

Uncommon Oncogenic Drivers in NSCLC

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Oncogene mutations and therapeutic options

Oncogene	Mutation prevalence	Therapy	Predicted response rate
EGFR	Asians 30-40%/ Caucasian 10- 20%	EGFR TKIs (most mutations)/pan-HER inhibitors	Erlotinib 60-80% Gefitinib 70% Afatinib 60% Osimertinib 50-60% (T790M)
ALK	1-7%	ALK inhibit 5	Crizotinib 50-60% Ceritinib 60% Alectinib 60% Brigatinib 60% Lorlatinib 48%
ROS1	1.7%, higher in	lors	Crizotinib 60-70% Ceritinib 60%
BRAF	2%	BRAF/MEK inhibitors	Dabrafenib 30% Dabraf/trametinib 60%
NTRK	<1%	Crizotinib/Larotrectinib/ NTRK inhibitors	Larotrectinib 76%
RET	1.7% (15% in EGFR/ALK/KRAS-)	RET inhibitors	Cabozantinib 40% Vandetinib 20%
MET	10%	Crizotinib/MET inhibitors	Crizotinib 25%
HER2	2%	Trastuzumab; pan-HER inhibitors	Dacomitinib 12% CityofHope Ado-trastuzumab 20%; TDM-1 44%

Why Does Testing Matter? Survival by Use of Targeted Therapy



The ultimate goal of genomic testing is to use the information generated to select therapies and improve outcomes



ROS1 Rearrangements in NSCLC (1% NSCLC)



ROS1

- First discovered in NSCLC in 2007
- Also found in some GBMs, cholangiocarcinomas, gastric, ovarian & other tumor types
- Activated by chromosomal rearrangement, leading to constitute kinase activation and oncogene addiction
- No overlap with ALK





Summary of ROS1 Anti-Tumor Efficacy with Crizotinib in PROFILE 1001 Study



Shaw et al. NEJM 371(21): 1963-71, 2014; updated at European Cancer Congress April 11,2019



Efficacy of ceritinib in NSCLC harboring ROS1 Rearrangement

32 patients; Ceritinib 750 mg QD, ORR –62% (Crizotinib naïve 67%; 2 patients with prior crizotinib – no response)

mPFS -19.3 m (in Crizotinib naïve), 9.3 m for all patients;

mDOR – 21 m; **mOS – 24 m**



Treatment –related AE's – (majority grade 1-2 were diarrhea, nausea, anorexia; most common grade 3-4 fatigue, increased LFT's); only 1 pt discontinued Tx due to generalized weakness and anorexia);



Lorlatinib in ROS1 positive NSCLC

- 47 pts, 13 crizotinib naïve, 34 crizotinib treated.
- ORR 36.2% in all cohorts ; RR in crizotinib naïve 61.5% and crizotinib treated 26.5%.
- Responses lasted as long as 10 months 5 crizotinib naïve and 5 crizotinib pretreated.
- RR in brain mets 56% with duration lasting at least 12 months for 5 patients (4 of whom were previously exposed to crizotinib).

- Common adverse events: hypercholesterolemia 83% and hypertriglyceridemia 60%, neurocognitive and mood effects triggered by the drug can be managed by dose interruption and reduction

BRAF mutations occur in multiple tumor types



Illustration of RAS–RAF–MEK–ERK MAP kinase signaling pathway.



- As a member of the Ras/mitogenactivated protein kinase signalling pathway, BRAF lies downstream of KRAS, and directly phosphorylates ERK.
- The pathway culminates in the transcription of genes favouring proliferation and survival.

BRAF mutations in NSCLC



Relative distribution of 'driver' mutations in lung adenocarcinoma BRAF – 2-4% and 50% are BRAF-V600E



Relative distribution of BRAF mutations in NSCLC.

BRAF mutations more commonly found in current or former smokers.

Paik P et al JCO 2011

Response of BRAF V600E mutant NSCLC to vemurafenib/ dabrafenib therapy



Pre vemurafenib

2 weeks post vemurafenib (960mg po bid)

Gautschi et al JTO 2012



Vemurafenib in BRAF V600E-Mutant Lung Cancer (20 patients)





Dabrafenib in BRAF V600E-Mutant Lung Cancer



Dabrafenib +Trametinib 1st Line in *BRAF* V600E-Mutant Lung Cancer





BRAF V600E NSCLC Treated with Dabrafenib and Trametinib



August 2012

June 2014



Courtesy of B. Johnson

NTRK Gene Fusions are Oncogenic and Signal Through Canonical Downstream Pathways

- The neurotrophic receptor tyrosine kinase genes NTRK1, NTRK2, and NTRK3 encode the tropomyosin receptor kinase (TRK) proteins TRKA, TRKB, and TRKC, respectively.
- After embryogenesis, TRK expression is limited primarily to the nervous system, where these kinases help regulate pain, proprioception, appetite, and memory.
- Recurrent chromosomal fusion events involving the carboxy-terminal kinase domain of TRK and various upstream amino-terminal partners have been identified across diverse cancers that occur in children and adults.
- TRK fusions lead to overexpression of the chimeric protein, resulting in constitutively active, ligand-independent downstream signaling.
- Biologic models and early clinical evidence suggest that these fusions lead to oncogene addiction regardless of tissue of origin and, in aggregate, may be implicated in up to 1% of all solid tumors



TRK Fusions Found in Diverse Cancer Histologies



Estimated 1,500–5,000 patients harbor TRK fusion-positive cancers in the United States annually



Methods to detect TRK Fusions

- Several modalities:
 - DNA & RNA NGS, FISH, IHC
- Large NTRK introns (compared to ALK, ROS1, RET) make DNA-based detection challenging
- Loxo/Ventana developing Pan-TRK IHC companion diagnostic (CDx)
- NGS "universal" CDx tests under FDA review include TRK fusion detection*

*FoundationOne, Oncomine Universal Dx



Pan-TRK IHC detects expression, shared among TRK fusions

More info: www.TRKtesting.com



Larotrectinib: A Selective TRK Inhibitor

Larotrectinib

- Larotrectinib is the first and only selective pan-TRK inhibitor in clinical development
- Highly potent against TRKA, TRKB, TRKC
 - 5–11 nM IC₅₀ in cellular assays
- Highly selective
- Development timeline
 - March 2015: 1st TRK-fusion patient treated
 - July 2016: breakthrough therapy designation
 - February 2017: pivotal enrollment complete





Efficacy of Larotrectinib: In TRK-Fusion Positive Cancers in Adults and Children

Diversity of cancers treated - 17 unique types Breast Infantile Appendix _ 2% **Pancreatic** Inflammatory myofibromatosis **Peripheral nerve** 2% 2% myofibroblastic kidney sheath tumor 2% tumor 4% 2% Sarcoma, NOS Salivary gland 4% 22% **Myopericytoma** 4% Cholangiocarcinoma_ Infantile fibrosarcoma (IFS) 4% 13% Spindle cell sarcoma 5% GIST 5% Thyroid Melanoma 9% 7% ung Colon 7% 7%



TRK fusions were identified by NGS or by FISH

TRK Inhibition in NTRK-Rearranged Tumors





Drilon et al, Cancer Discovery 2017; Hyman ASCO 2017; Farago et al, JTO 2016; Drilon et al NEJM 2018



SQSTM1-NTRK1 lung cancer patient





Baseline





Cycle 4

45F NSCLC & paraneoplastic hypertrophic osteoarthropathy

> Prior therapy: platinum/pemetrexed

Larotrectinib ongoing in month 8, resolution of paraneoplastic symptoms





Larotrectinib—AEs

	Treatment-emergent AEs (%)*					Trea	Treatment-related AEs (%)		
	Grade 1	Grade 2	Grade 3	Grade 4	Total	Grade 3	Grade 4	Total	
Fatigue	15	18	5	_	38	1	-	18	
Dizziness	22	4	2	—	27	1	-	20	
Nausea	20	5	2	-	26	2	-	18	
Anemia	8	9	9	-	26	3		10	
Vomiting	18	6		-	24		-	13	
Increased AST	16	4	3	-	23	1		18	
Constipation	20	2	1		22	_		12	
Cough	18	2			21			2	
Increased ALT	14	2	4	-	20	4	-	17	
Diarrhea	14	5	1		20	—	2 	6	
Dyspnea	10	6	2	_	18	_	-		

7 (13%) patients required dose reductions – all maintained tumor regression (1 CR, 5 PR, 1 SD) on reduced dose. No discontinuations for adverse events.





Emerging targets



EMERGING BIOMARKERS TO IDENTIFY NOVEL THERAPIES FOR PATIENTS WITH METASTATIC NSCLC

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RET rearrangements	Cabozantinib ^{6,7} Vandetanib ⁸
ERBB2 (HER2) mutations	Ado-trastuzumab emtansine ⁹
Tumor mutational burden (TMB)*	Nivolumab + ipilimumab ¹⁰ Nivolumab ¹¹

*TMB is an evolving biomarker that may be helpful in selecting patients for immunotherapy. There is no consensus on how to measure TMB.

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MET in NSCLC

- *MET* is a proto-oncogene that encodes for the transmembrane *MET* tyrosine receptor kinase
- Through ligand binding to HGF(hepatocyte growth factor), signaling pathways such as PI3K/AKT, MAPK, NF-kB, and STATs (signal transducer and activator of transcription proteins) are activated, which leads to cell proliferation and invasion
- Protein over-expression and phosphorylation are the most common forms of MET-positive NSCLC, but responses to therapy have been varied
- *MET* amplification occurs in less than 5% of lung adenocarcinoma; *MET* exon 14 alterations are found in 4 % of lung adenoca and predominantly associated with older age(median 73) and smoking history. *MET* gene rearrangement is uncommon, but the kinase fusion KIF5B-MET has been reported in adenoca.
- Multitargeted TKIs have been used to target MET in lung cancer (e.g., cobazantinib, crizotinib, merestinib) and a variety of TKIs with increased sensitivity are also under investigation (e.g., salvolitinib, tepotinib, capmatinib, sitravatinib, AMG337, tivantinib)
- A phase II study of tepotinib in patients with *MET* exon 14 skipping mutations is ongoing – preliminary data 60% RR.



Crizotinib in MET-amplified lung cancers

Multicenter phase 1 expansion cohort Crizotinib 250 mg twice daily **Primary endpoint:** overall response

2018	Low <i>MET</i>	Intermediate <i>MET</i>	High <i>MET</i>
	(<i>MET/CEP7</i> 1.8-2.2)	(<i>MET/CEP7</i> >2.2-<4.0)	(<i>MET/CEP7</i> ≥4.0)
	n=3	n=14	n=20
Overall response	33.3 %	14.3 %	40 %
	(95%Cl 0-84)	(95%Cl 0-64)	(95%Cl 22-96)
Medan DoR m	12.1	3.7	5.5
Median PFS m	1.8	1.9	<mark>6.7</mark>



MET amplification determined by FISH



Crizotinib in *MET*ex14-altered lung cancers

Multicenter phase 1 expansion cohort Crizotinib 250 mg twice daily

Primary endpoint: overall response

69 patients, Overall response rate (ORR) 32% (95% CI: 22–69), 3 – CR, 18 –PRs mPFS – 7.3m, m TTR – 7.6 weeks





Responses to Crizotinib Can Occur in High-Level *MET*-Amplified Non–Small Cell Lung Cancer Independent of *MET* Exon 14 Alterations



before crizotinib.

2 months on crizotinib.

B) **FISH analysis** on a central nervous system resection specimen with MNNG HOS Transforming gene (*MET*) (SpectrumRed) and chromosome centromere 7 (*CEP7*) (SpectrumGreen) **showing** *MET* **gene amplification** (mean *MET* copies per cell = 20.53; mean *CEP7* copies per cell = 2.07; *MET/CEP7* ratio = 9.94).





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Several genomic alterations activate RET in cancer

RET Fusions



RET Mutations

b RET nonsynonymous point mutations



Nature Reviews | Clinical Oncology



RET Rearrangements

- intact tyrosine kinase domain fused to an upstream gene partner
 - most common: KIF5B
 - others: CCDC6, NCOA4, TRIM33, KIAA1468
- result in ligand-independent dimerization and downstream growth pathway activation
- oncogenic in vitro and in vivo
- <u>1-2% NSCLC, more likely to be present in</u> younger, never-smokers with adenocarcinoma





Multikinase inhibitors in RET-rearranged lung cancers

From Baseline Change -20 -30 -40 RET Statu KIF5B-RET -50 Other RET 100 ORR=17% (3/18) 80 SD >6M: 28% (5/18) Sum of longest diameter, num decrease from baseline (%) 60 40 20 13 -20 10 -4011 naxir -60 -80 20 10 Maximum tumor shrinkage from baseline (%) ο -10 -20 -30 -40 KIF5B-RET -50 CCDC6-RET -60 Unknown-RET -70 -80

Multicenter phase 2 trial Primary endpoint: response Lenvatinib ORR 16%, mPFS– 7.3m

Korean phase 2 trial Primary endpoint: response Vandetanib ORR 18%, mPFS – 4.5 m

Japanese phase 2 trial (LURET) Primary endpoint: response Vandetanib ORR 53%, mPFS – 4.7m



RET Inhibitors—Efficacy Summary

Agent	RET testing	n	ORR (%)	PFS (months)	OS (months)
Cabozantinib (Drilon, ASCO 2015)	FISH/NGS	Stage I, 16	38	7	10
Cabozantinib (Gautschi, ASCO 2016)	FISH/NGS/RT-PCR	13	31	3.6	4.9
Vandetanib (Sato, ASCO 2016)	FISH/RT-PCR	19/17	47/53	4.7	47% 1-year
Vandetanib (Lee, ASCO 2016)	FISH confirmed	18	17	4.5	11.6
Vandetanib (Gautschi, ASCO 2016)	FISH/NGS/RT-PCR	11	18	2.9	10.2
Sunitinib (Gautschi, ASCO 2016)	FISH/NGS/RT-PCR	9	22	2.2	6.8
Lenvatinib (Velcheti, ESMO 2016)	NGS	25	16	7.3	NR
Any RET inhibitor (Gautschi, ASCO 2016)	FISH/NGS/RT-PCR	41	23	2.9	6.8 ₩ĭ

More selective RET inhibition is active in *RET*-altered cancers—BLU 667



Responses were seen both in multikinase inhibitor pre-treated and TKI-naïve lung and thyroid cancer patients.



Efficacy of LOXO-292 regardless of prior therapy



Note: Three patients not displayed due to treatment discontinuation prior to first post-baseline response assessment; *Denotes patient with 0% maximum change in tumor size; †Includes alectinib, cabozantinib, lenvatinib, pazopanib, ponatinib, RXDX-105, sitravatinib, sorafenib, and vandetanib; April 2, 2018 cut-off



🕅 Cityof Hope



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Oncogenic alterations: *HER2* mutations





TDM-1 (Ado-trastuzumab) in HER2- Mutant NSCLC

HER2 expression



HER2 mutation



ORR 44% (8/18, 95% CI 22-69%)



Median PFS was 4 months (95% CI 3.0 to NR, n=18 with 13 events)

Li J Clin Oncol 2018



HER2 TKIs in *HER2*-activated lung cancers



Kris M et al., Ann Oncol 2015 Jul; 26 (7): 1421-27 Median PFS 3 months



AFATINIB:

0/13 responses in prospective trial/PFS 3 months (Smit el al. ASCO 2017 Abstract #9070) 3/22 responses in retrospective series (Lai et al. ASCO 2017 Abstract #9071)



HER2 mutant NSCLC treated with chemotherapy and *HER2*-targeted drugs retrospective cohort study.

European EUHER2 cohort

Treatment	n	ORR	DC	PFS median	OS median
First-line: without HER2- targeting treatment	93	43.5%	70.7%	6 (5; 7.1)	24 (19.1; 36.4)
Second-line: without HER2- targeting treatment	52	10%	36%	4.3 (3.1; 5)	19.4 (9.6; 24.7)
EGFR-TKI	26	7.6%	26.8%	2.99 (1.87; 4.47)	20.14 (7.14; 32.95)
Trastuzumab combination, T- DM1	58	50.9%	75.5%	4.8 (3.4; 6.5)	13.3 (8.1; 15)
Neratinib, lapatinib, and afatinib	29	7.4%	55.5%	3.4 (2.4; 4)	6.5 (4.7; 30.6)



HER2-directed agent	HER2 alteration	n	ORR (%)	PFS (months)	OS (months)
Dacomitinib (Kris MG et al. Ann Oncol 2015)	mutation or amplification	30 (26 mut/ 4 amp)	12 mut/ 0 amp	3 mut	9
Afatinib (De Grève, 2012; Mazières, 2013; De Grève, 2015; Li,2015)	mutation	17 case reports	NA	1.8-10	NA
Lapatinib (Lopez-Chavez A et al. J Clin Oncol 2015)	mutation or amplification	6	0	NA	NA
Neratinib + temsirolimus (Besse B et al. ESMO 2014)	mutation	14	21	4	NA
Any therapy (Mazières J et al. Ann Oncol 2016)	mutation	101	23	6	23.4
Trastuzumab combination, T- DM1 (Mazières J et al. Ann Oncol 2016)	mutation	58	50.9%	4.8	13.3
Any HER2 therapy (Mazières J et al. Ann Oncol 2016)	mutation	65	50	5.1	

Identifying the target in HER2-activated lung cancers



- Significant heterogeneity exists in the molecular aberrations in *HER2* in lung cancers
- Variable effectiveness of HER2 kinase inhibitors reflects the diversity in alterations
- Define important characteristics
 - Type of mutation
 - presence and degree of HER2 amplification
 - HER2 protein expression, and
 - concurrent pathway activation
- SUMMIT study (neratinib), importance of concurrent pathway activation¹



Conclusions—Emerging targeted therapy

- *MET* exon14 is a promising alteration with multiple MET inhibitors in clinical development
- *RET* alterations have had responses to multitargeted TKIs and more specific RET-targeted agents are in ongoing trials
- *HER2* demonstrates heterogeneous mutations with variable responses to current targeted therapies
- Greatest barrier to treatment and enrollment in trials is testing—liquid biopsies more common eligibility in trials



Thank you!

Questions?



