positive cells, and the number of patients with antigen-positive cancer are considered to be alternative criteria [31]. On the basis of our results, $p53_{161}$, $hTERT_{461}$, $WT\text{-}1_{235}$, and $VEGFR2_{169}$ are considered the most optimal epitopes that satisfy all of the above criteria for peptide vaccine therapy in pancreatic adenocarcinoma patients. Although $MAGE\text{-}A3_{195}$ showed immunogenicity, its expression did not appear to be high in pancreatic adenocarcinoma tissue [32]. Therefore, it may be a candidate for cancer vaccine therapy when MAGE-A3 is confirmed to be overexpressed in pancreatic cancer tissue.

A mutation in the p53 gene and overexpression of the p53 protein have been reported previously in pancreatic adenocarcinoma [33], and all pancreatic cancer cell lines and specimens used in our study expressed p53. Some strategies targeting p53 have been proposed over the last decade [34]. As peptide vaccine therapy, the wild-type p53 peptide is well preserved in mutant p53 because most mutations in the p53 gene are missense mutations, and are considered to be one of the attractive targets as a cancer antigen. The frequencies of the CTL response against HLA-A24-restricted $p53_{161}$ investigated by the ELISPOT assay in head and neck carcinoma and hepatocellular carcinoma were shown to be 35 and 10 %, respectively [35, 36]. Although the frequency of 7 % in our study is lower, given the difference according to the primary tumor site or balance between sensitivity and specificity, induced CTLs showed cytotoxic activity against pancreatic adenocarcinoma cell lines, which suggested that p53 may be an attractive target in patients with pancreatic cancer.

hTERT is widely overexpressed in various cancer cells including pancreatic cancer [37], which is consistent with our results. A clinical trial demonstrated that GV1001, a HLA class II epitope corresponding to the hTERT (611–626) fragment, was immunogenic in pancreatic cancer patients [38]. Another previous study evaluating T cell responses to several hTERT epitopes in patients with hepatocellular carcinoma [39] demonstrated that $hTERT_{461}$- and $hTERT_{324}$-specific CTLs were induced in 5 (6.9 %) and 9 (12.5 %) of 72 patients, respectively. In the current study, these frequencies were equivalent and the killing of pancreatic cancer cell lines was demonstrated, which suggested that these epitopes also had immunogenicity in pancreatic cancer patients.

Peptide vaccine therapies using $WT\text{-}1_{235}$ and $VEGFR2_{169}$ combined with gemcitabine have already been conducted in pancreatic adenocarcinoma patients [23, 24]. We clarified that $WT\text{-}1_{235}$- and $VEGFR2_{169}$-specific CTLs induced from PBMCs showed cytotoxicity for human pancreatic cancer cell lines, and the results of further investigations are anticipated.

We performed phenotypic analysis of TAA-derived epitope-specific T cells to determine the most appropriate epitope for immunotherapy in patients with pancreatic adenocarcinoma. Epitope-specific tetramer$^+$ cells in PBMCs were also found in patients without IFN-γ ELISPOT responses, which was consistent with the findings of previous studies [39, 40] and suggested the existence of dysfunctional epitope-specific T cells. Epitope-specific tetramer$^+$ cells were also identified at a very low frequency in PBMCs from healthy volunteers and increased in CTLs induced with TAA-derived peptides, which was also consistent with previous studies in which TAA-specific tetramer$^+$ T cells were detectable in samples from healthy donors [41] or the in vitro stimulation of PBMCs with the epitopes derived from TAA could induce TAA-specific CTLs in healthy volunteers [42], even though the precise mechanism has not yet been clarified. Phenotypic analysis showed that the frequency of T cells with each memory and effector phenotype depended on the patient and also that peptide-specific memory T cells existed in PBMCs of patients with pancreatic adenocarcinoma. Because T cells with the memory phenotype exert stronger antitumor effects by secondary stimulation with the antigen, our results suggest that an additional immunological approach such as that consisting of a TAA-derived protein or peptide, recombinant virus, and engineered tumor cells to boost T cell function may be useful to enhance host antitumor immune responses.

Another purpose of this study was to identify the factors influencing immune responses. Our results suggested that the frequencies of the lymphocyte subsets in peripheral leukocytes were very important in the induction of TAA-specific CTLs. Although the relationship between cancer, inflammation, and immunity has already been documented [43], the precise mechanism has yet to be fully understood. One of the speculated reasons why PBMC from patients with lymphocytopenia could not induce a good immune response in our study is that the release of inhibitory immunological cytokines such as transforming growth factor β or IL-10 from pancreatic adenocarcinoma tissue decreases lymphocyte counts and impairs the function of lymphocytes both systemically and in the microenvironment [44]. It was also reported that lymphocyte counts and CTL responses were prognostic markers in advanced cancer cases receiving peptide vaccine therapy [45, 46]. Our results showing a correlation between the T cell response and outcomes in pancreatic adenocarcinoma patients corresponded to these previous findings, which indicate that restricting the objective to those with an adequate lymphocyte subset could lead to a clinical trial with favorable outcomes.

A limitation of this study was the lack of data for the clinical response. Tumor shrinkage or survival benefits are not always observed in all patients who exhibit immune responses. Further, clinical studies using peptides that could induce TAA-specific CTLs are needed to confirm our findings.

In conclusion, we simultaneously compared T cell responses to various TAA-derived epitopes in patients with pancreatic adenocarcinomas; our results suggested that $p53_{161}$, $hTERT_{461}$, $WT\text{-}1_{235}$, and $VEGFR2_{169}$ were the most suitable epitopes for cancer vaccine therapy.

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Comparison of hepatic arterial infusion chemotherapy and sorafenib in elderly patients with advanced hepatocellular carcinoma: A case series

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Abstract. Sorafenib and hepatic arterial infusion chemotherapy (HAIC) are both indicated for unresectable hepatocellular carcinoma (HCC). In this study, we compared the efficacy and safety of HAIC to that of sorafenib in elderly patients with HCC. Eligible patients included those aged ≥70 years, with histologically or clinically confirmed advanced HCC. A total of 12 patients received sorafenib (800 mg per day) and 8 patients received HAIC with 5-fluorouracil (300 mg/m^2 on days 1-5 and 8-12) with or without cisplatin (20 mg/m^2 on days 1 and 8), with interferon-α (3 times per week for 4 weeks). The response rate was significantly higher in patients treated with HAIC (37.5%) compared to that in patients treated with sorafenib (no response). The median overall survival (18.6 and 11.7 months) and progression-free survival (4.0 and 5.0 months) were similar between the sorafenib and HAIC groups, respectively. In the sorafenib group, 58.3% of the patients discontinued treatment compared to none in the HAIC group. The most frequent adverse event leading to discontinuation of sorafenib was anorexia. Similar to sorafenib, HAIC appears to be a feasible treatment and may also have the advantage of an adequate safety profile for elderly patients with advanced HCC. Further study of HAIC in a larger population of elderly patients is required to assess its potential as an alternative to sorafenib for HCC.

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Key words: hepatic arterial infusion chemotherapy, interferon, sorafenib, hepatocellular carcinoma, elderly patients, alternative treatment

Introduction

Hepatocellular carcinoma (HCC) is the most common neoplasm worldwide (1). HCC principally develops on a background of chronic liver disease, particularly cirrhosis caused by hepatitis C or hepatitis B virus infection (1). In Japan, the median age of patients with HCC has been increasing gradually since 1986 (2). Elderly cancer patients often present with multiple comorbidities and age-related changes in the pharmacokinetics and pharmacodynamics of anticancer drugs that may affect chemotherapeutic regimens (3). The clinical benefits of treatment of elderly patients with advanced HCC remain unclear. A previously published study demonstrated that investigations in elderly patients were less intense, that such patients were more likely to receive conservative therapy and that the median survival was worse compared to that among younger patients (4). However, the treatments for HCC have progressed significantly over the last few years and Mirici-Cappa *et al* (5) demonstrated that the overall applicability of radical or effective HCC treatment may not be affected by age. Moreover, Suda *et al* (2) suggested that the therapeutic approach to HCC should not be restricted by patient age.

Sorafenib is an oral tyrosine kinase inhibitor that targets multiple molecular pathways. In a pivotal study, sorafenib provided an overall survival (OS) advantage in patients with advanced HCC, with the median survival increasing by ~3 months in sorafenib-treated patients, compared to those receiving placebo therapy (6). Sorafenib is the only globally approved drug for the treatment of HCC; however, it is not curative and is only indicated for Child-Pugh class A patients who have preserved hepatic function. Hepatic arterial infusion chemotherapy (HAIC) is an alternative option for advanced HCC and, based on the Japanese HCC management guidelines, it is recommended for patients with the same indications for sorafenib (7). Although HAIC is widely used in Japan, as it tends to be associated with a favorable response rate (RR) in patients with HCC, randomized controlled trials have not been conducted and there is currently no evidence of a survival benefit for HAIC. HAIC may reduce HCC stage (8) and is indicated for patients exhibiting a moderate reduction in hepatic reserve function (9). In patients who achieve a complete response (CR) with HAIC, a long-term survival benefit was reported (10,11). The efficacy of sorafenib treatment in elderly patients with advanced HCC has been investigated in several studies (12-16); however, to the best of our knowledge, there are no available reports regarding the efficacy of HAIC in such patients and there are currently no satisfactory strategies for the management of advanced HCC as a function of age. The aim of this study was to compare the feasibility and safety of HAIC to those of sorafenib in elderly patients with advanced HCC.

Patients and methods

Patients. We retrospectively analyzed data from elderly patients with advanced unresectable HCC, who were treated at our hospital between March, 2002 and June, 2013. Eligible patients included those aged ≥70 years with histologically or clinically confirmed advanced HCC. HCC was considered as unresectable in patients who presented with severe vascular invasion or multiple intrahepatic lesions (i.e., ≥5 nodules), or in those with progressive disease (PD) following surgical or locoregional therapy intervention. A total of 20 eligible patients were identified.

The study protocol was approved by our Institutional Review Board and informed consent was obtained from all the patients prior to treatment.

Treatment. In the HAIC group (n=8), an implantable drug delivery system was used for arterial infusion of the chemotherapeutic agents. Between February, 2003 and March, 2009, HAIC consisted of 5-fluorouracil (5-FU) at a dose of 300 mg/m^2/day for 5 days during the 1st and 2nd weeks, combined with intramuscular or subcutaneous administration of interferon-α 3 times per week for 4 weeks. Interferon-α dosing consisted of either natural interferon-α, 5 million units; recombinant interferon-α, 12 million units; or interferon-α 2b, 3 million units. From April, 2009 onwards, HAIC was performed with 5-FU plus cisplatin (CDDP) at a dose of 20 mg/m^2/day on days 1 and 8, combined with intramuscular interferon-α administration, as described above (17). The treatment cycle was repeated until disease progression or unacceptable drug toxicity.

In the sorafenib group (n=12), a limited number of patients received sorafenib 200-600 mg/day as an initial dose. In the absence of adverse events (AEs), the dose of sorafenib was increased to 400 mg twice daily. Treatment was discontinued on the same basis as in the HAIC group. However, if the performance status and liver function of patients with PD was preserved, sorafenib was continued until the occurrence of severe AEs in order to prevent rapid tumor growth associated with treatment cessation.

Response assessment. Tumor response was determined using dynamic computed tomography or magnetic resonance imaging, according to Response Evaluation Criteria in Solid Tumors, version 1.1. RR was defined as the combined percentages of patients experiencing a CR and those with a partial response (PR). Tumor control rate (TCR) was defined as the combined percentages of patients experiencing CR, PR and stable disease (SD). HAIC was evaluated every 6 or 8 weeks and sorafenib treatment was evaluated every 4 or 12 weeks. OS was calculated from the date of treatment initiation to the date of the last follow-up or death. Progression-free survival (PFS) was calculated from the date of treatment initiation to the date

Table I. Clinical characteristics of patients treated with sorafenib and hepatic arterial infusion chemotherapy (HAIC).

Variables	Sorafenib (n=12)	HAIC (n=8)	P-value
Age (years)	80.2±5.4	74.9±3.4	0.039[a]
Gender (M/F)	6/6	6/2	NS[b]
White cell count ($x10^2/\mu l$)	48.0±13.2	59.4±27.4	NS[a]
Lymphocyte count ($x10^2/\mu l$)	14.6±8.5	14.9±6.2	NS[a]
Platelet count ($x10^4/\mu l$)	16.7±6.1	14.1±6.7	NS[a]
PT-INR	1.10±34.6	1.16±0.19	NS[a]
ALT (IU/l)	35.5±0.12	41.9±0.19	NS[a]
Total bilirubin (mg/dl)	0.67±0.40	0.76±0.27	NS[a]
Albumin (g/dl)	3.5±0.4	3.3±0.8	NS[a]
Cirrhosis (Child-Pugh A/B/C)	10/2/0	4/4/0	NS[b]
TNM stage (I/II/III/IV-A/IV-B)	0/2/3/2/5	0/2/3/2/1	NS[c]
Largest tumor (mm)	42.3±21.2	49.7±28.2	NS[a]
AFP	2,027±5,219	279±418	NS[a]

Results are expressed as means ± standard deviation. [a]Mann-Whitney U test. [b]Fisher's exact test. [c]Chi-square test. M, male; F, female; NS, non-significant; PT-INR, prothrombin time-international normalized ratio; ALT, alanine aminotransferase; Child-Pugh, Child-Pugh classification; TNM, tumor-node-metastasis; AFP, α-fetoprotein.

Table II. Comparison of best response between sorafenib and hepatic arterial infusion chemotherapy (HAIC).

Response	Sorafenib (n=12)	HAIC (n=8)	P-value
CR	0 (0.0)	1 (12.5)	NS
PR	0 (0.0)	2 (25.0)	NS
SD	6 (50.0)	4 (50.0)	NS
PD	6 (50.0)	1 (12.5)	NS
RR (CR+PR)	0 (0.0)	3 (37.5)	0.049[a]
TCR (CR+PR+SD)	6 (50.0)	7 (87.5)	NS

Values are presented as no. (%). [a]Fisher's exact test. NS, non-significant; CR, complete response; PR, partial response; SD, stable disease; PD, progressive disease; RR, response rate; TCR, tumor control rate.

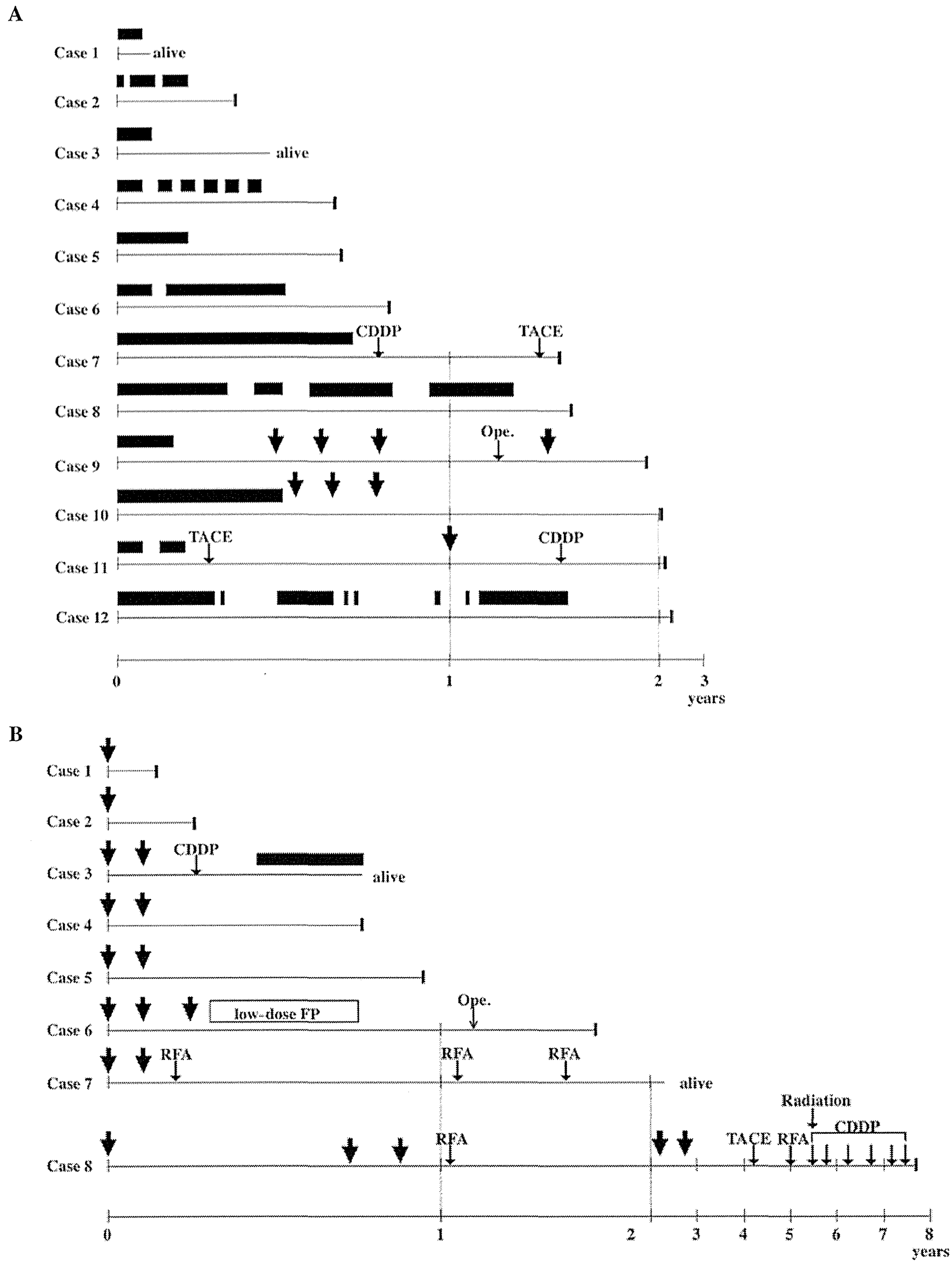

Figure 1. Clinical course of (A) the sorafenib and (B) hepatic arterial infusion chemotherapy (HAIC) groups. The best clinical responses were complete response in 1 patient (case 8) in the HAIC group, partial response in 2 patients (cases 6 and 7) in the HAIC group, stable disease in 10 patients (cases 1, 6, 9, 10, 11 and 12 in the sorafenib group and cases 2, 3, 4 and 5 in the HAIC group) and progressive disease in 7 patients (cases 2, 3, 4, 5, 7 and 8 in the sorafenib group and case 1 in the HAIC group). Although patients 1 and 3 in the sorafenib group and patients 3 and 7 in the HAIC group remained alive, other patients succumbed to the disease at the indicated time points. Closed bars, sorafenib administration. Arrows, HAIC. CDDP, cisplatin infusion; TACE, transcatheter arterial chemoembolization; Ope., operation; low-dose FP, continuous 5-fluorouracil and low-dose cisplatin infusion; RFA, radiofrequency ablation.

of the last follow-up or PD. Drug-related AEs were evaluated according to the Common Toxicity Criteria for Adverse Events, version 4.0 (Japan Clinical Oncology Group/Japan Society of Clinical Oncology edition).

Additional therapy. Of the 20 patients, 8 received additional treatment, including surgery, radiofrequency ablation (RFA), transcatheter arterial chemoembolization (TACE), HAIC using 5-FU and low-dose CDDP without interferon-α administration (low-dose FP), arterial CDDP infusion and irradiation therapy.

Statistical analyses. The results are expressed as means ± standard deviation. The differences between the two groups were examined for statistical significance using the Mann-Whitney U test, the Fisher's exact test and the Chi-square test. The survival curves for OS and PFS were analyzed using the Kaplan-Meier method and the differences were evaluated using a log-rank test. The 95% confidence intervals (CIs) of median OS and median PFS were calculated. P<0.05 was considered to indicate a statistically significant difference.

Results

Patient characteristics. The baseline patient clinical characteristics are summarized in Table I. The mean age of the sorafenib group was significantly higher compared to that of the HAIC group (P=0.039). There were no significant differences by blood cell counts, blood coagulation tests, biochemical tests, or Child-Pugh classifiction. In addition, a comparison of tumor-related background factors between the two groups did not reveal any significant differences in TNM stage, main tumor diameter, or serum α-fetoprotein levels.

Clinical response. The mean daily dose and duration of sorafenib treatment were 544 mg and 5.3 months, respectively. The mean number of treatment cycles in the HAIC group was 1.8 (~2.2 months). The treatment responses are summarized in Table II. The RR was significantly different between the two groups, as patients in the sorafenib group failed to respond to treatment (P=0.049). However, there was no significant difference in TCR between the two groups. Two patients in the HAIC group achieved a sustained CR after receiving additional RFA: one initially achieved a CR in response to HAIC and the other initially demonstrated a PR in response to HAIC.

Clinical course and additional therapy. Fig. 1 shows the clinical course of patients who were treated with sorafenib (Fig. 1A) or HAIC (Fig. 1B). In the sorafenib group, treatment was discontinued in 11 patients; for 7 patients (patients 2, 3, 4, 5, 7, 9 and 11), this was due to drug-related AEs, whereas the remaining patients (patients 6, 8, 10 and 11) developed PD. In the HAIC group, none of the patients discontinued 5-FU and CDDP infusion, but interferon-α administration was discontinued in 1 patient (patient 1). Four patients in each group (patients 7, 9, 10 and 11, Fig. 1A; and patients 3, 6, 7 and 8, Fig. 1B) received various additional therapies, including arterial CDDP infusion (patients 7 and 11, Fig. 1A; and patients 3 and 8, Fig. 1B); operation (patient 9, Fig. 1A; and patient 6, Fig. 1B); TACE (patients 7 and 11, Fig. 1A; and patient 8, Fig. 1B); low-dose FP (patient 6, Fig. 1B); RFA (patients 7 and 8, Fig. 1B); and radiation therapy (patient 8, Fig. 1B). Patients 9 and 10 (Fig. 1A) underwent HAIC immediately after sorafenib failure, whereas patient 3 (Fig. 1B) received sorafenib immediately after HAIC failure. Overall, no patients in the sorafenib group demonstrated a curative response following these treatments, whereas for 3 patients in the HAIC group, the additional treatment was significantly curative (P=0.049).

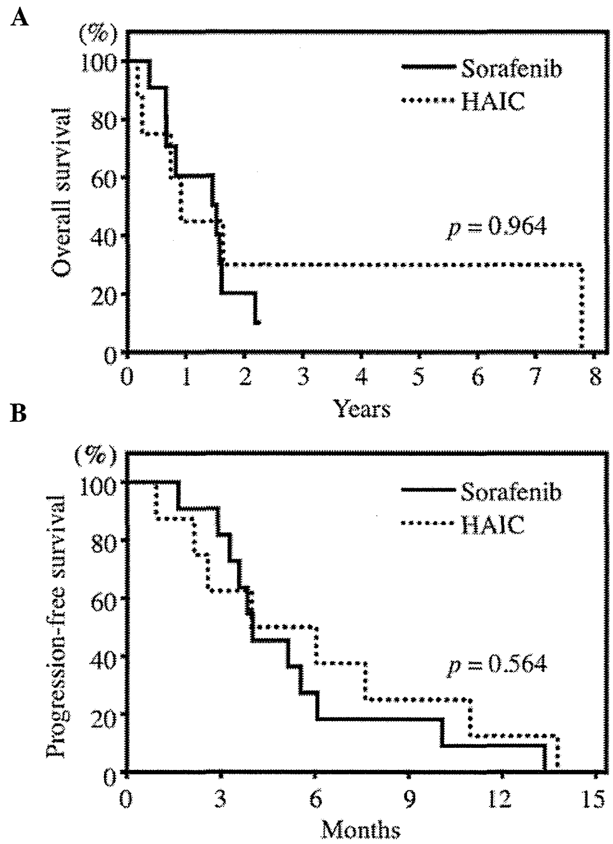

Figure 2. Kaplan-Meier analysis of (A) overall survival and (B) progression-free survival according to sorafenib and hepatic arterial infusion chemotherapy (HAIC). The P-value was calculated using the log-rank test.

Survival. The median OS of the total patient population was 17.8 months (0.93-94.7 months). The median OS was 18.6 months (95% CI: 13.8-23.4) and 11.7 months (95% CI: 0-31.5) in the sorafenib and HAIC groups, respectively (Fig. 2A). The median PFS was 4.0 months (95% CI: 2.1-5.9) and 5.0 months (95% CI: 2.6-7.4) in the sorafenib and HAIC groups, respectively (Fig. 2B). The median OS and PFS were not significantly different between the two groups (P=0.964 and 0.562, respectively).

Safety. The major AEs are listed in Table III. A total of 7 patients (58.3%) in the sorafenib group discontinued treatment due to grade 3 AEs [4 patients, anorexia; and 1 patient each with hand-foot (HF) syndrome, ascites and hepatic encephalopathy], whereas no patients demonstrated intolerance to HAIC. The discontinuation rate in the sorafenib group was significantly higher compared to that in the HAIC group (P=0.015). Among sorafenib-treated patients, the most frequent AEs were mild in severity (grade 1/2) and included HF syndrome, anorexia, hypoalbuminemia and diarrhea. Grade 3 AEs included HF syndrome, anorexia and hypertension. One Child-Pugh class A patient developed hepatic failure (hepatic encephalopathy) and sorafenib was discontinued. There were no grade 4 AEs. Among HAIC group patients, the most frequent AEs were mostly mild in severity (grade 1/2) and included decreased platelet count, anemia, fever, malaise, anorexia, hypoalbuminemia, decreased white blood cell count and decreased neutrophil count. In total, 6 hematological

Table III. Adverse events.

	Sorafenib (n=12) Grade (CTCAE v4.0)						HAIC (n=8) Grade (CTCAE v4.0)					
Adverse events	1	2	3	4	Any	3-4	1	2	3	4	Any	3-4
Anemia	4	1			5 (41.7)	0	2	5			7 (87.5)	0
Decreased WBC		1			1 (8.3)[a]	0	2	3	1		6 (75.0)[a]	1 (12.5)
Decreased neutrophil count		1			1 (8.3)[a]	0	3	2	1		6 (75.0)[a]	1 (12.5)
Decreasedlatelet count	4	3	1		8 (66.7)	1 (8.3)	3		3	1	7 (87.5)	4 (50.0)
Malaise	5	2			7 (58.3)	0	4	3			7 (87.5)	0
Fever					0[b]	0	6	1			7 (87.5)[b]	0
Anorexia	2	4	3		9 (75.0)	3 (25.0)	3	4			7 (87.5)	0
Nausea	1				1 (8.3)	0	2				2 (25.0)	0
Vomiting					0	0					0	0
Diarrhea	2	7			9 (75.0)	0	2				2 (25.0)	0
Mucositis	1	2			3 (25.0)	0		1			1 (12.5)	0
Hand-foot syndrome	4	1	4		9 (75.0)[a]	4 (33.3)					0[a]	0
Hepatic encephalopathy			1		1 (8.3)	1 (8.3)					0	0
Ascites		3			3 (25.0)	0					0	0
Bleeding					0	0					0	0
Cardiological					0	0					0	0
Hypertension	2	3	3		8 (66.7)[a]	3 (25.0)					0[a]	0
Pancreatitis					0	0					0	0
Infection		1			1 (8.3)	0		2			2 (25.0)	0
Hyperbilirubinemia	2	1			3 (25.0)	0	2				2 (25.0)	0
Hypoalbuminemia	2	8			10 (83.3)	0	1	5			6 (75.0)	0
Increased AST	6				6 (50.0)	0	2				2 (25.0)	0
Increased ALT	3				3 (25.0)	0	1				1 (12.5)	0
Increased creatinine	1				1 (8.3)	0	1	2			3 (37.5)	0
Increased serum amylase	3	2			5 (41.7)	0					0	0

The values represent number of events and the parenthetical data represent percentage values. [a]P<0.01; [b]P<0.001 (Fisher's exact test). CTCAE v4.0, Common Terminology Criteria for Adverse Events, version 4.0; WBC, white blood cell; AST, aspartate aminotransferase; ALT, alanine aminotransferase.

AEs of grade 3/4 were recorded in 4 patients. In the HAIC group, 1 patient (12.5%) experienced catheter occlusion as a catheter-related complication. In addition, 5 patients in the sorafenib group changed Child-Pugh class from A to B, whereas none of the patients in the HAIC group changed Child-Pugh class. These changes were mostly caused by the development of hypoalbuminemia in sorafenib-treated patients; there was no significant change in the prothrombin time-international normalized ratio (PT-INR).

Discussion

In the present study, we demonstrated the feasibility and safety of HAIC in elderly patients with advanced HCC. Several previous studies demonstrated the efficacy and safety of sorafenib in elderly patients (12,14-16); however, to the best of our knowledge, there are no studies performing a comparison of efficacy and safety between sorafenib and HAIC in elderly patients with HCC. It should be noted that the definition of 'elderly' may be controversial. We selected the cut-off age of 70 years, as the majority of age-related changes occur after this age (3). There are some studies available comparing sorafenib and HAIC for the treatment of HCC, but they were not performed in elderly patients (18,19).

In the present study, the RR of the HAIC group was significantly higher compared to that of the sorafenib group, but the TCR was similar between the two groups. Our findings were concurrent with those of previous studies of interferon-α-containing HAIC that demonstrated a RR of 24.6-73.0% (11,17,20-24), indicating that interferon-α-containing HAIC is a feasible treatment for elderly patients with advanced HCC.

An important finding of the present study is that, in the HAIC group, over a third of the patients achieved a CR or PR and, among these patients, 3 achieved long-term survival with additional curative therapy. This observation has important implications in understanding the indications for HAIC in elderly patients. There were no significant differences in median OS and PFS between the two groups. The median PFS with sorafenib was similar to that reported by previous investigations in elderly patients, but the median OS was longer (12,14-16). The reasons underlying the prolongation of OS in the sorafenib group in the present study are unknown, but one possibility is that the sorafenib group included 2 patients who received HAIC immediately after disease progression, which may skew the data. Two patients in the HAIC group achieved a CR after additional RFA. Other studies have demonstrated that a CR may improve long-term survival, although this was demonstrated in elderly patients (10,11).

The rate of treatment discontinuation due to severe AEs was significantly higher in the sorafenib group compared to that in the HAIC group. Multiple AEs have been associated with 5-FU, CDDP and interferon-α therapy; however, life-threatening AEs rarely occur, even in patients with liver cirrhosis (11,17,20,23). In this study, AEs in HAIC-treated patients were more severe than previously reported (11,17,20,23), particularly thrombocytopenia, although none resulted in treatment discontinuation or required any additional management. The evaluation of AEs in this patient population may be challenging, as the majority of the patients already presented with pancytopenia due to underlying liver cirrhosis. However, a high AE-induced discontinuation rate was apparent among sorafenib-treated patients, mostly as a result of anorexia or hypoalbuminemia, which may lead to ascites. In the present study, patients with a mean age of 80.2 years comprised 75% of all the grades of anorexia. This is concordant with the observations of Morimoto *et al* (13), who indicated that the incidence of anorexia was significantly higher among patients aged ≥75 years. Our results and those of Morimoto *et al* (13) differ from the results of the SHARP and Asia-Pacific trials (6,25); however, in those studies, the age and incidence of all-grade anorexia was 64.9 years (mean) and 51 years (median) and 14 and 12.8%, respectively (6,25). The results of those studies and our present results suggest that elderly patients are more prone to sorafenib-induced anorexia. In addition, Montella *et al* (15) suggested that the changes reported in Child-Pugh scores, as a result of changes in hypoalbuminemia and PT-INR, appeared to be associated with liver function and worsening of cirrhosis, rather than to the drugs administered. However, in the elderly patients in this study, the PT-INR did not change, suggesting preserved hepatic protein synthesis, indicating that hypoalbuminemia may be associated with the anorexia, rather than liver dysfunction. Accordingly, the results of the present study suggest that hypoalbuminemia is an important AE in elderly patients. In summary, HAIC may be a safer option compared to sorafenib for the treatment of elderly patients with HCC.

There were several limitations in the interpretation of the data presented in this study. First, the retrospective design and limited number of patients enrolled may give rise to selection bias. The mean age of the sorafenib group was higher compared to that of the HAIC group, which may explain why the incidence of AEs was higher in the sorafenib group. Moreover, according to the initial response to treatment, additional therapies were performed without limitation, which may affect OS. All the patients in the sorafenib group who received additional therapies developed PD or severe AEs, while some of the patients in the HAIC group who received additional therapies achieved a CR or PR. However, in part, the present study provided significant information regarding the management of HCC in elderly patients.

In conclusion, HAIC appears to be a feasible and safe treatment option for elderly patients with advanced HCC. However, further study of HAIC in a larger population of elderly patients is required to assess its potential as an alternative option for HCC management.

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A peptide antigen derived from EGFR T790M is immunogenic in non-small cell lung cancer

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Abstract. Lung cancer is the leading cause of cancer-related deaths worldwide. Epidermal growth factor receptor-tyrosine kinase inhibitors (EGFR-TKIs), such as gefitinib and erlotinib, have demonstrated marked clinical activity against non-small cell lung cancer (NSCLC) harboring activating epidermal growth factor receptor (EGFR) mutations. However, in most cases, patients develop acquired resistance to EGFR-TKI therapy. The threonine to methionine change at codon 790 of EGFR (EGFR T790M) mutation is the most common acquired resistance mutation, and is present in ~50% cases of TKI resistance. New treatment strategies for NSCLC patients harboring the EGFR T790M mutation are required. We evaluated the immunogenicity of an antigen derived from EGFR with the T790M mutation. Using BIMAS we selected several EGFR T790M-derived peptides bound to human leukocyte antigen (HLA)-A*02:01. T790M-A peptide (789-797) (IMQLMPFGC)-specific cytotoxic T lymphocytes (CTLs) were induced from peripheral blood mononuclear cells (PBMCs) of HLA-A2$^+$ healthy donors. An established T790M-A-specific CTL line showed reactivity against the NCSLC cell line, H1975-A2 (HLA-A2$^+$, T790M$^+$), but not H1975 (HLA-A2$^-$, T790M$^+$), and the corresponding wild-type peptide (ITQLMPFGC)-pulsed T2 cells using an interferon-γ (IFN-γ) enzyme-linked immuno spot (ELISPOT) assay. This CTL line also demonstrated peptide-specific cytotoxicity against H1975-A2 cells. This finding suggests that the EGFR T790M mutation-derived antigen could be a new target for cancer immunotherapy.

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Abbreviations: aAPC, artificial antigen-presenting cell; ELISPOT, enzyme-linked immuno spot; HLA, human leukocyte antigen; IFN-γ, interferon-γ; MAPK, mitogen-activated protein kinase; PBMC, peripheral blood mononuclear cell; PI3K, phosphatidylinositol 3-kinase; PFS, progression-free survival; STAT, signal transducer and activator of transcription

Key words: acquired resistance, CTL epitope, EGFR T790M, immunotherapy, non-small cell lung cancer

Introduction

Lung cancer is the leading cause of cancer-related deaths worldwide (1). Non-small cell lung cancer (NSCLC) accounts for ~80% of all lung cancer cases. Despite recent development in treatment agents, the prognosis for lung cancer patients remains poor (2).

Overexpression of epidermal growth factor receptor (EGFR) is observed in various malignancies, including lung cancer (3). EGFR activation induces many intracellular signaling pathways, such as the mitogen-activated protein kinase (MAPK), phosphatidylinositol 3-kinase (PI3K), and signal transducer and activator of transcription (STAT) pathways, which cause tumor cell proliferation and survival (4). The EGFR pathway is an appropriate target for cancer therapy, and several agents that block this pathway have been developed. In particular, epidermal growth factor receptor-tyrosine kinase inhibitors (EGFR-TKIs), such as gefitinib and erlotinib, demonstrated marked clinical activity against NSCLC harboring an activating EGFR mutation (5-9). However, patients develop acquired resistance to EGFR-TKIs almost without exception (10). A secondary mutation, resulting in a threonine to methionine change at codon 790 of EGFR (EGFR T790M), is the major mechanism of EGFR-TKI resistance (10,11). Additionally, some reports suggest that the EGFR T790M mutation may not be rare and may exist in a small population of in tumor cells before TKI treatment (12-14). Moreover, a pre-existing T790M mutation was associated with shorter progression-free survival (PFS) in patients receiving TKI treatment (13,14). At this time, no standard treatment for EGFR mutant patients with acquired resistance has yet been established, and novel strategies for overcoming this resistance issue are required.

Immunotherapy for NSCLC patients is considered to be a potentially feasible option, because of its high specificity and low toxicity against normal tissues; indeed, several tumor-associated antigen (TAA)-targeted phase 2/3 studies are ongoing (15). However, unfortunately, the results of a TAA-based vaccine therapy study were unsatisfactory (16). One concept for improving the effect of cancer vaccine therapy is to target mutated antigen-derived epitopes. It has been reported that various mutated epitopes were recognized by tumor-reactive T cells (17,18), suggesting that the mutated epitope was potentially immunogenic and thus might function as an immunotherapeutic target. There are few studies of immunotherapy targeting the EGFR T790M mutation. Here, we hypothesized that EGFR T790M-harboring cancer cells could be targeted by activated immune cells, and attempted to assess the immunogenicity of the EGFR T790M mutation-derived antigen *in vitro*. In the present study, we identified the human leukocyte antigen (HLA)-A2-restricted EGFR T790M mutation-derived epitope. Our results suggest that immunotherapy targeting the EGFR T790M mutation-derived antigen may be a novel treatment option for NSCLC patients with the T790M mutation. The combination of immunotherapy and EGFR-TKI therapy also may be a novel strategy for prevention of T790M-mediated resistance.

Materials and methods

Cell lines. The human NSCLC cell line H1975 was provided by Professor Seiji Yano (Kanazawa University, Ishikawa, Japan). H1975-A2 (H1975 transfected with HLA-A2) was provided by Dr Tetsuro Sasada (Kurume University, Fukuoka, Japan). Artificial APC-A2 (aAPC-A2) cells, which were generated by transduction of HLA-A*02:01, CD80, and CD83 molecules into K562 cells, were provided by Dr Naoto Hirano (Dana-Farber Cancer Institute, Boston, MA, USA). T2 cells (HLA-A*02:01, TAP$^-$) and human NSCLC cell line 11-18 were purchased from Riken (Saitama, Japan). These cell lines were cultured in RPMI-1640 (Sigma Chemical Co., St. Louis, MO, USA), supplemented with 10% FBS (Gibco-BRL, Carlsbad, CA, USA), 100 U/ml penicillin, and 100 μg/ml streptomycin in a humidified atmosphere containing 5% CO_2.

PBMC collection. Peripheral blood samples were collected from four HLA-A*02:01-positive healthy donors, after informed consent was obtained. Peripheral blood mononuclear cells (PBMCs) were isolated by density centrifugation using Ficoll-Hypaque (Pharmacia, Uppsala, Sweden) and frozen in liquid nitrogen until use.

Epitope prediction and synthesis. The epitope prediction software BIMAS (http://www-bimas.cit.nih.gov/molbio/hla_bind/) was used to predict peptides that could bind to HLA-A2. EGFR T790M mutation-derived peptides (purity >95%) were purchased from Scrum, Inc. (Tokyo, Japan). H-2 Kb-restricted ovalbumin (OVA) (257-264) (SIINFEKL) peptide (AnaSpec, Inc., Fremont, CA, USA) was used as a negative control in the peptide-binding assay. HLA-A2-restricted cytomegalovirus (CMV) (495-503) (NLVPMVATV) peptide was used as a positive control peptide, and an HLA-A2-restricted HIV-gag (77-85) (SLYNTYATL) peptide (American Peptide Company, Sunnyvale, CA, USA) as an irrelevant peptide in cytotoxic T lymphocyte (CTL) assays.

Peptide-binding assay. After incubation in culture medium at 26˚C overnight, T2 cells were washed with PBS and suspended in 1 ml Opti-MEM (Invitrogen Life Technologies, Carlsbad, CA, USA) with peptide (100 μg/ml), followed by incubation at 26˚C for 3 h and then at 37˚C for 2.5 h. After washing with PBS, HLA-A2 expression was measured using a BD FACSCanto II flow cytometer (BD Biosciences, San Jose, CA, USA) using a FITC-conjugated HLA-A2 (MBL Co., Ltd., Aichi, Japan)-specific monoclonal antibody. Mean fluorescence intensity (MFI) was analyzed using the FlowJo software (Tomy Digital Biology Co., Ltd., Tokyo, Japan). An OVA peptide was used as a negative control. A CMV peptide was used as a positive control peptide.

Generation of DCs. CD14$^+$ cells were isolated from PBMCs using human CD14 microbeads (Miltenyi Biotec GmbH, Bergisch Gladbach, Germany). Immature dendritic cells (DCs) were generated from CD14$^+$ cells using IL-4 (10 ng/ml; PeproTech, Inc., Rocky Hill, NJ, USA) and granulocyte-macrophage colony-stimulating factor (GM-CSF) (10 ng/ml; PeproTech, Inc.) in RPMI-1640 supplemented with 10% FBS. Maturation of DCs was induced by prostaglandin E2 (PGE2) (1 μg/ml; Sigma Chemical Co.) and tumor necrosis factor-α (TNF-α) (10 ng/ml; PeproTech, Inc.).

Induction of peptide-specific CTLs. CD8$^+$ cells were isolated using human CD8 microbeads (Miltenyi Biotec GmbH) from PBMCs. CD8$^+$ cells (2x10^6 cells/well) were stimulated with peptide-pulsed (10 μg/ml) 100-Gy-irradiated autologous mature DCs (1x10^5 cells/well) in RPMI-1640 containing 10% heat-inactivated human AB serum. After 1 week, these cells were stimulated twice weekly with peptide-pulsed (10 μg/ml) 200-Gy-irradiated aAPC-A2 cells (1x10^5 cells/well). Supplementation with 10 IU/ml IL-2 (Proleukin; Novartis, Basel, Switzerland) and 10 ng/ml IL-15 (PeproTech, Inc.) was performed at 3-4-day intervals between stimulations.

IFN-γ ELISPOT assay. Specific secretion of interferon-γ (IFN-γ) from human CTLs in response to stimulator cells was assayed using the IFN-γ enzyme-linked immuno spot (ELISPOT) kit (BD Biosciences), according to the manufacturer's instructions. Stimulator cells were pulsed with peptide for 2 h at room temperature and then washed three times. Responder cells were incubated with stimulator cells for 20 h. The resulting spots were counted using an ELIPHOTO counter (Minerva Tech, Tokyo, Japan).

CD107a assay and generation of a CTL line. CD8$^+$ cells isolated using human CD8 microbeads from cultured cells were incubated with peptide-pulsed T2 cells at a ratio of 2:1 for 3.5 h at 37˚C. CD107a-specific antibodies (BD Biosciences) were included in the mixture during the incubation period. CD8$^+$ CD107a$^+$ cells were sorted using a FACSAria II cell sorter (BD Biosciences). Sorted CTLs were stimulated, and the CTL line was established as described previously (19).

Cytotoxicity assay. Cytotoxic capacity was analyzed using the Terascan VPC system (Minerva Tech). The CTL line

Table I. Predicted EGFR T790M-derived peptides binding to HLA-A2.

Peptide name	Position	Length	Sequence	BIMAS score[a]
T790M-A	789-797	9	IMQLMPFGC	35.378
T790M-B	790-799	10	MQLMPFGCLL	51.77
T790M-C	788-797	10	LIMQLMPFGC	24.921
T790M-D	789-797[b]	9	IMQLMPFGV	495.288
T790M-E	789-797[c]	9	IMQLMPFGL	152.124
T790M-Awt	789-797	9	ITQLMPFGC	0.68

[a]Binding scores were estimated using the BIMAS software (http://www-bimas.cit.nih.gov/molbio/hla_bind/). [b,c]The cysteine (C) residue at position 797 was mutated to valine (V) and leucine (L), respectively. EGFR T790M, threonine to methionine change at codon 790 of EGFR.

was used as the effector cell type. Target cells were labeled in calcein-AM (Dojindo Molecular Technologies, Inc., Kumamoto, Japan) solution for 30 min at 37˚C. The labeled cells were then co-cultured with the effector cells for 4-6 h. Fluorescence intensity was measured before and after the culture period, and specific cytotoxic activity was calculated using the following formula: % cytotoxicity = {1 - [(average fluorescence of the sample wells - average fluorescence of the maximal release control wells)/(average fluorescence of the minimal release control wells - average fluorescence of the maximal release control wells)]} x 100%.

Results

*Assessment of EGFR T790M-derived peptide binding to HLA-A*02:01 molecules.* As the candidates of HLA-A*02:01-restricted EGFR T790M-derived CTL epitopes, we selected five 9- or 10-mer peptides with high predicted HLA-A*02:01-binding scores, calculated using BIMAS software. Three of the five EGFR T790M-derived peptides had higher binding scores than the corresponding wild-type peptides. Some studies have reported that modified peptides with single amino acid substitutions exhibit improved affinity for HLA molecules and enhanced immunogenicity (20-22); thus, we also designed two modified peptides. These modified peptides with a substitution of Cys for Val (T790M-D) or Leu (T790M-E) at codon 797 showed higher binding scores (Table I).

Using the HLA-A2 TAP-deficient T2 cell line, the binding affinity of the five synthetic peptides to HLA-A2 was assessed. A peptide-binding assay showed that three EGFR T790M-derived peptides were able to bind to HLA-A*02:01 molecules. In particular, the binding capability of the T790M-A peptide to HLA-A*02:01 molecules was higher than that of the corresponding wild-type peptide. This result suggests that the single amino acid substitution at codon 790 improved the binding affinity for HLA-A*02:01 molecules. The binding affinities of two mutated peptides (T790M-D and -E) to HLA-A*02:01 were equivalent to that of the CMV peptide used as a positive control (Fig. 1).

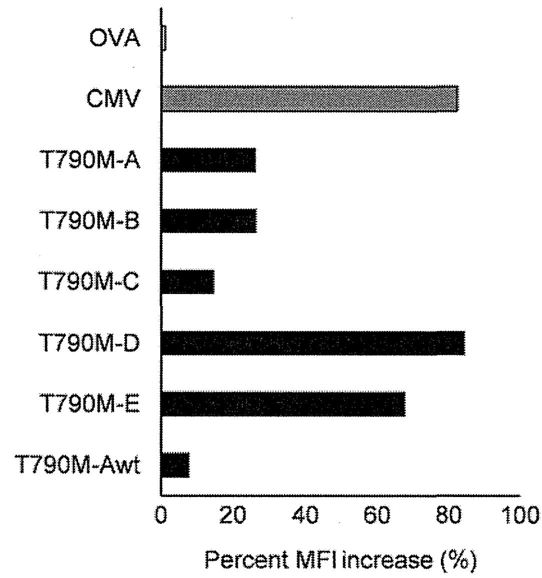

Figure 1. Binding of threonine to methionine change at codon 790 of EGFR (EGFR T790M)-derived peptides to human leukocyte antigen (HLA)-A2 molecule. A T2 binding assay was performed using a FACS system. An ovalbumin (OVA) peptide was used as a negative control. The bars show percent increases in mean fluorescence intensity (MFI). The average of two independent experiments is shown. (Percent MFI increase) = (MFI with the given peptide - MFI without peptide)/(MFI without peptide) x 100.

Induction of EGFR T790M-derived peptide-specific CTLs from human PBMCs. To evaluate the immunogenic potential of the five predicted HLA-A*02:01-binding peptides derived from EGFR T790M, we attempted to induce peptide-specific CTLs from human PBMCs obtained from four healthy donors. Several reports have shown the usefulness of artificial antigen-presenting cells (aAPCs) for the induction and expansion of peptide-specific CTLs from PBMCs (23,24). Thus, we attempted to induce such CTLs using aAPCs. $CD8^+$ cells were isolated from human PBMCs using human CD8 microbeads, and then stimulated with peptide-pulsed DCs for 1 week and subsequently, stimulated twice weekly with peptide-pulsed aAPC-A2 (Fig. 2A). As shown in Fig. 2B, ELISPOT assays revealed that T790M-A (789-797) (IMQLMPFGC)-specific CTLs were induced from PBMCs from all four donors. Also, induction of T790M-B (790-799) (MQLMPFGCLL)-specific CTLs were induced from PBMCs from two of the four healthy donors. However, stimulation with three other peptides, including modified peptides, did not induce peptide-specific CTLs. These results suggest that T790M-A (789-797) and T790M-B (790-799) have immunogenic potential and that

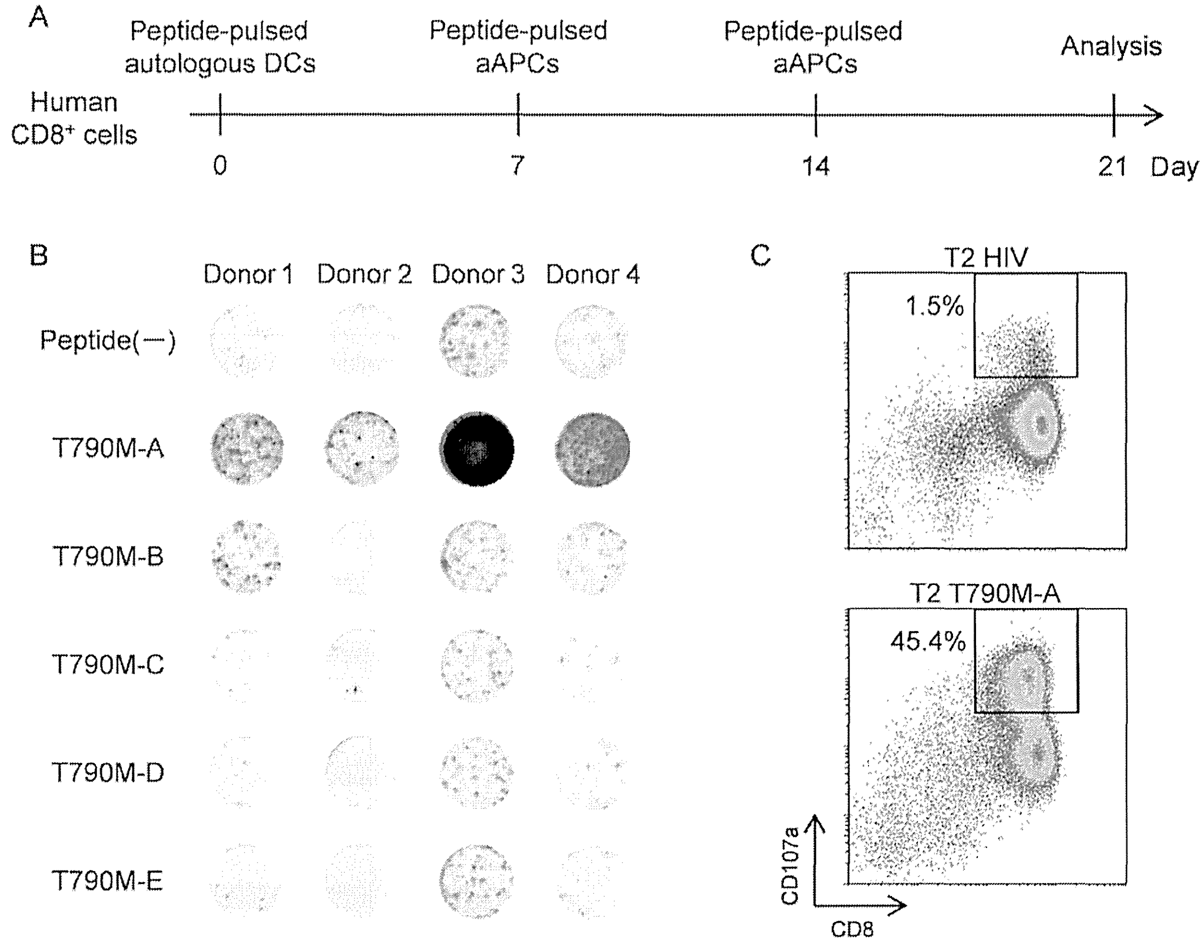

Figure 2. Induction of threonine to methionine change at codon 790 of EGFR (EGFR T790M)-derived peptide-specific cytotoxic T lymphocytes (CTLs) from peripheral blood mononuclear cells (PBMCs) of healthy donors. (A) Induction schedule of peptide-specific CTLs. $CD8^+$ cells ($2x10^6$ cells) isolated by anti-human CD8 microbeads from PBMCs were incubated with 10 μg/ml peptide-pulsed autologous dendritic cells (DCs) ($1x10^5$ cells) on day 0, followed by incubation with 10 μg/ml peptide-pulsed artificial antigen-presenting cell (aAPCs) ($1x10^5$ cells) on days 7 and 14. Peptide specificity was assessed by interferon-γ (IFN-γ) enzyme-linked immuno spot (ELISPOT) assay on day 21. (B) IFN-γ ELISPOT assay was carried out (effector, $1x10^5$ cells/well; target, $1x10^5$ cells/well) in duplicate at least three times independently; representative data are shown. (C) T790M-A-specific CTLs of healthy donor 3 were incubated with 10 μg/ml peptide-pulsed T2 cells (E:T = 2:1) for 3.5 h in the presence of an anti-human CD107a antibody. $CD8^+$ $CD107a^+$ cells were sorted using a FACSAria II cell sorter, which resulted in establishment of a T790M-A-specific CTL line.

CTLs specific for these peptides can be induced from human PBMCs. Given the effective induction of T790M-A (789-797) peptide-specific CTLs, we performed further analysis of the T790M-A peptide.

Generation of EGFR T790M-A-specific CTL line from human PBMCs. Next, we attempted to generate a purified T790M-A (789-797)-specific CTL line. Because the surface mobilization of CD107a is useful for identifying and isolating functional tumor-reactive T cells (25), we performed a CD107a assay to generate a purified T790M-A (789-797)-specific CTL line. Cultured cells stimulated by T790M-A peptide-pulsed DCs and aAPC-A2 *in vitro* were incubated with peptide-pulsed T2 cells at a ratio of 2:1 for 3.5 h at 37˚C in the presence of an anti-CD107a antibody. More frequent $CD107a^+$ cells were observed when CTLs were co-cultured with T790M-A peptide-pulsed T2 cells compared to HIV-peptide-pulsed T2 cells, and $CD8^+$ $CD107a^+$ cells were sorted as a purified, peptide-specific CTL line using a FACSAria II cell sorter (Fig. 2C). A purified T790M-A-specific CTL line was established from healthy donor 3.

Cross-reactivity of the T790M-A-specific CTL line with other EGFR T790M-derived peptides. To assess its cross-reactivity with other EGFR T790M-derived peptides, the T790M-A-specific CTL line was cultured with T2 cells pulsed with each peptide, and IFN-γ production was measured by ELISPOT assay. The T790M-A-specific CTL line specifically recognized T2 cells pulsed with T790M-A (789-797) but not non-peptide-pulsed T2 cells. The T790M-A-specific CTL line did not recognize T2 cells pulsed with the T790M-A (789-797) wild-type (ITQLMPFGC) peptide. Also, T2 cells pulsed with T790M-B, -D, and -E were not recognized by the T790M-A-specific CTL line (Fig. 3A). However, the T790M-A-specific CTL line showed cross-reactivity with T2 cells pulsed with T790M-C.

Next, we evaluated the cytolytic activity of the T790M-A-specific CTL line against cognate peptide-pulsed T2 cells. The T790M-A-specific CTL line specifically lysed T790M-A peptide-pulsed T2 cells but not HIV-peptide-pulsed T2 cells (Fig. 3B). These results suggest that the T790M-A-specific CTL line showed cross-reactivity against some EGFR

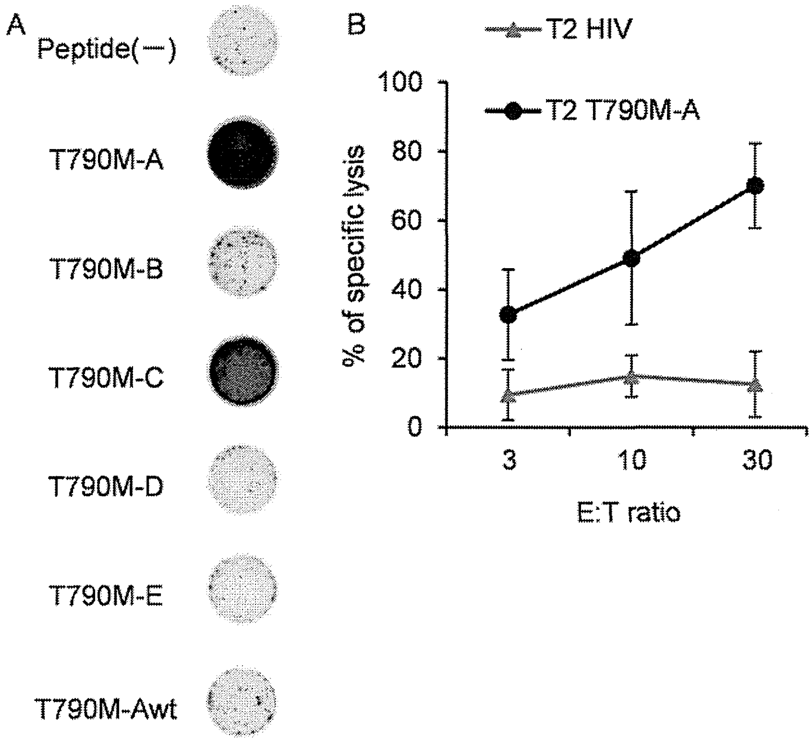

Figure 3. Cross-reactivity of the T790M-A-specific CTL line with threonine to methionine change at codon 790 of EGFR (EGFR T790M)-derived peptides. (A) Interferon-γ (IFN-γ) enzyme-linked immuno spot (ELISPOT) assay against T2 cells pulsed with each peptide. T2 cells pulsed with EGFR T790M-derived peptides (EGFR T790M-A, -B, -C, -D, -E, and Awt) were used as the target (effector $1x10^4$ cells/well, target $1x10^4$ cells/well). The assays were carried out in duplicate wells, and representative data are shown. (B) Cytotoxicity of the T790M-A-specific CTL line against T790M-A peptide-pulsed T2 cells. HIV-peptide-pulsed T2 cells were used as a negative control. Data are presented as means ± SD of three independent batches.

T790M-derived peptides, but not the corresponding wild-type EGFR-derived peptide. This cross-reactivity seems to be favorable for efficacy against EGFR T790M$^+$ cancer cells.

The T790M-A-specific CTL line recognizes and lyses HLA-A2$^+$ T790M$^+$ NCSLC cells. Next, we assessed the ability of the T790M-A-specific CTL line to recognize the HLA-A2$^+$ T790M$^+$ NCSLC cell line. This CTL line was incubated with 11-18 (T790M$^-$, HLA-A2$^+$), T790M-A-pulsed 11-18, H-1975 (T790M$^+$ HLA-A2$^-$), or H-1975-A2 (T790M$^+$ HLA-A2$^+$), and IFN-γ production was evaluated. We confirmed that the T790M-A-specific CTL line recognized peptide-pulsed 11-18 and H-1975-A2, but not 11-18 and H-1975, cells by IFN-γ ELISPOT assay (Fig. 4A). Similar data were obtained using CTLs from healthy donor 1 stimulated with T790M-A peptide-pulsed DC and aAPC-A2 *in vitro*, which were not purified by the CD107a assay (data not shown).

To evaluate the function of the T790M-A-specific CTL line against H1975-A2, a CD107a assay was performed. CD107a$^+$ cells were detected more frequently in culture with H-1975-A2 than with H-1975 cells (Fig. 4B).

Finally, we investigated the cytotoxic activity of the T790M-A-specific CTL line against H-1975-A2. Target cells were labeled with calcein-AM and co-cultured with the effector cells for 4-6 h. The T790M-A-specific CTL line showed cytotoxic activity against H1975-A2 cells, but not H1975 cells (Fig. 4C). These results suggest that the T790M-A-specific CTL line can recognize NSCLC cells harboring the EGFR T790M mutation in an HLA-A2-restricted manner.

Discussion

Mutated antigens associated with tumor cell progression and survival or drug resistance represent novel targets for cancer vaccine therapy. Warren *et al* evaluated computationally the antigenic potential of somatic mutations that occur in human cancers (26). They showed that several gene mutation-derived epitopes have immunogenic potential, at least computationally. Moreover, point mutations within the ABL kinase domain of the *BCR-ABL* gene are the most common causes of resistance to imatinib in chronic myeloid leukemia (CML) patients (27). Cai *et al* reported that the mutated *BCR-ABL* gene was associated with a TKI-resistance-generated CTL epitope in CML patients (28). These results suggest new immunotherapeutic approaches based on a TKI-resistant mutation-derived neoantigen. That is, mutations associated with acquired resistance to TKI therapy can be targeted by immune-based treatment strategies. This strategy may be an option to treat the gene mutation-mediated drug-resistant cancer cells. In the present study, we demonstrated the immunogenicity of antigens from mutated EGFR that are involved in TKI resistance in NCSLC.

TAAs can be classified into several categories, such as cancer-testis (CT) antigens, overexpressed antigens, differentiation antigens, and mutated antigens. Of these, only mutated antigens are unique, because they are not expressed in normal tissues. Previous reports have shown that peptide vaccine therapy can occasionally induce ineffective CTL responses, contrary to expectations (29-31). One possibility is

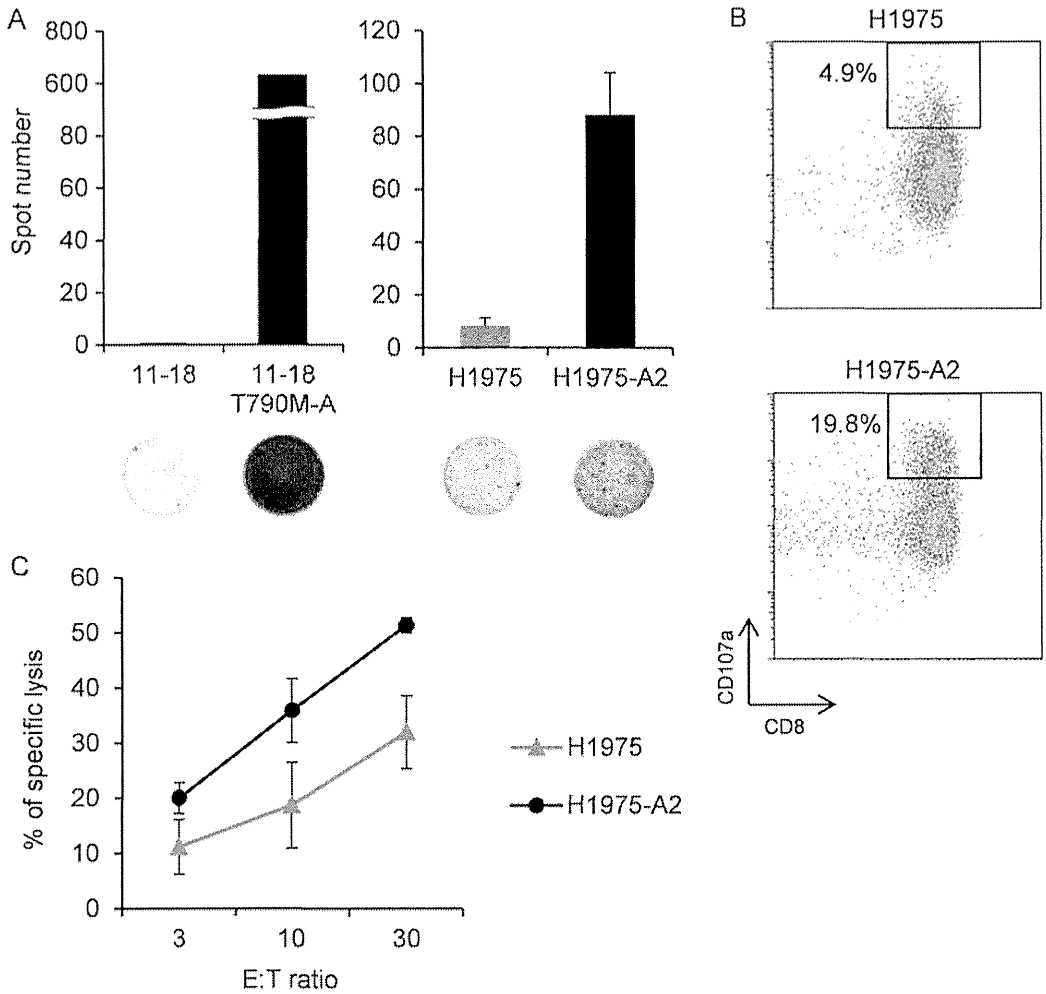

Figure 4. Reactivity of the T790M-A-specific CTL line against non-small-cell lung cancer (NSCLC) cells with or without the T790M mutation. (A) Interferon-γ (IFN-γ) enzyme-linked immuno spot (ELISPOT) assay results for the T790M$^+$ and T790M$^-$ NSCLC lines. Left: 11-18 and T790M-A peptide-pulsed (10 μg/ml) 11-18 cells were used as the targets (effector 1×10^5 cells/well, target 1×10^5 cells/well). Right: H-1975 and H1975-A2 cells were used as the targets (effector, 5×10^4 cells/well; target, 5×10^4 cells/well). The bars indicate the IFN-γ ELISPOT counts. (B) CD107a assay of the T790M$^+$ NSCLC line (E:T = 2:1). CD8$^+$ CD107a$^+$ cells were gated. (C) Cytotoxicity against the T790M$^+$ NSCLC cell line at the indicated effector/target ratios. Data are presented as means ± SD of three independent batches.

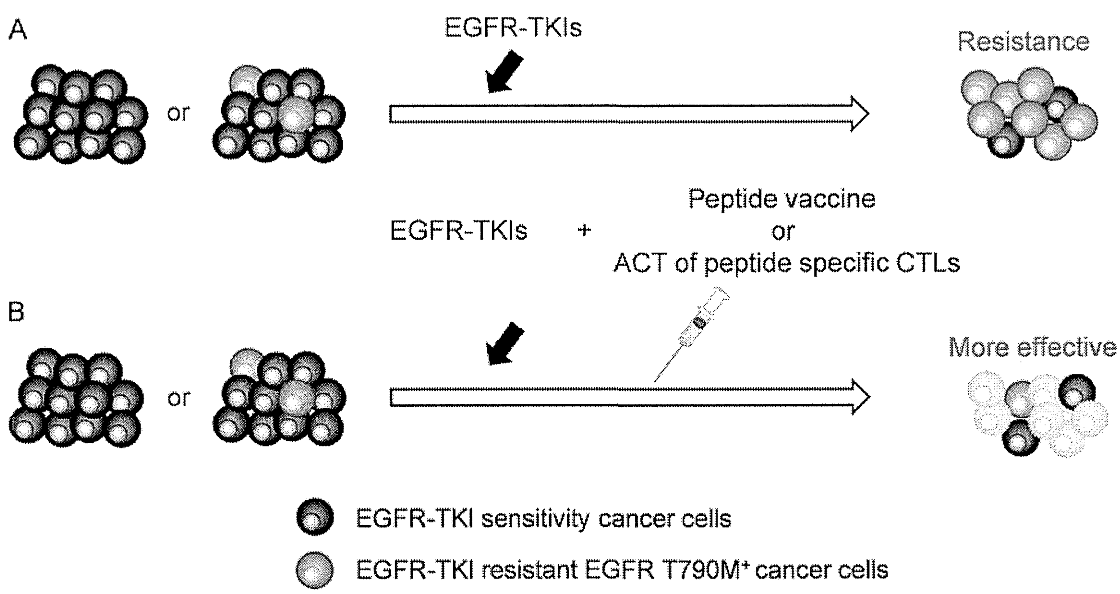

Figure 5. Combination therapy of epidermal growth factor receptor-tyrosine kinase inhibitor (EGFR-TKI) with T790M-targeted immunotherapy. (A) Generally, cancer cells develop acquired resistance to EGFR-TKI. (B) TKI-resistant cells harboring the T790M mutation were targeted by immunotherapy. This combination therapy may be effective against cancers with and without the threonine to methionine change at codon 790 of EGFR (EGFR T790M) mutation.

that the induced antigen-specific CTLs have a low affinity, and thus recognize only target cells pulsed with high concentrations of the peptide and not naturally presented epitopes on tumor cells. Several EGFR-derived CTL epitopes have been identified (32,33); however, the frequency of high-avidity EGFR-specific CTLs seems to be low in patients with EGFR-expressing cancers, because EGFR is a self-antigen that induces tolerance. The ability of low-avidity CTLs to recognize antigen-expressing tumor cells is considered to be weak. However, mutation-derived antigens are not self-antigens; thus, they would not be expected to induce immunotolerance, and so may have high immunogenicity. Indeed, in melanoma patients who experienced dramatic therapeutic effects after adoptive cell therapy with tumor-infiltrating lymphocytes (TILs), the mutated antigen-derived epitope was immunodominant and was recognized by tumor-reactive T cells (34,35).

In the present study, BIMAS was used to select EGFR T790M-derived candidate peptides that bind to HLA-A*02:01 according to computer algorithms, and T790M-A-specific CTLs could be induced from PBMCs of all four healthy donors by stimulation with peptide-pulsed DCs and aAPCs. Amino acid substitution of anchor residues (at position 2 and the C-terminus for HLA-A2) can alter the binding affinity (36-38). Leucine and methionine are the preferred anchor residues at position 2 of HLA-A2 (36,37). T790M-A (IMQLMPFGC) harbors a substitution of threonine to methionine at the anchor site, which confers immunogenicity. Also, valine and leucine are the preferred anchor residues at the C-terminus (36,37).

Then, we designed the modified peptides, T790M-D (IMQLMPFGV, substitution of cysteine to valine at the C-terminus) and T790M-E (IMQLMPFGL, substitution of cysteine to leucine at the C-terminus). These peptides bound to the HLA-A*02:01 molecule strongly (Fig. 1), but could not induce specific CTLs. T790M-D and -E are not self-antigens, being similar in this respect to T790M-A; this difference may be due in part to the difference in the frequency of peptide-specific CTL precursors. To confirm that the predicted candidate peptides are naturally presented peptides on tumor cells, peptide-specific CTL clones or lines induced by the peptides must recognize the tumor cells. A mass spectrometry (MS)-based method facilitates identification of peptide presentation by tumor cells (39). In this study, we confirmed the peptide-specific recognition of tumor cells by a peptide-specific CTL line, but not a CTL clone. However, CTL lines may contain distinct CTL clones that recognize irrelevant peptides, leading to apparent tumor reactivity (40). To avoid misleading tumor recognition and to evaluate the antigen-specific response of a CTL line, we used a peptide-specific CTL line established by CD107a sorting. An IFN-γ ELISPOT assay suggested that the specific CTL line recognized NSCLC cells harboring the EGFR T790M mutation in an HLA-A*02:01-restricted manner.

The T790M-A-specific CTL line did not show activity against the corresponding wild-type peptide. This suggests that EGFR T790M-targeted immunotherapy has no effect on NSCLC prior to EGFR-TKI treatment, with the exception of any pre-existing population of T790M-harboring cells, at least theoretically. Thus, consideration of combination therapy, EGFR-TKI and EGFR T790M-targeted immunotherapy, seems reasonable. Several studies have suggested that combination therapy could improve the efficacy of cancer immunotherapy. For instance, some chemotherapeutic agents can lead to upregulation of TAA expression or improvement of tumor cell resistance to specific CTLs (41). Use of an EGFR-TKI or anti-EGFR antibody augments the IFN-γ-induced expression of MHC classes I and II by A431 malignant human keratinocytes (42). Moreover, gefitinib improved the cytotoxic activity of natural killer cells against H1975 by modulating the interaction between NK cells and cancer cells, and by inhibiting STAT3 expression (43). These results indicate that the combination of EGFR-TKI and immunotherapy may have synergistic activity against NSCLC cells. The concept of combination therapy is shown in Fig. 5. Adding EGFR T790M-targeted immunotherapy to EGFR-TKI treatment could control the progression of cancer cells harboring T790M.

Yamada *et al* reported two HLA-A2-restricted EGFR T790M-derived CTL epitopes (790-799 MQLMPFGCLL and 788-798 LIMQLMPFGCL) (44). In addition to these epitopes, we identified the HLA-A*02:01-restricted CTL epitope T790M-A (789-797 IMQLMPFGC). We found that a T790M-A-specific CTL line established from human PBMCs had the ability to recognize and lyse the HLA-A*02:01$^+$ T790M$^+$ NCSLC cell line, and importantly, did not show cross-reactivity with the corresponding wild-type EGFR peptide. These results suggest that the EGFR T790M-A-specific CTL line recognizes single amino acid substitutions, leading to a low level of auto-immune reaction. The combination of an EGFR-TKI and T790M-targeted immunotherapy may be useful for treatment of NSCLC with the T790M mutation.

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Hepatology Research

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Original Article

Multicenter validation study of anti-programmed cell death-1 antibody as a serological marker for type 1 autoimmune hepatitis

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Aim: Recently, serum levels of anti-programmed cell death-1 (anti-PD-1) antibodies have been reported to be useful for the discrimination of type 1 autoimmune hepatitis (AIH) from drug-induced liver injury (DILI) and to be associated with clinical features of type 1 AIH. This multicenter study aimed to validate the usefulness of serum anti-PD-1 antibody as a serological marker for type 1 AIH.

Methods: Serum samples before the initiation of corticosteroid treatment were obtained from 71 type 1 AIH patients and 37 DILI patients. Serum levels of anti-PD-1 antibodies were measured by indirect enzyme-linked immunosorbent assay.

Results: Serum levels of anti-PD-1 antibodies were higher in type 1 AIH patients than in DILI patients ($P < 0.001$). The receiver–operator curve analysis showed that serum levels of anti-PD-1 antibodies were useful for the discrimination of type 1 AIH from DILI (area under the curve, 0.80). On the other hand, the multivariate Cox proportional hazard model showed that positivity for serum anti-PD-1 antibody, probable diagnosis based on the revised scoring system proposed by the International Autoimmune Hepatitis Group, and prothrombin activity of less than 60% were associated with the later normalization of serum transaminase levels. During the clinical course, the disease relapsed more frequently in patients positive for serum anti-PD-1 antibody (36% vs 11%).

Conclusion: This study suggests that serum anti-PD-1 antibody is useful for the diagnosis of type 1 AIH as an auxiliary diagnostic marker, and that serum levels of anti-PD-1 antibodies reflect clinical features of type 1 AIH.

Key words: autoantibody, autoimmune hepatitis, drug-induced liver injury, programmed cell death-1, validation

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INTRODUCTION

AUTOIMMUNE HEPATITIS (AIH) is a progressive inflammatory liver disorder characterized by histological interface hepatitis, elevation of serum immunoglobulin G (IgG) level, circulating autoantibodies and good response to immunosuppressive treatment.[1,2] The pathogenesis of AIH has not been fully revealed yet. Elevated serum IgG levels and positivity for serum antinuclear antibody (ANA) are hallmarks for the diagnosis of type 1 AIH; however, the diagnosis has been made based on the scoring systems for lack of specific diagnostic markers for AIH.[1,2]

Recently, serum anti-programmed cell death-1 (anti-PD-1) antibody has been reported to be useful for the discrimination of type 1 AIH from drug-induced liver injury (DILI) as an auxiliary diagnostic marker and to be associated with clinical features of type 1 AIH.[3] PD-1 is a co-stimulatory molecule expressed on activated T and B cells and has inhibitory properties. Anti-PD-1 antibody enhances the proliferation of allogeneic T cells.[4] PD-1-deficient mice thymectomized 3 days after birth develop massive hepatic necrosis with the appearance of serum ANA,[5] and this hepatitis responds well to corticosteroid treatment.[6] In addition, a recent clinical trial using anti-PD-1 antibody as an immunotherapeutic agent for advanced cancer shows the development of hepatitis, which responds well to corticosteroid treatment, as an adverse event.[7] Dysfunction of PD-1 may be associated with the pathogenesis of AIH.

This study aimed to validate the usefulness of serum anti-PD-1 antibody for the diagnosis of type 1 AIH and to confirm the association of serum anti-PD-1 antibody with the disease severity, response to corticosteroid treatment and the disease relapse.

METHODS

Ethics

THIS RETROSPECTIVE VALIDATION study complied with the Declaration of Helsinki and was approved by the institutional review board at Okayama University Graduate School of Medicine, Dentistry and Pharmaceutical Sciences.

Patients and serum samples

This study was carried out by the Intractable Hepato-Biliary Disease Study Group of Japan, sponsored by the Ministry of Health, Welfare and Labor of Japan. Serum samples before the initiation of corticosteroid treatment and clinical data were obtained from 71 type 1 AIH patients and 37 DILI patients, diagnosed in the following eight hospitals: Ehime University Hospital, Fukushima Medical University Hospital, Shinshu University Hospital, Teikyo University Hosiptial, Kyushu Medical Center, University of Fukui Hospital, Yamagata University Hospital, and Kochi Medical School Hospital.

For each patient, the following clinicopathological features were collected by the review of medical records: age, sex, laboratory data (white blood cell count, hemoglobin concentration, platelet count, bilirubin, aspartate aminotransferase, alanine aminotransferase [ALT], prothrombin activity, IgG, ANA) at the diagnosis, histological staging of liver fibrosis, initial dose of corticosteroid, timing of the normalization of serum ALT levels and timing of relapse. Clinical features of the study population are shown in Table 1. Collected serum samples were sent to Okayama University and stored at −30°C until use.

All type 1 AIH patients underwent liver biopsy. Type 1 AIH was diagnosed based on the revised scoring system proposed by the International Autoimmune Hepatitis Group.[1] DILI was diagnosed based on the diagnostic criteria of the Digestive Disease Week – Japan 2004 workshop,[8] the usefulness of which in the diagnosis of DILI has been confirmed by a study with a large sample size.[9]

Criteria for relapse in type 1 AIH

Relapse was defined as an increase in serum ALT levels to more than twofold of the upper normal limit (>60 IU/L), following the normalization of serum ALT levels (≤30 IU/L) with medical treatment.

Indirect enzyme-linked immunosorbent assay (ELISA)

Serum levels of anti-PD-1 antibodies were measured by indirect ELISA using the Protein Detector ELISA Kit (Kirkegaard & Perry Laboratories, Gaithersburg, MD, USA) in Okayama University.[3] All serum samples were tested in duplicate.

Briefly, 96-well U-bottom microtiter plates (Greiner Bio-One, Baden, Germany) were coated with 100 μL of 1 μg/mL recombinant PD-1 (Abnova, Taipei, Taiwan) in phosphate-buffered saline (PBS) at room temperature for 1 h. Unbound antigen was removed, non-specific binding sites were blocked by incubation with 1% bovine serum albumin (BSA) in PBS, and the wells were incubated with 100 μL of human sera diluted 1:20 in PBS with 1% BSA for 1 h. Thereafter, the wells were incubated with anti-human IgG diluted 1:1000 in PBS with 1% BSA, covalently linked to alkaline phosphatase, and the reaction was visualized by adding 100 μL of a substrate buffer (5-bromo-4-chloro-3-indolyl phosphate/nitro blue tetrazolium). The optical densities at 630 nm (OD_{630nm}) were read with a Model 680 microplate reader (Bio-Rad, Richmond, CA, USA). In