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Investigating the clinical and molecular characteristics of class II and III BRAF mutations and their response to anti-EGFR therapy in MSS CRC: A comprehensive analysis.

Ibrahim Halil Sahin¹, Joanne Xiu², Moh'd M. Khushman³, Emily Palumbo², Benjamin Adam Weinberg⁴, Mehmet Akce⁵, Aatur D. Singhi¹, Phoenix D. Bell¹, Anup Kasi⁶, Anthony F. Shields⁷, Matthew James Oberley², George W. Sledge Jr²., John Paul Y.C. Shen⁸, Anwaar Saeed¹, Mohamedtaki Tejani ⁹ ¹University of Pittsburgh Medical Center, Pittsburgh, PA; ²Caris Life Sciences, Phoenix, AZ; ³Washington University of Kansas Cancer Center, ⁷Barbara Ann Karmanos Cancer Institute, Detroit, MI; ⁸The University of Texas MD Anderson Cancer Center, Houston, TX; ⁹ Advent Health Cancer Institute

Significance and Background

BRAF mutations represent a highly heterogeneous group of molecular alterations seen in colorectal cancer (CRC).

Class I BRAF mutation (V600) render aggressive biology to CRC and poor response to EGFR blockade therapy.

Currently there are limited data on clinical and molecular features of class II and III BRAF mutations and their response to EGFR blockade therapy.

In this large comprehensive cohort study, we investigated the clinical and molecular characteristics of BRAF mutation classes and their impact on clinical outcomes in a large cohort of patients with mismatch proficient-microsatellite stable CRC.

Methods

A total of 24,327 pMMR/MSS CRC specimens were profiled by nextgeneration sequencing (592-gene, NextSeq; WES, WTS NovaSeq) (Caris Life Sciences, Phoenix, AZ).

BRAF mutations were detected by NGS and classified using published literature (Sahin et al. JCO OP 2021).

Interferon gamma signature (Cristescu et al. 2018) and MAPK pathway activity score (MPAS) (Wagle et al 2018) were calculated using RNA expression data (TPM: Transcript per million).

Beal-world overall survival information was obtained from insurance claims and calculated from tissue collection to last contact, while posttreatment survival from first of treatment to last contact.

Kaplan-Meier estimates were calculated for molecularly defined cohorts using Cox-proportional hazard analysis. Significance was determined as p values of <0.05.

Table 1. Demographic and clinical characteristics of patients

Gender	
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Figure 2. A) Overall OS outcomes of patients with BRAF WT, class I, II and IIII mutations B) those
without anti-EGFR therapy, C) Class I vs III D) Class I vs II

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	0.8
	Event-free Proportion 6.0 9.0

0.2

0.0





	MSS Class 1	MSS Class 2	MSS Class 3	MSS WT	Total	P values
Female	720 (6.73%)	60 (0.56%)	145 (1.36%)	9776 (91.36%)	10701	<0.0001
Male	548 (4.02%)	72 (0.53%)	178 (1.31%)	12828 (94.14%)	13626	
/ledian Age	66	64	63	62	62	<0.0001
Age IQR	57-74	55-70	53-72	52-70	53-71	
or Pacific Islander	24 (3.19%)	3 (0.40%)	8 (1.06%)	718 (95.35%)	753	<0.0001
White	840 (6.55%)	70 (0.55%)	175 (1.36%)	11744 (91.54%)	12829 (
· African American	60 (1.86%)	15 (0.47%)	43 (1.33%)	3104 (96.34%)	3222	
Other	51 (4.36%)	4 (0.34%)	17 (1.45%)	1097 (93.84%)	1169	
Unknown	293 (4.61%)	40 (0.63%)	80 (1.26%)	5941 (93.50%)	6354	
oanic or Latino	119 (4.22%)	17 (0.60%)	35 (1.24%)	2651 (93.94%)	2822	<0.0001
spanic or Latino	865 (5.82%)	75 (0.50%)	201 (1.35%)	13727 (92.33%)	14868	
Unknown	284 (4.28%)	40 (0.60%)	87 (1.31%)	6226 (93.81%)	6637	
Left-sided	361 (2.64%)	59 (0.43%)	172 (1.26%)	13058 (95.66%)	13650	<0.0001
Right-Sided	541 (10.26%)	34 (0.64%)	83 (1.57%)	4617 (87.53%)	5275	
Fransverse	130 (13.04%)	4 (0.40%)	7 (0.70%)	856 (85.86%)	997	
ther/Unclear	236 (5.36%)	35 (0.79%)	61 (1.38%)	4073 (92.46%)	4405	
Colon	709 (7.05%)	54 (0.54%)	120 (1.19%)	9176 (91.22%)	10059	<0.0001
Liver	186 (3.60%)	35 (0.68%)	72 (1.39%)	4873 (94.33%)	5166	
Rectum	70 (2.14%)	12 (0.37%)	58 (1.78%)	3124 (95.71%)	3264	
Lung	33 (2.48%)	9 (0.68%)	18 (1.35%)	1270 (95.49%)	1330	
Peritoneum	85 (8.99%)	5 (0.53%)	16 (1.69%)	839 (88.78%)	945	
ymph Node	38 (5.97%)	2 (0.31%)	12 (1.88%)	585 (91.84%)	637	
nclear/Other	147 (5.02%)	15 (0.51%)	27 (0.92%)	2737 (93.54%)	2926	







■CMS2 ■CMS3 ■CMS4

Figure 1. CMS classification of BRAF classes and BRAF WT CRC











A total of 1268, 132, and 323 patients with class I, II, and III BRAF mutations were identified. Class I BRAF mutations were significantly lower in African Americans (1.8%), and patients with class II and III had significantly higher leftsided tumors compared to patients with class I BRAF mutations (Table 1).

Class I BRAF mutations were significantly enriched with (CMS1) (Class I, II) and III: 47% vs. 13% vs. 18%) while class II and III BRAF mutations presented with more often CMS2 subtype (canonical) compared to class I (2%, 30% and 29%, p<0.05).

Class I BRAF and KRAS/NRAS mutations were nearly mutually exclusive (0.5%), while KRAS mutation incidences were 13% and 27.4% for class II and class III (p<0.001), respectively.

Batients with class II and III mutations had significantly better overall survival compared to patients with class I mutations (p<0.0001) and worse overall survival compared to wild-type BRAF pts. (P<0.01, Figure 1A). This was also observed among patients who did not receive anti-EGFR therapy (p<0.001 Figure 1B).

Among patients treated with anti-EGFR, patients with class II and III BRAF mutations had significantly better post-anti-EGFR survival compared to class I BRAF mutants (14.5 months vs 10.4 months P<0.01)

Cetuximab score was significantly lower for class I compared to Class II and III BRAF mutations (p<0.05) (Figure 3).

Conclusion

Bratients with class II and III BRAF mutated CRC present with clinically and biologically distinct diseases compared to patients with class I BRAF mutations, and they have improved outcomes compared to patients with class I, albeit worse than those with BRAF WT.

While KRAS mutations are mutually exclusive with class I BRAF mutations, they can be concurrently seen with class II and III BRAF mutations, and class II and III BRAF mutations carry distinct CMS signatures compared to class I BRAF mutations.

Class II and III BRAF mutations have better cetuximab scores compared to class I, and improved post-EGFR therapy survival outcomes were noted in the class II & III combined cohort.

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