Original Study

Clinical Relevance of *EGFR*- or *KRAS*-mutated Subclones in Patients With Advanced Non–small-cell Lung Cancer Receiving Erlotinib in a French Prospective Cohort (IFCT ERMETIC2 Cohort - Part 2)

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Abstract

Detecting driver mutations belongs now to the best practices in advanced/metastatic non–small-cell lung cancer. New molecular techniques are highly sensitive. In non–small-cell lung cancer treated with erlotinib (n = 228), we report that *EGFR*- and *KRAS*-mutated subclones had a prognostic value, but not minor KRAS-mutated subclones. Molecular techniques must be sensitive but not under 1% of mutated tumor cells.

Introduction: Evaluation of *EGFR* Mutation status for the administration of EGFR-TKIs in non-small cell lung Carcinoma (ERMETIC) was a prospective study designed to validate the prognostic value of *EGFR*/*KRAS* mutations in patients with advanced non–small-cell lung cancer (NSCLC), all receiving a first-generation tyrosine kinase inhibitor, erlotinib. ERMETIC2 was an ancillary project evaluating the clinical value of common *EGFR*/*KRAS*-mutated subclones regarding prognosis using highly sensitive molecular detection methods. **Materials and Methods:** Tumor samples from 228 patients with NSCLC (59% adenocarcinoma, 37% women, and 19% never/former smokers) were available for reanalysis using alternative highly sensitive molecular techniques. A multivariate Cox model was used for prognostic analysis. **Results:** Using alternative highly sensitive techniques, 16 *EGFR* and 51 *KRAS* supplementary mutations were newly identified, all still exclusive, leading to an overall rate of 12.3% (n = 28) and 33.3% (n = 76), respectively. Using real-time polymerase chain reaction (hybridization probe), they were significantly associated with progression-free survival ($P = .02$) and overall survival (OS) ($P = .01$), which were better for *EGFR*-mutated patients for progression-free survival (hazard ratio [HR], 0.46; 95% confidence interval [CI], 0.28-0.78) and OS (HR, 0.56; 95% CI, 0.31-1), and worse for *KRAS* mutations and OS (HR, 1.63; 95% CI, 1.09-2.44). Using the most sensitive technique detection for *KRAS*—clamp polymerase chain reaction—*KRAS* mutated subclones did not impact OS. **Conclusions:** *KRAS* and *EGFR* mutations were detected in higher proportions by alternative highly sensitive

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molecular techniques compared with direct Sanger sequencing. However, minor *KRAS*-mutated subclones offered no prognostic value when representing less than 1% of the tumor cells.

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Introduction

Epidermal growth factor receptor tyrosine kinase inhibitors (EGFR-TKIs), erlotinib, gefitinib, and afatinib, are authorized worldwide as first-line treatment for patients with advanced or metastatic non–small-cell lung cancer (NSCLC) with *EGFR*-activating mutations in their tumor.[1-3] Recently, the third-generation EGFR-TKI, osimertinib, has been validated as the standard of care for patients with T790M-positive NSCLC in whom disease had progressed during first-line EGFR-TKI therapy.[4] And more recently, osimertinib showed efficacy superior to that of standard first-/second-generation EGFR-TKIs in the first-line treatment of *EGFR* mutation-positive advanced NSCLC.[5]

Molecular tumor testing is actually mandatory for selecting first-line treatment in patients with advanced or metastatic NSCLC.[6-9] Yet no *EGFR* mutation assay is currently specifically recommended by the United States Food and Drug Administration, the European Agency for the Evaluation of Medicinal Products, or the European Society of Medical Oncology to inform treatment decisions.[10,11] Direct sequencing has for many years been considered the gold standard for testing, yet its sensitivity can limit its use to routinely somatic tumor testing, and alternative more sensitive molecular methods, targeted or not, have often since replaced this approach.[12] Furthermore, next-generation sequencing (NGS) or droplet digital polymerase chain reaction (ddPCR) are developed in molecular platforms. All these highly sensitive molecular methods should be able to detect mutated subclones (5% of mutated cells) to minor subclones (< 1% of mutated cells), thus raising the question of the prognostic/predictive value of such mutated different subclones.

Although *KRAS* is not a target for therapy, lung cancer molecular analyses often test for *EGFR* as well as *KRAS* mutations. In the Caucasian NSCLC population, *EGFR* and *KRAS* mutations are found in 11% and 29% of the patients, respectively.[3,7] These mutations are often mutually exclusive, hence why some authors have even proposed a step-by-step algorithm using *KRAS* mutation testing as the first step to rule out the presence of an *EGFR* mutation, in case of using targeted alternative molecular methods. Furthermore, *KRAS* mutations appear to affect an heterogeneous population with different prognostic/predictive values depending on the type of nucleotide base substitution, regarding EGFR-TKI treatment.[13,14] Finally, several studies have distinguished patients with *EGFR* mutations from those with non-*EGFR* mutated tumors, yet including *KRAS*-mutated tumors. In our study, we evaluated what impact the mutation detection threshold has on the prognostic value of erlotinib efficacy.

The ERMETIC (Evaluation of *EGFR* Mutation status for the administration of EGFR-TKIs in non-small cell lung Carcinoma) study, designed and supported by the French Collaborative Thoracic Cancer Intergroup, funded by the French National Cancer Institute, reported that formaldehyde-fixed paraffin-embedded specimens may be suitable sources for DNA analysis by means of genomic Sanger sequencing, providing rigorous preanalytical quality control standards are respected.[9,12] Since that publication, ERMETIC centers have switched to alternative molecular methods. The first step of

Table 1 Patients' Characteristics

	Frequency N = 228	Percentage, %
Age, y		
< 60	84	37
60-69	82	36
≥ 70	62	27
Gender		
Female	82	36
Male	146	64
Performance status		
0	36	17
1	98	46
2 or 3	77	37
Missing	17	
Histology		
Squamous cell	48	21
Adenocarcinoma	131	57
Others	49	21
Initial disease stage		
I-II-IIIA	48	21
IIIB	32	14
IV	147	65
Missing	1	
Initial number of metastatic sites		
0 or 1	107	47
2	65	29
3 or more	54	24
Missing	2	
Localization of metastasis		
Brain	62	27
Bone	79	35
Lung	105	46
Geographical origin		
Two European parents	201	88
Others	27	12
Smoking status		
Never	41	18
Former	150	66
Current	35	15
Missing	2	

Table 2 *EGFR* and *KRAS* Mutations in the Population (n = 228)
2A. Categorization of Mutation Status in the Population (n = 228)

N = 228 (%)	Direct Sequencing	New Mutations by Alternative Molecular Techniques (Including KRAS_SH)	New *KRAS* Mutation by Clamped PCR (KRAS_PNA)	Total
EGFR	12 (5.3)	16 (7.0)		28 (12.3)
KRAS	25 (11.0)	20 (8.8)	31 (13.6)	76 (33.3)
Wild type				124 (54.4)

Abbreviations: *KRAS*, AT_SH = alternative technique by hybridization probe (SH assay); *KRAS*, AT_PNA = alternative technique by clamp-PCR (SH + PNA assay); PCR = polymerase chain reaction; PNA = peptide nucleic acid.

ERMETIC2 consisted of a nationwide technological evaluation of this new *EGFR/KRAS* testing using NSCLC cell line DNA with various allele proportions. We demonstrated that the best threshold of mutation detection was obtained using allele-specific amplification-based technologies, with cutoff values of 5% and 1% for clamped PCR with peptide nucleic acid (PNA).[15] We report the prognosis-based clinical impact of this new strategy on 228 ERMETIC patients with available tumor samples reanalyzed using these techniques.

Patients and Methods

Patients and Tumor Samples

The ERMETIC prospective observational study included 522 patients with advanced NSCLC, either newly treated with erlotinib or before erlotinib administration.[6] A preliminary study revealed that *EGFR* and *KRAS* mutations identified using Sanger direct sequencing were independent markers of outcome in this population.[6] A subgroup of 228 patients provided sufficient samples for a second round of common *EGFR* and *KRAS* mutation screening using the alternative molecular methods selected after ERMETIC2 – part 1.[12]

Biological Assessment

The methods used were previously described.[12] Briefly, we used fragment analysis for *EGFR* exon 19 assessment, and targeted molecular techniques based on allele-specific amplification: probe-specific detection, TaqMan assay for *EGFR* exon 21 L858R mutation, and hybridization probe (SH assay), without PNA (KRAS_SH), or with PNA as clamp-PCR strategy (KRAS_PNA) for *KRAS* mutations.

Statistical Analysis

Endpoint definitions were as previously defined.[6] Survival rates were estimated using the Kaplan-Meier method with 95% confidence intervals (CIs). Impact on survival was quantified using Cox models and hazard ratios with 95% CIs. Variables with a *P*-value < .20 in univariate analysis were included into the multivariate analysis. A backwards selection process was undertaken with the final model, including all variables with *P*-values < .05.

Results

Patient Characteristics

The population consisted of patients with samples available for both *EGFR* and *KRAS* mutation analyses, excluding patients with insufficient material for simultaneous analysis of both genes or with non-amplifiable samples. Clinical characteristics of the patients (Table 1) did not differ from those with sample not available for this second part of the study (data not shown).

EGFR/KRAS Status

When tumors (n = 228) were tested by Sanger direct sequencing, the overall mutation rate was 16.2% (12 [5.3%] and 25 [11.0%] *EGFR* and *KRAS* mutations, respectively). When the same tumors (n = 228) were tested by alternative molecular methods, the overall mutation rate was 45.6% (28 [12.2%] and 76 [33.3%] *EGFR* and *KRAS* mutations, respectively), with 67 new mutations found (16 in *EGFR* and 51 in *KRAS*), including 60.8% (31/51) for *KRAS* mutations identified using the clamp-PCR strategy (Tables 2A and 2B). Details of *EGFR* and *KRAS* mutations by techniques are described in Table 3.

Survival Analysis: Progression-free Survival (PFS) and Overall Survival (OS)

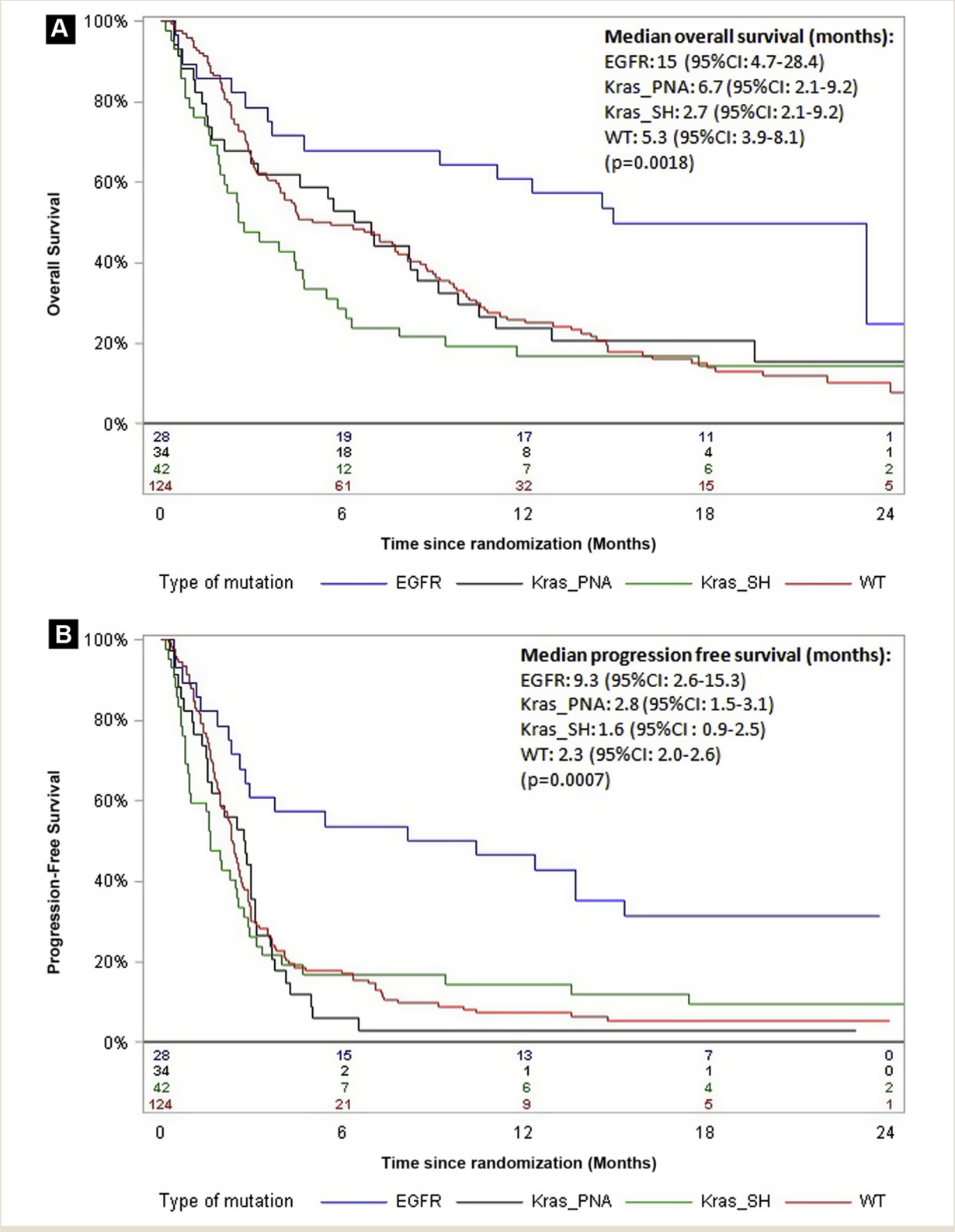
No differences in OS or PFS were observed between the initial and reanalyzed ERMETIC populations (data not shown). Patients with *KRAS*-mutated tumors were categorized according to the

Table 2B Number of Mutations by Technique

Technique	*EGFR*, AT FA (del19), n	*EGFR*, AT TaqMan (L858R), n	Total No. Mutations, n (%)
EGFR-SQC (n = 12)	6	6	12 (5.3)
New *EGFR* mutations (n = 16)	9	7	16 (7)
All *EGFR* mutations	15	13	28 (12.2)
Technique	***KRAS*, AT_SH**	***KRAS*, AT_PNA**	**Total No. Mutations, n (%)**
KRAS-SQC (n = 25)	22	3	25 (11)
New *KRAS* mutations (n = 51)	20	31	51 (22.4)
All *KRAS* mutations	42	34	76 (33.3)

Abbreviations: *EGFR*, SQC = direct sequencing; *EGFR*, *AT* = alternative technique (Del19: fragment analysis; L858R: probe-specific detection by TaqMan assay); *KRAS*, SQC = direct sequencing; *KRAS*, AT_SH = alternative technique by hybridization probe (SH assay); *KRAS*, AT_PNA = alternative technique by clamp-PCR (SH + PNA assay); PCR = polymerase chain reaction; PNA = peptide nucleic acid.

Figure 1 Survival Curves for Patients in the ERMETIC Re-analyzing Models According to Detection Technique. A, Overall Survival; B, Progression-free Survival



Abbreviations: CI = confidence interval; *EGFR* status = fragment analysis for *EGFR* exon 19 and TaqMan assay for *EGFR* L858R analysis; ERMETIC = Evaluation of *EGFR* Mutation status for the administration of EGFR-TKIs in non-small cell lung Carcinoma; *KRAS* status = real-time polymerase chain reaction with hybridization probe (KRAS_SH) or clamped polymerase chain reaction with peptide nucleic acid (KRAS_PNA); WT = wild-type for *EGFR* and *KRAS* mutations.

Table 3 Detail of *EGFR* and *KRAS* Mutations Detected by Molecular Methods (n = 104)

ID-ERMETIC	*EGFR*, SQC	*EGFR*, AT	*KRAS*, SQC	*KRAS*, AT_SH	*KRAS*, AT_PNA
490	WT	WT	G12A	G12A	G12A
130	WT	WT	G12A	G12A	G12A
110	WT	WT	G12A	G12A	G12A
150	WT	WT	G12C	G12C	G12C
320	WT	WT	G12C	G12C	G12C
217	WT	WT	G12C	G12C	G12C
478	WT	WT	G12C	G12C	G12C
75	WT	WT	G12C	G12C	G12C
429	WT	WT	G12C	WT	G12C
421	WT	WT	G12D	G12D	G12D
282	WT	WT	G12D	G12D	G12D
222	WT	WT	G12D	G12D	G12D
247	WT	WT	G12V	G12V	G12V
203	WT	WT	G12V	G12V	G12V
296	WT	WT	G12V	G12V	G12V
31	WT	WT	G12V	G12V	G12V
415	WT	WT	G12V	G12V	G12V
473	WT	WT	G12V	G12V	G12V
48	WT	WT	G12V	G12V	G12V
215	WT	WT	G12V	G12V	G12V
259	WT	WT	G12V	WT	G12V
259	WT	WT	G12V	WT	G12V
475	WT	WT	M	G12F	G12F
96	WT	WT	M	G12C	G12C
388	WT	WT	M	G12F	G12F
226	WT	WT	WT	G12D	G12D
512	WT	WT	WT	G12V	G12V
446	WT	WT	WT	M	M
465	WT	WT	WT	G12D	G12D
527	WT	WT	WT	G12D	G12D
522	WT	WT	WT	G13D	G13D
426	WT	WT	WT	G12V	G12V
206	WT	WT	WT	G12C	G12C
245	WT	WT	WT	G12V	G12V
151	WT	WT	WT	G12C	G12C
184	WT	WT	WT	G12V	G12V
335	WT	WT	WT	G12C	G12C
384	WT	WT	WT	G13V	G13V
456	WT	WT	WT	G12V	G12V
285	WT	WT	WT	G12A	G12A
80	WT	WT	WT	G12S	G12S
101	WT	WT	WT	G12C	G12C
191	WT	WT	WT	M	M
244	WT	WT	WT	G12C	G12C
286	WT	WT	WT	G12V	G12V
291	WT	WT	WT	WT	G12D
303	WT	WT	WT	WT	G12C
413	WT	WT	WT	WT	G12S
118	WT	WT	WT	WT	G12C
205	WT	WT	WT	WT	G13D
393	WT	WT	WT	WT	G13D
123	WT	WT	WT	WT	G12D
391	WT	WT	WT	WT	G12S
230	WT	WT	WT	WT	G12D

Table 3 Continued

ID-ERMETIC	*EGFR*, SQC	*EGFR*, AT	*KRAS*, SQC	*KRAS*, AT_SH	*KRAS*, AT_PNA
220	WT	WT	WT	WT	G12D
234	WT	WT	WT	WT	G12S
214	WT	WT	WT	WT	G12D
132	WT	WT	WT	WT	G12C
453	WT	WT	WT	WT	G12V
469	WT	WT	WT	WT	G12R
200	WT	WT	WT	WT	G12R
254	WT	WT	WT	WT	G13C
190	WT	WT	WT	WT	G12C
367	WT	WT	WT	WT	G12C
34	WT	WT	WT	WT	G12S
183	WT	WT	WT	WT	G12S
382	WT	WT	WT	WT	G12D
401	WT	WT	WT	WT	G13S
436	WT	WT	WT	WT	G12C
29	WT	WT	WT	WT	G12V
443	WT	WT	WT	WT	G12R
173	WT	WT	WT	WT	G12V
243	WT	WT	WT	WT	M
276	WT	WT	WT	WT	G12D
368	WT	WT	WT	WT	G13C
366	WT	WT	WT	WT	G12F
287	Del19	Del19	WT	WT	WT
375	Del19	Del19	WT	WT	WT
515	L858R	L858R	WT	WT	WT
233	Del19	Del19	WT	WT	WT
319	WT	L858R	WT	WT	WT
392	WT	Del19	WT	WT	WT
464	WT	Del19	WT	WT	WT
545	WT	Del19	WT	WT	WT
529	Del19	Del19	WT	WT	WT
269	WT	Del19	WT	WT	WT
78	WT	Del19	WT	WT	WT
412	WT	L858R	WT	WT	WT
135	Del19	Del19	WT	WT	WT
364	WT	Del19	WT	WT	WT
381	L858R	L858R	WT	WT	WT
260	WT	L858R	WT	WT	WT
344	Del19	Del19	WT	WT	WT
68	L858R	L858R	WT	WT	WT
534	L858R	L858R	WT	WT	WT
162	WT	L858R	WT	WT	WT
378	WT	L858R	WT	WT	WT
174	WT	L858R	WT	WT	WT
87	L858R	L858R	WT	WT	WT
121	WT	Del19	WT	WT	WT
196	WT	L858R	WT	WT	WT
242	WT	Del19	WT	WT	WT
361	L858R	L858R	WT	WT	WT
474	WT	Del19	WT	WT	WT

Abbreviations: *EGFR*, SQC = direct sequencing; *EGFR*, *AT* = alternative technique (Del19: fragment analysis; L858R: probe-specific detection by TaqMan assay); *KRAS*, SQC = direct sequencing; *KRAS*, AT_SH = alternative technique by hybridization probe (SH assay); *KRAS*, AT_PNA = alternative technique by clamp-PCR (SH + PNA assay); M = mutation with no precision of the type of mutation; PCR = polymerase chain reaction; PNA = peptide nucleic acid; WT = wild type.

Table 4 Multivariate Cox Model for Survival Analysis (n = 224)

	Overall Survival			Progression-free Survival		
	HR	95% CI	*P* Value	HR	95% CI	*P* Value
Mutation						
WT	1[a]		.01	1[a]		.02
EGFR mutation	0.56	0.31-1.00		0.46	0.28-0.78	
KRAS mutation (PNA)	1.08	0.69-1.69		1.17	0.77-1.77	
KRAS mutation (SH)	1.63	1.09-2.44		1.10	0.74-1.65	
Age, y						
< 60	–	–	–	1[a]	–	.07
60-69	–	–	–	0.72	0.50-1.03	
≥ 70	–	–	–	0.66	0.45-0.97	
Performance status						
0	1[a]	–	$< 10^{-4}$	1[a]	–	.0006
1	1.52	0.93-2.47		1.86	1.17-2.94	
2 or 3	3.17	1.90-5.28		2.68	1.66-4.33	
Missing	1.31	0.62-2.80		1.75	0.86-3.56	
Histology						
Adenocarcinoma	1[a]	–	.06	1[a]	–	.03
Squamous cell	1.60	1.07-2.38		1.10	0.75-1.62	
Others	1.31	0.90-1.90		1.60	1.12-2.27	
Initial number of metastatic sites						
0 or 1	1[a]	–	$< 10^{-4}$	1[a]	–	.0014
2	1.47	1.02-2.13		1.53	1.07-2.19	
3 or more	2.50	1.67-3.74		1.93	1.33-2.80	
Lung metastasis (2MD)						
No	1[a]	–	.10	–	–	–
Yes	0.76	0.54-1.06		–	–	–
Geographical origin						
Two European parents	1[a]	–	.09	–	–	–
Others	0.62	0.36-1.08		–	–	–
Smoking status (2MD)						
Never	1[a]	–	.15	1[a]	–	.07
Former	1.27	0.80-2.03		1.68	1.08-2.62	
Current	1.76	0.99-3.13		1.73	0.98-3.05	

Abbreviations: CI = confidence interval; *EGFR* = fragment analysis (exon 19) and TaqMan assay for L858R; HR = hazard ratio; KRAS_SH = real-time polymerase chain reaction (qPCR) with hybridization probe; KRAS_PNA = clamped PCR with peptide nucleic acid (PNA); 2MD = missing data; WT = wild-type EGFR and wild-type KRAS.
[a]Reference class.

mutation detection method, SH assay with or without clamp-PCR strategy (*KRAS*_SH vs. *KRAS*_PNA). The median OS was 15 months (95% CI, 4.7-28.4 months), 6.7 months (95% CI, 2.1-9.2 months), 5.3 months (95% CI, 3.9-8.1 months), and 2.7 months (95% CI, 2.1-9.2 months) for *EGFR*-mutated tumors, *KRAS_PNA*-mutated tumors, *EGFR/KRAS* wild-type (WT) tumors, and *KRAS*_SH-mutated tumors, respectively ($P = .0018$) (Figure 1A). The median PFS was 9.3 months (95% CI, 2.6-15.3 months), 2.8 months (95% CI, 1.5-3.1 months), 2.3 months (95% CI, 2.0-2.6 months), and 1.6 months (95% CI, 0.9-2.5 months) for patients with *EGFR*-mutated, *KRAS*_PNA-mutated, WT, and *KRAS*_SH-mutated tumors, respectively ($P = .0007$) (Figure 1B). The 1-year survival rates were 60.7% (95% CI, 42.4%-76.4%), 25.8% (95% CI, 18.9%-34.2%), 23.5% (95% CI, 12.4%-40%), and 16.7% (95% CI, 8.3%-30.6%) for these 4 groups, respectively. The clinical characteristics significantly associated with prognosis (OS, PFS) were the same as for the initial population (Table 4 and data not shown). After adjusting for clinical factors, multivariate analysis of mutation status remained significantly associated with OS ($P = .01$) and PFS ($P = .02$), which were better for *EGFR*-mutated patients for PFS (hazard ratio [HR], 0.46; 95% CI, 0.28-0.78) and OS (HR, 0.56; 95% CI, 0.31-1), and worse for *KRAS* mutations for OS (HR, 1.63; 95% CI, 1.09-2.44) (Table 4). Using the most sensitive technique detection for *KRAS*—clamp PCR—*KRAS* mutated subclones did not impact OS. *EGFR* mutation significantly decreased the risk or death by 44%, and the risk of progression or death by 54% in patients treated with erlotinib. *KRAS* mutations detected by SH (KRAS_SH) significantly increased the risk of death, by 63%.

Conversely, *KRAS* mutations detected by clamp-PCR strategy (KRAS_PNA) did not increase the risk of death.

Type of KRAS Mutation

No prognostic value was related to the alteration type (transition/transversion) or mutation location (codon 12 or 13) among the 76 *KRAS*-mutated patients.

Discussion

The prognostic or predictive value afforded by driver-mutated subclones and minor sub-clones in NSCLC and other cancer types is still open to debate. With the development of high throughput and extremely sensitive methods, such as NGS, clamp-based PCR, or ddPCR, establishing a cutoff is now mandatory. The clinical value of low allele frequency detection needed to be assessed regarding 2 issues: Can it rescue mutation testing for small biopsies with low tumor-cell content and high stromal component? Does it have any clinical value?

This study was designed to reanalyze paraffin-embedded NSCLC tumor samples using alternative molecular techniques currently employed in France and many laboratories worldwide thanks to their cost-efficiency for analysis of recurrent genetic alterations, requiring low amounts of DNA from formaldehyde-fixed paraffin-embedded samples. We described 16 and 51 new *EGFR* and *KRAS* mutations, respectively, after reanalysis. In the ERMETIC initial population, *EGFR* status impacted both PFS and OS, whereas *KRAS* status only impacted OS.[9,12] Similar results were observed for *EGFR* mutation in the reanalyzing study. In contrast, though, *KRAS* status analyzed by PCR using hybridization probes remained predictive of OS, the more sensitive clamped PCR method that identified low mutated subclones failed to impact prognosis, raising the question of these minor subclones clinical relevance for patient care.

The number of newly-detected *EGFR* mutations in our study proved relatively small, suggesting that *EGFR* mutations are present in the majority of tumor cells or associated with an amplification of the mutated allele in NSCLC, as previously described.[16,17] We demonstrated that, by using sensitive methods, we may be able to reattempt detection of an *EGFR* alteration, an important capability for treatment decisions. All our patients receiving EGFR-TKIs were correctly treated, although the mutation was not identified in the initial ERMETIC study; hence, why no modification of *EGFR* prognostic value was observed between initial and reanalyzing ERMETIC studies. In the latest study, testing was performed using methods with a 10% to 5% detection threshold for fragment analysis of *EGFR* exon 19 deletions and for PCR using TaqMan probes of *EGFR* L858R mutations.[15] Therefore, we deduce that the new *EGFR*-mutated cases were related to the tumor cell content being low, initially under the level of detecting *EGFR* mutation by direct sequencing. The unpredictable variability in *EGFR* copy number and therefore in *EGFR* WT/mutant allelic ratio justifies using sensitive methods to identify patients with *EGFR*-mutated tumors.

The situation is probably more complex for *KRAS* mutations in the setting of NSCLC,[7,13] with *KRAS*-mutated subclones previously described in NSCLC.[18] All the 25 *KRAS* mutations detected by direct sequencing in the initial population were detected by alternative molecular techniques in the reanalyzing population (internal positive controls). Among the remaining cases, 45 (19.7%) were positive for *KRAS* mutations using PCR with hybridization probes, and 76 (33.3%) were detected using more sensitive clamped PCR (no cases with concomitant *EGFR* mutation). However, this increased sensitivity did not detect any minor subclones as having prognostic impact. Our results suggest that patients with *KRAS*-mutated subclones, using 1% as a cutoff (clamp-PCR), behave as with WT mutations. Such absence of clinical relevance of *KRAS*-mutated minor subclones was previously described in advanced colorectal cancer treated with anti-EGFR therapy.[19] In NSCLC, it appears that such sensitive methods are not necessarily useful, achieving approximately 1% detection rate for *KRAS* mutations.

Conclusion

Highly sensitive molecular methods increased the number of *EGFR* and *KRAS* mutations in NSCLC tumors. For common *EGFR* mutations, this increase is lower and correlated with classical prognostic values (OS, PFS) in first-line EGFR-TKI-treated patients with NSCLC. For *KRAS* mutation, detection of mutated subclones (5%) is associated with survival (OS) but not the minor subclones (< 1%). Our study demonstrated that if more sensitive techniques could detect new mutated cases, it is not necessary to have a too low cutoff for such analysis. Threshold cutoff for mutation analysis must be taken into account for new molecular techniques such as NGS or ddPCR.

Clinical Practice Points

- Detecting driver mutations now belongs to the best practices in advanced/metastatic NSCLC. New molecular techniques are highly sensitive.
- Highly sensitive molecular methods increased the number of *EGFR* and *KRAS* mutations in NSCLC tumors. For common *EGFR* mutations, this increasing is lower with classical prognostic (OS, PFS) values. For *KRAS* mutation, the detection of mutated subclones is associated with survival (OS) but not the minor subclones.
- Molecular techniques must be sensitive but not under 1% of mutated tumor cells.

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Disclosure

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