Table 4. Summary of Survival and Response

Survival/ Response	Before Amrubicin Dose Revision		After Amrubicin Dose Revision	
	IP Arm (n = 97)	AP Arm (n = 94)	IP Arm (n = 45)	AP Arm (n = 48)
ORR				
No.	72 of 97	70 of 93*	30 of 44*	39 of 47*
%	74.2	75.3	68.2	83.0
PFS				
Median	6.0	5.3	5.4	5.0
95% CI	5.5 to 6.6	4.9 to 5.7	4.8 to 6.4	4.7 to 5.7
OS				
Median	17.7	14.9	18.0	15.6
95% CI	13.9 to 22.1	13.1 to 16.8	12.2 to NE	12.4 to 20.7

Abbreviations: AP, amrubicin plus cisplatin; IP, irinotecan plus cisplatin; NE, not estimable; ORR, overall response rate; OS, overall survival; PFS, progression-free survival.
*One patient excluded because of no measurable lesions.

DISCUSSION

The outcomes in our study did not satisfy the primary end point, showing OS in the AP arm to be significantly inferior to that in the IP arm. The MST for AP was favorable (15 months), reproducing the outcomes obtained in the phase I/II study. The MST for IP was approximately 5 months beyond that shown in JCOG 9511. AP may simply be inferior to IP in the first line in that the platinum–topoisomerase I inhibitor partnership between cisplatin and irinotecan may be more synergistic. Although there was only a 0.5-month difference in median PFS, the IP arm displayed a much longer MST (ie, postprogression survival of IP arm was longer); two conceivable reasons for this are the advancements in support therapy and the influence of poststudy treatment.

Table 5. Poststudy Therapy

Chemotherapy	Second Line		Third Line	
	IP Arm (n = 127)	AP Arm (n = 122)	IP Arm (n = 84)	AP Arm (n = 87)
IP	7	10	0	3
Irinotecan	3	24	7	19
Cisplatin, irinotecan, and etoposide	10	13	2	2
Carboplatin plus irinotecan	1	4	0	9
Irinotecan plus other	0	1	3	4
Amrubicin	61	2	34	12
AP	0	4	0	1
Carboplatin plus amrubicin	1	0	0	0
Cisplatin plus etoposide	9	11	4	1
Carboplatin plus etoposide	22	29	25	24
Etoposide	1	0	0	0
Carboplatin, etoposide, and other	0	1	0	0
Topotecan	12	23	6	5
Carboplatin	0	0	0	1
Carboplatin plus other	0	0	1	4
Other	0	0	2	2

Abbreviations: AP, amrubicin plus cisplatin; IP, irinotecan plus cisplatin.

The incidence of the greatest toxicity concern in JCOG 9511, grade 3 to 4 diarrhea, was 7.7% in this study (16.0% in JCOG 9511). The incidence of diarrhea was lower, which was most likely the result of advances in support therapy. That said, the impact of poststudy treatment should garner the most attention as a reason for the inability to demonstrate survival extension or noninferiority in our study.

Analysis of subsequent therapies administered in this study revealed that ultimately, two thirds of all patients in the IP arm received single-agent amrubicin as a subsequent therapy. There was no difference between the two arms in terms of the percentage of patients who received subsequent therapies, suggesting that amrubicin, used in a large percentage of patients in the IP arm as postprotocol therapy, contributed to an extension in OS.

Several studies have examined the use of amrubicin as secondary treatment for SCLC.[15-18] A phase II study by Inoue et al[15] comparing amrubicin with topotecan, considered to be standard secondary treatment, indicated the possibility that amrubicin might be superior to topotecan. A phase III study conducted by Jotte et al[16] did not show any significant difference between topotecan and amrubicin as second-line chemotherapy in terms of OS (MST: amrubicin, 9.2 months; topotecan, 9.9 months; HR, 0.89; 95% CI, 0.73 to 1.06); however, outcomes with amrubicin were significantly better in terms of RR and PFS, and OS was better in subanalysis only among patients experiencing refractory relapse (MST: amrubicin, 6.2 months; topotecan, 5.7 months; HR, 0.77; 95% CI, 0.79 to 1.0; $P = .047$). Although topotecan is the most evidence-based second-line therapy for SCLC,[19,20] amrubicin has come into widespread use in Japan as a result of many reports on its use among Japanese patients (ie, RR and PFS compare favorably, and survival is quite respectable).

Amrubicin is a topoisomerase II inhibitor, suggesting that it may not be effective in patients for whom etoposide (also topisomerase II inhibitor) or EP has failed. Irinotecan is a topoisomerase I inhibitor, and amrubicin may be effective in those for whom IP has failed (unlike in those for whom EP has failed). Accordingly, the possibility remains that the frequent use of amrubicin in poststudy treatment may have extended survival even beyond that expected. This may be a reason why IP therapy showed significantly better survival than AP therapy in our study. In this phase III trial, AP proved to be inferior to IP, but the results seen here do not negate the activity of this agent in SCLC and perhaps underscore the particular value of amrubicin as second- or third-line therapy in this setting.

The AP arm showed reproducible, favorable survival in the form of 15-month MST and noninferiority to EP in a phase III study conducted in China (MST: AP, 11.79 months; EP, 10.28 months),[21] suggesting that AP is rather effective. However, considering that hematotoxicity and FN, even after reduction of the dose to 35 mg/m^2, were relatively serious, and considering the excellent effect of amrubicin monotherapy in relapse treatment, we are unable to recommend AP as standard first-line therapy for ED-SCLC. Therefore, IP therapy showed favorable OS and toxicity profile, indicating, as expected, its continuing presence as one of the standard first-line therapies for ED-SCLC in Japan.

AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST

Although all authors completed the disclosure declaration, the following author(s) and/or an author's immediate family member(s) indicated a financial or other interest that is relevant to the subject matter under consideration in this article. Certain relationships marked with a "U" are those for which no compensation was received; those relationships marked with a "C" were compensated. For a detailed description of the disclosure categories, or for more information about ASCO's conflict of interest policy, please refer to the Author Disclosure Declaration and the Disclosures of Potential Conflicts of Interest section in Information for Contributors.

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GLOSSARY TERMS

Topoisomerase I: An enzyme that acts on the topology of native DNA by changing the supercoiled structure of DNA. Topoisomerase I makes a nick in one DNA strand, twists it around the other, and religates the nicked strand.

Topoisomerase II: An enzyme that catalyzes the ATP-dependent transport of one segment of DNA duplex through another DNA duplex. Topoisomerases change the topology of DNA by controlling the essential functions of separating intertwined daughter chromosomes.

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Appendix

Overall survival (OS) was defined as the time from random assignment to death resulting from any cause and censored at the last follow-up date. Progression-free survival (PFS) was defined as the interval from random assignment to diagnosis of progression or death resulting from any cause and censored at the last date on which progression-free status was evaluated.

The response rate was the proportion of patients evaluated as having a complete or partial response as overall response among all eligible patients with evaluable lesions. Proportion of grade 3 to 4 diarrhea was defined the number of patients who experienced at least one grade 3 to 4 diarrhea event by Common Terminology Criteria for Adverse Events (version 3) from the first day of protocol treatment to 30 days after protocol treatment. Quality of life was compared in terms of a proportion of patients whose quality-of-life scores improved during protocol treatment.

CIs for OS and PFS proportions were estimated using Greenwood's formula, and those of median OS and median PFS were estimated using the method of Brookmeyer and Crowley. Hazard ratios were estimated using Cox regression.

Multiplex genomic profiling of non-small cell lung cancers from the LETS phase III trial of first-line S-1/carboplatin versus paclitaxel/carboplatin: results of a West Japan Oncology Group study

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ABSTRACT:

Archival formalin-fixed, paraffin-embedded (FFPE) tumor specimens were collected from advanced NSCLC patients enrolled in LETS phase III trial comparing first-line S-1/carboplatin with paclitaxel/carboplatin and subjected to multiplex genotyping for 214 somatic hotspot mutations in 26 genes (LungCarta Panel) and 20 major variants of *ALK*, *RET*, and *ROS1* fusion genes (LungFusion Panel) with the Sequenom MassARRAY platform. *MET* amplification was evaluated by fluorescence in situ hybridization. A somatic mutation in at least one gene was identified in 48% of non–squamous cell carcinoma and 45% of squamous cell carcinoma specimens, with *EGFR* (17%), *TP53* (11%), *STK11* (9.8%), *MET* (7.6%), and *KRAS* (6.2%). Mutations in *EGFR* or *KRAS* were associated with a longer or shorter median overall survival, respectively. The LungFusion Panel identified *ALK* fusions in six cases (2.5%), *ROS1* fusions in five cases (2.1%), and a *RET* fusion in one case (0.4%), with these three types of rearrangement being mutually exclusive. Nine (3.9%) of 229 patients were found to be positive for de novo *MET* amplification. This first multiplex genotyping of NSCLC associated with a phase III trial shows that MassARRAY-based genetic testing for somatic mutations and fusion genes performs well with nucleic acid derived from FFPE specimens of NSCLC tissue.

INTRODUCTION

Lung cancer is the leading cause of death related to cancer worldwide,with non–small cell lung cancer (NSCLC) accounting for 85% of lung cancer cases (1). Advanced or metastatic NSCLC has been treated with platinum-based chemotherapies in a manner dependent on tumor histological features, with consideration given to the balance between the modest efficacy and side effects of such treatment. Over the last decade, however, substantial progress has been made in the development of genotype-based targeted therapies for advanced NSCLC. The success of epidermal growth factor receptor (EGFR) tyrosine kinase inhibitors (TKIs) in the treatment of *EGFR* mutation–positive advanced NSCLC established a proof of concept that molecularly targeted agents are far more effective than conventional chemotherapy when administered to the appropriate genetically defined patient population (2-7). Somatic mutations in other genes including *KRAS*, *HER2*, *PIK3CA*, *BRAF*, and *DDR2* have also been investigated as potential targets for genotype-based treatment approaches in NSCLC (8). More recently, the anaplastic lymphoma kinase (ALK) TKI crizotinib was approved with a companion diagnostic test for the treatment of a relatively small (up to 3 to 5%) subset of patients with advanced NSCLC who harbor *ALK* rearrangements (9-11). The subsequent discovery of *ROS1* and *RET* rearrangements as potentially treatable targets suggested that several chromosomal translocations and corresponding gene fusions may serve as a driving force for NSCLC (12-16). These findings have highlighted the genetic diversity of NSCLC, which can no longer be considered a single disease. Furthermore, the coexistence of different genetic alterations and therapeutic targets in NSCLC patients can profoundly affect the response to therapy (17). The clinical implementation of genomic profiling for NSCLC with high-throughput and multiplex genotyping tests is thus warranted in order to prioritize appropriate therapies for individual patients (18).

We have previously presented the results of the Lung Cancer Evaluation of TS-1 (LETS) study (19, 20). This multicenter randomized phase III trial demonstrated the noninferiority of the combination of S-1 and carboplatin compared with that of paclitaxel and carboplatin in terms of overall survival (OS) for chemotherapy-naïve patients with advanced NSCLC. Our West Japan Oncology Group (WJOG) has now embarked on multiplex genomic analyses of the archival formalin-fixed, paraffin-embedded (FFPE) tumor specimens collected from the patients enrolled in the LETS study. The primary platform for genotyping of tumors adopted in the present study is the Sequenom MassARRAY system, which combines multiplex polymerase chain reaction (PCR) analysis with single-base primer extension, followed by analysis of the primer extension products by matrix-assisted laser desorption-ionization (MALDI)–time-of-flight (TOF) mass spectrometry. We thus conducted high-throughput genotyping of 214 somatic hotspot mutations in 26 genes (LungCarta Panel) (Supplementary Table S1) as well as of 20 major variants of *ALK*, *RET*, and *ROS1* fusion genes (LungFusion Panel). Given that recent preclinical and clinical studies have also implicated de novo *MET* amplification as an oncogenic driver (21-23), we also evaluated *MET* amplification in available tumor specimens by fluorescence in situ hybridization (FISH).

RESULTS

Patients and sample collection

FFPE specimens obtained at diagnosis were available for 304 (53.9%) of the 564 patients enrolled in the LETS study. Most (229 out of 304, 75.3%) of the specimens were obtained by transbronchial biopsy. Nine specimens contained no tumor cells and were excluded from further analysis. The remaining 295 specimens were subjected to extraction of DNA and RNA, yielding median amounts of 504 ng (range, 33 to 25,230 ng) and 516 ng (range, 6 to 32,795 ng), respectively. The numbers of evaluable patients were 275 for somatic gene mutations (LungCarta Panel), 240 for fusion gene characterization (LungFusion Panel), and 229 for *MET* amplification (FISH) (Figure 1). The characteristics of these groups of patients, including the efficacy results, were similar overall

Table 1. Characteritics and outcome for patients subjected to molecular analyses compared with those for the intention-to-treat (ITT) population of the LETS study

	Somatic mutation analysis (n = 275)	Fusion gene analysis (n = 240)	*MET* amplification analysis (n = 229)	ITT population (n = 564)
Characteristic				
CBDCA+PTX/CBDCA+S-1	136 (49%)/139 (51%)	117 (49%)/123 (51%)	113 (49%)/116 (51%)	282 (50%)/282 (50%)
Median age (range), years	63 (36–74)	64 (36–74)	63 (36–74)	64 (36–74)
Male/female	211 (77%)/64 (23%)	184 (77%)/56 (23%)	178 (78%)/51 (22%)	433 (77%)/131 (23%)
ECOG PS 0/1	76 (28%)/199 (72%)	63 (26%)/177 (74%)	62 (27%)/167 (73%)	177 (31%)/387 (69%)
Clinical stage IIIB/IV	68 (25%)/207 (75%)	59 (25%)/181 (75%)	60 (26%)/169 (74%)	136 (24%)/428 (76%)
Nonsmoker/smoker	49 (18%)/226 (82%)	44 (18%)/196 (82%)	38 (17%)/191 (83%)	104 (18%)/460 (82%)
Outcome				
PFS hazard ratio (95% CI)	0.88 (0.70–1.12)	0.95 (0.74–1.24)	0.83 (0.64–1.09)	1.04 (0.86–1.22)
OS hazard ratio (95% CI)	0.93 (0.71–1.21)	0.85 (0.64–1.13)	0.91 (0.68–1.21)	0.96 (0.79–1.15)

Abbreviations: CBDCA, carboplatin; PTX, paclitaxel; ECOG, Eastern Cooperative Oncology Group; PS, performance status; PFS, progression-free survival; CI, confidence interval; OS, overall survival.

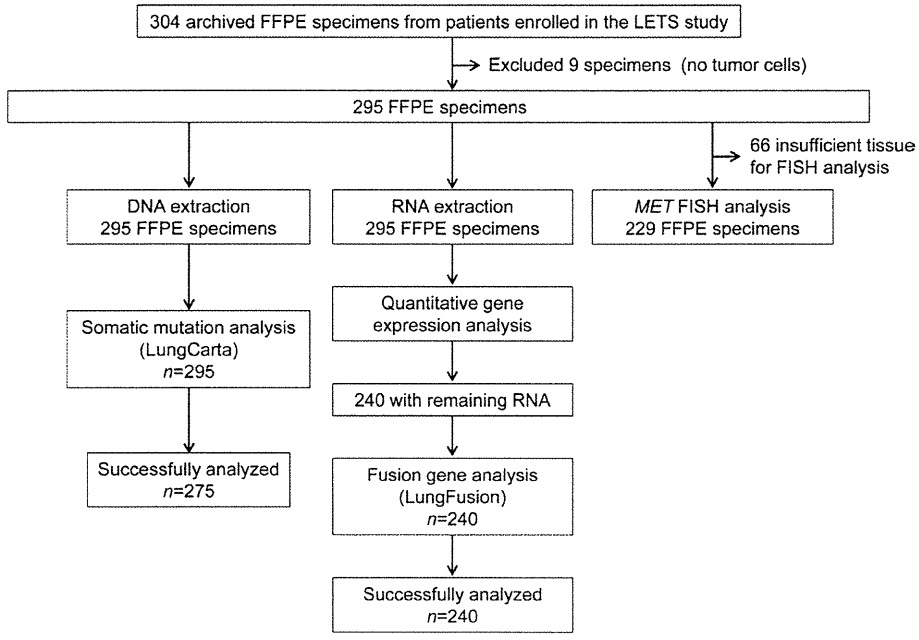

Figure 1: CONSORT diagram for the study. Of the FFPE specimens obtained from 304 advanced NSCLC patients (54%) enrolled in the LETS study, 9 specimens contained no tumor cells and the remaining 295 specimens were subjected to extraction of DNA and RNA. In addition, 229 FFPE specimens were analyzed for *MET* amplification by FISH.

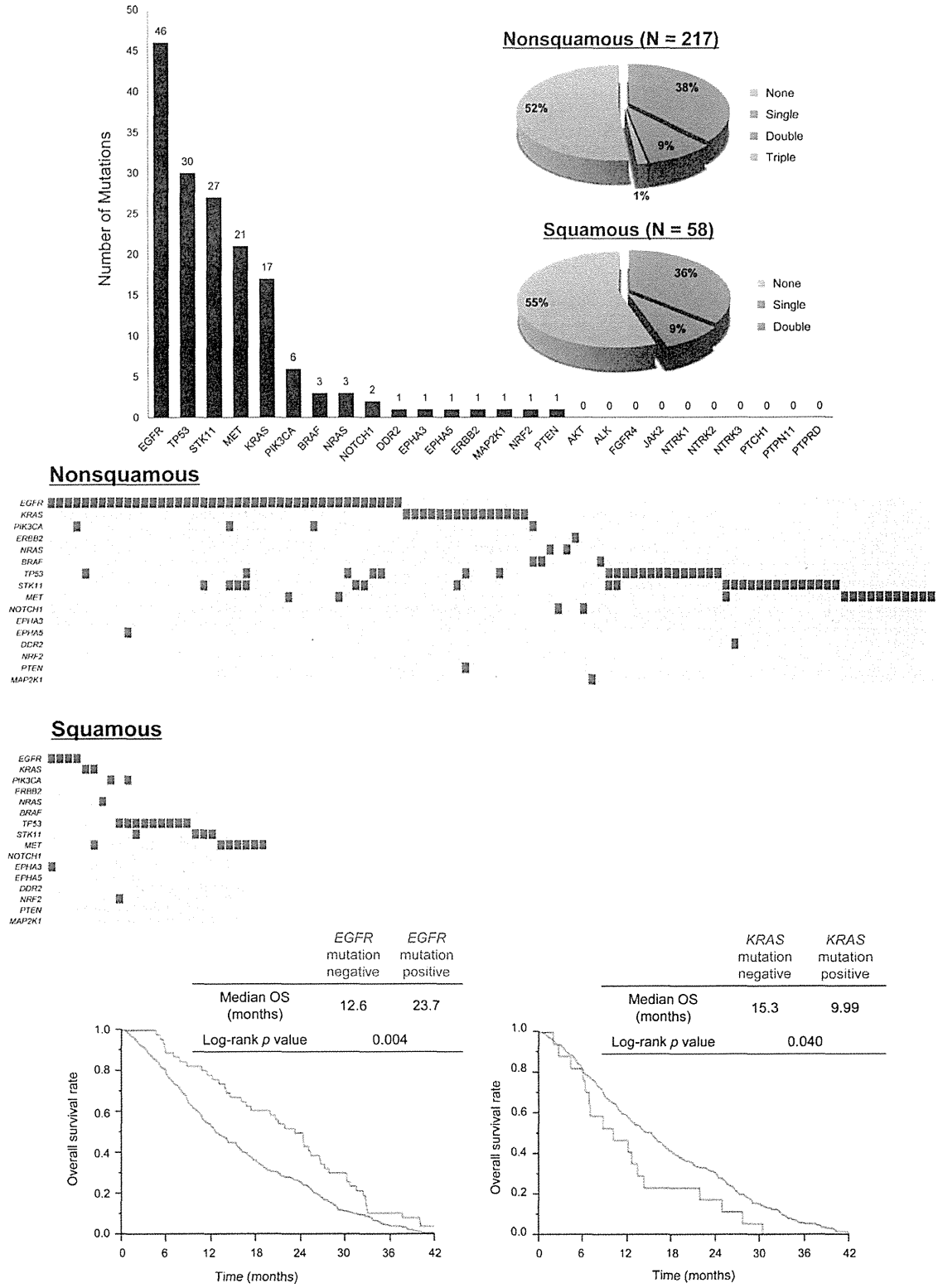

Figure 2: Analysis of somatic gene mutations in FFPE specimens from advanced NSCLC patients. A, The pie charts show the distribution for the number of mutations detected in specimens according to tumor histology. B, Number of mutations in each of the 26 analyzed genes for the 275 specimens that were successfully genotyped. C, Mutational profiles for the patients harboring at least one mutation. D, OS analysis for advanced NSCLC patients according to *EGFR* mutation and *KRAS* mutation status.

to those of the intention-to-treat population (Table 1).

Analysis of somatic gene mutations

Of the 295 specimens referred for somatic mutation analysis, 275 (93.2%) provided mutational profiles with a >90% success rate for genotyping (Figure 1). Somatic mutations in at least one gene were identified in 105 (48%) of the 217 patients with non–squamous cell carcinoma (non-SCC) and in 26 (45%) of the 58 patients with SCC. Twenty-five (9.1%) specimens (20 non-SCC, 5 SCC) were positive for mutations in two genes, and three non-SCC tumors each had mutations in three genes (Figure 2A). Overall, we identified *EGFR* mutations in 46 patients (17%), *TP53* mutations in 30 (11%), *STK11* mutations in 27 (9.8%), *MET* mutations in 21 (7.6%), *KRAS* mutations in 17 (6.2%), *PIK3CA* mutations in 6 (2.2%), *BRAF* and *NRAS* mutations in 3 each (1.1%), *NOTCH1* mutations in 2 (0.7%), and *DDR2*, *EPHA3*, *EPHA5*, *ERBB2*, *MAP2K1*, *NRF2*, and *PTEN* mutations in 1 each (0.4%) (Figure 2B). Among the 46 patients with *EGFR* mutations, 15 individuals (33%) had a deletion in exon 19 and 24 individuals (52%) had a point mutation (L858R or L861Q) in exon 21, whereas three patients had point mutations in exon 18, two had point mutations in exon 19, and two had mutations in exon 20 (Supplementary Table S2). Mutation profiles for patients harboring at least one mutation are shown in Figure 2C. *EGFR* and *KRAS* mutations were mutually exclusive. Of the 46 patients with *EGFR* mutations, three also harbored *PIK3CA* mutations. Four patients with *KRAS* mutations also had an additional mutation in *STK11*, in *TP53* and *PTEN*, in *TP53*, or in *MET*.

The median OS of *EGFR* mutation–positive patients was significantly longer than that of patients without *EGFR* mutations (23.7 vs. 12.6 months, $P = 0.004$) (Figure 2D). Conversely, patients with *KRAS* mutations had a significantly shorter median OS than did those with wild-type *KRAS* (9.99 vs. 15.3 months, $P = 0.040$) (Figure 2D).

Fusion gene characterization

We previously established an assay system based on the MassARRAY platform for detecting *EML4-ALK* in FFPE biopsy specimens of advanced NSCLC (24). In the present study, we further developed a new multiplex system for MassARRAY assays (LungFusion Panel) focused on the capture of 20 major variants of *ALK*, *RET*, and *ROS1* fusion genes (Supplementary Tables S3 to S5). The LungFusion Panel assays detected plasmid DNA corresponding to the 20 different fusion variants with the expected mass spectra (Supplementary Figure S1), with the lower threshold for detection ranging from 5 to 60 copies (Supplementary Table S6).

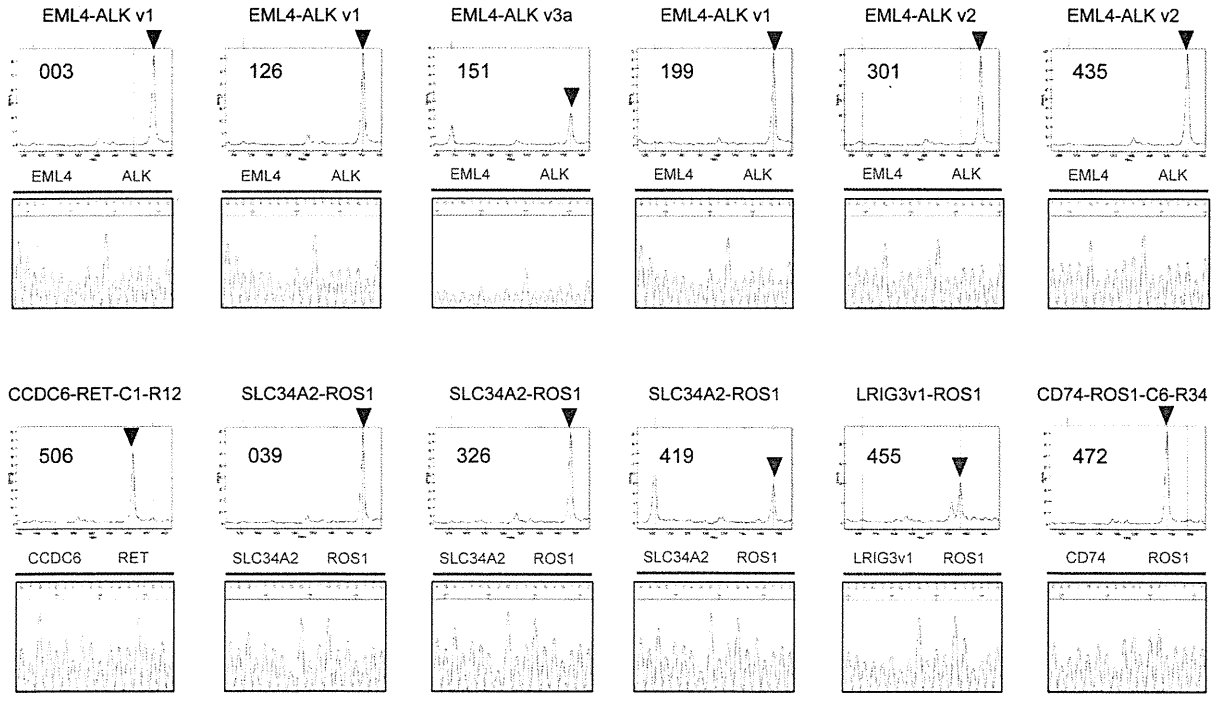

Figure 3: Detection of *ALK*, *RET*, and *ROS1* fusion genes in FFPE specimens of advanced NSCLC. Arrowheads indicate mass spectrometry peaks corresponding to the indicated fusion genes. The variants of these fusions identified with the LungFusion Panel were validated by direct sequencing.

Table 2. Clinicopathologic characteristics of the 12 patients with fusion gene–positive NSCLC
Ad: Adenocarcinoma, Sq: Squamous cell carcinoma

Fusion gene	Age (years)	Sex	Smoking history	Tumor histology	Clinical stage	Concomitant mutations
EML4-ALK v1	70	F	No	Ad	IV	*STK11* (F354L)
EML4-ALK v1	50	M	Yes	Ad	IV	*MET* (N375S)
EML4-ALK v3a	55	M	Yes	Sq	IIIB	None
EML4-ALK v1	56	M	Yes	Ad	IV	None
EML4-ALK v2	57	F	No	Sq	IIIB	None
EML4-ALK v2	50	F	Yes	Ad	IIIB	*STK11* (F354L)
CCDC6-RET	58	F	No	Ad	IV	None
SLC34A2-ROS1	74	M	Yes	Ad	IV	*KRAS* (G12V)
SLC34A2-ROS1	65	F	No	Ad	IV	*EGFR* (L858R), *PIK3CA* (E542K), *STK11*(F354L)
SLC34A2-ROS1	58	M	Yes	Ad	IV	*KRAS* (G12A)
LRIG3v1-ROS1	65	M	Yes	Other	IV	None
CD74-ROS1	53	M	Yes	Ad	IIIB	None

All 240 specimens referred for analysis with the LungFusion Panel were tested successfully. The LungFusion assay followed by direct sequencing identified *ALK* fusions in six cases (three *EML4-ALK* variant 1, two *EML4-ALK* variant 2, and one *EML4-ALK* variant 3a), a *CCDC6-RET* fusion in one case, and *ROS1* fusions in five cases (three *SLC34A2-ROS1*, one *LRIG3v1-ROS1*, and one *CD74-ROS1*) (Figure 3). The frequencies of *ALK*, *RET*, and *ROS1* rearrangements were 2.5%, 0.4%, and 2.1%, respectively, and these three types of rearrangement were mutually exclusive. Clinicopathologic characteristics of the 12 fusion-positive patients are shown in Table 2. Although these patients tended to be younger than the fusion-negative patients (median age of 58 vs. 64 years), there was no statistically significant difference in age, sex distribution, smoking history, tumor histological type, or

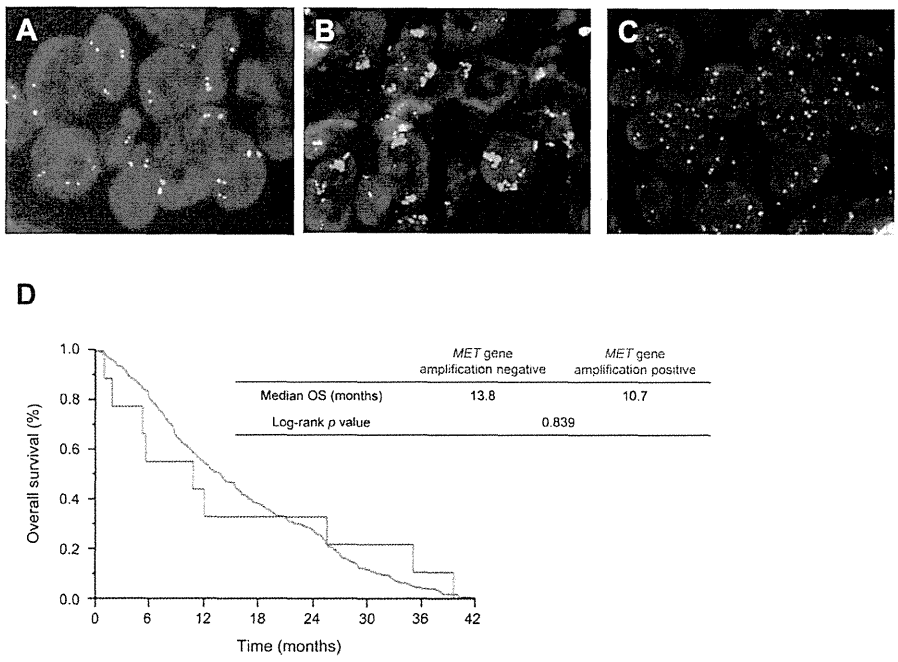

Figure 4: FISH analysis of de novo *MET* amplification in advanced NSCLC and survival analysis according to *MET* amplification status. A–C, Representative FISH images for specimens negative (A) or positive (B and C) for *MET* amplification. Green and red signals correspond to CEN7p and the *MET* locus, respectively. D, OS according to de novo *MET* amplification status in advanced NSCLC patients.

Table 3. Clinicopathologic characteristics of the nine patients with *MET* amplification–positive NSCLC

Age (years)	Sex	Smoking history	Tumor histology	Clinical stage	Concomitant mutations
54	M	Yes	Ad	IV	None
71	F	No	Ad-sq	IV	*TP53* (R248Q), *STK11* (F354L)
54	M	Yes	Ad	IV	*TP53* (R273L)
57	M	Yes	Ad	IV	None
59	M	No	Ad	IV	*EGFR* (E709A, G719S)
64	M	Yes	Ad	IV	None
46	M	Yes	Ad	IV	None
54	M	Yes	Ad	IV	None
72	M	Yes	Ad	IV	None

disease stage between these two groups. Among the *ALK* fusion–positive patients, two individuals had concurrent *STK11* (F354L) mutations and one had a *MET* (N375S) mutation (Table 2). Among the five *ROS1* fusion–positive patients, two individuals also had a *KRAS* mutation (G12V or G12A) and one had *EGFR* (L858R), *PIK3CA* (E542K), and *STK11* (F354L) mutations (Table 2). The median OS was 19.5 and 13.8 months ($P = 0.89$) for fusion-positive and fusion-negative patients, respectively.

MET amplification

MET copy number was evaluated by FISH in 229 cases and was detected in 9 cases (3.9%) (Figure 4A–C), among which the median gene copy number was 8.8 (range, 6.1 to 15.3). All *MET* amplification–positive patients had non-SCC (5.2%, 9 of 174 patients) and most were male and smokers (Table 3). Two of these patients had a *TP53* mutation, either alone or together with an *STK11* mutation, and one patient had two *EGFR* mutations (E709A + G719S) (Table 3). Although the median OS tended to be shorter for *MET* amplification–positive patients than for amplification-negative patients (10.7 vs. 13.8 months), this difference was not statistically significant (Figure 4D).

DISCUSSION

As the number of molecularly targeted therapies for molecularly defined subsets of patients with NSCLC increases, there is an increasing need for high-throughput genotyping tests to evaluate the corresponding genetic abnormalities. The successful clinical application of such tests will depend on attainment of robust performance with minute samples derived from the FFPE tumor material collected for pathological diagnosis. In the present study, we tested FFPE specimens of NSCLC tissue for multiple genetic abnormalities simultaneously with the use of multiplex assay panels based on Sequenom's MassARRAY platform. The LungCarta Panel encompasses 214 distinct mutations in 26 genes previously annotated in NSCLC. Although collection of tumor material was not mandatory in the LETS study, FFPE archival tumor specimens were obtained from more than half of the advanced NSCLC patients enrolled in the study. Although most of the collected specimens were obtained by transbronchial biopsy and were small in size, >90% were successfully genotyped, thus satisfying the dual requirements of pathological diagnosis and multiplex analysis of somatic mutations with a single biopsy sample. We detected mutations in at least one gene in about half of the tested subjects, consistent with previous studies performed with other platforms (25). The frequency of *EGFR* mutations in our study (17%) is lower than that previously determined for Japanese patients with NSCLC (26). Given that *EGFR* mutation tests have been commercially available with insurance coverage since 2007 in Japan, the reason for this difference is likely that many *EGFR* mutation–positive patients were not enrolled in the LETS study because EGFR-TKIs were available as a first-line treatment option. The bias toward a higher percentage of wild-type *EGFR* patients may also have affected the observed incidence of other somatic mutations, including both those that are nonoverlapping or associated with *EGFR* mutations. The 6% prevalence of *KRAS* mutations in our cohort is also lower than the frequency reported for Caucasian patients, consistent with the previously described ethnic differences in the incidence of *KRAS* mutations (26). We also retrospectively evaluated the influence of *EGFR* or *KRAS* genotype on survival outcome for the advanced NSCLC patients enrolled in the LETS study. *EGFR* mutation–positive patients had a significantly superior OS compared with individuals with wild-type *EGFR*, likely because most mutation-positive patients received EGFR-TKIs as second-line or later chemotherapy. On the other hand, patients who had tumors with wild-type *KRAS* had a significantly better survival compared with those who had

KRAS mutations. Given that some patients with wild-type *KRAS* had *EGFR* mutations or *ALK*, *RET*, or *ROS1* fusion genes, however, we also compared the survival outcome of *KRAS* mutation–positive patients with that of wild-type *KRAS* patients negative for these treatable targets. Although *KRAS* mutation–positive patients showed a trend toward a shorter survival compared with those negative for *KRAS* and *EGFR* mutations as well as for fusion genes (9.99 vs. 12.9 months, $P = 0.113$) (Supplementary Figure S2), the negative prognostic value of *KRAS* mutations remains uncertain on the basis of the data in the present study.

Several oncogenic gene fusions have recently been identified in NSCLC. *EML4-ALK* was the first such fusion detected in NSCLC, with its discovery in 2007 (9) being followed by the identification of *ROS1* and *RET* fusions in 2012 (12-15). Although the frequency of each of these types of fusion gene is only ~1 to 5% in unselected NSCLC patients, the affected patient subsets are treatable with corresponding kinase inhibitors. A break-apart FISH assay is the FDA-approved diagnostic test to screen for *ALK* rearrangement in NSCLC. FISH is thus currently considered the standard diagnostic technology for gene rearrangement, but its high cost and requirement for technical expertise limit its clinical application. Furthermore, timely acquisition of genotype information including oncogenic gene fusion status is required to guide rapid initiation of appropriate molecularly targeted therapies. The development of novel platforms that allow simultaneous screening for *ALK*, *ROS1*, and *RET* fusions is thus urgently needed. In the present study, we extended the MassARRAY technique to develop a multiplex screen (LungFusion Panel) designed to assess RNA isolated from FFPE biopsy specimens for *ALK*, *ROS1*, and *RET* fusion genes simultaneously. In this initial proof-of-concept effort, we confirmed robust performance of the LungFusion assay with 240 FFPE clinical samples obtained from advanced NSCLC patients, revealing a prevalence of 2.5%, 2.1%, and 0.4% for *ALK*, *ROS1*, and *RET* fusion genes, respectively. We also confirmed the mutual exclusivity of these three types of fusion gene. Of note, we found that three of five *ROS1* fusion–positive patients harbored concurrent actionable oncogenic somatic mutations of *EGFR*, *PIK3CA*, or *KRAS*. A 65-year-old woman who had never smoked had adenocarcinoma harboring *SLC34A2-ROS1* as well as *EGFR* (L858R) and *PIK3CA* (E542K) mutations. Two previous studies of Asian populations also detected coexistence of *EGFR* mutations and *ROS1* rearrangements in NSCLC patients (27, 28). Given that our cohort was also exclusively Japanese, the high prevalence of *EGFR* mutations in Asian patients with NSCLC may increase the chance for detection of coexistence of these two types of genetic alterations. As far as we are aware, the above-mentioned 65-year-old woman in our cohort is the first reported patient with both a *ROS1* fusion and a *PIK3CA* mutation. We also detected *KRAS* mutations (G12V or G12A) in two *SLC34A2-ROS1*–positive patients, with coexistence of *ROS1* rearrangement and *KRAS* mutation not having been previously described. Further studies are warranted to investigate whether the overlap between these oncogenes is clinically relevant and might affect the choice of optimal therapy.

We have previously shown that inhibition of MET signaling either with the small-molecule MET and ALK inhibitor crizotinib or by RNA interference targeted to MET mRNA resulted in marked antitumor effects in *MET* amplification–positive NSCLC cell lines both in vitro and in vivo (21). Furthermore, NSCLC patients with de novo *MET* amplification have shown a pronounced clinical response to crizotinib (22, 23), which was originally developed as a TKI for c-MET. These preclinical and clinical findings suggest that de novo *MET* amplification is an oncogenic driver for, and therefore a valid target for the treatment of, NSCLC. The clinicopathologic profile of advanced NSCLC patients with de novo *MET* amplification remains largely unknown, however. Several studies performed with different methods and different criteria for definition of gene amplification have reported a frequency of de novo *MET* amplification in NSCLC ranging from 2% to 20% (29). In the present study, we applied strict guidelines of the American Society of Clinical Oncology/College of American Pathologists for the definition of gene amplification and thereby identified 9 out of 229 advanced NSCLC patients (3.9%) as having de novo *MET* amplification. Eight of these nine patients had adenocarcinoma and one had adenosquamous carcinoma histology. Although most of the nine patients were male and smokers, no specific clinicopathologic feature was significantly associated with de novo *MET* amplification. The notion that tumors positive for de novo *MET* amplification, *EGFR* mutations, or oncogenic (*ALK*, *ROS1*, *RET*) fusions are distinct biological entities was supported by our finding that, with one exception, these genetic alterations were mutually exclusive.

There are several potential limitations to our study. First, although we detected significant survival differences between advanced NSCLC patients positive or negative for *EGFR* or *KRAS* mutations, the analysis did not take into account other prognostic factors and should be interpreted within the context of its retrospective nature. Second, although the LungCarta Panel encompasses >200 mutations across 26 cancer genes, important gene mutations may be present outside of the selected hotspot regions. Given that the MassARRAY system involves multiple primer sets for both PCR amplification and primer extension, the addition of new mutations to existing panels is straightforward but still requires effort. Lastly, we performed molecular testing with a single biopsy specimen, which may not be representative of all sites within a tumor.

In summary, the present study constitutes the

first multiplex genotyping analysis of patients with advanced NSCLC enrolled in a phase III clinical trial. Such an approach will be important for future evaluation of the clinical impact of specific genetic alterations and predictive biomarkers. Our data indicate that MassARRAY-based multiplex genetic testing both for somatic mutations and for *ALK*, *ROS1*, and *RET* fusion genes performed well with nucleic acid (DNA and RNA) extracted from FFPE tumor specimens obtained from patients with advanced NSCLC.

METHODS

Patients and sample collection

The design and results of the LETS study have been described previously [19,20]. In brief, the study subjects comprised patients aged 20 to 74 years with a histopathologic diagnosis of stage IIIB or IV NSCLC, an Eastern Cooperative Oncology Group (ECOG) performance status of 0 or 1, and preserved function of major organ systems. They had not previously received chemotherapy, and they were randomly assigned in a 1:1 ratio to treatment with either carboplatin plus S-1 or carboplatin plus paclitaxel. The present study was designed retrospectively after completion of the first interim analysis of the LETS trial and was approved by the institutional ethics committee of each of the participating institutions. Archival FFPE tumor specimens were collected for diagnosis from the participants of the LETS study at 22 centers and were shipped to Kinki University Faculty of Medicine.

Sample processing

The collected FFPE specimens underwent histological review, and only those containing sufficient tumor cells as revealed by hematoxylin-eosin staining were subjected to nucleic acid extraction. DNA and RNA were purified with the use of an Allprep DNA/RNA FFPE Kit (Qiagen, Valencia, CA). The isolated RNA was subjected to reverse transcription with the use of a High Capacity cDNA Reverse Transcription Kit (Applied Biosystems, Foster City, CA). The DNA and RNA samples were analyzed in the following order of priority: (1) multiplex analysis of somatic gene mutations (LungCarta Panel; Sequenom, San Diego, CA), (2) quantitative analysis of gene expression (results to be described elsewhere), and (3) characterization of *ALK*, *ROS1*, and *RET* fusion genes (LungFusion Panel).

Mutation detection by mass spectrometry

The genes in the LungCarta Panel are listed in Supplementary Table S1. Multiplex PCR was performed in a volume of 5 μL containing 1 U of Hotstart Taq polymerase (Sequenom), 1.1 to 10 ng of genomic DNA, the LungCarta PCR primer pool(Sequenom), and 500 μmol of each deoxynucleoside triphosphate (dNTP). The PCR protocol included incubation at 95°C for 15 min; 45 cycles of incubation at 94°C for 20 s, 56°C for 30 s, and 72°C for 60 s; and a final incubation at 72°C for 3 min. Unincorporated dNTPs were deactivated by incubation with 0.5 U of shrimp alkaline phosphatase (Sequenom) at 37°C for 40 min, after which the enzyme was inactivated by incubation for 5 min at 85°C. Single-base primer extension was performed with the LungCarta extension primer pool (Sequenom), 0.2 μL of mass-modified dNTPs (Sequenom), and 1.15 U of Thermosequenase enzyme (Sequenom). The extension protocol included incubation at 94°C for 30 s; 60 cycles of incubation at 94°C for 5 s, 52°C for 5 s, and 80°C for 5 s; and a final incubation at 72°C for 3 min. After the addition of a cation-exchange resin to remove residual salt followed by 41 μL of water, the extension products were spotted onto a matrix pad (3-hydroxypicolinic acid) of a SpectroCHIP II (Sequenom) for analysis with a Bruker MALDI-TOF mass spectrometer. Spectra were processed with SpectroREADER software (Sequenom) and transferred to the MassARRAY Typer 4 Analyzer (Sequenom) for further analysis.

Fusion gene detection by mass spectrometry

PCR and extension primers were designed to specifically amplify the breakpoint junction regions for 20 types of fusion gene (Supplementary Tables S3–S5) with the use of MassARRAY Assay Designer 3.1 (Sequenom). The detection technique has been described previously.[25] Reverse-transcribed cDNA was subjected to PCR in a volume of 5 μL containing 1 U of Taq polymerase (Sequenom), 500 μmol of each dNTP, and 200 nmol of each PCR primer. The PCR protocol included incubation at 95°C for 15 min; 45 cycles of incubation at 94°C for 20 s, 56°C for 30 s, and 72°C for 60 s; and a final incubation at 72°C for 3 min. Unincorporated dNTPs were deactivated by incubation with 0.5 U of shrimp alkaline phosphatase (Sequenom) at 37°C for 40 min, after which the enzyme was inactivated by incubation for 5 min at 85°C. Single-base primer extension was performed with the LungFusion extension primer pool (depending on the mass), 0.2 μL of mass-modified dNTPs (Sequenom), and 1 U of iPLEX enzyme (Sequenom). The extension protocol included incubation at 94°C for 30 s; 40 cycles of incubation at 94°C for 5 s, 52°C for 5 s, and 80°C for 5 s; and a final incubation at 72°C for 3 min. After the

addition of a cation-exchange resin to remove residual salt followed by 41 μL of water, the extension products were spotted onto a matrix pad (3-hydroxypicolinic acid) of a SpectroCHIP II (Sequenom) for analysis with a Bruker MALDI-TOF mass spectrometer. Spectra were processed with SpectroREADER software (Sequenom) and then transferred to the MassARRAY Typer 4 Analyzer (Sequenom) for further analysis.

Control vectors containing fusion sequences were constructed by In-Fusion PCR cloning (Clontech, Palo Alto, CA), with the exception of those for *EML4-ALK*, which were constructed as described previously [24]. Data analysis was performed with MassARRAY Typer software, version 4.0 (Sequenom). Positive samples were confirmed by subcloning and sequencing with the pTA2 vector (Toyobo, Osaka, Japan) and M13 universal primers.

FISH

FISH was performed to determine *MET* copy number in FFPE tumor specimens with the use of a c-Met/CEN7p Dual Color FISH Probe (GSP Laboratory, Kawasaki, Japan), where CEN7p is the centromeric region of chromosome 7p. After screening of all sections, images of tumor cells were captured and recorded, and the signals for at least 50 random nuclei were counted for an area in which individual cells were recognized in each of at least 10 representative images. Nuclei with a disrupted boundary were excluded from the analysis. Gene amplification was strictly defined on the basis of a mean *MET*/CEN7p copy number ratio of >2.2, as previously described (30). Polysomy or an equivocal *MET*/CEN7p ratio (1.8 to 2.2) was thus scored as negative for amplification.

Statistical analysis

OS in patients for each biomarker analysis was estimated with the Kaplan-Meier method and analyzed with a Cox proportional-hazard model. Differences in OS between genotypes were evaluated with the log-rank test. All statistical analysis was performed with SAS for Windows, release 9.2 (SAS Institute, Cary, NC), and JMP software (version 10, SAS Institute). A P value of <0.05 was considered statistically significant.

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A single-arm confirmatory study of amrubicin therapy in patients with refractory small-cell lung cancer: Japan Clinical Oncology Group Study (JCOG0901)

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ABSTRACT

Objectives: We conducted an open-label, multicenter, single-arm study to confirm the efficacy and safety of amrubicin (AMR), a topoisomerase II inhibitor, for treating refractory small-cell lung cancer (SCLC).
Patients and methods: Patients with chemotherapy-refractory SCLC received 40 mg/m^2 AMR for 3 consecutive days, every 21 days. The primary endpoint was the overall response rate (ORR) and the secondary endpoints were progression-free survival (PFS), overall survival (OS), and safety.
Results: Between November 2009 and February 2011, 82 patients were enrolled. Each patient received a median of four treatment cycles (range, 1–22 cycles). ORR was 32.9% [$P < 0.0001$ by the exact binomial test for the null hypothesis that ORR $\leq$ 10%; 95% confidence interval (CI), 22.9–44.2%]. The median PFS and OS periods were 3.5 months (95% CI, 3.0–4.3 months) and 8.9 months (95% CI, 7.6–11.3 months), respectively. Significant differences in ORR (21.4% *v* 45.0%; $P = 0.034$), PFS (median, 2.9 *v* 5.1 months; $P = 0.0009$), and OS (median, 7.9 *v* 13.1 months; $P = 0.0128$) were observed between patients previously treated with etoposide and others. Neutropenia was the most common grade 3 or 4 adverse events (93.9%), and febrile neutropenia developed in 26.8% patients. No treatment-related death occurred.
Conclusions: AMR monotherapy can be considered an effective and safe treatment option for refractory SCLC. Previous chemotherapy with etoposide may influence AMR efficacy.

1. Introduction

Small-cell lung cancer (SCLC) is the most rapidly growing lung cancer subtype and patient prognosis is extremely poor [1]. Although most SCLC patients respond to initial treatment, long-term survival is low. Unfortunately, disease progression or relapse occurs in almost all advanced-stage SCLC patients and in the majority of early-stage SCLC patients [2–6]. Response to subsequent chemotherapy depends on responsiveness to previous induction

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chemotherapy and the interval between cessation of initial therapy and disease progression [7,8].

Overall response rates (ORRs) of 21–38% and median overall survival (OS) of 6.9–11.7 months were reported in chemotherapy-sensitive SCLC patients after treatment with topotecan, a topoisomerase I inhibitor [8,9]. A previous randomized study demonstrated similar efficacy and improved tolerability of topotecan compared with cyclophosphamide, doxorubicin, and vincristine [10]. Topotecan is also considered as a treatment option for chemotherapy-refractory SCLC; however, low ORRs (0–11%) and OS (median, 4.7–5.4 months) have been reported [8,9,11]. Thus, a standard chemotherapy for the treatment of refractory SCLC has not yet been established. However, effective treatment must be developed to improve prognosis for SCLC patients.

Amrubicin (AMR), a fully synthetic 9-aminoanthracycline, is metabolized in the body to the active metabolite amrubicinol, which has higher antitumor activity than AMR. Both AMR and amrubicinol, which are topoisomerase II inhibitors, exhibit antitumor activities against various human tumors in xenograft models and have shown no risk of typical anthracycline cardiotoxicity [12]. In subgroup analyses of small phase II studies, AMR showed promising activity in patients with refractory SCLC with ORR of 17–50% and median OS of 5.3–10.3 months [9,13].

Accordingly, the results of previous studies indicated that AMR may be useful for treating refractory SCLC. Therefore, we conducted this study to confirm the efficacy and safety of AMR, a topoisomerase II inhibitor, for treating refractory SCLC. A phase III trial was preferred to evaluate the effectiveness of AMR therapy; however, other than AMR therapy, there was no promising treatment under development for refractory SCLC at that time. As second-best evidence that was not from a randomized controlled trial, we designed a nonrandomized single-arm confirmatory study to evaluate whether AMR therapy can be considered as a standard treatment for refractory SCLC.

2. Patients and methods

2.1. Study design

This was an open-label, multicenter, single-arm confirmatory study involving 25 institutions in Japan. The study protocol was approved by the Japan Clinical Oncology Group (JCOG) Protocol Review Committee and the institutional review board of each participating institution.

2.2. Eligibility criteria

Patients were required to have histologically or cytologically documented SCLC, and were refractory to treatment with one or two previous chemotherapy regimens, at least one of which was platinum based. Refractory disease was defined as no response to previous chemotherapy, disease progression on chemotherapy, or disease progression <90 days of completing previous chemotherapy after confirming a complete response (CR) or partial response (PR). Other inclusion criteria included age of 20–74 years, Eastern Cooperative Oncology Group performance status of 0–1, measurable disease, no history of chemotherapy with AMR, no history of surgery for SCLC, no thoracic radiation therapy ≤4 weeks before registration, adequate baseline organ function [leukocyte count ≥ 3000/mm^3, absolute neutrophil count ≥ 1500/mm^3, hemoglobin ≥ 9.0 g/dL, platelet count ≥ 100,000/mm^3, total bilirubin ≤ 2.0 mg/dL, aspartate aminotransferase (AST) and alanine aminotransferase (ALT) levels ≤ 100 IU/L, serum creatinine level ≤ 2.0 mg/dL, PaO_2 under room air ≥ 60 mmHg, and electrocardiographic findings within normal range]. Written informed consent was obtained from all patients. Patients were ineligible if they had active concomitant malignancy, massive pleural or pericardial effusion, symptomatic brain metastasis, or severe comorbidities such as active infections, uncontrolled hypertension, severe heart disease, uncontrolled diabetes mellitus, bowel obstruction, psychiatric disease, severe emphysema, interstitial pneumonia, or pulmonary fibrosis. Patients having systemic steroid medication and pregnant or breast feeding women were also excluded.

2.3. Treatment

Treatment was started within 1 week after enrollment in the study. Patients received AMR at 40 mg/m^2/day for 3 consecutive days, every 21 days. The treatment was repeated until disease progression, intolerable toxicity, or patient refusal. The dose of AMR was decreased to 35 mg/m^2/day if any of the following were observed during the previous course: leukocyte count <1000/mm^3, platelet count <20,000/mm^3, grade 3 febrile neutropenia, or grade 3 nonhematological toxicity (except nausea, anorexia, weight loss, creatinine, hyponatremia, hyperglycemia or alopecia). A second dose reduction to 30 mg/m^2/day was made in subsequent cycles on the basis of the same criteria. In cases of grade 4 nonhematological toxicity or continued toxicity that would have required a third dose reduction, the protocol treatment was terminated.

Patients received full supportive care as required, including transfusion of blood products. The protocol specified that granulocyte colony-stimulating factor (G-CSF) should be used in accordance with the national health insurance coverage of Japan, indications for G-CSF administration were as follows: (a) when fever (in principal over 38 °C) was observed with a neutrophil count of ≤1000/mm^3; (b) when a neutrophil count of 500/mm^3 was observed; (c) during the previous course, if fever (in principal over 38 C) with a neutrophil count of ≤1000/mm^3 was observed, or if a neutrophil count of 500/mm^3 was observed, then after completing the same chemotherapy, if a neutrophil count of ≤1000/mm^3 was observed. There was no restriction for subsequent chemotherapy after disease progression in this study.

2.4. Evaluation

The Response Evaluation Criteria in Solid Tumors guidelines (ver. 1.0) was used to evaluate tumor response [14]. Computed tomography was performed at baseline and at least every two cycles. Confirmation of a CR or PR was required at least 4 weeks after the first documentation of a response. Independent review of tumor response was performed for patients with any extent of tumor shrinkage. Three reviewers, including a diagnostic radiologist, were assigned as an independent review panel. Adverse events were recorded and graded using the Common Terminology Criteria for Adverse Events (ver. 3.0). Evaluation of cardiotoxicity was performed as needed, as judged by the physician.

2.5. Study endpoints and statistical analysis

The primary endpoint in this study was ORR, which was calculated as confirmed response (CR + PR) according to independent assessments. We believe that tumor shrinkage is essential to improve prognosis for refractory SCLC. Furthermore, previous studies for refractory SCLC showed large variations in survival times [8,9,11,13]. Because ORR with slight variation was considered a hard endpoint, we used ORR as the primary endpoint. As secondary endpoints, we evaluated progression-free survival (PFS) and OS as effectiveness endpoints and the incidence of an adverse event as a safety endpoint. We hypothesized that if the ORR of AMR therapy was high enough compared with that of topotecan therapy, AMR

could be considered as a standard treatment option. The sample size was set as $N = 80$ to achieve a power of at least 80% with a one-sided alpha of 0.05, and expected and threshold values for the primary endpoint of 20% and 10%, respectively. Survival was estimated using the Kaplan–Meier method and subgroups were compared using the log-rank test.

For AMR therapy to be considered as a standard option for patients with refractory SCLC, its safety and survival should also be equal or superior to those of topotecan therapy. According to the results of previous topotecan studies [8,9,11], anticipated values were 2.0–3.0 months for median PFS and 5.0–7.5 months for median OS, and a proportion of treatment-related deaths (≤5%) was also anticipated. The Fisher's exact test was used to compare categorical data. All analyses were performed using SAS release 9.1 statistical software (SAS Institute, Cary, NC, USA).

3. Results

3.1. Patient characteristics

From November 2009 to February 2011, a total of 82 patients (17 women and 65 men; median age, 66 years; age range, 44–74 years) from 25 Japanese institutions were enrolled in this study. All 82 patients were eligible for analysis of the efficacy and safety of AMR. Patient characteristics are listed in Table 1. All 82 patients received prior platinum-based chemotherapy, including pretreatment with irinotecan-containing chemotherapy regimens ($n = 47$, 57.3%) and etoposide-containing chemotherapy regimens ($n = 42$, 51.2%). Thirteen of these patients had received thoracic radiation therapy concurrently or sequentially with chemotherapy.

Each patient received a median of four AMR treatment cycles (range, 1–22 cycles), and 18 (22.0%) had a cumulative AMR doses exceeding 750 mg/m^2. Reasons for off-protocol included disease progression ($n = 67$), unacceptable toxicity ($n = 8$), and patient refusal possibly related to adverse events ($n = 7$). AMR dose reduction was required in 31 patients (37.8%), and the dose was decreased by two levels in seven patients (8.5%).

Table 1
Patient characteristics ($N = 82$).

Characteristics	Patients	
	n	%
Age (years)		
Median	66	
Range	44–74	
Gender		
Female	17	20.7
Male	65	79.3
ECOG performance status		
0	34	41.5
1	48	58.5
Disease extent at entry		
Limited disease	6	7.3
Extensive disease	76	92.7
No. of prior chemotherapy regimens		
1	72	87.8
2	10	12.2
Prior chemotherapy regimen (multiple choices)		
Cisplatin-containing	62	75.6
Carboplatin-containing	26	31.7
Cisplatin and carboplatin-containing	6	7.3
Irinotecan-containing	47	57.3
Etoposide-containing	42	51.2
Topotecan-containing	3	3.7
Response to prior chemotherapy		
Complete response	3	3.7
Partial response	58	70.7
Stable disease	4	4.9
Progressive disease	17	20.7
History of thoracic radiation therapy		
No	69	84.1
Yes	13	15.9

Abbreviation: ECOG, Eastern Cooperative Oncology Group.

Table 2
Response to amrubicin in the intent-to-treat population.

Response	Number of patients	%
CR	2	2.4
PR	25	30.5
SD	37	45.1
PD	16	19.5
Not evaluable	2	2.4
Overall response rate (CR + PR)	27	32.9
95% CI[a]		22.9–44.2

Abbreviations: CR, complete response; PR, partial response; SD, stable disease; PD, progressive disease; CI, confidence interval.
[a] Calculated by the exact method.

3.2. Response

Independent reviews of tumor response were performed for 39 patients with any extent of tumor shrinkage. Among the total study population, CR was achieved in two patients (2.4%), PR in 25 (30.5%), stable disease (SD) in 37 (45.1%) after two courses, and progressive disease (PD) in 16 (19.5%). The response was not evaluable in two patients (2.4%) as a result of early termination of the treatment protocol. One patient refused further treatment after one cycle of AMR therapy, and the other terminated therapy because of poor performance status. Thus, for AMR therapy, an ORR of 32.9% was observed in our study population ($P < 0.0001$ by the exact binomial test for the null hypothesis that ORR ≤10%; 95% CI, 22.9–44.2%) (Table 2).

In a subset analysis of response to AMR, ORR was lower in patients treated with etoposide than in others (21.4% *v* 45.0%, respectively; $P = 0.034$) (Table 3). No remarkable difference in ORR was observed according to demographic characteristics [age,

Table 3
Subset analysis of response to amrubicin.

Characteristics	Number of patients	Response rate (%)	*P*
Age (years)			
44–70	61	32.8	1.00
≥71	21	33.3	
Gender			
Female	17	47.1	0.25
Male	65	29.2	
ECOG performance status			
0	34	35.3	0.81
1	48	31.3	
Disease extent at entry			
Limited disease	6	16.7	0.66
Extensive disease	76	34.2	
No. of prior chemotherapy regimens			
1	72	36.1	0.15
2	10	10.0	
Prior treatment with irinotecan			
No	35	25.7	0.25
Yes	47	38.3	
Prior treatment with etoposide			
No	40	45.0	0.034
Yes	42	21.4	
Response to prior chemotherapy			
CR/PR	61	36.1	0.42
SD/PD	21	23.8	
History of thoracic radiation therapy			
No	69	33.3	1.00
Yes	13	30.8	

Abbreviations: ECOG, Eastern Cooperative Oncology Group; CR, complete response; PR, partial response; SD, stable disease; PD progressive disease.

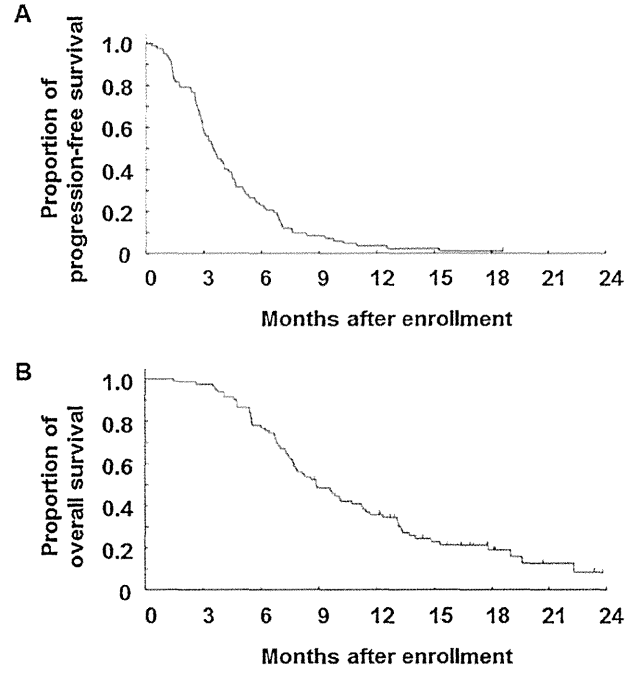

Fig. 1. (A) Progression-free survival and (B) overall survival of patients treated with amrubicin ($n = 82$).

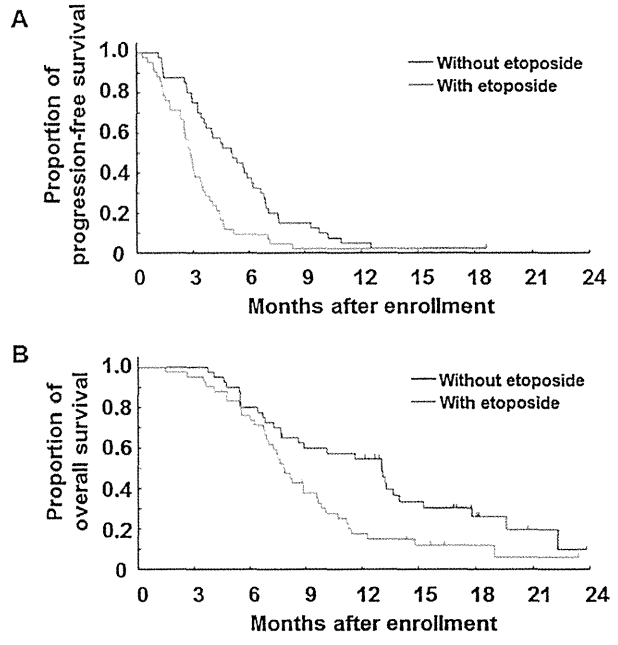

Fig. 2. (A) Progression-free survival and (B) overall survival in patients previously treated with etoposide ($n = 42$) and those not treated with etoposide ($n = 40$).

gender, performance status, disease extent at entry, number of prior chemotherapy regimens, prior treatment with irinotecan, response to prior chemotherapy (CR/PR *v* SD/PD), or history of thoracic radiation therapy].

3.3. Survival

At the cutoff date for data collection, the median follow-up time was 8.8 months in all registered patients (range, 1.5–23.8 months). Of the 82 patients, 81 (98.8%) were observed until disease progression and 66 (80.5%) until death. The median PFS for all 82 patients was 3.5 months (95% CI, 3.0–4.3 months) and the PFS at 6 months was 23.2% (95% CI, 14.7–32.7%; Fig. 1A). The median OS for all 82 patients was 8.9 months (95% CI, 7.6–11.3 months) and the 1-year survival was 35.7% (95% CI, 25.4–46.1%; Fig. 1B).

PFS was shorter in patients previously treated with etoposide than in others (median, 2.9 *v* 5.1 months; hazard ratio, 2.11; 95% CI, 1.35–3.30; $P = 0.0009$; Fig. 2A), as was OS (median, 7.9 *v* 13.1 months; hazard ratio, 1.86; 95% CI, 1.13–3.06; $P = 0.0128$; Fig. 2B).

3.4. Safety

The most common adverse events were hematological toxicities, including grade-3 or -4 neutropenia (93.9%), leukopenia (85.4%), anemia (25.6%), and thrombocytopenia (20.7%; Table 4). Grade-3 febrile neutropenia developed in 22 patients (26.8%). Nonhematological toxicities were generally mild and no evidence of cardiotoxicity of AMR was found in this study (Table 4). Pneumonitis was observed in nine patients (grade 4, $n = 1$; grade 3, $n = 2$; grade 2, $n = 3$; and grade 1, $n = 3$), and seven (grade 4, $n = 1$; grade 3, $n = 2$; grade 2, $n = 2$; and grade 1, $n = 2$) discontinued treatment because of unacceptable toxicity levels. The incidence rate of pneumonitis was higher in patients with history of thoracic radiation therapy than in others (38.5% *v* 5.8%, respectively), but one grade 4 pneumonitis case was observed in a patient without a history of thoracic radiation therapy.

Table 4
Grade 3 or 4 adverse events in patients treated with amrubicin ($N = 82$) (CTCAE v3.0).

Adverse event	Grade 3		Grade 4		≥Grade 3	
	n	%	*n*	%	*n*	%
Leukopenia	48	58.5	22	26.8	70	85.4
Anemia	19	23.2	2	2.4	21	25.6
Thrombocytopenia	12	14.6	5	6.1	17	20.7
Neutropenia	18	22.0	59	72.0	77	93.9
Febrile neutropenia	22	26.8	0	0.0	22	26.8
Hyperglycemia	11	16.4	0	0.0	11	16.4
Hyponatremia	9	11.0	4	4.9	13	15.9
Infection	5	6.1	1	1.2	6	7.3
Dyspnea	3	3.7	1	1.2	4	4.9
Elevated ALT level	4	4.9	0	0.0	4	4.9
Elevated AST level	3	3.7	0	0.0	3	3.7
Anorexia	3	3.7	0	0.0	3	3.7
Pneumonitis	2	2.4	1	1.2	3	3.7
Fatigue	1	1.2	0	0.0	1	1.2
Weight loss	1	1.2	0	0.0	1	1.2
Nausea	1	1.2	0	0.0	1	1.2
Sensory neuropathy	1	1.2	0	0.0	1	1.2

Abbreviations: ALT, alanine transaminase; AST, aspartate aminotransferase; CTCAE, Common Terminology Criteria for Adverse Events.

G-CSF was administered to 51 (62.2%) patients and blood transfusions were necessary in 9 (11.0%). No treatment-related death was observed in this study.

4. Discussion

This single-arm confirmatory study was conducted to confirm the efficacy and safety of AMR in patients with refractory SCLC. In the present study, the primary endpoint was the ORR, which was 32.9%. This data supported the result that the ORR of AMR therapy was significantly better than that of topotecan therapy, in accordance with that previously reported in a randomized phase II study by Inoue et al. [9]. A possible limitation of this study is related to its design, which was not a randomized phase III study, but rather a nonrandomized single-arm confirmatory study. Although there was potential for selection bias as a result of this study design, ORR