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厚生労働科学研究費補助金

創薬基盤推進研究事業

次世代型コンパニオン診断薬の創出に向けた橋渡し研究

平成 26 年度　総括・分担研究報告書

研究代表者　西尾　和人

平成 27（2015）年　3 月

別紙１

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別紙３

厚生労働科学研究費補助金（創薬基盤推進研究事業）
総合研究報告書

次世代型コンパニオン診断薬の創出に向けた橋渡し研究

研究代表者　西尾　和人
近畿大学医学部ゲノム生物学教室　教授

研究要旨
IonPGM および MassArray を応用した Multiplex 体細胞変異診断薬の基本設計を完了し、良好な基本性能試験成績ならびに良好な feasibility 試験結果を得た。申請に向けた当局との事前相談の結果を踏まえて、臨床性能試験の実施、承認申請に向け、準備している。

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後藤　功一（国立がん研究センター東病院呼吸器内科　科長）
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A．研究目的

次世代型コンパニオン診断薬として、複数の遺伝子異常を同時に測定するテクノロジーを共同開発し、当該企業による薬事承認申請を行うこと。
平成 26 年度の目標は LungFusion /LungCarta）については、GMP 製造移管（近大，臨床検査薬企業）、SOP 整備（近大，臨床検査薬企業）を行う。PGM Fusion Panel については、基本性能試験（近大）、GMP 製造移管（近大，臨床検査薬企業）を行う。NCCE Panel については feasibility 試験、GMP 製造、SOP 整備の工程による開発を進め、最終年度（平成 27 年度）に臨床性能試験を開始することを目標とする。

B．研究方法

シーケノム社（現アジェナ・バイオサイエン社）による MassArray を用いた Lung Fusion kit およびライフテクノロジーズ社（現サーモフィッシャーサイエンティフィック社）による IonPGM を用いた PGM Fusion Panel について、Feasibility 試験終了後、速やかにキットデザイン等につき PMDA の助言を受け、その助言に基づき基本性能試験、GMP レベルでの製造移管、診断薬企業との連携により迅速に実施し、承認プロセスに関するデータ整備、資料整備を進めた。ライフテクノロジーズ社（現サーモフィッシャーサイエンティフィック社）による IonPGM を用いた NCCE Panel について既承認および臨床開発が進行中の肺腺癌分子標的薬の効果予測に有用な 10 遺伝子のゲノム DNA 断片を特異的に濃縮し、ライフテクノロジーズ社 Ion PGM による解析が可能なターゲットキャプチャーシステムを設計した。ゲノム DNA 上の逆位・転座を自動的に検出する独自のコンピュータープログラムを設計した。国立がん研究センターに保有する希少ドライバー変異陽性の肺がん細胞株 8 株のゲノム DNA を用いてターゲットキャプチャーシークエンス及び変異検出を行った。

（倫理面への配慮）
Feasiblilty 試験の実施に当たっては、各実施機関の倫理委員会の承認を得た後、個人情報保護等に配慮し実施した。

C．研究結果

近畿大学による Lung Fusion kit(MassARRAY，アジェナ・バイオサイエン社との共同研究)、PGM Fusion Panel（IonPGM，サーモフィッシャーサイエンティフィック社），および国立がん研究センターによる NCCE Panel(IonPGM，サーモフィッシャーサイエンティフィック社)について、キットデザインの確定と細胞株および臨床検体を用いた feasibility 試験を実施し、いず

れのキットも良好な結果を得た。

Lung Fusion kit については、アジェナ・バイオサイエン社と近畿大学とが共同研究契約を締結し、PMDA の薬事戦略相談事前面談での助言に基づき、MassArray の feasibility 試験を実施し、オーストラリアでの feasibility 試験と連携し、データの取り纏めを行った。それを基に、アジェナ社と基本性能試験を開始した。事前相談内容を踏まえた対応としては、1 対 1 対応が基本であるとの認識から、マルチ診断薬においても、対応する分子標的薬とのコンパニオン診断としての可能性を、当該製薬企業と協議した。また、事前面談での指摘を踏まえて、機器を含むキットの全体の構成を示すこととし、下記 1-3 に示す項目の整備を行った。

1. 診断キットの工程の明確化: RNA 抽出から cDNA 化の工程について検証、最適化を行った。
2. 基本性能試験の実施: 臨床サンプル 450 例での基本性能試験をブリスベンにて実施し、最終版のパフォーマンスデータを取得、現在、ドキュメントを作成中である。本データは first priority として、日本における承認申請に用いる。
3. 医療機器申請: FDA 申請を行い、承認済みである。

次世代シーケンサーIonPGM を用いた PGM Fusion Panel の feasibility 試験では実臨床レベルのサンプルでの実施成功率は 96%と良好であった。海外アカデミアと共同での feasibility 試験の結果は、2014 年アメリカ癌学会で報告され、この結果を基に、キットデザインの確定、SOP の確定を行った。また企業との共同による基本性能試験、キットの GMP 製造移管を行った。これらの結果を基に、サーモフィッシャーサイエンティフィック社は、PGM Fusion Panel の欧州 CE-IVD の承認を得た。また、遺伝子解析装置として Ion PGM Dx の医療機器化を完了した。

NCCE Panel については、培養細胞株 8 株(PC9, II-18, H1075, HT-29, H1048, HCC78, H2228, LC2/ad) のゲノム DNA 各 250 ng から、*RET, ALK, ROS1* 融合遺伝子、*EGFR, KRAS, ERBB2, BRAF, PIK3CA, AKT, MAP2K1* の活性型点変異周辺計 26,183 bp を特異的にハイブリダイゼーションによって濃縮し、Ion 318 chip を用いた Ion PGM シークエンサー上で 8 サンプルを同時解析した。平均 depth は 1500 以上、On target rate は 60%以上と良好なシークエンス性能を示した。独自に開発した融合遺伝子探索プログラムを併用して変異解析を行ったところ各細胞株における既知の変異を正確に診断できた。前年度に実施した細胞株及び臨床検体の融合遺伝子探索の予備検討結果とあわせ、NCCE Panel の基本設計が完成した。診断薬化を図るため (株) 理研ジェネシスと共同研究契約を結び、NCCE Panel プロトタイプの基本性能試験を行った。これらの結果をふまえ医療機器、体外診断薬の承認の可能性について (独) 医薬品医療機器総合機構と薬事戦略相談の事前相談に臨み、助言を得た。

D. 考察

次世代シークエンス技術、MassArray の利用により Multiplex 体細胞変異の診断は充分に実施可能であった。マルチ診断薬については、薬事法上の規制およびコンパニオン診断に関するガイダンスとの整合性につき、議論の最中である。本プロジェクトの進捗に伴い、規制上との整合性については、規制当局との綿密な連携により進めていく必要があり、次年度にも事前相談、対面助言を受ける予定である。

本研究で実施している、feasibility 試験の実績は、当該企業における日本での承認申請に対する重要な動機づけとなると考えられる。今後、計画内容を忠実に実行し、キット開発に関する PMDA の薬事戦略相談事前面談・対面助言を今後も継続的に行い、平成 27 年度におけるマルチプレックス診断薬の臨床性能試験の実施に向け積極的に推進する。

E. 結論

3 つのマルチ診断薬について、いずれも良好な基本性能試験成績と良好な feasiblility 試験結果を得た。

申請に当たって、当局との事前相談を実施し、有益な助言を得た。これらを踏まえて、臨床性能試験の実施に向け、準備を継続する。

F. 健康危険情報

特記なし。

G. 研究発表

(発表誌名巻号・頁・発行年等も記入)

1. 論文発表

1. Okamoto I, Sakai K, Morita S, Yoshioka H, Kaneda H, Takeda K, Hirashima T, Kogure Y, Kimura T, Takahashi T, Atagi S, Seto T, Sawa T, Yamamoto M, Satouchi M, Okuno M, Nagase S, Takayama K, Tomii K, Maeda T, Oizumi S, Fujii S, Akashi Y, Nishino K, Ebi N, Nakagawa K, Nakanishi Y, Nishio K. 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. Oncotarget, 5(8): 2293-304, 2014.

2. 学会発表

1. Magdaleno SS, Nishio K, et al. The OncoNetwork Consortium: A global

collaborative research study on the development and verification of an Ion AmpliSeq RNA gene lung fusion panel. American Association for Cancer Research 104th Annual Meeting 2014, San Diego, 2014.4.5-9.

2. Cienfuegos J, Nishio K, et al. Verification of an Ion AmpliSeq™ RNA Fusion Lung Cancer Research Panel, workflow, and analysis solution: an OncoNetwork collaborative research study. The 64th Annual Meeting of the American Society of Human Genetics, San Diego, 2014.10.18-22.
3. Tsuchihara K, et al, Development and Validation of a DNA Based Test for Guiding Therapy in Lung Cancer by Seiconductor-based Next Generation Sequencer. AMP 2014 Annual Meeting, National Harbor, MD., 2014.11.15.

H. 知的財産等の出願・登録状況（予定を含む。）

1. 特許取得
   1. 次世代 DNA シークエンスデータを用いた融合遺伝子融合点検出プログラム(予定)
   2. 融合遺伝子探索プログラム(特願2015-007103)

2. 実用新案登録
   該当なし

3. その他

厚生労働科学研究費補助金（創薬基盤推進研究事業）
分担研究報告書

LungFusion /LungCartaにおけるFeasibility試験・キットデザインの確定・基本性能試験に関する研究

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研究分担者	冨田秀太	近畿大学医学部ゲノム生物学教室・講師
研究分担者	武田真幸	近畿大学医学部腫瘍内科・講師

研究要旨
IonPGMおよびMassArrayによるMultiplex体細胞変異診断薬（PGM Fusion Panel およびLung Fusion kit)の基本設計を完了させ、海外アカデミアと共同でのfeasibility 試験を実施した。Feasibility 試験の結果に基づきPGM Fusion Panelについては、海外でのCE-IVD承認を得た。国内では規制当局の助言を得て、臨床性能試験の準備を整えた。

A．研究目的

IonPGMおよびMassArrayを用いて、肺癌分子標的薬のコンパニオン診断のためのマルチ診断薬の開発を行う。Feasibility試験、キットデザインの確定、GMP製造、SOP整備の工程による開発を進め、最終年度には臨床性能試験を開始するための環境を整える。

B．研究方法

Feasibility試験終了後速やかにキットデザイン等につきPMDAの助言を受け、その助言に基づき基本性能試験、GMPレベルでの製造移管、診断薬企業との連携により迅速に実施し、承認プロセスに関するデータ整備、資料整備を進めた。

（倫理面への配慮）
Feasibility試験の実施に当たっては、施設の倫理委員会の承認の得て実施した。

C．研究結果

平成25年度に実施したPMDA薬事戦略相談事前面談の結果を受け、シーケノム社（現アジェナ・バイオサイエン社）、ライフテクノロジーズ社（現サーモフィッシャーサイエンティフィック社）と共同研究契約を締結した。平成26年度はアジェナ・バイオサイエン社と共同で、MassArrayのfeasibility 試験を実施し、オーストラリアでのfeasibility 試験と連携し、データの取り纏めを行った。それを基に、アジェナ社と基本性能試験を開始した。また、近畿大学医学部において継続的に実施した次世代シーケンサーIonPGM を用いたPGM Fusion Panelのfeasibility試験では実臨床レベルのサンプルでの実施成功率は96%と良好であった。海外アカデミアと共同でのfeasibility 試験の結果は、2014年アメリカ癌学会で報告され、この結果を基に、キットデザインの確定、SOPの確定を行った。また企業との共同による基本性能試験、キットのGMP製造移管を行った。これらの結果を基に、サーモフィッシャーサイエンティフィック社は、PGM Fusion Panelの欧州CE-IVDの承認を得た。また、遺伝子解析装置としてIon PGM Dxの医療機器化を完了した。

D．考察

臨床サンプルからのRNAサンプルを用いたfeasibility試験において、良好な成功率を得たことから、実臨床レベルで充分に使用可能であると考えられる。GMP移管等もスムーズに推移している。結果の判別のためのソフトウエアの最終確定を進めており、H27年度の半ばに完了する予定である。最終年度の臨床性能試験の実施に向け立案、承認を得る段階にある。

E．結論

IonPGMおよびMassArrayによるPGM Fusion Panelおよびlung Fusion kitは良好な基本性能およびfeasibility が示され、体外診断薬の為の臨床性能試験の実施に向け、順調に推移している。

F．健康危険情報

特記なし。

G． 研究発表

（発表誌名巻号・頁・発行年等も記入）

1. 論文発表

1. Okamoto I, Sakai K, Morita S, Yoshioka H,

Kaneda H, Takeda K, Hirashima T, Kogure Y, Kimura T, Takahashi T, Atagi S, Seto T, Sawa T, Yamamoto M, Satouchi M, Okuno M, Nagase S, Takayama K, Tomii K, Maeda T, Oizumi S, Fujii S, Akashi Y, Nishino K, Ebi N, Nakagawa K, Nakanishi Y, Nishio K. 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. Oncotarget, 5(8): 2293-304, 2014.

2. 学会発表

1. Magdaleno SS, Nishio K, et al. The OncoNetwork Consortium: A global collaborative research study on the development and verification of an Ion AmpliSeq RNA gene lung fusion panel. American Association for Cancer Research 104th Annual Meeting 2014, San Diego, 2014.4.5-9.
2. Cienfuegos J, Nishio K, et al. Verification of an Ion AmpliSeq™ RNA Fusion Lung Cancer Research Panel, workflow, and analysis solution: an OncoNetwork collaborative research study. The 64th Annual Meeting of the American Society of Human Genetics, San Diego, 2014.10.18-22.

H. 知的財産等の出願・登録状況（予定を含む。）

1. 特許取得
該当なし

2. 実用新案登録
該当なし

3. その他

厚生労働科学研究費補助金（創薬基盤推進研究事業）
分担研究報告書

NCCEパネルの設計、基本・臨床性能試験に関する研究

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研究要旨
次世代シークエンス技術を応用したMultiplex体細胞変異診断薬（NCCE Panel）の基本設計を完了させ、独自に開発した融合遺伝子探索プログラムの知財化を行った。医療機器、体外診断薬としての承認を目指し診断薬企業との共同研究を開始した。今後規制当局の助言を得て臨床性能試験の準備を進める。

A．研究目的

次世代シークエンス技術を応用し肺癌分子標的療法の治療効果を予測する複数の遺伝子異常を同時に測定可能なMultiplex体細胞変異診断薬（NCCE Panel）のfeasibility試験、GMP製造、SOP整備の工程による開発を進め、最終年度（平成27年度）に臨床性能試験を開始することを目標とする。

B．研究方法

既承認および臨床開発が進行中の肺腺癌分子標的薬の効果予測に有用な10遺伝子のゲノムDNA断片を特異的に濃縮し、ライフテクノロジーズ社Ion PGMによる解析が可能なターゲットキャプチャーシステムを設計した。ゲノムDNA上の逆位・転座を自動的に検出する独自のコンピュータープログラムを設計した。国立がん研究センターに保有する希少ドライバー変異陽性の肺がん細胞株8株のゲノムDNAを用いてターゲットキャプチャーシークエンス及び変異検出を行った。

C．研究結果

培養細胞株8株(PC9, II-18, H1075, HT-29, H1048, HCC78, H2228, LC2/ad) のゲノムDNA各250 ngから、*RET, ALK, ROS1*融合遺伝子、*EGFR, KRAS, ERBB2, BRAF, PIK3CA, AKT, MAP2K1*の活性型点変異周辺計26,183 bpを特異的にハイブリダイゼーションによって濃縮し、Ion 318 chipを用いたIon PGMシークエンサー上で8サンプルを同時解析した。平均depthは1500以上、On target rateは60%以上と良好なシークエンス性能を示した。独自に開発した融合遺伝子探索プログラムを併用して変異解析を行ったところ各細胞株における既知の変異を正確に診断できた。前年度に実施した細胞株及び臨床検体の融合遺伝子探索の予備検討結果とあわせ、NCCE Panelの基本設計が完成した。診断薬化を図るため（株）理研ジェネシスと共同研究契約を結び、NCCE Panelプロトタイプの基本性能試験を行った。これらの結果をふまえ医療機器、体外診断薬の承認の可能性について（独）医薬品医療機器総合機構と薬事戦略相談の事前相談に臨み、助言を得た。

D．考察

次世代シークエンス技術の利用によりMultiplex体細胞変異の診断は可能であった。今後臨床性能試験における、適切な検体数、感度、特異度等を設定する。また肺腺癌の希少ドライバー遺伝子異常の陽性例が検出されているゲノムスクリーニング研究LC-SCRUMと連動した研究計画の立案を進める必要がある。

E．結論

NCCE Panelの良好な基本性能が証明された。今後、規制当局の助言を得て最終年にGMP製造移管、SOP整備を進め、臨床性能試験の立案を行う。

F．健康危険情報

特記なし。

G．研究発表

学会発表

1. Tsuchihara K, et al., Development and Validation of a DNA Based Test for Guiding Therapy in Lung Cancer by Seiconductor-based Next Generation Sequencer. AMP 2014 Annual Meeting, National Harbor, MD., 2014.11.15.

H．知的財産等の出願・登録状況（予定を含む。）

1. 特許出願
融合遺伝子探索プログラム（特願2015-007103）

別紙４

研究成果の刊行に関する一覧表

雑誌

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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.

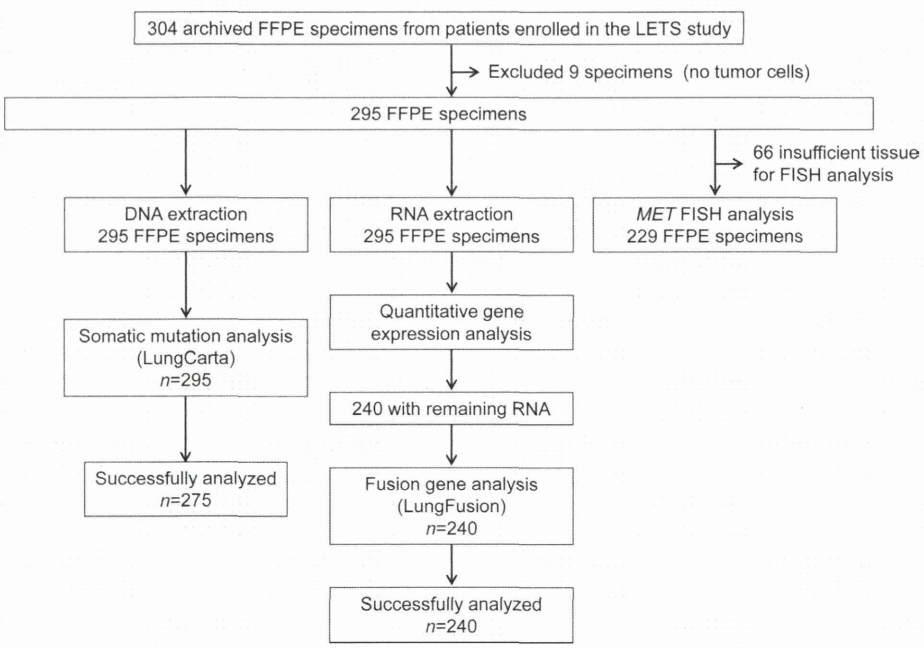

Figure 1: CONSORT diagram for the study. Of the FFPE specimens obtained from 304 advanced NSCLC patients (54%) enrolled in the LETS study, 9 specimens contained no tumor cells and the remaining 295 specimens were subjected to extraction of DNA and RNA. In addition, 229 FFPE specimens were analyzed for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

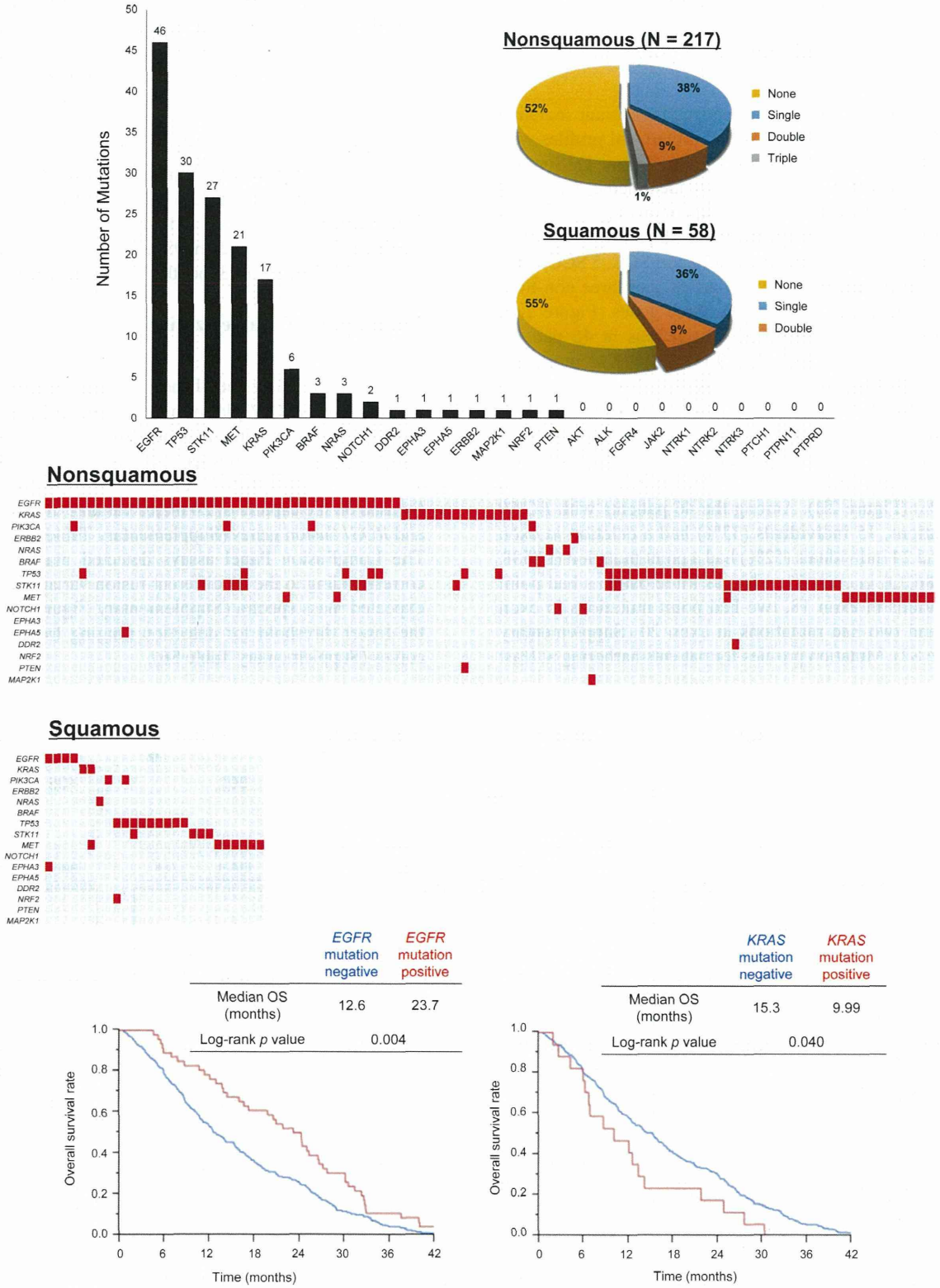

Figure 2: Analysis of somatic gene mutations in FFPE specimens from advanced NSCLC patients. A, The pie charts show the distribution for the number of mutations detected in specimens according to tumor histology. B, Number of mutations in each of the 26 analyzed genes for the 275 specimens that were 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).

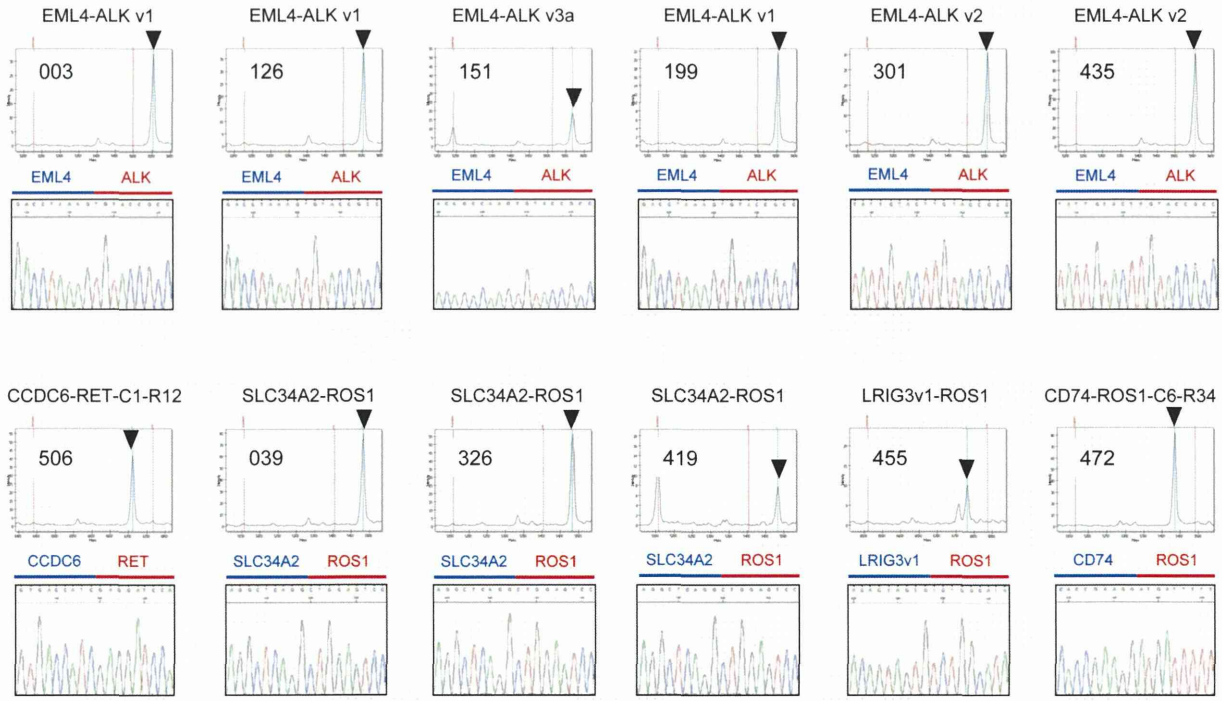

Figure 3: Detection of *ALK*, *RET*, and *ROS1* fusion genes in FFPE specimens of advanced NSCLC. Arrowheads indicate mass spectrometry peaks corresponding to the indicated fusion genes. The variants of these fusions identified with the LungFusion Panel were validated by direct sequencing.

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

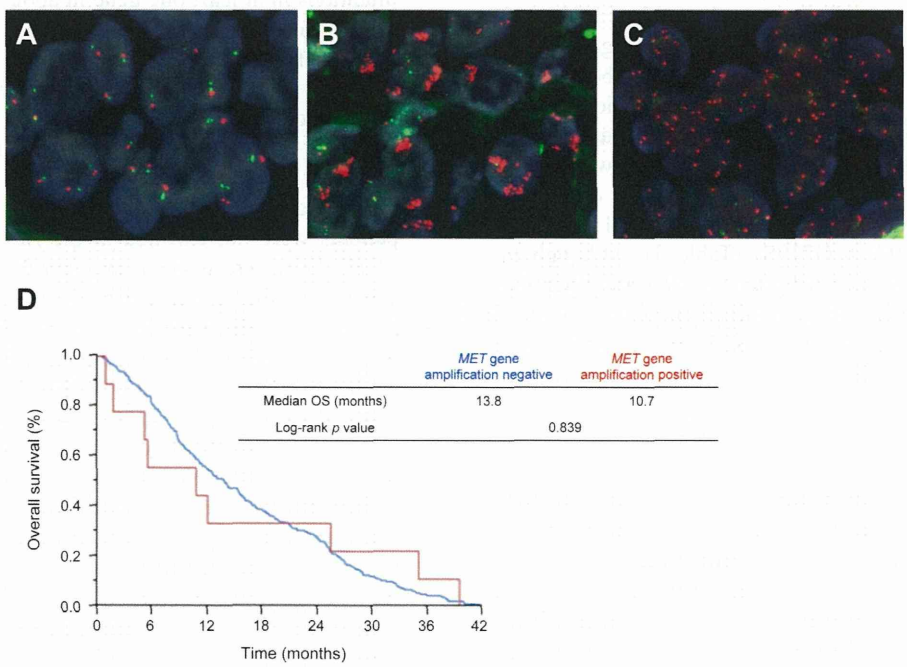

Figure 4: FISH analysis of de novo *MET* amplification in advanced NSCLC and survival analysis according to *MET* amplification status. A–C, Representative FISH images for specimens negative (A) or positive (B and C) for *MET* amplification. Green and red signals correspond to CEN7p and the *MET* locus,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