



Novel Molecularly Targeted Therapies and Biomarkers in Advanced Colorectal Cancer

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Objectives

- Discuss important clinicopathologic features underlying the biology of colorectal cancer
- Describe varying sequences of therapies in management of metastatic colorectal cancer
- Describe biomarkers that guide selection and personalization of therapies for patients with advanced colorectal cancer




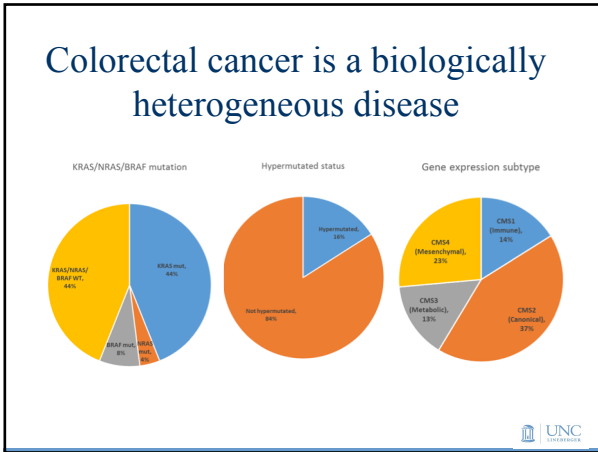
Colorectal cancer is a leading cause of cancer death in the U.S.

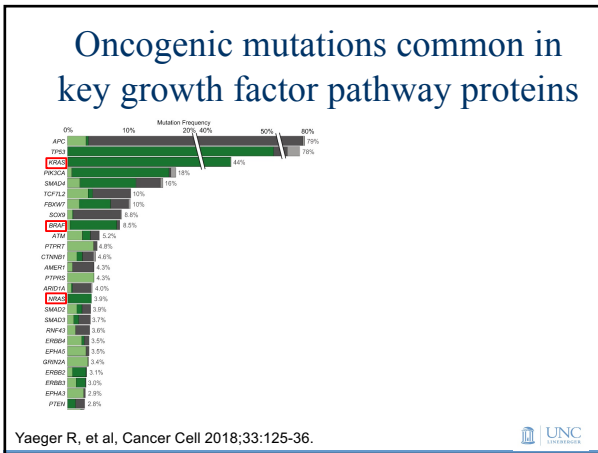
Estimated Deaths

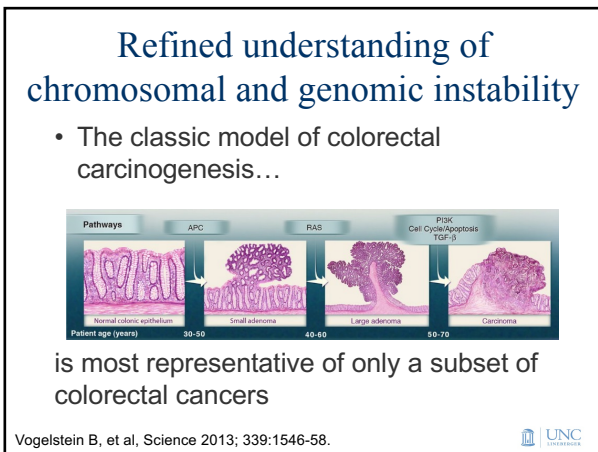
Males			Females		
Lung & bronchus	83,550	28%	Lung & bronchus	70,500	25%
Prostate	29,430	9%	Breast	40,920	14%
Colon & rectum	27,390	8%	Colon & rectum	23,240	8%
Pancreas	23,020	7%	Pancreas	21,310	7%
Liver & intrahepatic bile duct	20,540	6%	Ovary	14,070	5%
Leukemia	14,270	4%	Uterine corpus	11,350	4%
Esophagus	12,850	4%	Leukemia	10,100	4%
Urinary bladder	12,520	4%	Liver & intrahepatic bile duct	9,660	3%
Non-Hodgkin lymphoma	11,510	4%	Non-Hodgkin lymphoma	8,400	3%
Kidney & renal pelvis	10,010	3%	Brain & other nervous system	7,340	3%
All Sites	323,630	100%	All Sites	286,010	100%

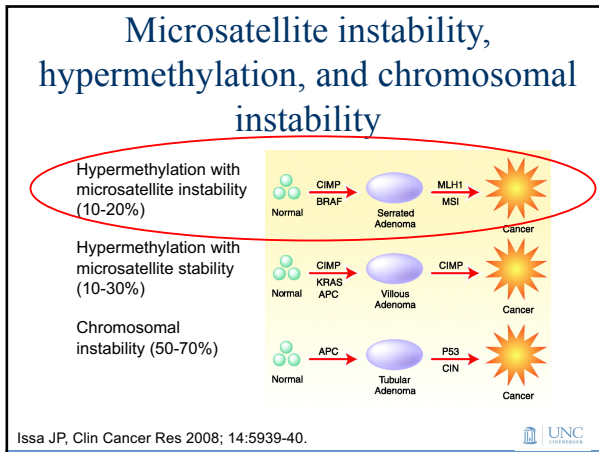
Siegel RL, et al. CA Cancer J Clin 2018; 68:7-30

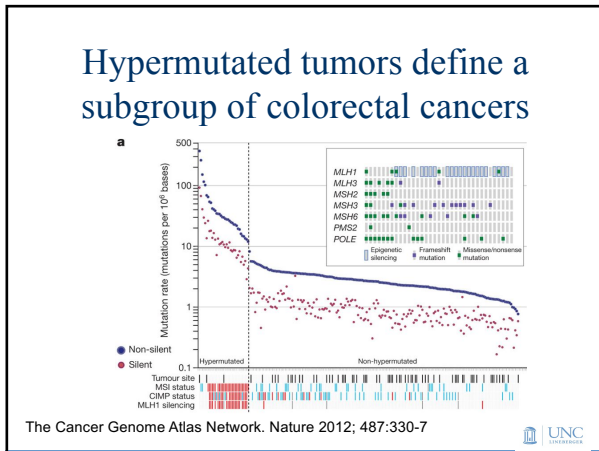












- ### Multiple etiologies of hypermutated colorectal cancers
- Microsatellite instability due to deficiency of mismatch repair protein
 - Germline mutation (Lynch syndrome / HNPCC)
 - Epigenetic silencing via methylation of MLH1 promoter
 - DNA polymerase ϵ (POLE) or δ (POLD1) proofreading domain mutation
- Yaeger R, et al, Cancer Cell 2018;33:125-36.

Tests for microsatellite instability / deficient mismatch repair

Immunohistochemistry

Microsatellite stable

Microsatellite unstable

Polymerase chain reaction

There is 96% concordance between IHC and PCR, but 11.8% of MSI-High tumors by PCR had discordant IHC – often in cases of HNPCC where mutations do not abrogate nuclear staining.

Bartley AN, et al. Cancer Prev Res (Phila) 2012; 5:320-7.

Scarpa A, et al. Microsatellite Instability - Defective DNA Mismatch Repair: ESMO Biomarker Factsheet

Next generation sequencing to infer MSI

- 99.4% concordance with MSKCC sequencing panel
- 97% concordance with Foundation One sequencing (95 microsatellite loci).

Orthogonal testing
● Diabry
● Insearve

Table 1. Validation: CGP MSI method is 97% concordant with PCR and IHC-based methods

	PCR MSI-H	IHC MSI-H	CGP MSI-High
MSKCC (N=14)	14	14	14
FO (N=14)	14	14	14

Concordance for 95 microsatellite loci: overall concordance rate is 97% (28/29). Sensitivity is 97% (28/29). Specificity is 97% (1/1).

2 discrepant 100 microsatellite samples are correct calls, the overall concordance rate is 94% (26/28). Sensitivity is 94% (26/28). Specificity is 94% (1/1).

“The clinical validity of the qualitative MSI designation has not been established.”

Middha S, et al. JCO Precis Oncol 2017

Hall MJ, et al. GI ASCO 2016

Case 1

- A previously healthy 60 year old male presents after colonoscopy for iron deficiency anemia revealed moderately differentiated adenocarcinoma in the ascending colon. He has no significant family history of colorectal cancers. Initial staging CT scans revealed multiple bilobar liver metastases and peritoneal carcinomatosis. The patient has an excellent performance status.

Poll

Which of the following tests is not recommended to send tumor tissue for?

- A) BRAF codon 600 mutation
- B) Assessment of microsatellite stability, by mismatch repair protein staining and/or MSI testing by PCR
- C) PD-L1 immunohistochemistry using 22C3 antibody
- D) KRAS exons 2, 3, and 4 mutations
- E) NRAS exons 2, 3, and 4 mutations



Answer

Which of the following tests is not recommended to send tumor tissue for?

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- C) PD-L1 immunohistochemistry using 22C3 antibody
- D) KRAS exons 2, 3, and 4 mutations
- E) NRAS exons 2, 3, and 4 mutations



Case continued

- This patient with moderately differentiated adenocarcinoma of the ascending colon was found to have intact nuclear staining of MLH1, MSH2, MSH6, and PMS2 on immunohistochemistry. Testing for KRAS, NRAS, and BRAF mutations revealed no mutations.



Poll

Out of the following choices, which of the following treatments would be the best first-line therapy?

- A) Pembrolizumab
- B) FOLFIRI + Bevacizumab
- C) FOLFOX + Panitumumab
- D) CAPOX + Ziv-aflibercept
- E) Trifluridine + Tipiracil



Answer

Out of the following choices, which of the following treatments would be the best first-line therapy?

- A) Pembrolizumab
- B) FOLFIRI + Bevacizumab**
- C) FOLFOX + Panitumumab
- D) CAPOX + Ziv-aflibercept
- E) Trifluridine + Tipiracil



First-line chemotherapy of metastatic colorectal cancer

Chemo backbone

- FOLFOX or CAPOX
- FOLFIRI
- 5FU/leucovorin or capecitabine if less fit



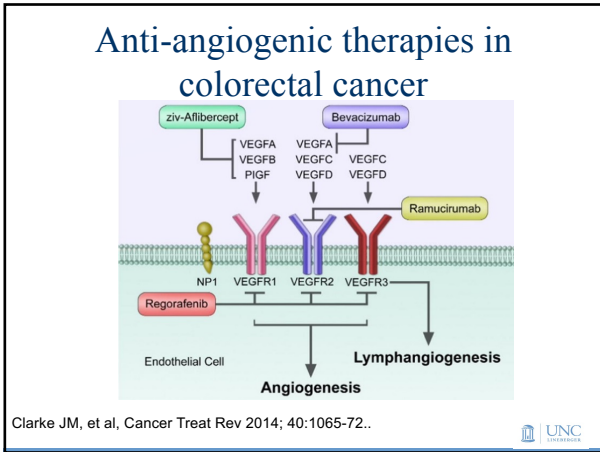
Biologic agent

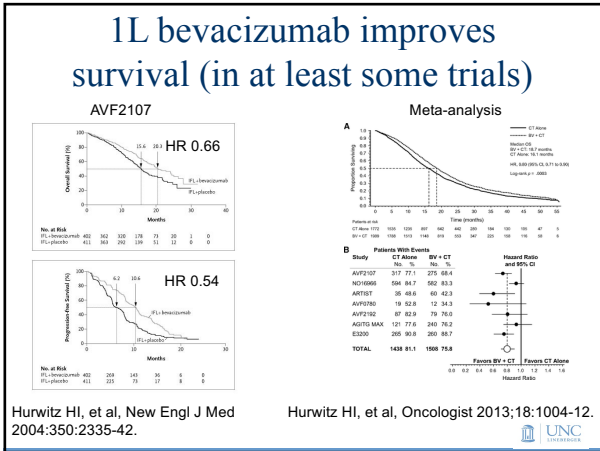
- Bevacizumab
- Anti-EGFR antibody (Cetuximab or Panitumumab) if RAS WT and left-sided primary

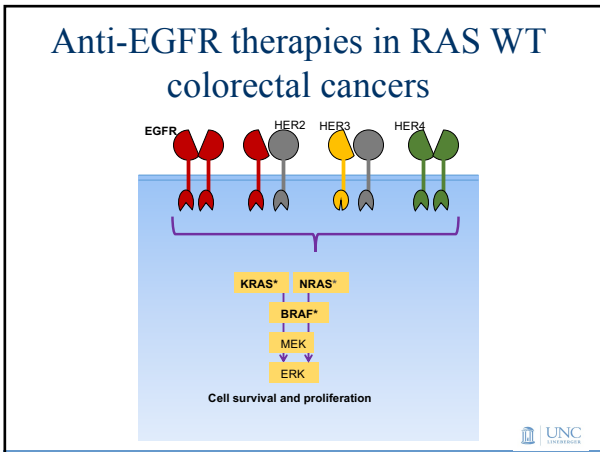
In certain circumstances

FOLFOXIRI ± bevacizumab



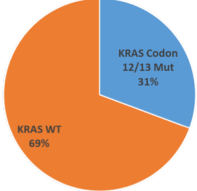






KRAS codons 12 and 13 mutations are most common

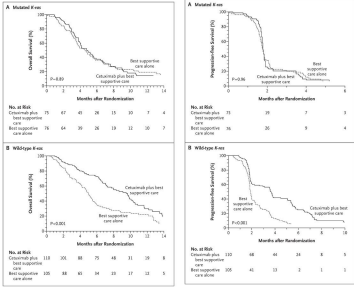
- Studies find 30-40% KRAS codon 12/13 mutations



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KRAS mutation is predictive biomarker for resistance to anti-EGFR



HR 0.55 (95% CI 0.41-0.74)
Interaction p=0.01 between KRAS and treatment

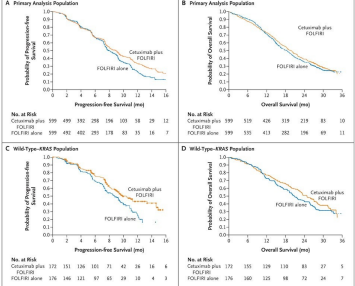
HR 0.40 (95% CI 0.30-0.54)
Interaction p<0.001 between KRAS and treatment

Karapetis CS, et al, N Engl J Med 2008; 359:1757-65

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KRAS mutation is predictive biomarker for resistance to anti-EGFR



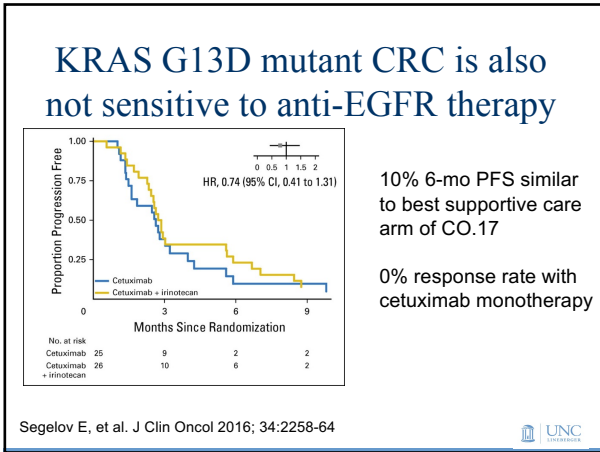
HR 0.68 (95% CI 0.50-0.94)

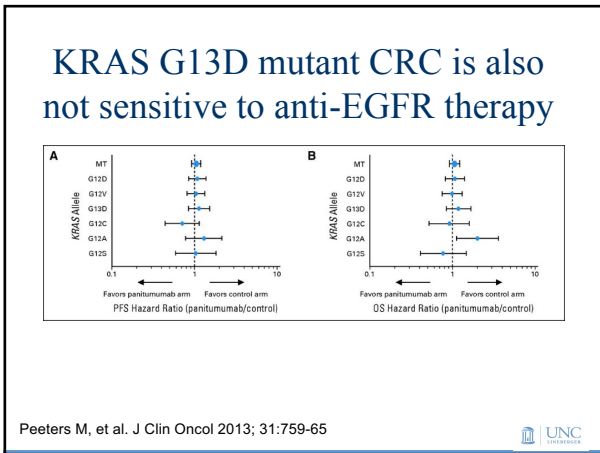
HR 0.84 (95% CI 0.64-1.11)

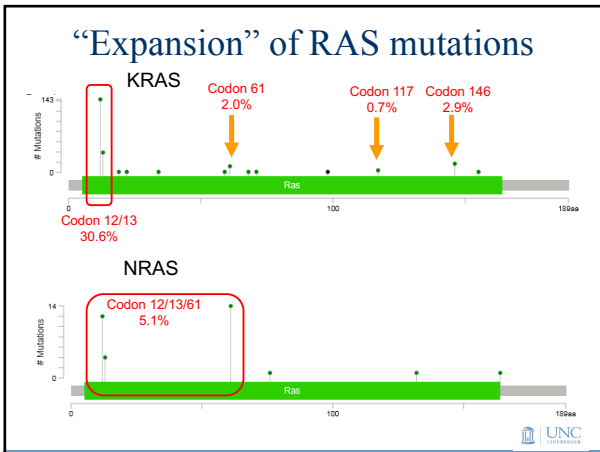
Van Cutsem E, et al, N Engl J Med 2009;360:1408-17

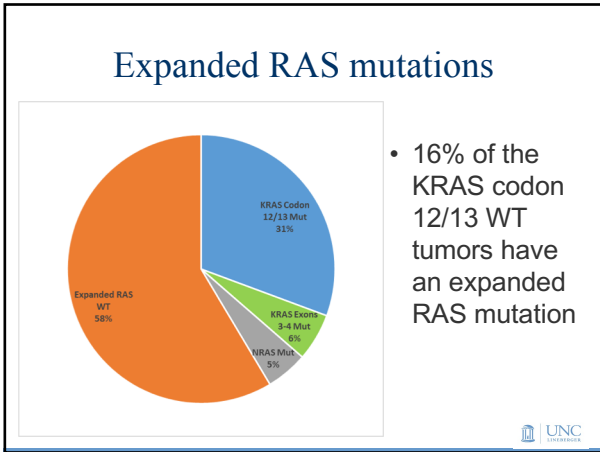
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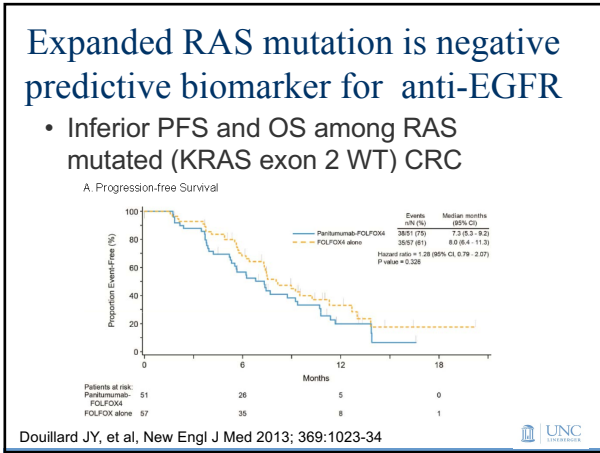


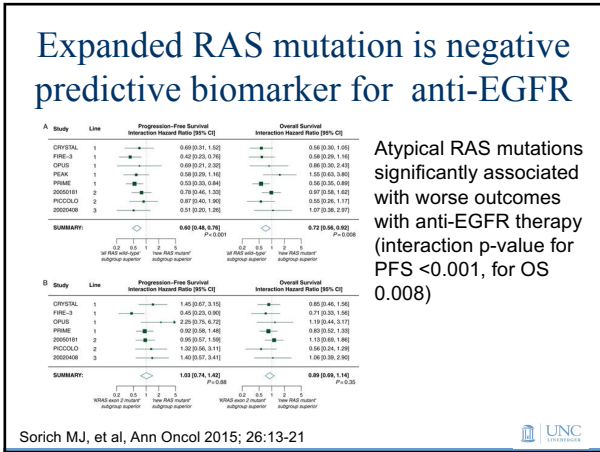






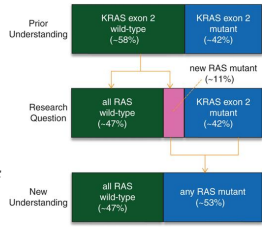






Expanded RAS mutation testing is now standard of care

- Expanded RAS mutation (KRAS and NRAS codons 12, 31, 59, 61, 117, 146) is predictive for lack of benefit of anti-EGFR therapy



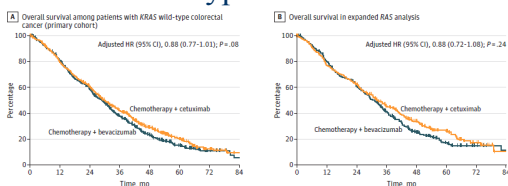
Sorich MJ, et al, Ann Oncol 2015; 26:13-21



Is there an optimal first-line biologic for RAS WT colorectal cancer?



CALGB/SWOG 80405 showed no significant difference between bevacizumab vs cetuximab in KRAS wild-type cancer

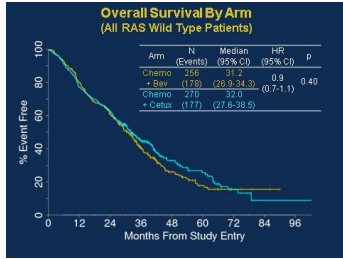


No. of patients at risk	0	12	24	36	48	60	72	84
Chemotherapy + bevacizumab	559	442	317	187	94	42	10	3
Chemotherapy + cetuximab	578	450	338	215	122	55	15	2

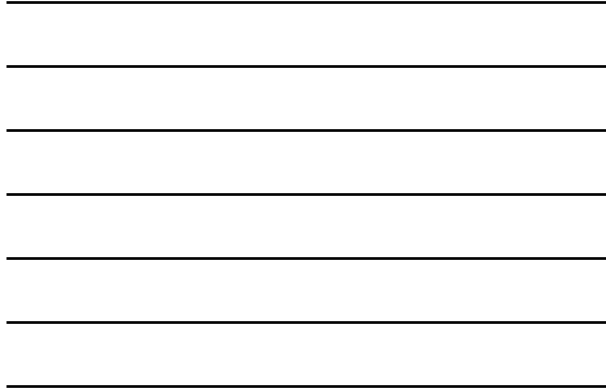
Venook AP, et al, JAMA 2017; 317:2392-2401



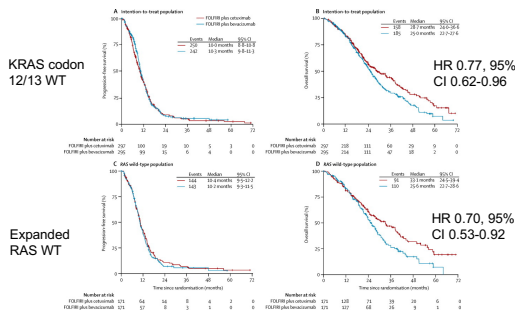
80405 also showed no difference by expanded RAS WT



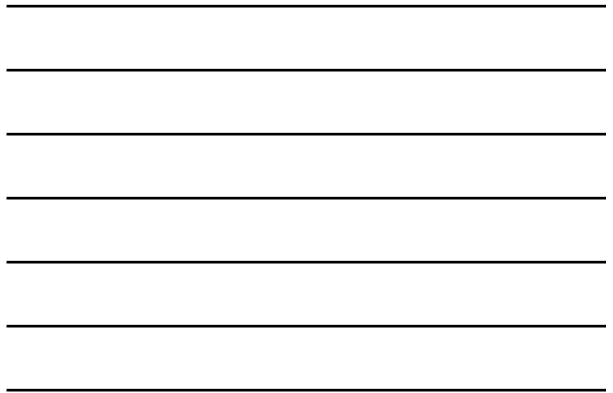
Lenz HJ, et al, Ann Oncol 2014; 25 suppl_4, abstract 501O



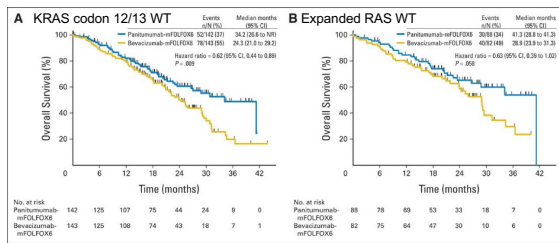
But FIRE-3 did show survival benefit in favor of cetuximab



Heinemann V, et al, Lancet Oncol 2014; 15:1065-75



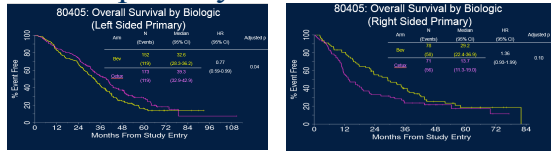
PEAK showed survival benefit in favor of panitumumab



Schwartzberg LS, et al, J Clin Oncol 2014; 32:2240-7.



Markedly worse survival among right-sided primary with 1L cetuximab



BIOLGIC	SIDE OF PRIMARY	HAZARD RATIO	P (adjusted*)
Any biologic	Cetux v Bev, left	1.81 (1.15, 2.84)	P _{adj} = 0.009
	Cetux v Bev, right	0.62 (0.32, 1.23)	
FFS	Left	1.94 (1.28, 2.95)	P _{adj} = 0.001
	Right	0.64 (0.35, 1.09)	
Cetux v Bev	Left	0.77 (0.59, 1.00)	0.04
	Right	1.39 (0.93, 1.99)	
OS	Left	0.64 (0.46, 0.90)	0.15
	Right	1.39 (0.93, 1.99)	
PFS	Left	1.39 (0.93, 1.99)	0.10
	Right	1.64 (1.12, 2.42)	

*Adjusted for baseline, protocol chemotherapy, post-adjuvant therapy, prior RT, age, sex, synchronous disease, in place primary, best maintenance

Venook AP, et al, J Clin Oncol 2016; 34 suppl15, abstract 3504

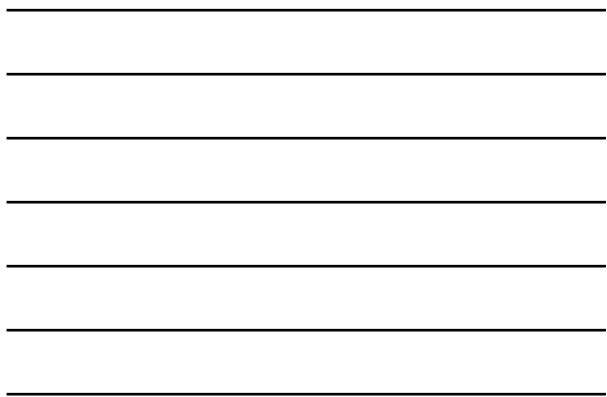


80405 Results with Expanded RAS and BRAF testing

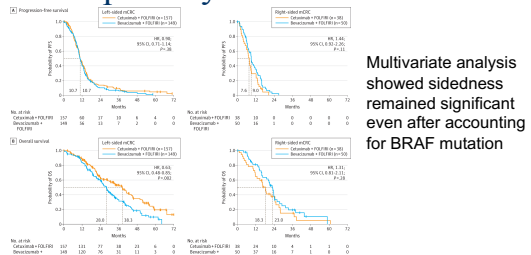
	Left sided Median OS (95% CI)	Right sided Median OS (95% CI)	Log-rank p- value	Adjusted HR (95% CI)
Total population (n=728)	32.9 (30.7-35.3)	19.6 (7.0-23.6)	<0.0001	1.39 (1.03-1.88)
All RAS/BRAF WT (n=225)				
Bevacizumab (n=91)	38.7 (34.3-42.3)	34.4 (23.6-62.0)	0.918	0.62 (0.32-1.23)
Cetuximab (n=96)	40.3 (34.0-48.3)	18.4 (14.2-30.1)	0.003	1.68 (0.85-3.34)
BRAF Mutant				
Bevacizumab (n=23)	12.0 (4.8-14.5)	23.7 (7.9-36.9)	0.035	
Cetuximab (n=16)	9.6 (8.6-NE)	5.8 (1.9-11.7)	0.508	

Adjusted Cox proportional HR for side 1.392 (1.032-1.878)

Venook AP, et al, J Clin Oncol 2017; 35 suppl, abstract 3503



Markedly worse survival among right-sided primary with 1L cetuximab



Multivariate analysis showed sidedness remained significant even after accounting for BRAF mutation

Among right-sided CRC, FOLFIRI + cetuximab is also not superior to FOLFIRI alone by PFS (p=0.66) or OS (p=0.76)

Tejpar S, et al, JAMA Oncol 2017; 3:194-201.



Summary of First-Line Trials for all-RAS WT

	Right-sided Median OS	Left-sided Median OS
80405 (n=474)	N=149	N=325
Cetuximab	13.6 (11.3-19.0)	39.3 (32.9-42.9)
Bevacizumab	29.2 (22.4-36.9)	32.6 (28.3-36.2)
FIRE-3 (n=394)	N=88	N=306
Cetuximab	18.3	38.3
Bevacizumab	23.0	28.0
PEAK (n=143)	N=36	N=107
Panitumumab	17.5 (9.1-30.7)	43.4 (31.6-63.0)
Bevacizumab	21.0 (6.0-29.0)	32.0 (26.0-47.4)

Venook AP, et al, J Clin Oncol 2016; 34 suppl15, abstract 3504; Tejpar S, et al, JAMA Oncol 2017; 3:194-201; Boeckx N, et al, Ann Oncol 2017; 28:1862-8.



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Bevacizumab	29.2 (22.4-36.9)	32.6 (28.3-36.2)	p=0.50
FIRE-3 (n=394)	N=88	N=306	
Cetuximab	18.3	38.3	p<0.001
Bevacizumab	23.0	28.0	p=0.04
PEAK (n=143)	N=36	N=107	
Panitumumab	17.5 (9.1-30.7)	43.4 (31.6-63.0)	p=0.007
Bevacizumab	21.0 (6.0-29.0)	32.0 (26.0-47.4)	p=0.004

Venook AP, et al, J Clin Oncol 2016; 34 suppl15, abstract 3504; Tejpar S, et al, JAMA Oncol 2017; 3:194-201; Boeckx N, et al, Ann Oncol 2017; 28:1862-8.



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Bevacizumab	29.2 (22.4-36.9)	32.6 (28.3-36.2)	p=0.10	
FIRE-3 (n=394)	N=88	N=306		
Cetuximab	18.3	38.3	p=0.28	Interaction p=0.009
Bevacizumab	23.0	28.0	p=0.002	
PEAK (n=143)	N=36	N=107		
Panitumumab	17.5 (9.1-30.7)	43.4 (31.6-63.0)	p=0.33	p=0.31
Bevacizumab	21.0 (6.0-29.0)	32.0 (26.0-47.4)		

Venook AP, et al, J Clin Oncol 2016; 34 suppl15, abstract 3504; Tejpar S, et al, JAMA Oncol 2017; 3:194-201; Boeckx N, et al, Ann Oncol 2017; 28:1862-8.

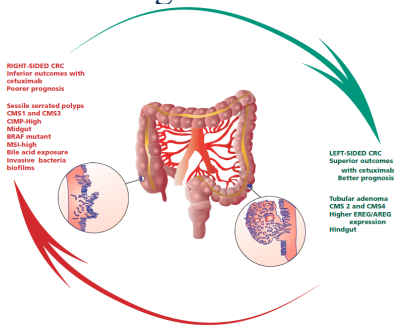


Conclusions for selecting a first-line biologic therapy for RAS WT

- Confirm wild-type in extended RAS (KRAS and NRAS exons 2,3,4)
- Do not use anti-EGFR based therapy for right-sided primary
- Consider first-line anti-EGFR (vs. bevacizumab) based therapy for left-sided primary
- If has BRAF mutation consider different strategy



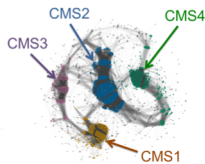
Primary side is a clinical surrogate for biologic differences



Lee MS, et al, J Natl Compre Canc Netw 2017; 15:411-9



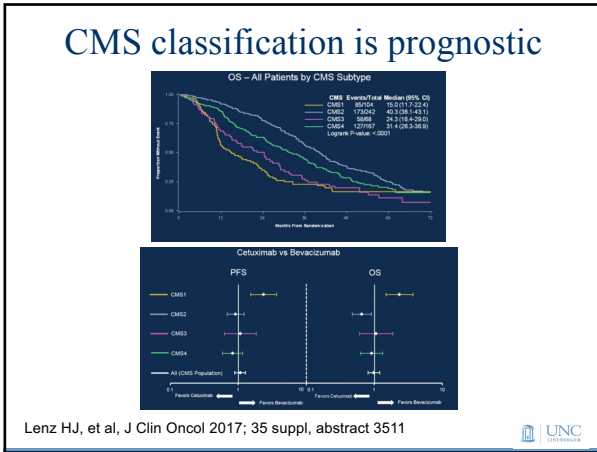
Consensus Molecular Subtypes (CMS) as a potential biomarker

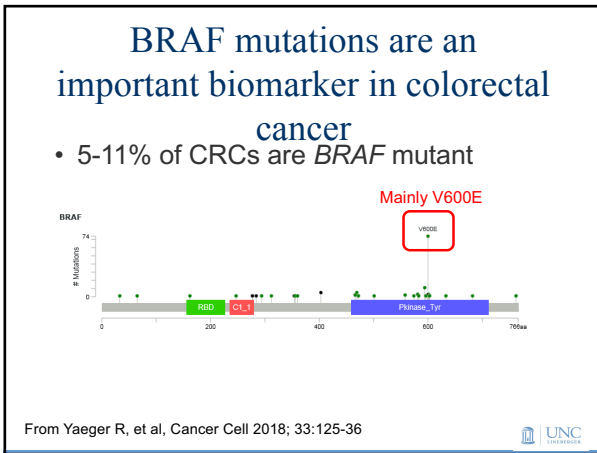


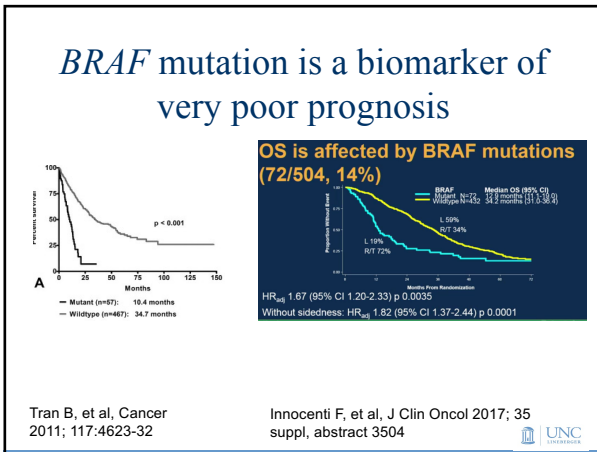
CMS1 Microsatellite	CMS2 Conventional	CMS3 Methylation	CMS4 Mesenchymal
14%	37%	13%	23%
MSI, CIMP high, hypermutation	SCNA high	Mixed MSI status, SCNA low, CIMP low	SCNA high
BRAF mutations		KRAS mutations	
Immune infiltration and activation	WNT and MYC activation	Metabolic deregulation	Stromal infiltration, TGF- β activation, angiogenesis
Worse survival after relapse			Worse relapse-free and overall survival

Guinney J, et al, Nat Medicine 2015; 21:1350-6.









Targeted approaches to target BRAF V600 mutant CRC

- Seek clinical trials!
- Multilevel pathway inhibition is promising approach

Progression-free survival by treatment arms

Time from randomization, months	0.4*	0.17††	1.1*
Median PFS	13.0 (9.4-16.6)	4.2 (3.4-5.0)	14.0 (11.4-16.6)

Dabrafenib + Trametinib + Panitumumab 21% response rate

- Ongoing phase III BEACON CRC trial of encorafenib + binimetinib +/- cetuximab vs chemo/cetuximab

Corcoran RB, et al, Cancer Discov 2018; 8:428-43



Targeted approaches to target BRAF V600 mutant CRC

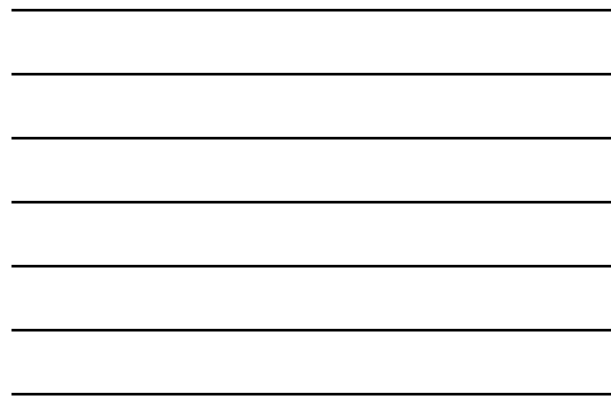
- Consider vemurafenib + cetuximab + irinotecan if no prior anti-EGFR therapy

	N	Events	Median	95% Conf Int
Cetuximab + Irinotecan	50	48	2.0	(1.8 - 2.1)
Vemurafenib + Cetuximab + Irinotecan	49	40	4.5	(3.6 - 5.7)

HR = 0.48 (95% CI 0.31 - 0.75)
P = 0.001

- Median OS 9.6 mo vs 5.9 mo, HR 0.73 (0.45-1.17) but limited by crossover

Kopetz S, et al, J Clin Oncol 2017; 35 suppl, abstract 3505



BRAF mutations are not all equivalent

Class	Codons	% BRAF Mutations
Class I: Kinase activity activated	V600	78.4%
Class II: Kinase activity activated	G464, G466, G469, N581, L597, A598, K601	6.1%
Class III: Kinase activity impaired	G466, D594, G596	15.5%

More dependent on receptor signaling in preclinical models; Clinical relevance unclear

Jones JC, et al, J Clin Oncol 2017; 35:2624-30



HER2 amplification appears targetable from preliminary trial data

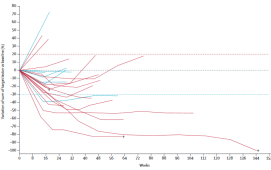
HERACLES: Trastuzumab + Lapatinib

- ORR 30% (95% CI 13-47)
- PFS 21 wk (95% CI 16-32)

MyPathway: Trastuzumab + Pertuzumab


- ORR 37.5% (95% CI 21.1-56.2)

Hurwitz H, et al, J Clin Oncol 2017; suppl 4: Abstract 676



S1613: Randomized phase II trial of trastuzumab + pertuzumab vs cetuximab + irinotecan for HER2 amplified, RAS/BRAF WT previously treated metastatic CRC

Sartore-Bianchi A, et al, Lancet Oncol 2016;17:738-46



Rare but potentially actionable gene fusions in CRC

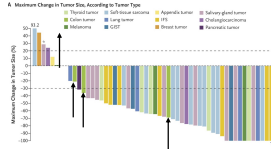
NTRK fusion

- 0.5% of CRC
- 4/55 subjects in the pivotal larotrectinib trial had colon cancer

ALK fusion


- 0.2% of CRCs
- Case reports of responses with ceritinib

Yakirevich E, et al, Clin Cancer Res 2016;22:3831-40.



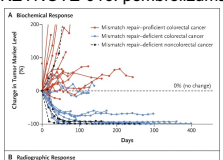
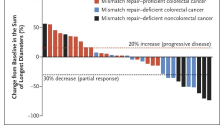
ALK, ROS1, and NTRK fusions are in 0.2-2.4% of CRC and are more common in elderly, right-sided, RAS WT, MSI-High cancers

Pietrantonio F, et al, J Natl Cancer Inst 2017; 109:



MSI-High is a key predictive biomarker for immune checkpoint inhibitors

KEYNOTE-016: pembrolizumab





Pembrolizumab granted accelerated FDA approval for MSI-High CRC following treatment with 5FU, oxaliplatin, irinotecan

All MSI-High (n=149)	
Complete response rate	7.4%
Partial response rate	32.2%
ORR (95% CI)	39.6% (31.7-47.9)
Median duration of response	Not reached

MSI-High CRC (n=90)	
ORR	36%
Range of duration of response	1.6+ to 22.7+ mo

Le DT, et al, New Engl J Med 2015; 372:2509-20



The enigma of immuno-oncology in MSS colorectal cancer

- POLE mutant cancer may respond to pembrolizumab (Gong J, et al, J Natl Compr Canc Netw 2017;15:142-7)
- Recent negative phase III IMblaze370 trial of atezolizumab + cobimetinib vs atezolizumab vs regorafenib
- Key question is how to increase lymphocyte infiltration into “immune deserts” of T cell devoid tumors (Le DT, et al, Cancer Immunol Res 2017;5:942-9)



Summary of molecular biomarker testing guidelines for standard of care

- Test KRAS and NRAS codons 12, 13, 59, 61, 117, and 146 for patients being considered for anti-EGFR therapy
- Test for BRAF p.V600 mutation for prognostic stratification
 - Insufficient evidence for BRAF p.V600 mutation as predictive biomarker against anti-EGFR therapy
- Test for mismatch repair status for identification of patients at high risk for Lynch syndrome and/or prognostic stratification *(and for immune checkpoint inhibitor therapy)*
- Though metastatic/recurrent tissue is preferred for biomarker testing, in their absence, primary tumor tissue is acceptable and should be used.

Sepulveda AR, et al, J Clin Oncol 2017;35:1453-86

(my addendum given subsequent FDA approval)



Other non-standard potentially actionable findings for chemo-refractory patients

Always consider clinical trials!

Molecular Profile	Frequency	Therapy Options
BRAF V600E Mutant	5-11%	Cetuximab + Vemurafenib + Irinotecan *
BRAF non-V600 Mutant	<1%	? RTK inhibition for class III
HER2 Amplified	5%	Trastuzumab + Lapatinib Trastuzumab + Pertuzumab
NTRK fusion	<0.5%	TRK inhibitor
ALK fusion	<0.5%	? ALK inhibitor
POLE mutation with hypermutated status	<1%	? Anti-PD1 antibody

* Listed in NCCN guidelines

? Based on case reports or preclinical data, though compelling rationale