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Randomized trial of drip infusion versus bolus injection of vinorelbine for the control of local venous toxicity

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Summary Vinorelbine is a moderate vesicant that is well known to cause local venous toxicity such as drug induced-phlebitis. We conducted a prospective randomized trial to determine whether a 1-min bolus injection (1 min bolus) of vinorelbine reduced the incidence of local venous toxicity compared with a 6-min drip infusion (6 min infusion). Non-small cell lung cancer patients who were to receive chemotherapy containing vinorelbine were randomly assigned to receive either 6 min infusion or 1 min bolus of the drug. All infusions were administered through a peripheral vein. Local venous toxicity was evaluated at each infusion up to two cycles. Eighty-three patients were randomized into the study and 81 of them assessable for analysis. One hundred thirty-eight infusions to 40 patients in 6 min infusion and 135 infusions to 41 patients in 1 min bolus were delivered. Vinorelbine induced-local venous toxicity was observed in 33% of patients in 6 min infusion and 24% in 1 min bolus. There was no statistically significant difference between the two arms ($P = 0.41$). The incidence of local venous toxicity per infusions was 16% (22 of 138 infusions) in 6 min infusion and 11% (15 of 135 infusions) in 1 min bolus ($P = 0.47$). No severe local venous toxicity was seen in either arm. In this study, the administration of in 1 min bolus of vinorelbine did not significantly reduce the incidence of local venous toxicity compared with 6 min infusion. Further studies for the control of local venous toxicity of vinorelbine are warranted.

1. Introduction

Vinorelbine is a second-generation semi-synthetic vinca alkaloid whose antitumor activity is related to its ability to depolymerize microtubules and disrupt the mitotic spindle apparatus [1]. Vinorelbine has been shown to have clearly higher activity and lower neurotoxicity than the other vinca

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alkaloids, and is currently one of the most active agents for the treatment of non-small cell lung cancer (NSCLC) or other solid tumors [2–4].

Vinorelbine is most commonly administered through a peripheral vein as drip infusion over a period of between 6 and 10 min [5]. However, vinorelbine is a moderate vesicant that is well documented to cause local venous toxicity such as drug induced-phlebitis and venous irritation, and its incidence of approximately 30% has been reported in patients who received vinorelbine via a 6–10 min drip infusion [6,7]. Although local venous toxicity is not life threatening, it can result in discomfort or pain and can be a disincentive of chemotherapy to the patients. Therefore local venous toxicity should be managed effectively to decrease patient discomfort.

Recently, a retrospective study on drug induced-phlebitis with bolus injection of vinorelbine has been reported. In the analysis of 39 patients who received the administration of bolus injection of vinorelbine, drug induced-phlebitis occurred in only 1 of 39 patients (2.6%). The results suggested that the administration of bolus injection of vinorelbine might decrease the incidence of drug induced-phlebitis when compared common drip infusion [8]. Furthermore, shortening the infusion time of vinorelbine has also been reported to reduce the incidence of drug induced-phlebitis [9], although a randomized trial evaluating the bolus injection of vinorelbine has not been performed.

We conducted a prospective randomized trial to determine whether a 1-min bolus injection (1 min bolus) of vinorelbine reduced the incidence of local venous toxicity compared with a 6-min drip infusion (6 min infusion). In addition, we assessed the incidence of acute lower back pain, which has been reported to occur in shorter time infusions of vinorelbine [10] as other toxicity.

2. Patients and methods

2.1. Patient eligibility

Patients who had histological or cytological evidence of cancer, and planned to receive vinorelbine-containing chemotherapy as peripheral infusion, were eligible for this study. The patients were required to be 20 years of age or older and have an Eastern Cooperative Oncology Group performance status (PS) of 0–2. Patients were excluded if they had previous treatment with vinorelbine, medical condition that required regular use of steroids, or were pregnant or nursing. All patients provided written informed consent before randomization for this study, and the study was approved by the institutional review board at the National Cancer Center.

2.2. Study design

This study was a randomized trial comparing 1 min bolus of vinorelbine with 6 min infusion for the control of local venous toxicity. The study was performed in the National Cancer Center Hospital East. Patients were randomly assigned to receive either 6 min infusion or 1 min bolus by a minimization method. Before randomization, patients were stratified by chemotherapy regimens (stratum I: vinorelbine plus cisplatin, stratum II: vinorelbine plus gemcitabine, stratum III: vinorelbine alone) and body mass index (BMI) (stratum I: normal (BMI < 24), stratum II: high (BMI 24 or more)). We reported previously that high BMI was associated with a significant increased risk of vinorelbine irritation [6].

2.3. Treatment plan

Patients received either 6 min infusion or 1 min bolus of vinorelbine. Vinorelbine was diluted in 50 ml (6 min infusion) or 20 ml (1 min bolus) normal saline, respectively. All infusions were administered through a peripheral vein and followed by flushing the vein with approximately 200 ml of fluid. The administration of other drugs for the prevention of local venous toxicity was not allowed. Vinorelbine-containing chemotherapy regimens consisted of vinorelbine 20–25 mg/m^2 on days 1 and 8 plus cisplatin 80 mg/m^2 on day 1 every 3 weeks, vinorelbine 20–25 mg/m^2 plus gemcitabine 1000 mg/m^2 on days 1 and 8 every 3 weeks, or vinorelbine 20–25 mg/m^2 alone on days 1, 8 and 15 every 4 weeks.

2.4. Outcome assessment

The primary endpoint of this study was the incidence of local venous toxicity per patient. Local venous toxicity was evaluated at each infusion up to two cycles and graded according to the National Cancer Institute Common Toxicity Criteria (NCI-CTC) version 2.0 for injection site reaction by attending physician: grade 0, none; grade 1, pain, itching or erythema; grade 2, pain or swelling, with inflammation or phlebitis; and grade 3, ulceration or necrosis that is severe or prolonged or requires surgery. After the administration of vinorelbine, patients self-recorded in personal dairies symptoms of pain, itching, swelling, blister, or ulceration at injection. The patient's dairies were also used for support of diagnosis of local venous toxicity. Local venous toxicity was categorized as positive or negative, with positive defined as experience of grade 1 or more local venous toxicity at least once during treatment. The secondary endpoint of this study was the incidence of local venous toxicity per infusions and other toxicity. The incidence of acute lower back pain, which was reported to occur in shorter time infusion of vinorelbine, and hematological toxicity were mainly assessed as the other toxicity, and graded according to NCI-CTC version 2.0.

2.5. Statistical analysis

The purpose of this study was to determine whether 1 min bolus of vinorelbine reduced the incidence of local venous toxicity compared with 6 min infusion. The calculation of sample size was based on the estimated incidence of local venous toxicity per patient in the two treatment groups. On the basis of previous reports [6,8], an incidence of local venous toxicity per patients of 30% in 6 min infusion and of 5% in 1 min bolus was assumed. To demonstrate this hypothesis with an alpha of 5% and a power of 80% in a two-sided test, thirty-five patients from each group were required. A total of 80 patients were projected to be accrued. All comparisons between proportions were performed by the Chi-square test

or Fisher's exact test, as appropriate. Multivariate analysis was performed by logistic regression procedure to determine the relationship between the incidence of local venous toxicity and the clinical variables. P values < 0.05 were considered significant. The reported P values were based on two-sided tests. Statistical analysis software (StatView-J Ver.5.0, Macintosh) was used for the analyses.

3. Results

3.1. Patient characteristics

Between October 2002 and April 2003, 83 patients were enrolled and randomly assigned into the study. Baseline patient characteristics according to treatment group are shown in Table 1. The two treatment groups were well balanced in regards to age, PS, chemotherapy regimens, and BMI. All patients had advanced NSCLC and no prior chemotherapy. Two patients were not assessable for analysis because they refused to receive chemotherapy after randomization.

Treatment delivery is shown in Table 2. One hundred and thirty-eight infusions to 40 patients in 6 min infusion and 135 infusions to 41 patients in 1 min bolus were delivered. There was no significant difference between the two arms for treatment delivery of vinorelbine.

3.2. The incidence of local venous toxicity

The incidence of local venous toxicity was 33% (95% confidence interval (CI), 18.6–49.1%) in 6 min infusion (13 of the 40 patients) and 24% (95% CI, 12.4–40.3%) in 1 min bolus (10 of the 41 patients) (Fig. 1a). There was no statistically significant difference between the two arms (P = 0.41; relative risk, 0.67; 95% CI, 0.25–1.77). In 6 min infusion, grade 1 local venous toxicity was observed in 12 patients, grade 2 in 1 patient; in 1 min bolus, grade 1 local venous toxicity was observed in 8 patients, grade 2 in 2 patients. No severe local venous toxicity was seen with both arms. The incidence of local venous toxicity per infusions was 16% in 6 min infusion (22 of 138 infusions) and 11% in 1 min bolus (15 of 135 infusions) (P = 0.47) (Fig. 1b).

The incidence of local venous toxicity according to chemotherapy regimens were 29% (18/60) in the vinorelbine plus cisplatin group, 22% (2/9) in the vinorelbine plus gemcitabine group, and 25% (1/4) in the vinorelbine alone group, respectively. The incidence of local venous toxicity in the normal BMI group was 30% compared with 24% in the high BMI group (P = 0.77). There was no statistically significant difference among the stratified factors. We used multivariate logistic regression analysis to determine the relationship

Table 2 Treatment delivery

	6 min drip infusion	1 min bolus injection
Evaluable patients	40	41
Vinorelbine infusions		
1	1	3
2	9	8
3	1	4
4	29	26
Total infusions	138	135
Vinorelbine (mg)/body Median (range)	39 (30–48)	40 (27–48)

Table 1 Baseline patients characteristics

Characteristic	6 min drip infusion (n = 41)		1 min bolus injection (n = 42)		P
	No.	%	No.	%	
Age (years)					
Median	65		65		0.37
Range	42–76		49–78		
Sex					
Male	29	71	36	86	0.10
Female	12	29	6	14	
ECOG performance status					
0/1	7/29	88	11/28	93	0.48
2	5	12	3	7	
Chemotherapy regimen					
Vinorelbine/cisplatin	35	85	35	83	0.95
Vinorelbine/gemcitabine	4	10	5	12	
Vinorelbine alone	2	5	2	5	
Body mass index					
Median (range)	21.7 (13.5–34.2)		21.2 (14.7–29.9)		0.79
Normal ≤ 24	31	76	31	74	
High > 24	10	24	11	26	

ECOG, Eastern Cooperative Oncology Group.

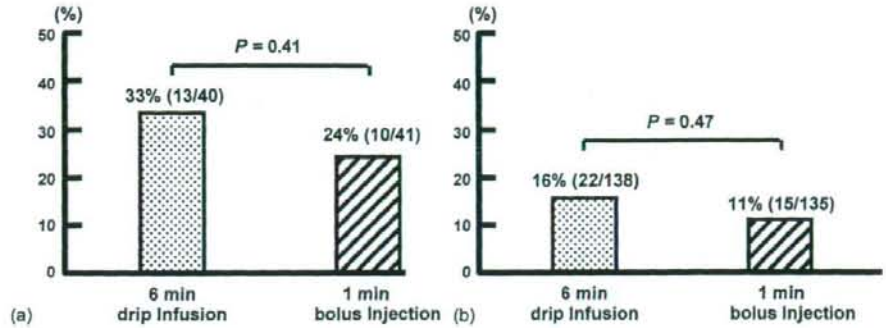

Fig. 1 The incidence of local venous toxicity: (a) per patient, (b) per infusions.

between local venous toxicity and the clinical variables (sex, age, chemotherapeutic regimen, BMI, the dose of VNR, and treatment arm). No significant correlations between the incidence of local venous toxicity and the clinical variables were found.

According to the patient's self-recorded diary, 43% (17/40) of patients in 6 min infusion had at least one symptom at injection site and 34% (14/41) of patients in 1 min bolus ($P = 0.43$).

3.3. Other toxicity

Acute lower back pain (>grade 1) was observed in 8% of 6 min infusion, and in 7% of 1 min bolus. There was no statistically significant difference between the two arms ($P > 0.99$). Grade 3/4 neutropenia and thrombocytopenia occurred with similar frequency in both arms.

4. Discussion

Local venous toxicity such as drug induced-phlebitis is one of the discomforting toxicities for patients in cancer chemotherapy. Vinorelbine is generally well tolerated and can be administered safely in an outpatient setting; however, it is a moderate vesicant with the potential to cause local venous toxicity. In our study, the incidence of local venous toxicity with the 6-min drip infusion of vinorelbine, which was used as control arm, was 33%, a similar frequency as found in past reports [6,7].

This is the first randomized study that evaluated the incidence of local venous toxicity with the bolus injection of vinorelbine. In this study, the administration of 1 min bolus of vinorelbine did not significantly reduce the incidence of local venous toxicity compared with 6 min infusion. The 24% rate of local venous toxicity with 1 min bolus of vinorelbine, which was observed in our study, was higher than anticipated in the study hypothesis. We speculate that our study hypothesis overestimated the incidence of local venous toxicity with 1 min bolus of vinorelbine because the previous reference reports were not prospective randomized studies [7,8]. Indeed, our study indicated that the administration of 1 min bolus of vinorelbine resulted in a non-statistically significant 27% reduction in rate of local venous toxicity compared with the 33% rate of 6 min infusion. We think that our study might have no under power to detect a clinically significant difference between the two treatment groups. In our study, an overall incidence of local venous toxicity was 28% although no severe local venous toxicity was seen. If a patient with only poor peripheral venous access receives the administration of vinorelbine, the use of implantable central venous access device should be considered. Moreover, the administration of 1 min bolus of vinorelbine has not been associated with an increased risk of acute lower back pain, which was previously reported to occur in shorter time infusions of vinorelbine [10]. Hematologic toxicity such as neutropenia and thrombocytopenia were also equivalent in both arms. In addition, we examined the clinical risk factors related to local venous toxicity of vinorelbine, but unfortunately there was no significant clinical risk factor in this study.

Two other randomized studies have been performed for the control of local venous toxicity of vinorelbine. Lazano et al. [9] compared the use of heparin-containing solution as anti-thrombotic effect [11] with 10-min infusion of vinorelbine. In their study, a population of 23 patients was randomized to arm A, in which vinorelbine plus 5000 U of heparin was diluted in 500 ml of normal saline and infused over 2 h, or arm B, in which vinorelbine was diluted in 50 ml of normal saline and infused over 10 min. Arm A with heparin was found to be inferior to arm B in terms of pain control at the injection site. Fasce et al evaluated the influence of infusion time of vinorelbine on local venous toxicity in a randomized cross-over trial [10]. Forty-eight patients with solid tumors were randomized to 6-min infusion or 20-min infusion of vinorelbine. Local venous toxicity was recorded in 23 patients (48%) in the 6-min infusion group, and in 26 patients (56%) in the 20-min infusion group, respectively. On the basis of their results, we used the administration of 6 min infusion of vinorelbine as the control arm in this study. The use of defibrotide [12,13] as another anti-thrombotic drug, or cimetidine [14], which was reported to inhibit histamine actions in endothelial cells by vinorelbine [15], have been investigated in an attempt to reduce the incidence of local venous toxicity of vinorelbine. However, there have been no randomized controlled trials to verify the benefit of these methods, and thus a randomized controlled study is needed to draw definitive conclusions about their efficacy.

In conclusion, our findings indicated that the incidence of local venous toxicity with 1 min bolus of vinorelbine was

higher than previously reported. In our study, the administration of 1 min bolus of vinorelbine did not significantly reduce the incidence of local venous toxicity compared with 6 min infusion. Further studies for the control of local venous toxicity of vinorelbine are warranted.

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Susceptibility to Lung Cancer and Genetic Polymorphisms in the Alcohol Metabolite-related Enzymes Alcohol Dehydrogenase 3, Aldehyde Dehydrogenase 2, and Cytochrome P450 2E1 in the Japanese Population

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BACKGROUND. It is believed that acetaldehyde plays an important role in alcohol-related carcinogenesis; although current epidemiologic studies have provided inconsistent findings on the association between alcohol consumption and the risk of lung cancer.

METHODS. To clarify the hypothesis that genetic polymorphisms in alcohol-metabolizing enzymes may influence susceptibility to lung cancer, the authors conducted a hospital-based case-control study and examined genetic polymorphisms in the alcohol dehydrogenase 3, aldehyde dehydrogenase 2 (*ALDH*$_2$), and cytochrome P450 2E1 genes in 505 patients with histologically confirmed lung cancer and in a group of 256 noncancer controls who provided complete cigarette and alcohol consumption histories. Genotyping was conducted by polymerase chain reaction-restriction fragment-length polymorphism assay.

RESULTS. A significant association was noted between alcohol consumption and lung cancer risk. Thus, using the median value for the controls as the cut-off point, the odds ratios (OR) for light and heavy drinkers were 1.76 and 1.95, respectively (P for trend = .012), compared with nondrinkers. In addition, there was a significant trend toward increased risk of lung cancer in drinkers with *ALDH*$_2$ variant alleles (P for trend <.0001). The adjusted OR for heavy drinkers was 6.15 compared with nondrinkers. Regarding associations between histologic type and genotypes, the *ALDH*$_2$ variant allele was significantly less common in patients who had adenocarcinoma compared with controls.

CONCLUSIONS. The current observations suggested a positive association between alcohol consumption and the risk of lung cancer. Drinking may increase the risk, especially among individuals who have the variant *ALDH*$_2$ alleles. ***Cancer* 2007;110:353–62.** *2007 American Cancer Society.*

KEYWORDS: lung cancer, alcohol consumption, case-control study, genetic polymorphism, alcohol dehydrogenase 3, aldehyde dehydrogenase 2, cytochrome P450 2E1.

Epidemiologic studies have provided inconsistent results regarding the associations between alcohol consumption and the risk of lung cancer. In general, therefore, the involvement of alcohol in lung cancer etiology has been regarded with skepticism, with any indication of an association being attributed in most instances to confounding factors, such as cigarette smoking.[1] It indeed is difficult to separate the effects of alcohol and smoking because, the 2 tend to be

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correlated, but this problem does not automatically exclude the possibility that there is a separate alcohol effect. A panel of experts commissioned by the World Cancer Research Fund and the American Institute for Cancer Research in 1997, after reviewing the epidemiologic evidence, concluded that alcohol intake *possibly* may increase lung cancer risk.[2] Although the mechanism by which alcohol may cause cancer remains obscure, many epidemiologic studies have identified chronic alcohol consumption as a significant risk factor for cancers of the oral cavity, pharynx, larynx, and esophagus in humans.[3] When investigating the role of alcohol-related carcinogenesis, most studies have concentrated on the type of alcoholic beverage consumed and the amount of daily intake, but this does not fully explain the variance in individual susceptibility to alcohol-related cancer.

Recent reports strongly implicate acetaldehyde, the first metabolite of ethanol, rather than alcohol itself, as responsible for the risk of developing alcohol-related cancers. It has been reported that acetaldehyde causes mutations by DNA adduct formation and inhibition of DNA repair. Moreover, drinking or inhaling acetaldehyde has mutagenic and carcinogenic effects and induced nasal and laryngeal carcinomas in experimental animals.[4–8]

Ethanol is primarily (80%) oxidized to acetaldehyde by alcohol dehydrogenase (*ADH*), and most of this acetaldehyde is then eliminated by aldehyde dehydrogenase (*ALDH*). However, ethanol and acetaldehyde also are metabolized through the microsomal ethanol-oxidizing system and the microsomal acetaldehyde-oxidizing system, and cytochrome P450 2E1 (*CYP2E1*) is a major contributor to those systems.[9,10] *CYP2E1* has high oxidation activity and is induced by long-term alcohol intake. These enzymes exhibit wide interindividual variability in their activity, suggesting that the variation may be caused by genetic polymorphisms.

There are several *ADH* subtypes, some of which have genetic variants with altered kinetic properties. ADH_3 is polymorphic, and the enzyme encoded by the ADH_3^1 allele metabolizes ethanol to acetaldehyde 2.5 times faster than that encoded by the ADH_3^2 allele.[11] $ALDH_2$ is a key enzyme in the elimination of acetaldehyde. In individuals with $ALDH_2^2$, a variant allele that is prevalent among East Asians (eg, 50% prevalence in Japan[12]), the activity of this enzyme is extremely low. The *CYP2E1* variant allele, which is detectable by *Rsa*I digestion (termed the c2 variant), corresponds to higher activity ethanol metabolism and is associated with greater alcohol consumption.[13–15] Individuals who have 1 or more ADH_3^1, $ALDH_2^2$, and *CYP2E1* c2 alleles accumulate more acetaldehyde in the blood after drinking ethanol and may be at increased risk for various alcohol-related diseases at similar levels of alcohol intake as individuals who do not carry these alleles. Because the ADH_3 variant allele is common in whites, and the $ALDH_2$ and *CYP2E1* variant alleles are found at high frequency in Asians, research on these genes is most advanced regarding alcohol-related diseases and alcohol metabolism.

The association between genetic polymorphisms in these enzymes and susceptibility to some types of cancer has been reported in case-control studies. The ADH_3^1 and $ALDH_2^2$ alleles are associated closely with alcohol-related cancers in the upper aerodigestive tract,[16–21] and systemic acetaldehydemia has been considered responsible for carcinogenesis in this locality. However, to our knowledge, there are no reports on associations between polymorphisms of *ALDH* and lung cancer risk. In relation to *ADH*, a negative association between genetic variation in ADH_3 and lung cancer has been reported recently.[22] *CYP2E1* is responsible primarily for the bioactivation of many low-molecular-weight, tobacco-specific carcinogens, including certain nitrosamines, such as *N*-nitrosodimethylamine and *N*-nitrosonornicotine. It is possible that the *CYP2E1* c2 variant not only may increase the blood concentration of acetaldehyde but also may activate these carcinogens more strongly. Activated nitrosamines have been linked to the development of numerous cancers. However, results from studies that evaluated the role of *CYP2E1* polymorphisms in relation to lung cancer have been discrepant.[23–28] Because previous investigations did not adjust for alcohol consumption and/or did not have sufficient power to distinguish the risk from alcohol consumption, these inconsistent findings may have been caused by variations in *CYP2E1* enzyme activity induced by ethanol.

We conducted a hospital-based case-control study to evaluate whether ADH_3, $ALDH_2$, or *CYP2E1* polymorphisms are associated with lung carcinogenesis. The primary endpoint of the current study was to clarify the association between each genetic polymorphism and the risk of lung cancer, controlling for the amount of alcohol consumed and smoking habits. Furthermore, associations between alcohol consumption and lung cancer risk in individuals with variant alleles, again controlling for smoking, and associations between these polymorphisms and histologic characteristics were evaluated.

MATERIALS AND METHODS

Participants

This study was approved by the Institutional Review Board and the Ethics Committee of the National

Cancer Center, Japan. The majority of eligible participants in this study were residents of Chiba and East Tokyo, and all were of Japanese nationality. Personal and clinical data from patients who participated in the Lung Cancer Database Project at the National Cancer Center Hospital East (NCCH-E) and the National Cancer Center Research Institute East were used in the current study. The database includes information on demographic factors, physical symptoms, psychological factors, and lifestyle factors (diet, smoking, etc) obtained from self-reported questionnaires and medical information from the patients' medical charts and blood, DNA, and urine specimens. All patients who were enrolled in the current study had primary lung cancer that was newly diagnosed with histologic or cytologic confirmation at the Thoracic Oncology Division of the NCCH-E, Japan, from September 1997 to June 2000. All patients provided their written informed consent prior to enrolment in this project. Unmatched controls were newly recruited individuals from the population with no history of cancer or other tumors who visited the Thoracic Oncology Division of NCCH-E from March 2002 to May 2003 and were confirmed as cancer-free by appropriate examinations (chest computed tomography scans, bronchofibroscopy, video-assisted thoracoscopic biopsy, etc). The major reasons for visiting the hospital were suspicions of lung cancer on chest x-ray or sputum cytology at their annual medical check-up or referral from other hospitals. Epidemiologic data were collected by personal interview. All individuals in the control group completed the same standardized questionnaire that was completed by the Lung Cancer Database Project participants, including detailed demographic information, history of cancer, occupational and residential history, and detailed information regarding alcohol and tobacco consumption. All participants provided their written consent.

Sample Collection and DNA Extraction

Four milliliters of peripheral venous blood were collected into heparinized tubes. Genomic DNA was purified from peripheral blood lymphocytes using a DNA isolation kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions and was stored at 80°C.

Polymorphism Analysis

ADH_3 and $ALDH_2$ genotyping was performed by using the polymerase chain reaction-restriction fragment-length polymorphism (PCR-RFLP) method. To prevent the amplification of closely related ADH_1 and ADH_2 genes, samples initially were digested with the *Nla*III restriction enzyme (TOYOBO, Osaka, Japan). A 145-base pair (bp) section of the ADH_3 gene was amplified by PCR using 200 ng of predigested genomic DNA with primers (sense, 5′-GCTTTAAGAGT AAATATTCTGTCCCC-3′; antisense, 5′-AATCTACCTCT zTTCCGAAGC-3′). The PCR product obtained in this manner then was digested directly with restriction enzyme *Ssp*I (TOYOBO). After polyacrylamide gel electrophoresis, ADH_3 alleles were visualized by ethidium bromide and were photographed under ultraviolet light. The ADH_3^1 allele produced fragments of 67 bp, 63 bp, and 15 bp; and the ADH_3^2 allele produced fragments of 131 bp and 15 bp.

A 134-bp fragment of the $ALDH_2$ gene was amplified by PCR according to a slightly modified method of Harada et al.[12] One hundred fifty nanograms of genomic DNA were mixed with 5 pmol of each primer (sense, 5′-CAAATTACAGGGTCAAGGGCT-3′; antisense: 5′-CCACACTCACAGTTTTCTCTT-3′) in a total volume of 50 μL that contained 50 μM deoxynucleotide triphosphate, 1.5 mM $MgCl_2$, and 1 U Taq DNA polymerase; Takara Shuzo, Kyoto, Japan). Thirty-five cycles (denaturation at 94°C for 15 seconds, annealing at 58°C for 1 minute and 30 seconds, and polymerization at 72°C for 30 seconds) were performed using a GeneAmp PCR system 9600 (PerkinElmer, Oak Book, Ill). After purification, each PCR product was digested with *Mbo*II (TOYOBO), electrophoresed on a 20% polyacrylamide gel, stained with ethidium bromide, and photographed. The $ALDH_2^1$ allele produced fragments of 125 bp and 9 bp, and the $ALDH_2^2$ allele produced fragments of 134 bp.

The *CYP2E1* genotypes ascribed to the *Rsa*I site in the 5′-flanking region also were identified as RFLPs by PCR. Genomic DNA (100 ng) was subjected to PCR with each primer (sense, 5′-ATCCACAAGTG ATTTGGCTG-3′; antisense, 5′-CTTCATACAGACCCTC TTCC-3′). PCR was performed for 35 cycles under the following conditions: 1 minute at 95°C for denaturation, 1 minute at 55°C for primer annealing, and 1 minute at 72°C for primer extension. The 412-bp fragment was digested with *Rsa*I (TOYOBO). The products that were yielded were fragments with 360 bp and 50 bp for c1/c1; 360 bp, 50 bp, and 410 bp for c1/c2; and 410 bp for c2/c2 detected by electrophoretic analysis in 5% polyacrylamide gels.

Statistical Analysis

Patient characteristic (see Table 1) were compared with characteristic in the control group by using the Student *t* test or the chi-square test. Odds ratios (ORs) and 95% confidence intervals (95% CIs) were obtained by unconditional logistic regression analy-

TABLE 1
Baseline Characteristics of Lung Cancer Cases and Controls

Characteristic	No. (%) Cases (n = 505)	Controls (n = 256)	P for difference
Mean age SD, y	64.8 8.3	63.5 10.2	.06*
Sex			
Men	360 (71.3)	126 (49.2)	
Women	145 (28.7)	130 (50.8)	<.0001†
Smoking status			
Never	140 (27.7)	129 (50.4)	
Past	97 (19.2)	64 (25)	
Current	268 (53.1)	63 (24.6)	<.0001†
Smoking amounts, pack-years			
Past			
<27	35 (36.1)	32 (50)	
27	62 (63.9)	32 (50)	.08†
Current			
<40	71 (26.5)	30 (47.6)	
40	197 (73.5)	33 (52.4)	.001†
Alcohol drinking habit, times/wk			
Seldom	116 (23)	118 (46.1)	
2	43 (8.5)	42 (16.4)	
3–6	96 (19)	22 (8.6)	
Daily	250 (49.5)	74 (28.9)	.0001†
Alcohol amounts, g/day			
0	120 (23.8)	119 (46.5)	
<31.6	154 (30.5)	65 (25.4)	
31.6	231 (45.7)	72 (28.1)	.0001†

SD indicates standard deviation.
* Determined using the Student *t* test.
† Determined using the chi-square test.

sis. In our regression models, we adjusted ORs for potential confounding variables, including age, sex, smoking status (never, past, current) or amounts smoked (pack-years) and alcohol consumed (none, light, heavy). Because differences in the amount of alcohol consumed (ethanol, in gram per day) were very large, we divided those who drank into 3 categories: nondrinkers, light drinkers (31.6 g per day), and heavy drinkers (>31.6 g per day). The amount of tobacco smoke exposure was calculated as pack-years (usual amount per day/20 × overall duration [years] of use). Participants were considered current smokers if they smoked up to 1 year before the date of diagnosis in the case group or up to the date of the interview for the control group. The average amount of daily ethanol intake was calculated in grams. Calculation of this value was based on an average ethanol content of 4-volume% in beer, 15-volume% in Japanese sake (rice wine), 25-volume% in Japanese spirits (syochu), 12-volume% in wine, and 40-volume% in spirits. Drinking frequency was assessed as 5 categories: less than once a week, 1 or 2 days a week, 3 or 4 days a week, 5 or 6 days a week, and daily. Categorical variables were compared with the chi-square test. ORs and 95% CIs were calculated by using logistic regression analysis adjusting for age, sex, smoking, and drinking. The Mantel extension test was used to evaluate linear trends across categories of alcohol consumption that were divided into 4 categories by quartiles for control. Resulting P values <.05 (2-tailed) were considered statistically significant. All statistical analyses were performed using the SAS statistical software package (SAS Institute Inc., Cary, NC).

RESULTS

In total 510 patients with lung cancer (cases) and 260 healthy controls participated in this study. Because of the lack of DNA samples or information on lifestyle, 9 participants were eliminated. Table 1 summarizes the baseline characteristics of selected variables for the lung cancer cases and controls. Age distribution was similar in both groups (mean, 64.8 years and 63.5 years, respectively); however, the cases were more likely than the controls to be men (71.3% and 49.2%), to be current smokers (53.1% and 24.6%) and heavy smokers, and to consume more alcohol. The proportions of those who consumed >31.6 g per day of ethanol and of daily drinkers were 45.7% and 49.5%, respectively, for cases and 28.1% and 28.9%, respectively, for controls. The median values from the control group for the 2 smoking amount categories were used as the cut-off values. The 3 categories of alcohol consumption were lifetime nondrinker, below the median intake, and above the median intake.

The frequency of ADH_3, $ALDH_2$, and *CYP2E1* genotypes and ORs among lung cancer cases and controls are presented in Table 2. After adjustment for age, sex, smoking amount, and amount of alcohol consumed, the ORs for individuals with the ADH_3, $ALDH_2$, and *CYP2E1* variant alleles, compared with individuals who were homozygous for the common allele, were 1.01, 0.73, and 0.93, respectively. Thus, there were no significant differences in the frequencies of any genotypes between cases and controls. The OR for carriers of the *CYP2E1* c2/c2 genotype, compared with the c1/c1 genotype, was 4.66 (P <.05). This genotype is not in Hardy-Weinberg equilibrium in the control population, the observed frequency is most likely an underestimate, and the finding of an association with lung cancer is most likely a false-positive result.

Without taking these genotypes into consideration, a direct association between alcohol consumption and lung cancer occurrence can be derived, as

TABLE 2
The Frequency of Alcohol Dehydrogenase 3, Aldehyde Dehydrogenase 2, and Cytochrome P450 2E1 Genotypes and Odds Ratios Among Lung Cancer Cases and Controls

Genotype	No. (%)		OR	
	Cases (n = 505)	Controls (n = 256)	Crude	Adjusted*
ADH_3				
C/C	459 (90.9)	227 (88.7)	1	1
C/V	44 (8.7)	29 (11.3)	0.75 (0.46–1.23)	0.71 (0.40–1.16)
V/V	2 (0.4)	0 (0)	—	—
C/V and V/V	46 (9.1)	29 (11.3)	0.78 (0.48–1.28)	0.74 (0.44–1.24)
$ALDH_2$				
C/C	319 (63.2)	134 (52.3)	1	1
C/V	168 (33.3)	108 (42.2)	0.65 (0.48–0.90)†	0.73 (0.52–1.03)
V/V	18 (3.6)	14 (5.5)	0.54 (0.26–1.12)	0.75 (0.35–1.59)
C/V and V/V	186 (36.8)	122 (47.7)	0.64 (0.47–0.87)†	0.73 (0.53–1.02)
CYP2E1				
C/C	300 (59.4)	147 (57.4)	1	1
C/V	175 (34.7)	106 (41.4)	0.81 (0.59–1.11)	0.83 (0.60–1.15)
V/V	30 (5.9)	3 (1.2)	4.90 (1.47–16.32)†	4.66 (1.36–16.0)†
C/V and V/V	205 (40.6)	109 (42.6)	0.92 (0.68–1.25)	0.93 (0.68–1.29)

OR indicates odds ratios; *ADH_3*, alcohol dehydrogenase 3; C, common allele; V, variant allele; *$ALDH_2$*, aldehyde dehydrogenase 2; *CYP2E1*, cytochrome P450 2E1.
* ORs were adjusted for age, sex, smoking amounts (pack-years), and alcohol amounts (ethanol: mg per day).
† $P < .05$.

shown in Table 3. Drinking was classified as none, light (31.6 g per day) or heavy (>31.6 g per day). When adjusted for age, sex, and smoking amounts, drinking imposed a significantly greater risk of lung cancer occurrence. The ORs for the light drinkers and heavy drinkers, compared with nondrinkers, were 1.76 and 1.95, respectively (P for trend = .012). Thus, the risk of lung cancer increases as the amount alcohol consumed increases.

ORs for developing lung cancer in association with the *ADH_3*, *$ALDH_2$*, and *CYP2E1* genotypes also are presented in Table 3. Similar to what was observed in all participants taken together, an increased risk for developing lung cancer also was observed among individuals who were homozygous for the common allele ADH_3^{1-1}. However, because there were too few *ADH_3* variant allele carriers to analyze any association between alcohol consumption and lung cancer risk for this allele, it was inappropriate to compare the ADH_3^2 and ADH_3^{1-1} genotypes.

The adjusted OR for the $ALDH_2^{1-1}$ group was 0.75 (95% CI, 0.39–1.42) in light drinkers and 0.46 (95% CI, 0.20–0.99) in heavy drinkers. In contrast, individuals with the $ALDH_2^2$ allele had a significantly greater risk of lung cancer; light drinkers had a 3.6-fold increased risk, and heavy drinkers had a 6.2-fold increased risk compared with nondrinkers (P for trend < .0001). These results indicate that, in individuals with the *$ALDH_2$* variant allele, continuous alcohol consumption is a strong risk factor for lung cancer.

The OR for the *CYP2E1* c1/c1 genotype was 1.81 (95% CI, 0.97–3.38) for light drinkers and 1.67 (95% CI, 0.86–3.21) for heavy drinkers. For individuals with the *CYP2E1* c2 allele, the OR was 1.74 (95% CI, 0.91–3.35) for light drinkers and 2.56 (95% CI, 1.16–5.65) for heavy drinkers (P for trend = .005). These results may indicate that individuals with the *CYP2E1* variant allele are in a high-risk group for lung cancer in heavy drinkers.

It must be emphasized that, because of differences in distribution according to sex between cases and controls, we analyzed relative risks only in men (Table 4). For baseline characteristics among men, higher consumption of alcohol and more smoking were observed, as expected. Regarding associations between alcohol consumption and lung cancer risk, drinking was associated with an increased risk of developing lung cancer in all participants. The adjusted OR for the light and drinkers, compared with nondrinkers, was 6.54 (95% CI, 3.13–13.7) and 6.58 (95% CI, 3.28–13.2), respectively. However, in individuals with active $ALDH_2^{1-1}$ genotypes, there was no association between alcohol consumption and lung cancer risk. In individuals with the inactive $ALDH_2^2$ alleles, the risk for lung cancer was 6.8-fold (95% CI, 2.72–17.1) for light drinkers and 9.3-fold (95% CI, 3.72–23.4) for heavy drinkers compared with nondrinkers (P for trend <.0001). The risk in men who were heavy drinkers was much greater compared with women and those who carried the active $ALDH_2^{1-1}$ genotype.

In individuals with the c2 allele, the risk of lung cancer for light drinkers (OR, 8.31; 95% CI, 2.67–25.9) and for heavy drinkers (OR, 9.93; 95% CI, 3.39–29.1) was increased compared with individuals who were homozygous for the *CYP2E1* c1 allele and compared with the risks in all men. However, it should be noted that, because of the low incidence of homozygosity for variant allele in the control group, statistical power was limited in this instance. Similar assessments also were made in women, but no significant associations between any genotype and lung cancer risk were observed (data not shown).

Table 5 shows the distribution of the *ADH_3*, *$ALDH_2$*, and *CYP2E1* genotypes according to tumor histology. The frequency of the ADH_3^2 allele for all histologic types was similar to the frequency observed in controls. The frequency of the $ALDH_2^2$ allele for squamous cell carcinomas, small cell carci-

TABLE 3
Odds Ratios of Developing Lung Cancer for Alcohol Dehydrogenase 3, Aldehyde Dehydrogenase 2, and Cytochrome P450 2E1 Genotypes Stratified by Drinking Amounts

			Drinkers						
	Nondrinkers		31.6 g/Day			>31.6 g/Day			
Genotype	No.*	Reference	No.*	OR (95% CI)†	P	No.*	OR (95% CI)†	P	P for trend‡
All	120/119	1	154/65	1.76 (1.12–2.75)	.014	231/72	1.95 (1.19–3.21)	.0085	.012
ADH_3									
C/C	112/105	1	141/60	1.59 (0.99–2.55)	.054	206/62	1.88 (1.10–3.21)	.02	.025
C/V and V/V	8/14	1	13/5	4.31 (0.912–20.38)	.065	25/10	3.28 (0.742–14.55)	.12	.17
$ALDH_2$									
C/C	57/41	1	99/39	0.75 (0.39–1.42)	.37	163/54	0.46 (0.2– 0.99)	.049	.03
C/V and V/V	63/78	1	55/26	3.63 (1.76–7.46)	.0005	68/18	6.15 (2.77–13.65)	<.0001	<.0001
CYP2E1									
C/C	72/61	1	95/36	1.81 (0.97–3.38)	.061	133/50	1.67 (0.86–3.21)	.13	.31
C/V and V/V	48/58	1	59/29	1.74 (0.91–3.35)	.097	98/22	2.56 (1.16–5.65)	.02	.005

OR indicates odds ratio; 95% CI, 95% confidence interval; *ADH_3*, alcohol dehydrogenase 3; C, common allele; V, variant allele; *$ALDH_2$*, aldehyde dehydrogenase 2; *CYP2E1*, cytochrome P450 2E1.

* The number of cases/number of controls.

† ORs were adjusted for age, sex, and smoking amount (pack-years).

‡ The Mantel extension test.

TABLE 4
Odds Ratios of Developing Lung Cancer for Alcohol Dehydrogenase 3, Aldehyde Dehydrogenase 2, and Cytochrome P450 2E1 Genotypes Stratified by Drinking Amounts Among Men

			Drinkers						
	Nondrinkers		31.6 g/Day			>31.6 g/Day			
Genotype	No.*	Reference	No.*	OR (95% CI)†	P	No.*	OR (95% CI)†	P	P for Trend‡
All	17/31	1	120/36	6.54 (3.13–13.65)	<.0001	223/59	6.58 (3.28–13.22)	.0001	<.0001
ADH_3									
C/C	15/27	1	110/34	6.14 (2.83–13.29)	<.0001	201/49	7.27 (3.44–15.36)	.0001	<.0001
C/V and V/V	2/4	1	10/2	23.31(1.41–286.0)	.028	22/10	5.43 (0.63–47.09)	.12	.47
$ALDH_2$									
C/C	5/2	1	72/16	1.47 (0.25–8.67)	.67	158/42	1.10 (0.20–6.23)	.91	.29
C/V and V/V	12/29	1	48/20	6.82 (2.72–17.13)	<.0001	65/17	9.33 (3.72–23.39)	.0001	<.0001
CYP2E1									
C/C	10/14	1	77/24	5.22 (1.95–13.94)	.0003	125/42	4.71 (1.85–12.05)	.0012	.08
C/V and V/V	7/17	1	43/12	8.31 (2.67–25.89)	.0001	98/17	9.93 (3.39–29.09)	.0001	<.0001

OR indicates odds ratio; 95% CI, 95% confidence interval; *ADH_3*, alcohol dehydrogenase 3; C, common allele; V, variant allele; *$ALDH_2$*, aldehyde dehydrogenase 2; *CYP2E1*, cytochrome P450 2E1.

* Values shown represent the number of cases/number of controls.

† OR were adjusted for age, sex, and smoking history (pack-years).

‡ Mantel extension test.

nomas, and other histologic types was similar to that observed in controls. However, the *$ALDH_2^2$* allele was significantly less common in patients with adenocarcinomas than in controls (36.1% vs 47.7%; $P = .018$). In contrast, the *CYP2E1* c2/c2 genotype was more common in patients with adenocarcinomas (5.8%) and small cell carcinomas (9.8%) than in controls (1.2%).

In this study, we observed that alcohol consumption was an independent risk factor for lung cancer after adjusting for the influence of smoking (P for trend = .012). Although we assumed that individuals who had the *ADH_3^{1-1}* genotype were at greater risk for lung cancer compared with individuals who had the *ADH_3^2* allele, there was no evidence of an association between lung cancer and the *ADH_3* genotype

TABLE 5
Distribution of Alcohol Dehydrogenase 3, Aldehyde Dehydrogenase 2, and Cytochrome P450 2E1 Genotype According to Histologic Findings

	No. (%)				
		Histologic type			
Genotype	Control group (n = 256)	Adenocarcinoma (n = 330)	Squamous cell (n = 100)	Small cell (n = 51)	Other (n = 24)
ADH_3					
C/C	227 (88.3)	297 (90)	91 (91)	48 (94.1)	23 (95.8)
C/V	29 (11.7)	31 (9.4)	9 (9)	3 (5.9)	1 (4.2)
V/V	0 (0)	2 (0.6)	0 (0)	0 (0)	0 (0)
P for difference*		.35	.52	.25	.28
$ALDH_2$					
C/C	134 (52.3)	211 (63.9)	54 (54)	36 (70.6)	18 (75)
C/V	108 (42.2)	104 (31.5)	45 (45)	13 (25.5)	6 (25)
V/V	14 (5.5)	15 (4.6)	1 (1)	2 (3.9)	0 (0)
P for difference*		.018	.17	.056	.083
CYP2E1					
C/C	147 (57.4)	197 (59.7)	59 (59)	31 (60.8)	13 (54.2)
C/V	106 (41.4)	114 (34.6)	37 (37)	15 (29.4)	9 (37.5)
V/V	3 (1.2)	19 (5.8)	4 (4)	5 (9.8)	2 (8.3)
P for difference*		.0067	.19	.001	.04

ADH_3 indicates alcohol dehydrogenase 3; C, common allele; V, variant allele; $ALDH_2$, aldehyde dehydrogenase 2; *CYP2E1C*, cytochrome P450 2E1.
* Chi-square test for comparison with controls.

in any analysis. Because the enzyme activity of $ALDH_2^2$ is extremely low, acetaldehyde accumulates after alcohol intake. We could not demonstrate any association of $ALDH_2$ genotypes with the risk of lung cancer after adjusting for smoking and the amount of alcohol consumed. However, we observed that individuals who had the $ALDH_2^2$ allele were at a significantly greater risk of lung cancer because of alcohol consumption, although there was a significant trend for lower levels of alcohol consumption in individuals who had the $ALDH_2^{1-1}$ genotype (P for trend = .03). We hypothesized that not only the differences in blood acetaldehyde concentrations but also the differences in enzyme activity on tobacco-specific carcinogens contribute to carcinogenesis. However, we produced no evidence that lung cancer risk is related to possession of the *CYP2E1* c2/c2 genotype or that the *CYP2E1* genotype modifies lung cancer susceptibility related to alcohol intake.

DISCUSSION

The control population for this study was recruited from the visitors to the NCCH-E. The majority of patients had false-positive chest x-rays at their annual check-up and had normal chest computed tomography scans, and they were not suffering from any respiratory illness. Furthermore, their family medical histories were similar to those expected in the ordinary Japanese population, although the number of current smokers among both men (42.9%) and women (6.9%) may have been somewhat lower than the average (46.8% and 11.1%, respectively, for 2003 according to the Announcement of the Ministry of Health, Labor, and Welfare). For these reasons, we believe that our control group was not at greater risk of cancer occurrence compared with the regular Japanese population. Moreover, it was not necessary to take into account any biases stemming from the selective inclusion only of consenting participants, because the great majority of both patients and controls agreed to participate in the study.

The data from the control group showed that individuals who had the $ALDH_2$ wild-type genotype consumed more alcohol than individuals who had the variant genotype. This may suggest that genetic polymorphisms of alcohol-metabolizing enzymes influence drinking habits, because consumption may be limited by the unpleasant reactions caused by the accumulation of acetaldehyde in individuals with $ALDH_2$ variant genotypes. Nonetheless, habitual drinking can increase consumption because of increased microsomal acetaldehyde-oxidizing system activation, further promoting the oxidation of acetaldehyde. The association between drinking habit and ADH_3 and *CYP2E1* genotypes remains uncertain.

Regarding correlations between smoking and drinking habits, the coexistence of smoking and

drinking increased the risk of lung cancer compared with nondrinkers who never smoked, particularly the OR for heavy smokers (>37 pack-years) and drinkers, which was 8.4 (95% CI, 2.3–30.2; $P = .0012$) in the light drinkers and 7.0 (95% CI, 2.1–23.4) in the heavy drinkers (data not shown).

The involvement of alcohol in lung cancer etiology has been controversial, although many epidemiologic studies have suggested positive associations between different parameters of alcohol consumption and lung cancer risk. In the current study, we have demonstrated that drinking is a strong risk factor for lung cancer that is dose-dependent and is stronger in men than in women. This same tendency was observed even in the genotype analysis, but none of the results indicated a significant association between lung cancer and drinking in women. Furthermore, no associations were observed between peripheral lung adenocarcinoma, drinking, and genotypes of alcohol metabolite-related enzymes in women.

The question of ethnicity in the distribution of the polymorphisms of these alcohol metabolite-related enzyme genes always must be considered. The ADH_3^2 allele is present in almost 60% of whites but is far more rare (5–10%) in Japanese. In contrast, the $ALDH_2^2$ allele is found only in Asians. The *CYP2E1* c2 allele is present in 35% to 56% of Japanese and Chinese, and in 2% to 5% of whites. In the current study, the frequency of variant alleles of each polymorphism was 9.9% for ADH_3, 40.5% for $ALDH_2$, and 41.3% for *CYP2E1*. This is consistent with previous studies in Japanese and other Asians.

We observed that the risk for lung cancer was increased significantly by alcohol consumption in a dose-dependent fashion in individuals with the $ALDH_2^2$ alleles. Previously, some Japanese studies also showed a strong genetic and environmental interaction between $ALDH_2^2$ and alcohol intake for the risk of developing esophageal and upper aerodigestive tract cancer.[18–21] In contrast, for individuals with the $ALDH_2^{1-1}$ genotype, there was an inverse association between alcohol consumption and the risk of lung cancer. These results suggest that increased acetaldehyde concentrations from a reduction in acetaldehyde oxidation caused by the presence of the $ALDH_2^2$ allele contribute to the development of lung cancer. Significantly higher blood acetaldehyde concentrations after drinking in individuals with the ADH_3^1 or $ALDH_2^2$ allele have been reported compared with the concentrations in individuals who lacked these alleles,[11,29] and it has been demonstrated that breath acetaldehyde levels are proportional to blood acetaldehyde levels. Indeed, Muto et al.[30] and Jones[31] observed significantly higher acetaldehyde levels in the breath from individuals with the $ALDH_2^2$ allele than in those without that allele. Therefore, exposure to higher concentrations of acetaldehyde in the lower respiratory tract may play a critical role in alcohol-related carcinogenesis. Regarding the influence of smoking, when adjusted for age, sex, and amount of alcohol consumed, the risks for developing lung cancer in current smokers were 1.5-fold greater for those with the inactive $ALDH_2$ genotype (data not shown) compared with nonsmokers. The lung cancer risk for individuals with the $ALDH_2^2$ allele was not increased further by smoking.

Although there have been some reports of a significant association between the ADH_3^1 allele and some types of upper aerodigestive tract cancer, this association has been controversial.[16,17,32–34] We failed to observe an association between ADH_3 gene polymorphisms and the development of lung cancer, most likely because of the limited statistical power from the low frequency of the variant allele in the Japanese population.

Several investigations[24,31,35,36] have indicated that the *CYP2E1* c2 allele is associated with susceptibility to some types of cancer. However, other investigators reported that carriers of the c2 allele had decreased susceptibility to a number of cancers[25–27,37] and reported no association between *CYP2E1* genotypes and cancer.[23,28,38] Discrepancies among these results may be caused by several factors, including differences in study design, sample size, and the populations' ethnicity. Statistical power usually is very limited in studies of the white population because of the extreme rarity of variant genotypes. Although *CYP2E1* enzyme activity is induced by certain chemicals, such as ethanol, large interindividual variation has been observed in its constitutive activity as well as after induction. Watanabe et al.[39] and Hayashi et al.[15] reported that the *Rsa*I variant c2 allele produced higher enzyme activity than the c1/c1 genotype in Japanese individuals, although this finding is itself controversial.[40–42] Highly activated *CYP2E1* induced by alcohol may play a more important role in the metabolic activation of several tobacco-specific procarcinogens, including various nitrosamines. It has been suggested that these low-molecular-weight carcinogens are associated with the development of peripheral adenocarcinoma. This finding is consistent with the results from our analysis of *CYP2E1* presented in Table 5. However, the *CYP2E1* c2/c2 genotype is not in Hardy-Weinberg equilibrium in the control population, the observed frequencies most likely are underestimates, and these findings of

an association with histologic type most likely are false-positive results. In our analysis of $ALDH_2$, the incidence of adenocarcinoma was high among individuals who had the wild-type genotype. Although a high incidence of squamous cell carcinoma was not observed, this result may imply that carcinogenesis caused by acetaldehyde occurs more in cancers other than adenocarcinoma as well as in esophageal and upper aerodigestive tract cancers.

A previous hospital-based study that was conducted in Japan failed to identify any association between the *RsaI* polymorphism and lung cancer, even when the analysis was stratified according to different histologic type.[28] A more recent study indicated that there was a significant decrease in overall lung cancer risk associated with the possession of at least 1 copy of the *CYP2E1 RsaI* variant allele, whereas there was no association between the *CYP2E1 RsaI* polymorphism and the histologic type of lung cancer.[27] However, none of the previous studies had adjusted for risk according to alcohol consumption levels, which strongly influence the activity of this enzyme. In the current study, we demonstrated that there is a difference between individuals who have the *CYP2E1 RsaI* c2/c2 genotype compared with individuals who have the common c1/c1 genotype, with an adjusted OR of 4.66 (95% CI, 1.36–16.0) for the former group. Because of the low incidence of homozygosity in controls, the genotype distribution was not in Hardy-Weinberg equilibrium in our control population. The increased lung cancer risk among individuals with the *CYP2E1* c2/c2 genotype likely was a false-positive result.

A correlation between the amount of alcohol consumed, genetic polymorphisms in the alcohol metabolite-related enzymes, and the stage of lung cancer was not observed in the current study, and we could not confirm that these factors were related to the aggressiveness of lung cancer. Furthermore, no associations were identified between the location of the primary cancer, the amount of alcohol consumed, and the genotype of these enzymes or between the risk for lung cancer and the type of alcoholic beverage consumed.

In summary, we report a significant association between amounts of alcohol consumed and susceptibility to lung cancer and that the risk of lung cancer in individuals with $ALDH_2$ variant alleles, but not with ADH_3 or *CYP2E1* variant alleles, apparently was enhanced more by alcohol intake than in individuals with common genotypes. Moreover, to our knowledge, this is the first report documenting an association between lung cancer and genetic polymorphisms of alcohol metabolite-related enzymes. Because the sample size was relatively small for the investigation of effects stratified by each genotype, the current findings should be confirmed in large-scale studies with greater statistical power.

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Phase II trial of carboplatin and paclitaxel in non-small cell lung cancer patients previously treated with chemotherapy

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Summary The purpose of this phase II trial was to evaluate the efficacy and toxicity of carboplatin plus paclitaxel in the treatment of advanced non-small cell lung cancer (NSCLC) previously treated with chemotherapy. Patients with a performance status (PS) of 0 or 1 who had received one or two previous chemotherapy regimens for advanced NSCLC were eligible. Paclitaxel 200 mg/m^2 was infused over 3 h and followed by carboplatin (area under the curve 6) infusion over 1 h, once every 3 weeks. Thirty patients were enrolled. A complete response was observed in 1 patient and a partial response in 10 patients, for an overall response rate of 36.7%. The median time to progression was 5.3 months. The median survival time was 9.9 months, and the 1-year survival rate was 47%. Hematological toxicity in the form of grade 3/4 neutropenia occurred in 54%, but grade 3 febrile neutropenia developed in only 3%. Non-hematological grade 3 toxicities were less frequent. There were no treatment-related deaths. The combination of carboplatin plus paclitaxel is an active and well-tolerated regimen for the treatment of NSCLC patients who have previously been treated with chemotherapy and have a good PS.

1. Introduction

Lung cancer remains a major cause of death from cancer in many countries. More than half of all patients diagnosed with non-small cell lung cancer (NSCLC) have advanced stage IIIB or IV disease at presentation, and patients with advanced NSCLC are candidates for systemic chemotherapy. Platinum-based chemotherapy is considered the standard first-line treatment for patients with advanced NSCLC, and prolongs survival, palliates symptoms, and improves quality of life [1,2]. Many patients with good performance status (PS) when progression occurs after first-line chemotherapy are suitable candidates for second-line chemotherapy [3].

The taxanes are an important class of new agents for the treatment of advanced NSCLC. Paclitaxel, in combination with carboplatin, is the most common regimen

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used as first-line chemotherapy for advanced NSCLC, and this combination has a more favorable toxicity profile and is more convenient to administer than other platinum-based regimens [4,5]. Docetaxel has been investigated more extensively than any other agent for second-line treatment of advanced NSCLC, and the results of two randomized phase III trials of second-line chemotherapy in patients with advanced NSCLC demonstrated that docetaxel monotherapy significantly improved survival compared with best supportive care or other single agents (vinorelbine or ifosfamide) [6,7].

Belani et al. recently reported that results of a phase III trial comparing a carboplatin plus paclitaxel regimen with a cisplatin plus etoposide regimen for first-line treatment of advanced NSCLC [8]. Carboplatin plus paclitaxel yielded a higher response rate (23% versus 15%), time to progression (121 days versus 111 days), and overall quality of life benefit than cisplatin plus etoposide, but the median survival time was better in the cisplatin plus etoposide arm than in the carboplatin plus paclitaxel arm (274 days and 233 days, respectively [$P=0.086$]). The authors reported that a substantially greater proportion of patients in the cisplatin plus etoposide arm received second-line chemotherapy with a taxane-containing regimen than in the carboplatin plus paclitaxel arm, and suggested that treatment with taxanes in a second-line setting may have had an impact on the survival in their study. Remarkably, more than half of the regimens that were used in the second-line setting of their study consisted of paclitaxel alone or carboplatin plus paclitaxel, not docetaxel. While the efficacy of paclitaxel-containing regimens as first-line chemotherapy for advanced NSCLC has been established in many randomized phase III trials [9], the data on the efficacy of paclitaxel-containing regimens in second-line settings are limited [10,11].

Based these considerations we conducted a phase II trial to evaluate the efficacy and toxicity of carboplatin plus paclitaxel in the treatment of advanced NSCLC previously treated with chemotherapy.

2. Patients and methods

2.1. Eligibility criteria

The inclusion criteria were: pathologically confirmed advanced NSCLC patients with measurable disease who had received one or two previous chemotherapy regimens for their disease. Patients were required to submit evidence of failure of prior chemotherapy. Patients who were previously treated with carboplatin or paclitaxel were excluded if the best response was progressive disease (PD). Patients who had received prior radiotherapy were eligible provided that at least 30 days had elapsed between the completion of radiotherapy and entry into the study. Patients were also required to be 20–75 years of age, have an Eastern Cooperative Oncology Group PS of 0 or 1, and have adequate organ function as indicated by the following parameters: absolute neutrophil count $\geq 1500\,mm^{-3}$, platelet count $\geq 100{,}000\,mm^{-3}$, hemoglobin $\geq 9.0\,g/dl$, AST and ALT $\leq 2.0\times$ the institutional upper normal limits, total bilirubin $\leq 1.5\,mg/dl$, creatinine $\leq 1.5\,mg/dl$, $PaO_2 \geq 65$ Torr. Exclusion criteria were: uncontrolled pleural or pericardial effusion, active concomitant malignancy, prior irradiation to areas encompassing more than a third of the pelvis plus spine, active infection, myocardial insufficiency or myocardial infarction within the preceding 6 months, uncontrolled diabetes mellitus or hypertension, any other condition that could compromise protocol compliance, pregnancy and/or breast-feeding. All patients were required to provide written informed consent before entry into the study. The study was approved by the institutional review board of our institution.

2.2. Treatment plan

Treatment was started within a week of entry into the study. Patients received paclitaxel $200\,mg/m^2$ diluted in 500 ml of 0.9% saline as a 3-h intravenous infusion followed by carboplatin (area under the curve [AUC] 6; Calvert formula) diluted in 250 ml of 5% glucose as a 1-h intravenous infusion, every 3 weeks. All patients were premedicated with dexamethasone (24 mg i.v.), famotidine (20 mg i.v.), and diphenhydramine (50 mg orally) 30 min before the paclitaxel infusion to prevent a hypersensitivity reaction. A 5-HT3-receptor antagonist was intravenously administered as an antiemetic before carboplatin. Therapy was continued for at least two cycles unless the patient experienced unacceptable toxicity or had PD. The maximum number of cycles of chemotherapy was six. In the event of grade 4 leukopenia or thrombocytopenia or of grade 3 neutropenic fever, the dose of carboplatin and paclitaxel was reduced to AUC 5 and $175\,mg/m^2$, respectively, in the following cycle of chemotherapy. The next cycle of chemotherapy was started if the neutrophil count was $\geq 1500\,mm^{-3}$, the platelet count $\geq 100{,}000\,mm^{-3}$, AST and ALT $\leq 100\,IU/l$, total bilirubin $\leq 2.0\,mg/dl$, creatinine $\leq 1.5\,mg/dl$, PS 0 or 1, and the patient was afebrile.

Pretreatment evaluation included a medical history, a physical examination, vital signs, height and body weight, PS, complete blood count, biochemical studies, arterial blood gas analysis, electrocardiogram, chest radiograph and computed tomography scan (CT), abdominal ultrasound or CT, and brain magnetic resonance imaging or CT. A complete blood count, biochemical studies, and chest radiograph were performed weekly during the first cycle of chemotherapy, and 2 weekly starting with the second cycle.

2.3. Response and toxicity assessment

Objective tumor response was assessed as complete response (CR), partial response (PR), stable disease ≥ 8 weeks (SD), or PD according to the Response Evaluation Criteria in Solid Tumors. Measurable lesions were defined as lesions whose longest diameter was ≥ 2 cm. Imaging studies were repeated every 4 weeks until the objective tumor response was confirmed. All responses were reviewed by an independent radiologist. Toxicity was graded using National Cancer Institute-Common Toxicity Criteria version 2.0.

2.4. Statistical analysis

The primary endpoint of this study was the response rate, defined as the proportion of patients whose best response was CR or PR among all enrolled patients in the intent-to-treat analysis. The secondary end points were toxicity and overall and progression-free survival (PFS) from the date of enrollment in this study.

According to Simon's minimax two-stage phase II study design, the treatment program was designed for a minimal response rate of 5% and to provide a significance level of 0.05 with a statistical power of 80% in assessing the activity of the regimen according to a 20% response rate. The upper limit for first-stage drug rejection was no response in 13 evaluable patients. The upper limit for second-stage drug rejection was three responses in 27 evaluable patients. Overall survival time was defined as the interval between enrollment in this study and death or the most recent follow-up visit. PFS was defined as the interval between enrollment in this study and the first documented PD, death, or the most recent follow-up visit. Survival was estimated by the Kaplan–Meier analysis method. All comparisons between proportions were performed by Fisher's exact test.

3. Results

3.1. Patient characteristics

Between October 2002 and November 2003, 30 patients were enrolled in this study, and their characteristics are shown in Table 1. Twenty-six (87%) patients were men, and 21 (70%) patients had adenocarcinoma. Median age was 60 years. The majority of the patients (93%) had received prior platinum-based chemotherapy, and seven (23%) patients had received two prior chemotherapy regimens. The platinum-based chemotherapy regimens that had been used were: cisplatin plus vinorelbine ($n=26$), cisplatin plus gemcitabine ($n=1$), and carboplatin plus gemcitabine ($n=1$). There were 15 (50%) responders to any of the prior chemotherapy regimens and 12 of them had experienced a response (CR/PR) to cisplatin-based chemotherapy. Twenty-one (70%) patients had a treatment-free interval of 3 or more months since the final dose of the prior chemotherapy regimen.

A total of 94 cycles of chemotherapy were administered, and the median number of cycles per patient was three (range, 1–6). Four patients had received only one cycle of treatment either because of toxicity (two patients, grade 3 rash), the patient's refusal (one patient), or PD (one patient).

3.2. Response and survival

Two patients were not evaluable for response because the protocol treatment had been terminated because of toxicity (grade 3 rash) during the first cycle of chemotherapy, and they subsequently received further chemotherapy without PD. There was 1 CR and 10 PRs among the 30 patients, and the objective response rate in the intent-to-treat analysis was 36.7% (95% confidence interval [CI], 19.9–56.1%) (Table 2). Treatment outcomes of all patients are listed in Table 3. The response rate of patients who experienced a response (CR/PR) to prior cisplatin-based chemotherapy was 43% (6/14), as opposed to 23% (3/13) among the non-response patients ($P=0.41$). The response rate of the patients who had received one prior chemotherapy regimen was 39% (9/23), as opposed to 28% (2/7) among the patients who had received two regimens ($P>0.99$). According to the treatment-free interval since the final dose of the prior chemotherapy regimen, the response rate of patients whose interval was 3 months or more was 33% (7/21), com-

Table 1 Patient characteristics

Characteristic	No. of patients (%)
Patients enrolled	30
Sex	
Male	26
Female	4
Age, years	
Median	60
Range	39–75
ECOG performance status	
0	7
1	23
Stage	
IIIB	11
IV	19
Histology	
Adenocarcinoma	21
Squamous cell carcinoma	7
Large cell carcnioma	2
Prior treatment	
Platinum-based chemotherapy	28 (93)
Docetaxel	5 (16)
Chest radiotherapy	4 (13)
No. of prior chemotherapy regimens	
1	23
2	7

Table 2 Treatment efficacy ($n=30$)

	No. of patients	%
Response		
Overall response rate	11	36.7
Complete response	1	3.3
Partial response	10	33.3
Stable disease	12	40
Progressive disease	5	16.7
Not evaluable	2	6.7
Survival		
Median (months)	9.9	
1 year (%)	47	
Progression-free survival		
Median (months)	5.3	

Table 3 Treatment outcomes of all patients

Patient No.	Prior first-line therapy		Prior second-line therapy		Time from last therapy (months)	CBDCA + PTX, best response	PFS (months)	Survival (months)
	Regimen	Best response	Regimen	Best response				
1	CDDP + VNR	SD	DOC	PD	1.8	SD	1.4	25.2
2	CBDCA + GEM	NE	Gefitinib	PD	0.8	PR	3.8	8.8
3	CDDP + VNR	SD	–		6.8	SD	7.6	18.1
4	CDDP + GEM	PR	–		9.5	PR	7.5	33.8+
5	CDDP + VNR	SD	–		4.8	SD	2.8	7.0
6	CDDP + VNR + DOC + RT	PR	–		6.0	PR	8.0	21.6
7	GEM + VNR	SD	–		23.0	PD	1.2	7.8
8	CDDP + VNR + RT	PR	–		13.6	SD	6.7	25.0+
9	CDDP + VNR	SD	–		5.0	SD	2.1	3.7
10	CDDP + VNR	SD	–		5.0	PD	1.2	6.7
11	CDDP + VNR	PR	–		8.9	NE	1.1	3.3
12	CDDP + VNR	SD	Gefitinib	CR	1.9	SD	6.3	6.3
13	CDDP + VNR	PR	–		5.4	NE	1.0	13.4
14	CDDP + VNR	PR	–		1.7	SD	4.8	5.7
15	CDDP + VNR + RT	PR	–		9.3	SD	5.0	15.7
16	CDDP + VNR	SD	–		2.8	PR	3.7	15.8
17	CDDP + VNR	SD	DOC + GEM	SD	3.8	SD	5.3	21.6+
18	CDDP + VNR + DOC + RT	PR	–		3.9	SD	4.5	9.0
19	CDDP + VNR	PR	–		12.9	PR	9.4	16.0
20	CDDP + VNR	PR	–		11.5	CR	24.8+	24.8
21	CDDP + VNR	PD	–		1.1	PR	9.2	23.6+
22	CDDP + VNR	SD	DOC	SD	4.5	PD	2.3	5.5
23	Gefitinib	SD	–		0.9	PR	8.8	12.7
24	CDDP + VNR	PR	–		11.1	PR	5.3	10.2
25	CDDP + VNR	PR	Gefitinib	PR	4.4	PR	5.5	9.9
26	CDDP + VNR	NE	–		11.7	PR	7.0	12.2
27	CDDP + VNR	PR	–		5.4	SD	6.2	9.4
28	CDDP + VNR	SD	–		0.8	PD	1.4	2.5
29	CDDP + VNR	PR	–		4.4	PD	0.2	8.4
30	Gefitinib	PD	CDDP + VNR	PD	0.9	SD	3.1	3.3

CBDCA, carboplatin; PTX, paclitaxel; PFS, progression-free survival; CDDP, cisplatin; VNR, vinorelbine; GEM, gemcitabine; DOC, docetaxel; RT, chest radiotherapy; SD, stable disease; NE, not evaluable; PR, partial response; PD, progressive disease; CR, complete response.