recent exposure to hepatotoxic drugs, and no stored sera available. They were followed every 3 months or more frequently, if indicated clinically, and their serum samples were monitored for liver biochemistry and serologic markers of HBV infection, including HBsAg, HBeAg, anti-HBe, HBV DNA and HBcrAg. Serum samples had been stored at -20°C until use.

Antiviral therapy was commenced immediately in the patients with: (1) significant fibrosis/cirrhosis detected by liver biopsy; and (2) evidence of decompensation, such as ascites, varices and hepatic encephalopathy.

To identify predictors of early HBeAg seroconversion, clinical, biological, virological and pathological data at the time

of liver biopsy were compared between patients who did and who did not achieve early HBeAg seroconversion, within 1 year after receiving liver biopsies, by univariate and multivariate analyses. Further, patients were stratified by independent factors for HBeAg seroconversion, and the cumulative incidence of HBeAg seroconversion was compared between groups using the Kaplan-Meier method. The study protocol complied with the Good Clinical Practice Guidelines and the 1975 Declaration of Helsinki, and was approved by the review board of the institution. Each patient gave a written informed consent before participating in this study.

Routine laboratory tests for HBV markers

Quantitative measurements of HBsAg and HBeAg were carried out using commercial enzyme-linked immunosorbent assay (ELISA) kits in the ARCHITECT ANALYSER i2000 (Abbott Japan Co., Ltd., Tokyo, Japan) in accordance with the manufacturers' instructions in Nagasaki Medical Center. The sensitivity of HBsAg assay ranged from 0.05 to 250 IU/ml. Sera with HBsAg >250 IU/ml were serially diluted 100-fold so as to include them within the dynamic range. HBeAg was quantified by a two-step immunoassay with use of chemiluminescence microparticles. Briefly, undiluted samples were mixed with paramagnetic beads coated with anti-HBe. After a washing step, conjugate and reactants were added for exciting emission of the light that is proportional to the concentration of HBeAg. The result was expressed by the ratio of relative light unit (RLU) of the sample to the cut-off RLU (S/CO). Samples with S/CO values >1.0 were regarded positive for HBeAg. Then, serial dilutions of the reference standard of PE HBeAg (Paul Ehrlich Institute, Langen, Germany) were used to define the linear range of the assay and create a reference curve for linear regression. The linear range was 0.024–100 PEIU/ml. A standard curve was produced, and linear regression was used to convert assay results into appropriate units (PEIU/ml). For samples that fell outside the linear range of the assay, the assay was performed on serial dilutions to ensure the linearity.

HBV DNA and HBcrAg

HBV DNA was determined by the COBAS Taqman HBV test (Roche Diagnostics K.K., Tokyo, Japan). Values under or over the detection range were recorded as 2.1 or 9.1 log copies/ml. HBcrAg was measured by the CLEIA HBcrAg assay kit (Fujirebio, Inc., Tokyo, Japan) in a fully automated analyzer (Lumipulse system, Fujirebio, Inc.). Values under or over the detection range were recorded as 3.0 or 7.0 log copies/ml. Assays for HBV DNA and HBcrAg were performed in a commercial clinical laboratory (SRL, Inc., Tokyo, Japan). Sera with values over the detection range were diluted to include them within the dynamic range.

Interferon-inducible protein 10 (IP-10)

IP-10 was quantified by the Invitrogen Human IP-10 ELISA (Invitrogen Corporation, Carlsbad, CA, USA) according to the manufacturer's protocol in Nagasaki Medical Center.

HBV genotyping

HBV DNA was extracted from serum (100 μl) with use of the SMITEST EX R&D extraction kit (MBL Co., Ltd., Nagoya, Japan). It was amplified for determination of genotypes by

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Table 1. Histological evaluation of liver biopsy specimens.

(A) Fibrosis staging			
Stage	Fibrosis		
0	None		
1	Enlarged, fibrotic portal tracts		
2	Periportal or portal-portal septa but intact architecture		
3	Fibrosis with architectural distortion without obvious cirrhosis		
4	Probable or definite cirrhosis		
(B) Inflammation grading			
Grade	Portal/periportal activity		Lobular inflammation
	Piecemeal necrosis	Lymphocyte aggregation	
0	None or minimal	None	None
1	Inflammation only	< 1/3 in portal triad	Inflammation alone
2	Mild	1/3–2/3 in portal areas	Focal necrosis or acidophil bodies
3	Moderate	> 2/3 in portal areas	Severe focal cell damages
4	Severe	Entire portal triad	Damage with bridging necrosis

the SMITEST HBV Genotyping Kit (MBL Co., Ltd.) based on hybridization with type-specific probes immobilized on a solid-phase support [24].

Precore stop codon (G1896A) and core promoter (A1762T/G1764A) mutations

A1896 mutation in the precore (PreC) region was detected by the enzyme-linked minisequence assay (SMITEST HBV PreC ELMA, Roche Diagnostics, Tokyo, Japan), and mutations in the core promoter (CP) region for T1762/A1764 by the enzyme-linked specific probe assay (SMITEST HBV Core Promoter Mutation Detection Kit, Roche Diagnostics K.K.). The results were recorded as “the wild-type” and “mutant types” dominantly expressed by HBV isolates [25].

Histological examination

Liver biopsy was taken by fine-needle aspiration (16G spony) guided by ultrasonography. Biopsy specimens were fixed in 10% neutral formalin, cut at 3- to 4- μ m thickness, and stained with Hematoxyline-Eosin and Azan-Mallory, as well as for silver to visualize reticulin fibers. Tissue sections were examined independently by two senior liver pathologists. For each biopsy specimen, a protocol was filled out for grading necro-inflammation and staging fibrosis by the criteria of Desmet et al. [26] and Scheuer [27] (Table 1). As for the portal activity, not only piecemeal necrosis, but also lymphocytic aggregation was categorized into 5 (0–4) grades in the respective area involved.

Statistical analysis

Continuous variables were compared between groups by the Mann-Whitney *U* test, and categorical variables by χ^2 and Fisher's exact tests. The cumulative incidence of HBeAg seroconversion was calculated using the Kaplan-Meier

method, and the difference was evaluated by the log-rank test. Multiple logistic regression analysis was performed to identify independent factors in significant association with early HBeAg seroconversion. A *p* value <0.05 was considered significant. Statistical analyses were performed using the SPSS version 17.0 software package (SPSS Inc., Chicago, IL, USA).

RESULTS

Baseline characteristics of patients

Among the 673 patients with HBsAg who had received liver biopsies in our hospital during 1991 through 2005, 234 (34.8%) patients who met the inclusion criteria were enrolled in this study. Demographic and laboratory characteristics at the time of liver biopsy are listed in Table 2. They had a median age of 37 years (range: 12–74), and 161 (69%) were men. Of them, 231 (99%) were infected with HBV of genotype C. The median serum ALT level at the baseline was 141 IU/l (range: 13–2644 IU/l), and the median duration of follow-up was 86.5 months (range: 12.0–213.0 months). During the follow-up, 91 (39%) received antiviral treatment, with interferon (IFN) or lamivudine, or the combination thereof.

Comparison of clinical features between patients with and without early HBeAg seroconversion

Early HBeAg seroconversion, within 1 year after receiving liver biopsies, was achieved by 58 of the 234 (24.8%) patients. In univariate analysis, factors predictive of early HBeAg seroconversion were: ALT (*p*=0.002), IP-10 (*p*=0.029), HBsAg (*p*=0.003), HBeAg (*p*<0.001), HBV DNA (*p*=0.001), HBcrAg (*p*<0.001), CP mutations (*p*=0.040), fibrosis (*p*=0.033) and lobular inflammation (*p*=0.002). Other factors including age, albumin, platelets, AFP, PreC mutation, cell infiltration and