



ASCO HIGHLIGHTS

31 MAYO - 4 JUNIO 2019



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Mutaciones de MET

Dra. Ana Laura Ortega

Con la colaboración de:



Bristol-Myers Squibb

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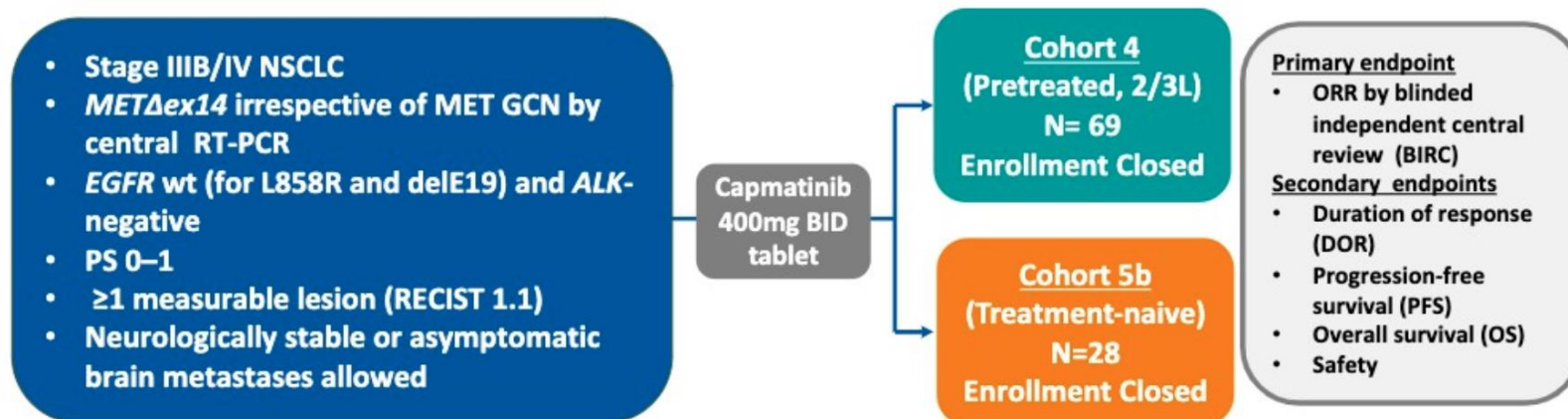
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Capmatinib in *MET Δ ex14*-mutated advanced non-small cell lung cancer (NSCLC): Efficacy data from the phase II GEOMETRY mono-1 study

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GEOMETRY mono-1: A phase II trial of capmatinib in patients with advanced NSCLC harboring *MET* exon14 skipping mutation



Study methodology:

- Cohort 4 and 5b are each analyzed separately and have independent statistical hypothesis
- Primary (ORR) and key secondary (DOR) endpoints based on BIRC including 2 parallel independent radiology reviewers (+ additional one for adjudication)
- Efficacy endpoints based on BIRC and investigator assessment per RECIST 1.1

Data cut off: April 15, 2019; median duration of follow-up for DOR: 9.7 months in Cohort 4 and 9.6 months in Cohort 5b
Additional data on *MET* mutated patients will be generated in Cohort 6 (2L; N~30) and Cohort 7 (1L; N~27)

Baseline characteristics

Baseline characteristics		Cohort 4 (2/3L) N = 69	Cohort 5b (1L) N = 28
Age (years)	Median (range)	71 (49-90)	71 (57-86)
Race, n (%)	Caucasian	49 (71.0)	24 (85.7)
	Asian	19 (27.5)	4 (14.3)
	Other	1 (1.4)	0
Sex, n (%)	Female/Male	40 (58.0)/29 (42.0)	18 (64.3)/10 (35.7)
Smoking history, n (%)	Never smoker	40 (58.0)	18 (64.3)
	Former smoker	27 (39.1)	9 (32.1)
	Current smoker	2 (2.9)	1 (3.6)
ECOG status, n (%)	0	16 (23.2)	7 (25.0)
	1	52 (75.4)	21 (75.0)
	2	1 (1.4)	0
Histology, n (%)	Adenocarcinoma	53 (76.8)	25 (89.3)
	Squamous	6 (8.7)	2 (7.1)
	Others*	10 (14.5)	1 (3.6)
Key metastatic site of cancer, n (%)	Brain [†]	11 (15.9)	3 (10.7)
	Liver	16 (23.2)	4 (14.3)
	Bone	41 (59.4)	16 (57.1)
	Adrenal	11 (15.9)	6 (21.4)
Concurrent MET amplification, n (%)	<4 GCN	18 (26.1)	4 (14.3)
	≥4-6 GCN	15 (21.7)	10 (35.7)
	≥6-<10	17 (24.6)	3 (10.7)
	≥10 GCN	11 (15.9)	4 (14.3)
	Missing	8 (11.6)	7 (25.0)

*all other histologies including 5 sarcomatoid/carcinosarcoma

[†]12 identified in medical history and 2 identified at baseline CT scan

Best overall response (pretreated cohort 4)

All responses confirmed per RECIST 1.1

Response rates consistent between BIRC and investigator assessment

	Cohort 4 (2/3L) N=69	
	BIRC	Investigator
Best overall response, n (%)		
Complete Response	0	1 (1.4)
Partial Response	28 (40.6)	28 (40.6)
Stable Disease	25 (36.2)	22 (31.9)
Non-CR/non-PD	1 (1.4)	2 (2.9)
Progressive Disease	6 (8.7)	7 (10.1)
Not evaluable*	9 (13.0)	9 (13.0)
Overall response rate (ORR) %, (95% CI)	40.6 (28.9, 53.1)	42.0 (30.2, 54.5)
Disease control rate (DCR) %, (95% CI)	78.3 (66.7, 87.3)	76.8 (65.1, 86.1)

*not qualifying for confirmed CR or PR and without SD after more than 6 weeks or progression within the first 12 weeks

BIRC, blinded independent review committee; CI, confidence interval; CR, complete response; DCR, disease control rate (CR+PR+SD+non-CR/non-PD); ORR, overall response rate (CR+PR); PD, progressive disease; PR, partial response; SD, stable disease

Best overall response (treatment naive cohort 5b)

All responses confirmed per RECIST 1.1

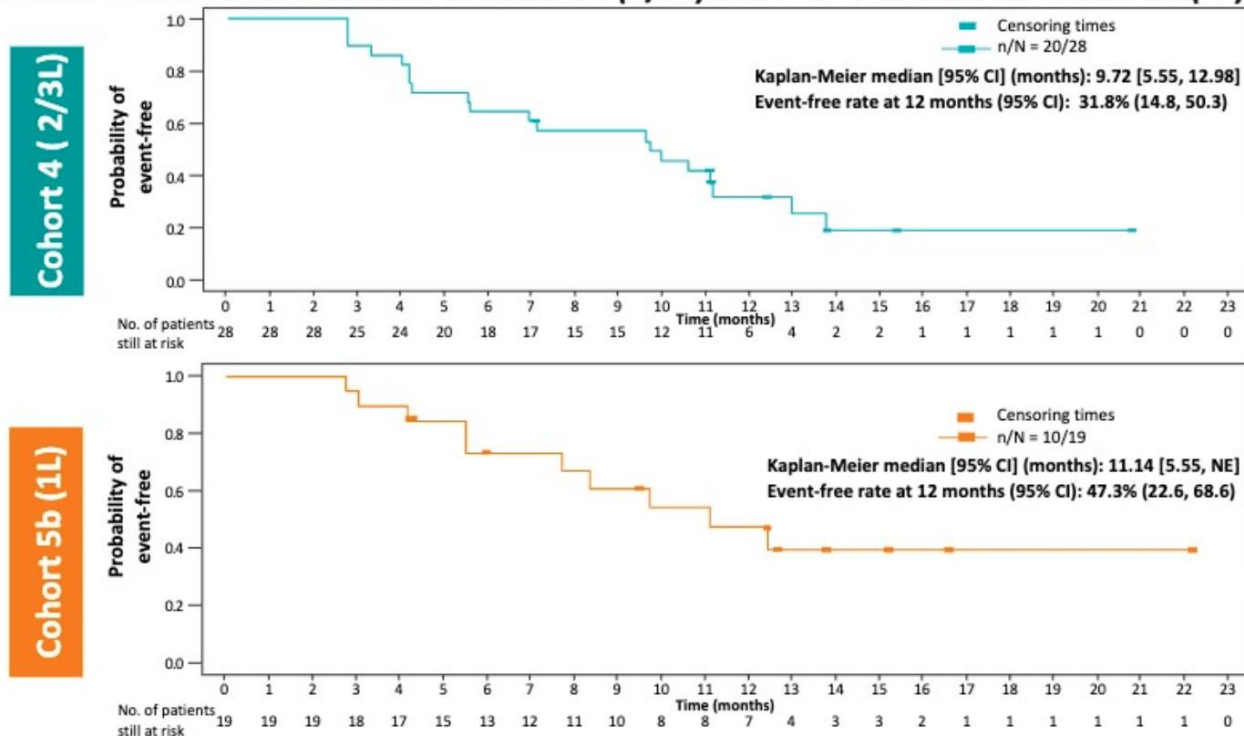
Response rates consistent between BIRC and investigator assessment

	Cohort 5b (1L) N=28	
	BIRC	Investigator
Best overall response, n (%)		
Complete Response	1 (3.6)	0
Partial Response	18 (64.3)	17 (60.7)
Stable Disease	8 (28.6)	10 (35.7)
Progressive Disease	1 (3.6)	1 (3.6)
Overall response rate (ORR) %, (95% CI)	67.9 (47.6, 84.1)	60.7 (40.6, 78.5)
Disease control rate (DCR) %, (95% CI)	96.4 (81.7, 99.9)	96.4 (81.7, 99.9)

BIRC, blinded independent review committee; CI, confidence interval; CR, complete response; DCR, disease control rate (CR+PR+SD+non-CR/non-PD); ORR, overall response rate (CR+PR); PD, progressive disease; PR, partial response; SD, stable disease

Duration of Response per BIRC

Median DOR was 9.72 months in Cohort 4 (2/3L) and 11.14 months in Cohort 5b (1L)

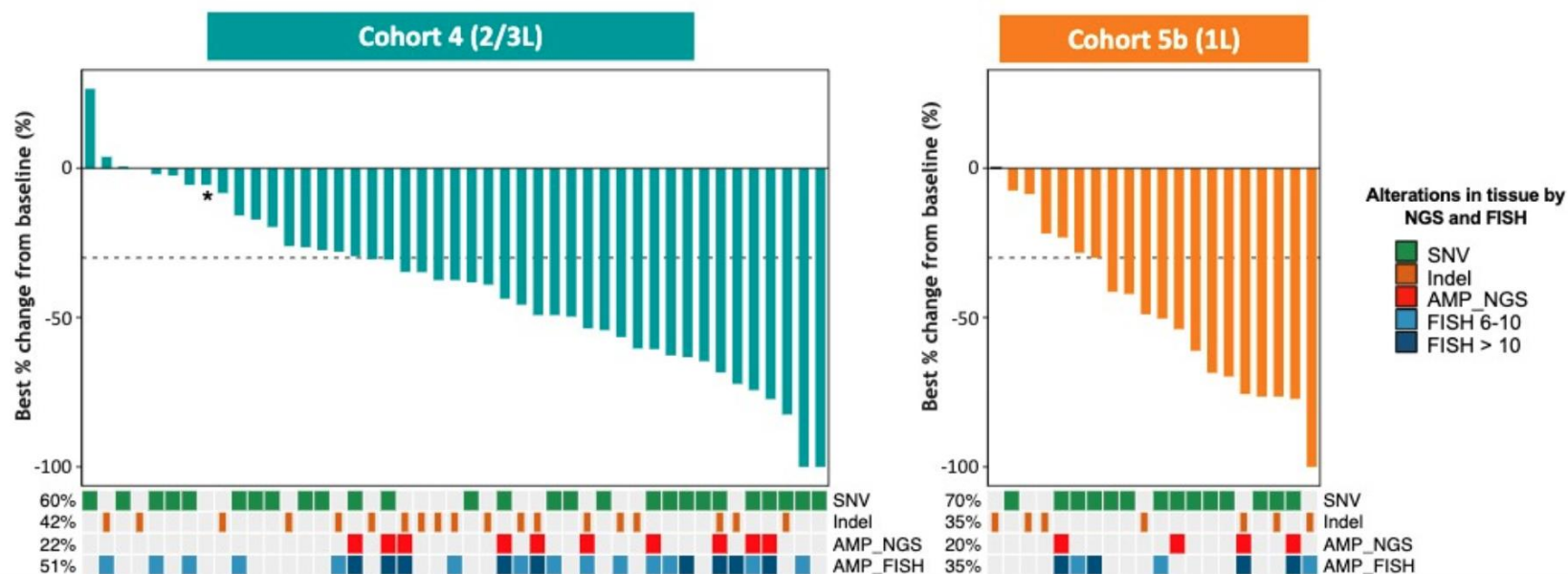


Median DOR per investigator was 8.31 months (95% CI: 4.34, 12.06) in Cohort 4 and 13.96 months (95% CI: 4.27, NE) in Cohort 5b

n is the number of events, N is the number of patients

Tumor shrinkage by *MET* alterations

- **Deep responses and DOR were observed independently of type of *MET* mutation (SNV, Indel) leading to METΔex14 or co-occurrence of *MET* amplification.**
- ***MET* mutations could be detected by both RT-PCR and NGS**
 - High concordance (99%) between NGS and RT-PCR[†] in detection of METΔex14 in tumor tissue



*Patient had noncanonical METΔex14 due to internal rearrangement and no known SNV or Indel variant

[†]73 tissue samples, Cohort 4=53 (Including 1 patient with a noncanonical METΔex14 rearrangement and no canonical variants), Cohort 5b=20.

SNV, Single nucleotide variant in MET leading to Ex14 skipping; Indel, Insertion or deletion leading to METEx14; AMP_NGS, amplification detected by FM NGS panel ≥ 6 GCN; AMP_FISH, MET FISH copy number

Phase II study of tepotinib in NSCLC patients with *MET*ex14 mutations

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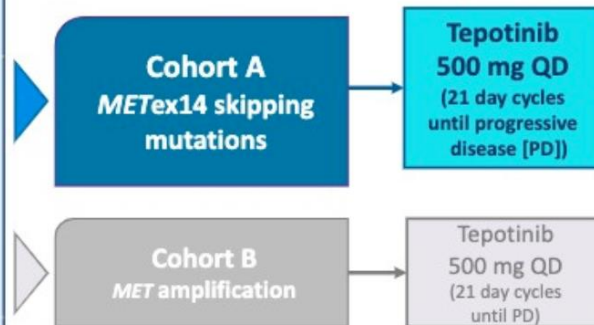
1. Memorial Sloan Kettering Cancer Center, New York, NY, USA; 2. CHU Bordeaux, service des maladies respiratoires, Bordeaux, France; 3. Lille University Hospital, University of Lille, Lille, France; 4. Vall d'Hebron Institute of Oncology (VHIO), Barcelona, Spain; 5. Saitama Cancer Center, Saitama, Japan; 6. CHU de Toulouse-Hopital Larrey, IUCT – Oncopole, Quai de livraison Pharmacie, Toulouse, France; 7. Pius-Hospital, University of Oldenburg, Oldenburg, Germany; 8. Vanderbilt-Ingram Cancer Center, Nashville, TN, USA; 9. ICO Rene Gauducheau Center, Saint-Herblain, France; 10. Antwerp Hospital University, Edegem, Belgium; 11. HU HM Madrid Sanchinarro, Madrid, Spain; 12. The University of Chicago, Chicago IL, USA; 13. Fondazione IRCCS - Istituto Nazionale dei Tumori, Milan, Italy; 14. Nagoya University Graduate School of Medicine, Nagoya, Japan; 15. Asklepios Lung Clinic, Munich-Gauting, Germany; 16. Dr Rosell Oncology Institute, Dexeus University Hospital, Quironsalud Group, Barcelona, Spain; 17. Kurume University Hospital, Kurume, Japan; 18. Tottori University Hospital, Yonago, Japan; 19. Merck KGaA, Darmstadt, Germany; 20. MD Anderson Cancer Center, The University of Texas, Houston, TX, USA

VISION study design

VISION is a single-arm, phase II trial of tepotinib in patients with NSCLC harboring MET alterations (NCT02864992)

Study Design

- Stage IIIB/IV NSCLC
 - All histologies (including squamous and sarcomatoid)
 - Exclusion of active brain metastases or brain as only measurable lesion
 - Tissue- or blood-based *MET* alterations (central lab testing)
 - A. *MET*ex14 skipping mutations detected:
 - Plasma, LBx (DNA based)
 - OR
 - Tissue, TBx (RNA based)
 - B. *MET* amplification only
 - 1st, 2nd, 3rd line of therapy
 - Prior anti-MET therapy was not allowed
 - Prior immunotherapy was allowed
- N = up to 120**



The trial aims for an ORR based on independent review in the range of 40–50% with a lower limit of the corresponding exact 2-sided 95% confidence interval (according to Clopper–Pearson) to exceed an ORR of 20%.

Selected Endpoints

Primary endpoint

- Objective response rate (ORR) by independent review

Secondary endpoints

- ORR by investigator assessment
- Duration of response
- Objective disease control
- Progression-free survival
- Overall survival
- Safety
- Health-related quality of life

We now report interim data including ORR assessed by independent review and select secondary endpoints

Baseline patient and tumor characteristics

Characteristic, n (%)		Tepotinib (N=87)*	Characteristic, n (%)		Tepotinib (N=87)*
Median age, years (range)		74.0 (39–89)	METex14-skipping mutation [§]	Positive in ctDNA (L+)	57 (65.5)
Sex	Male	47 (54.0)		Positive in tissue (T+)	58 (66.7)
			Histopathological classification	Adenocarcinoma	75 (86.2)
Race [†]	White	66 (75.9)		Squamous	7 (8.0)
	Asian	17 (19.5)		Sarcomatoid	1 (1.1)
Smoking history [‡]	Never smoker	38 (43.7)	Disease stage at study entry [‡]	IIIB	2 (2.3)
	Former smoker	38 (43.7)		IV	83 (95.4)
	Regular smoker	2 (2.3)	Brain metastases	Present	8 (9.2)
Prior lines of anticancer therapy	0	33 (37.9)			
	1	31 (35.6)	ECOG PS	0	22 (25.3)
	2	20 (23.0)		1	65 (74.7)
	3	3 (3.4)			

*All tepotinib-treated patients. †Other n=1; race not collected at site n=3. ‡Smoking history and Disease stage at study entry were missing for 9 and 2 patients, respectively.

§Numbers do not add up to 100% due to overlap of patients with both L+ and T+. Of 53 patients that were tested both with LBx and TBx, 29 were positive in both. ||Non-small cell lung cancer not otherwise specified n=1; poorly differentiated carcinoma n=1; adenosquamous n=1; missing n=1. ¶Non-target lesions. ECOG PS, Eastern Cooperative Oncology Group performance status.

Efficacy: Best overall response (IRC/Investigator)

Efficacy analysis includes patients having ≥2 post-baseline assessments or who discontinued treatment for any reason.

Tepotinib 500 mg QD	Liquid biopsy (L+)		Tissue biopsy (T+)	
	IRC (n=48)	Investigator (n=47)	IRC (n=51)	Investigator (n=51)
BOR by RECIST 1.1, n (%)				
Complete response	0 (0)	3 (6.4)	0 (0)	3 (5.9)
Partial response	24 (50.0)	23 (48.9)	23 (45.1)	25 (49.0)
Stable disease	8 (16.7)	5 (10.6)	14 (27.5)	11 (21.6)
Progressive disease	7 (14.6)	10 (21.3)	8 (15.7)	6 (11.8)
Not evaluable	9 (18.8)	6 (12.8)	6 (11.8)	6 (11.8)
ORR,* n (%) [95% CI]	24 (50.0) [35.2, 64.8]	26 (55.3) [40.1, 69.8]	23 (45.1) [31.1, 59.7]	28 (54.9) [40.3, 68.9]
mDOR, months [95% CI]	12.4 [5.8, ne]	17.1 [7.1, ne]	15.7 [9.0, ne]	14.3 [5.7, ne]
DCR,† n (%) [95% CI]	32 (66.7) [51.6, 79.6]	31 (66.0) [50.7, 79.1]	37 (72.5) [58.3, 84.1]	39 (76.5) [62.5, 87.2]

*ORR, objective response rate: confirmed complete response/partial response.

†DCR, disease control rate: confirmed complete response/partial response or stable disease lasting at least 12 weeks.

L+, METex14-skipping mutation-positive in ctDNA; T+, METex14-skipping mutation-positive in tissue.

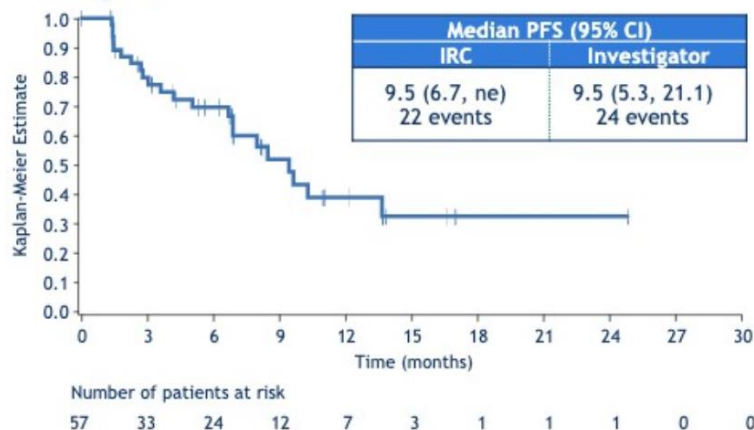
BOR, best overall response; CI, confidence interval; IRC, independent review committee; mDOR, median duration of response; ne, not estimable.

Efficacy: Progression-free survival

PFS across all treatment lines

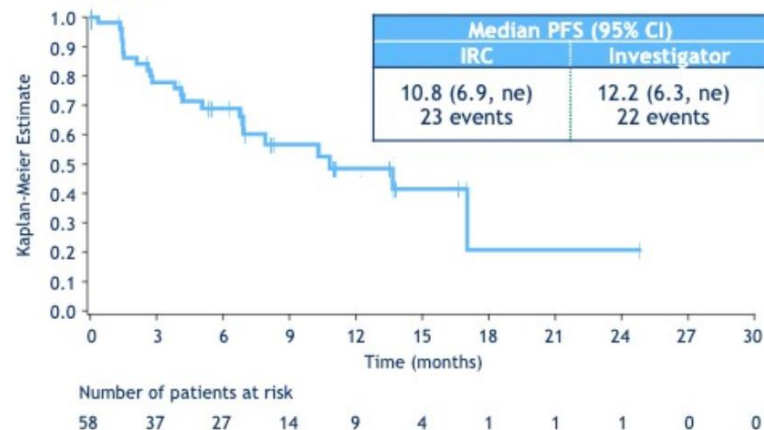
Liquid biopsy (L+) (n=57)

PFS by IRC



Tissue biopsy (T+) (n=58)

PFS by IRC



33/57 L+ patients and 31/58 T+ patients remain on treatment.

Median follow-up for PFS (IRC): 6.9 months (95% CI 5.5, 11.0).

L+, METex14-skipping mutation-positive in ctDNA; T+, METex14-skipping mutation-positive in tissue.

IRC, independent review committee; ne, not estimable; PFS, progression-free survival.

Primary and acquired resistance to MET inhibition in patients with *MET* exon 14-altered lung cancers

Robin Guo, Michael Offin, A. Rose Brannon, Andrew Chow, Lukas Delasos, Romel Somwar, Olivia Wilkins, Kerry Scott, Yuan Tian, Fabiola Cecchi, Todd A. Hembrough, Bob T. Li, Charles M. Rudin, Mark G. Kris, Maria E. Arcila, Natasha Rekhtman, Paul K. Paik, Marc Ladanyi, Ahmet Zehir, Alexander Drilon

Department of Medicine, Memorial Sloan Kettering Cancer Center, New York, NY; Department of Pathology, Memorial Sloan Kettering Cancer Center, New York, NY; Department of Radiology, Memorial Sloan Kettering Cancer Center, New York, NY; NantOmics, LLC, Rockville, MD; UConn Health, Farmington, CT

Methods

Patients

- Advanced non-small cell lung cancers
- *MET* exon 14 alteration
 - DNA/RNA-based next-generation sequencing (NGS) of tumor
- Received 1 or more MET tyrosine kinase inhibitors

Tumor NGS

- Targeted DNA NGS (MSK-IMPACT™/FoundationOne)
 - Before MET TKI (n=74)
 - Paired NGS at progression (n=14)
- Targeted RNA NGS (n=16, MSK-Solid Fusion™ Assay)

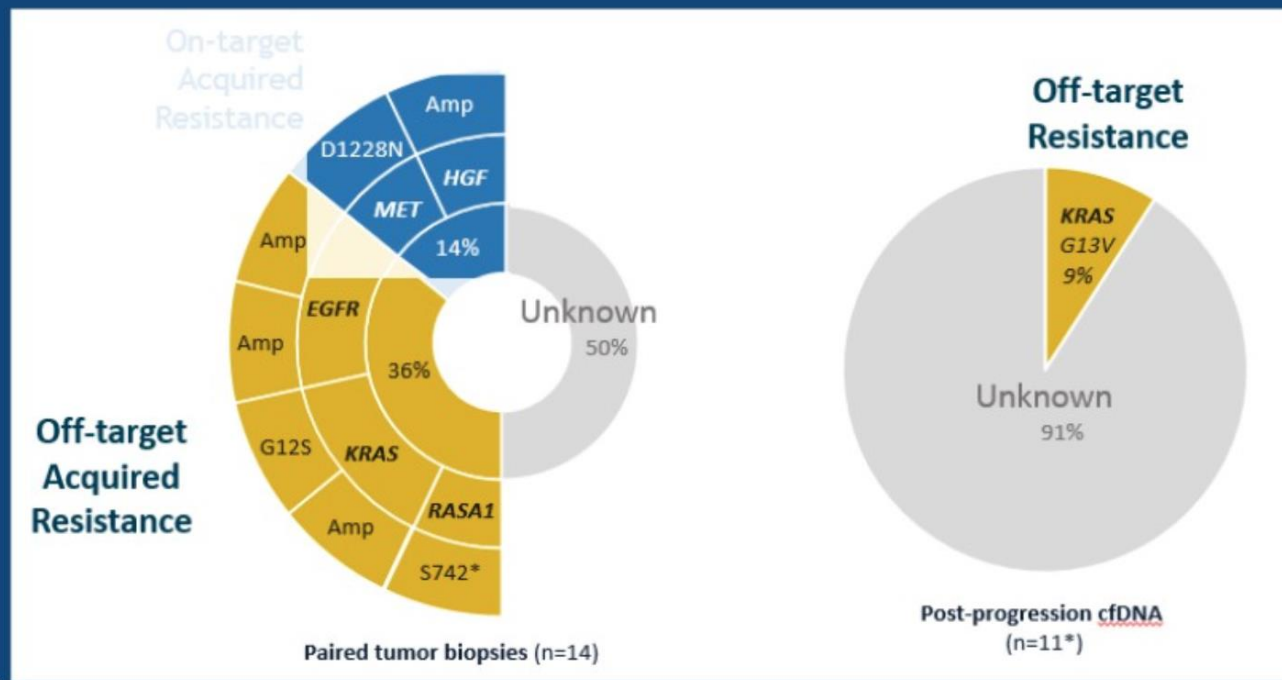
Tumor Protein Assessment

- Mass Spectrometry (NantOmics)
 - *MET* protein (n=16)
 - *KRAS* protein (n=16)
- *MET* Immunohistochemistry (n=8, SP44 Clone)

Clinicopathologic features of patients with advanced *MET* exon 14-altered lung cancers

All patients (n=75)		
Age, median (range)	73 years (44-91 years)	
Sex, % (n)	Female	52% (39)
Cigarette smoking, % (n)	Never	44% (33)
	Former or Current	56% (42)
Histology	Adenocarcinoma	77% (58)
	Sarcomatoid	11% (8)
	Other	12% (9)
Number of TKIs	1	76% (57)
	2 or more	24% (18)
MET TKI received	Crizotinib	91% (68)
	Other TKIs (never Crizotinib)	9% (7)

Acquired resistance involves on target and bypass pathways



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PRESENTED AT: **2019 ASCO**
ANNUAL MEETING

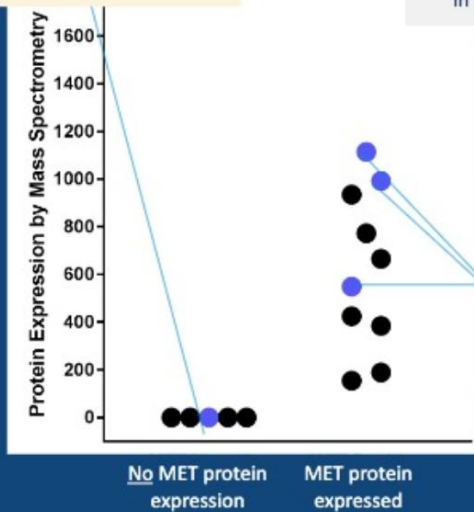
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PRESENTED BY: Karen Reckamp, MD, MS

Response to MET TKI by protein expression in *MET* ex14 NSCLC

DISCORDANT

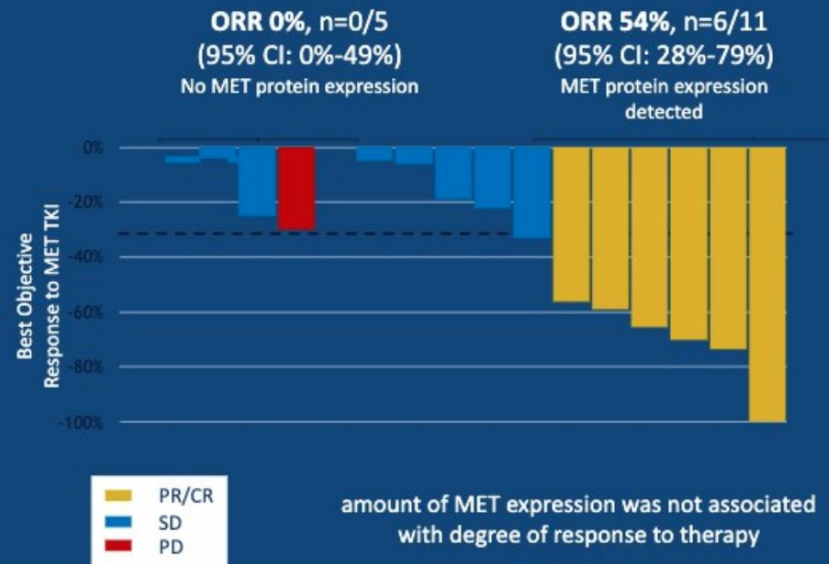
- *MET*ex14-altered in DNA
- *MET*ex14-altered in RNA
- *MET* protein not expressed



- *MET* exon14 alteration detected in RNA
- Insufficient tissue for RNA testing

CONCORDANT

- *MET*ex14-altered in DNA
- *MET*ex14-altered in RNA
- *MET* protein overexpressed



Guo R et al ASCO 2019

Increase Upfront NGS testing for NSCLC

- Growing number of actionable targets with approved therapies
- Cost effective
- Identify more patients with *MET* ex14
- Lead to additional targeted therapies for NSCLC

TABLE 3. Total Cost and Cost Difference Versus NGS

Medicare-Insured Patients (n = 2,066)		
Testing Strategy	Total Cost	Cost Difference v NGS
NGS	2,190,499	—
Sequential	3,721,368	1,530,869
Exclusionary	3,584,177	1,393,678
Hotspot panel	4,331,295	2,140,795

NOTE. Costs are given in 2017 US dollars.
Abbreviation: NGS, next-generation sequencing.

Pennell NA et al J Clin Oncol Precision Oncology 2019



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