

Published in final edited form as:

Clin Cancer Res. 2014 October 15; 20(20): 5322–5330. doi:10.1158/1078-0432.CCR-14-0332.

Mismatch repair status and *BRAF* mutation status in metastatic colorectal cancer patients: a pooled analysis of the CAIRO, CAIRO2, COIN and FOCUS studies

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Abstract

Purpose—To determine the prevalence and prognostic value of mismatch repair (MMR) status and its relation to *BRAF* mutation (*BRAF*^{MT}) status in metastatic colorectal cancer (mCRC).

Experimental Design—A pooled analysis of four phase III studies in first-line treatment of mCRC (CAIRO, CAIRO2, COIN and FOCUS) was performed. Primary outcome parameter was the hazard ratio (HR) for median progression-free survival (PFS) and overall survival (OS) in relation to MMR and *BRAF*. For the pooled analysis, Cox regression analysis was performed on individual patient data.

Results—The primary tumors of 3063 patients were analyzed, of which 153 (5.0%) exhibited deficient MMR (dMMR) and 250 (8.2%) a *BRAF*^{MT}. *BRAF*^{MT} was observed in 53 (34.6%) of patients with dMMR tumors compared to 197 (6.8%) of patients with proficient MMR (pMMR) tumors ($p < 0.001$). In the pooled data set, median PFS and OS were significantly worse for patients with dMMR compared to pMMR tumors (HR 1.33, 95% CI 1.12-1.57 and HR 1.35, 95% CI

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Conflict of interest: None of the authors have a conflict of interest to disclose.

1.13-1.61, respectively), and for patients with *BRAF*^{MT} compared to *BRAF* wild-type (*BRAF*^{WT}) tumors (HR 1.34, 95% CI 1.17-1.54 and HR 1.91, 95% CI 1.66-2.19, respectively). PFS and OS were significantly decreased for patients with *BRAF*^{MT} within the group of patients with pMMR, but not for *BRAF* status within dMMR, or MMR status within *BRAF*^{WT} or *BRAF*^{MT}.

Conclusions—Prevalence of dMMR and *BRAF*^{MT} in mCRC patients is low and both biomarkers confer an inferior prognosis. Our data suggest that the poor prognosis of dMMR is driven by the *BRAF*^{MT} status.

Keywords

dMMR; *BRAF*; metastatic colorectal cancer

INTRODUCTION

Colorectal cancer (CRC) is a heterogeneous disease arising through different pathways.(1, 2) Three molecular pathways are well known to be involved in the multistep process of colorectal carcinogenesis, including the chromosomal instability (CIN) pathway, the mutator pathway (microsatellite instability (MSI)), and the epigenetic instability pathway or CpG island Methylator Phenotype (CIMP), the latter of which has substantial overlap with the other two.

MSI is the result of a deficient DNA mismatch repair (dMMR) system. A germ line mutation in one of the mismatch repair genes, most often *MLH1* or *MSH2*, is the cause of dMMR in patients with Lynch syndrome, which comprises 0.8–5% of all CRCs.(3) dMMR is also observed in 10–20% of patients with sporadic CRC, of which the majority of dMMR tumors are due to inactivation of *MLH1* (~95%), caused by hypermethylation of the gene promoter, with *MSH2* and *MSH6* accounting for a smaller percentage.(3-5) These dMMR tumors have distinct features, such as origin in the proximal colon, prominent lymphocytic infiltrate, poorly differentiated morphology, mucinous or signet ring differentiation(6) and association with a favorable prognosis in early stage CRC(7). In metastatic CRC (mCRC) the prevalence of dMMR is low (3.5%).(8, 9) This supports the hypothesis that dMMR tumors have a reduced metastatic potential.(10, 11) Due to its lower frequency the prognostic role of dMMR in mCRC has not been properly evaluated thus far.

The presence of a *BRAF* mutation (*BRAF*^{MT}) in a dMMR tumor indicates a sporadic origin, and essentially excludes a diagnosis of Lynch syndrome.(12, 13) In CRC the overall prevalence of *BRAF*^{MT} is ~10%.(14) *BRAF*^{MT} has a negative prognostic impact, although this may be restricted to patients with proficient MMR (pMMR) tumors.(15, 16) Data on the role of *BRAF* in relation to MMR status in mCRC are scarce and are derived from small subsets of selected patients.

The current study was initiated to assess the role of MMR in relation to the *BRAF*^{MT} status in respect to prevalence and outcome in patients with mCRC who participated in four large prospective phase III studies: CAIRO(17), CAIRO2(18), COIN(19, 20) and FOCUS(21).

MATERIAL AND METHODS

Patients and treatment

Data were derived from mCRC patients included in four large phase III studies in first line treatment: CAIRO ([ClinicalTrials.gov](https://clinicaltrials.gov/ct2/show/study/NCT00312000) NCT00312000), CAIRO2 ([ClinicalTrials.gov](https://clinicaltrials.gov/ct2/show/study/NCT00208546) NCT00208546), COIN (ISRCTN 27286448) and FOCUS (ISRCTN 79877428), of which the results have been published previously.(17-21) Collection of formalin-fixed paraffin-embedded material (FFPE) of the primary tumor was part of the initial protocol in all four studies.

MMR status

For samples of both CAIRO studies, immunohistochemistry (IHC) was performed on FFPE tissue with antibodies against MMR proteins MLH1, MSH2, MSH6 and PMS2. In addition, MSI analysis was performed where there was an absence of MMR protein expression or equivocal IHC results. dMMR status was determined using two microsatellite markers (BAT 25 and BAT 26). If only one of these markers showed instability, the analysis was extended with four additional markers (BAT 40, D2S123, D5S346, and D17S250). A tumor was defined as dMMR if at least two of the six markers showed instability or pMMR if none of the markers showed instability. Tumors with only one of the markers showing instability were defined as dMMR-low and included in the pMMR category. For samples from the COIN study, dMMR status was assessed using two microsatellite markers (BAT25 and BAT26). If only one of these markers showed instability the tumor was defined as dMMR, and as pMMR if no instability was observed. For samples from the FOCUS study, dMMR status was based on loss of MLH1 and MSH2 protein expression, assessed by IHC. If either protein showed loss of expression, the tumor was defined as dMMR, and pMMR if no loss of expression was observed.

Hypermethylation status of the *MLH1* gene promoter

Hypermethylation of the *MLH1* gene promoter in patients with a dMMR tumor was analyzed in samples from the CAIRO and CAIRO2 studies only and therefore not included in the pooled analysis. The DNA methylation status of the *MLH1* promoter region was determined after bisulphite treatment of the DNA using the EZ DNA methylation KIT, ZYMO Research (Orange, CA, USA), as described previously.(8)

BRAF mutation status

The *BRAF* V600E mutation status was assessed in duplicate by high resolution melting (HRM) sequencing analysis for tumor material in the CAIRO study(22) and by direct sequencing analysis in the CAIRO2 study(23). For samples of the COIN and FOCUS studies, the *BRAF* V600E mutation status was determined by Pyrosequencing (and Sequenom in COIN), and verified by Sanger sequencing as described previously.(19, 24) Non-V600E *BRAF* mutations detected by these assays (n=19) were not included in the current analyses on outcome.

Statistical methods

Individual patient data were included in the pooled analysis. Progression free survival (PFS) was defined as the time from the date of randomization to first progression or death, whichever came first. Overall survival (OS) was defined as the time from randomization to the date of death. The primary outcome measure was the hazard ratio (HR) for PFS and OS in relation to MMR and *BRAF* mutation status. For PFS and OS all studies were included in a Cox regression model (proportional hazard model) by using the study as a factor in the model. In this way, dependence of the hazard on study could be modeled. The HR was corrected for study effect. Survival curves were plotted and log-rank tests were performed to compare survival for the different groups defined. A statistical interaction analysis for survival data of dMMR and *BRAF* status was performed. All analyses were conducted using the SAS system version 9.2; $p < 0.05$ was considered as statistically significant.

RESULTS

Study population and MMR / *BRAF* mutation status

Tumor and normal samples from 3063 out of 6155 randomized mCRC patients were available and suitable for analysis of both MMR and *BRAF* mutation status. Of these 3063 patients, 322 patients participated in the CAIRO study, 516 patients in the CAIRO2 study, 1461 patients in the COIN study and 764 patients in the FOCUS study.

The prevalence of MMR status and *BRAF* mutation status and their correlation are presented in Table 1 and 2, respectively. dMMR was found in tumors of 153 (5.0%) patients and 250 (8.2%) patients had a *BRAF*^{MT} (Table 1). There was no evidence of heterogeneity for the prevalence of dMMR and *BRAF*^{MT} in the four studies; $p=0.614$ and $p=0.943$, respectively (Table 1). A *BRAF*^{MT} was observed in 53 (34.6%) of patients with dMMR tumors compared to 197 (6.8%) of patients with pMMR tumors ($p < 0.001$) (Table 2). There was heterogeneity for the prevalence of combined MMR and *BRAF*^{MT} status between the four studies. In the CAIRO study, there were significantly more patients with a combined dMMR and *BRAF*^{MT} (dMMR / *BRAF*^{MT}) tumor compared to the other three studies ($p=0.002$) (Table 2).

Patient and tumor characteristics (sex, age, location of the primary tumor, performance status, number of metastatic sites involved) for the different subgroups defined by the combined MMR and *BRAF* mutation status are summarized in Supplementary Table 1. Hypermethylation of *MLH1* was the main cause of dMMR in both CAIRO and CAIRO2 studies (30 out of 45 patients), this was associated with a high frequency of *BRAF*^{MT} (73%) compared to tumors without *MLH1* hypermethylation (7%).

Survival data

The survival data of the individual studies, the pooled data set and the pooled analysis for patients with dMMR, pMMR, *BRAF*^{MT} and *BRAF*^{WT} tumors are presented in Table 3. The median PFS and OS were significantly worse for patients with dMMR compared to pMMR tumors (PFS: 6.2 versus 7.6 months, respectively, HR 1.33, 95% CI 1.12-1.57, $p=0.001$; OS: 13.6 versus 16.8 months, respectively, HR 1.35, 95% CI 1.13-1.61, $p=0.001$). Median PFS and OS were also significantly worse for patients with *BRAF*^{MT} compared to *BRAF*^{WT}

tumors (PFS: 6.2 versus 7.7 months, respectively, HR 1.34, 95% CI 1.17-1.54, $p < 0.001$; OS: 11.4 versus 17.2 months, respectively, HR 1.91, 95% CI 1.66-2.19, $p < 0.001$).

To determine a possible interaction between MMR and *BRAF* status, with respect to the survival, a Cox regression was performed by using the study as a factor in the model. For PFS and OS all studies were included in a Cox regression model (proportional hazard model) by using the study as a factor in the model. Results are presented for MMR status in a *BRAF*^{MT} and *BRAF*^{WT} background, and vice versa for *BRAF* status in a dMMR and pMMR background in table 4. Survival curves, as estimated by the Cox regression, are presented in Figure 1. In *BRAF*^{MT} tumors stratified by MMR status, there was no significant survival difference for patients with dMMR compared to pMMR tumors (PFS; 6.1 versus 6.2 months, respectively, HR 0.95, 95% CI 0.62-1.46, $p = 1.000$; OS; 11.7 versus 11.3 months, respectively, HR 1.05, 95% CI 0.68-1.63, $p = 1.000$). Also in *BRAF*^{WT} tumors stratified by MMR status, there was no significant survival difference for patients with dMMR compared to pMMR tumors (PFS: 6.3 versus 7.8 months, respectively, HR 1.32, 95% CI 1.00-1.75, $p = 0.051$; OS: 15.0 versus 17.3 months, respectively, HR 1.22, 95% CI 0.91-1.65, $p = 0.463$). In dMMR tumors stratified by *BRAF* status, there was no significant survival difference for patients with *BRAF*^{MT} compared to *BRAF*^{WT} tumors (PFS: 6.1 versus 6.3 months, respectively, HR 1.07, 95% CI 0.67-1.70, $p = 1.000$; OS: 11.7 versus 15.0 months, respectively, HR 1.51, 95% CI 0.93-2.46, $p = 0.155$). In pMMR tumors stratified by *BRAF* status, there was a significantly decreased median PFS and OS for patients with *BRAF*^{MT} compared to *BRAF*^{WT} tumors (PFS: 6.2 versus 7.8 months, respectively, HR 1.34, 95% CI 1.10-1.64, $p < 0.001$; OS: 11.3 versus 17.3 months, respectively, HR 1.94, 95% CI 1.57-2.40, $p < 0.001$) The test for interaction between dMMR and *BRAF*^{MT} was statistically not significant (PFS: HR 0.79, 95% CI 0.54-1.16, $p = 0.234$; OS: HR 0.78, 95% CI 0.52-1.15, $p = 0.211$).

DISCUSSION

This study presents the largest data set on the role of tumor MMR status and *BRAF* mutation status in respect to prevalence and outcome in a population of patients ($n = 3063$) with mCRC who participated in four prospective phase III studies. We found that dMMR and *BRAF*^{MT} in mCRC each have a low prevalence (5% and 8.2%, respectively), and that both biomarkers indicate a poor prognosis. Given the absence of a statistically significant interaction between *BRAF*^{MT} and dMMR, our data suggest that the poor prognostic value of dMMR is driven by the *BRAF*^{MT} status.

Several aspects of our study warrant further discussion. In this pooled analysis different methods for detecting dMMR were applied, which however have all been validated for the detection of dMMR in CRC. In both CAIRO studies, an approach based on test methods described in the Bethesda criteria, used for standard clinical practice for patients suspected for Lynch syndrome, has been applied.(25) The COIN study analyzed the BAT25 and BAT26 mononucleotide markers, which have a high sensitivity (94%) and specificity (98%), and the use of these two markers alone identifies 97% of MSI tumors.(26) The FOCUS study evaluated MLH1 and MSH2 protein expression by immunohistochemistry, which is a sensitive (92.3%) and specific (100%) method for screening for dMMR.(27)

We acknowledge that the difference in MMR detection methods represents a weakness of our study, however the comparable prevalence of the dMMR status among the four studies in this pooled analysis, ranging from 4.4% to 5.6% argues against this. The results from the individual studies show that the patient population with dMMR tumors is heterogeneous. The observed difference in the prevalence of a *BRAF*^{MT} in dMMR tumors suggests a possible difference in the origin of dMMR, sporadic versus hereditary. Unfortunately, data on the hypermethylation status of the *MLH1* gene promoter, which could differentiate between these two groups, are not available of all four studies.

Furthermore, different methods for detecting the *BRAF* V600E mutation were applied. HRM sequencing, Sanger sequencing and Pyrosequencing have all shown to be reliable methods(22, 28). Data from systematic studies to assess the test accuracy or reproducibility of the different techniques used for *BRAF* mutation testing are not available.

Another issue is the difference in availability of tumor samples among the trials. This is partly caused by non-availability of an extra paraffin-embedded block for DNA analysis, and partly due to non-resected primary tumors in patients with synchronous disease. In these patients often only a diagnostic biopsy was performed, which does not provide sufficient material for further molecular analysis for research purposes. This is an important, underexposed issue which may introduce a sample/case bias not only in our analysis, but in other translational studies in mCRC as well.

The low prevalence of dMMR in mCRC can be explained by the reduced potential of stage I-III dMMR tumors to metastasize.(10, 11) However the underlying mechanisms of this low metastatic potential are yet to be elucidated. It has been suggested that a greater immunoreactivity of dMMR tumors(29, 30) or decreased tumor cell viability due to excessive DNA damage(31) may play a role. In mCRC, data about the prevalence of *BRAF*^{MT} in dMMR tumors are scarce, but in line with our results.(32, 33) The strong inter-relationship between *BRAF*^{MT} and dMMR is well established in early stage CRC(14, 34), however the etiology of both alterations still needs to be elucidated.

We observed a higher prevalence of *BRAF*^{MT} in mCRC dMMR tumors (34.6%) than reported for early-stage dMMR CRC tumors (24%).(16) Patients with early-stage dMMR in general have a better prognosis compared to patient with early-stage pMMR, however within the group of dMMR, patients with *BRAF*^{MT} tumors have a worse prognosis.(35) Subsequently, this may lead to a shift in the dMMR / *BRAF*^{MT} ratio in mCRC patients. There is increasing evidence identifying *BRAF*^{MT} as a significant poor prognostic factor in early stage and mCRC.(18, 36-38) *BRAF* is an oncogene and it is known that the mutations constitutively activate the MAPK pathway for cell growth, in the absence of extracellular stimuli. However, by itself *BRAF* is not sufficient for cancer and must cooperate with other processes to induce the fully cancerous state.(39) Another explanation for the inferior prognosis of *BRAF*^{MT} tumors might be their distinct pattern of metastatic spread. Previous studies have demonstrated a significantly increased rate of peritoneal and distant lymph node metastases and a decreased rate of lung metastases compared to *BRAF*^{WT} tumors.(9, 40)

It has been speculated that the worse prognostic value of dMMR tumors in mCRC may be related to a difference in metastatic spread. Earlier studies showed a reduced rate of liver metastases for dMMR tumors in mCRC(40), and a higher incidence of peritoneal metastases, these factors are known to be related to prognosis.(41, 42) This was confirmed by a previous analysis of the COIN study (9), but these data are not available from the other studies of our analysis.

Lastly, due to the different treatment regimens among the four studies of this pooled analysis, the predictive role of dMMR and *BRAF*^{MT} in mCRC could not be addressed.

In conclusion, dMMR and *BRAF*^{MT} each have a low prevalence in mCRC, and both biomarkers confer a poor prognosis. Our data suggest that the poor prognosis of dMMR is driven by the *BRAF*^{MT} status. However, we caution against a firm conclusion on this issue since our study was not sufficiently powered to test this interaction.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

We thank the patients and their families who participated in all the studies and gave their consent for this research, and the investigators and pathologists who submitted samples for assessment. The CAIRO studies were conducted with the support of the network of the Dutch Colorectal Cancer Group (DCCG). The COIN and FOCUS studies were conducted with the support of Cancer Research UK, the UK Medical Research Council (MRC) and the National Cancer Research Networks.

Financial support: CAIRO: This study was supported by the Dutch Colorectal Cancer Group (DCCG), a grant support from the Commissie Klinisch Toegepast Onderzoek (CKTO) of the Dutch Cancer Foundation (KWF), unrestricted scientific grants from Roche, Aventis, Sanofi, and Pfizer, the Cornelis Visser Foundation and the framework of CTMM, the Center for Translational Molecular Medicine, DeCoDe project (grant 03O-101)

CAIRO2: This study was supported by the DCCG, and grants for data management and analysis from the CKTO of the Dutch Cancer Foundation and unrestricted research grants from Roche, Merck Serono, Sanofi-Aventis, and D&S
COIN: This study was supported by the Bobby Moore Fund from Cancer Research UK, Cancer Research Wales and the NISCHR Cancer Genetics Biomedical Research Unit. The COIN trial was funded by Cancer Research UK and the MRC. An unrestricted educational grant from Merck Serono provided additional support to this work and the trial.

FOCUS: This study was supported by Merck KGaA, Yorkshire Cancer Research, Leeds Experimental Cancer Medicine Center and the Leeds CRUK Center

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Statement of translational relevance

This is the first pooled analysis on individual patient data to assess the role of the mismatch repair (MMR) status in relation to the *BRAF* mutation status in respect to prevalence and outcome in patients with metastatic CRC (mCRC). These patients participated in four large randomized prospective phase III studies, namely the CAIRO, CAIRO2, COIN and FOCUS studies. We show that the prevalence of deficient MMR (dMMR) and *BRAF* mutation is low in mCRC patients. Both biomarkers confer an inferior prognosis. We observed a higher incidence of *BRAF* mutation in dMMR tumors than reported for early-stage dMMR CRC patients and our data suggest that the poor prognosis of dMMR is driven by *BRAF*^{MT} status.

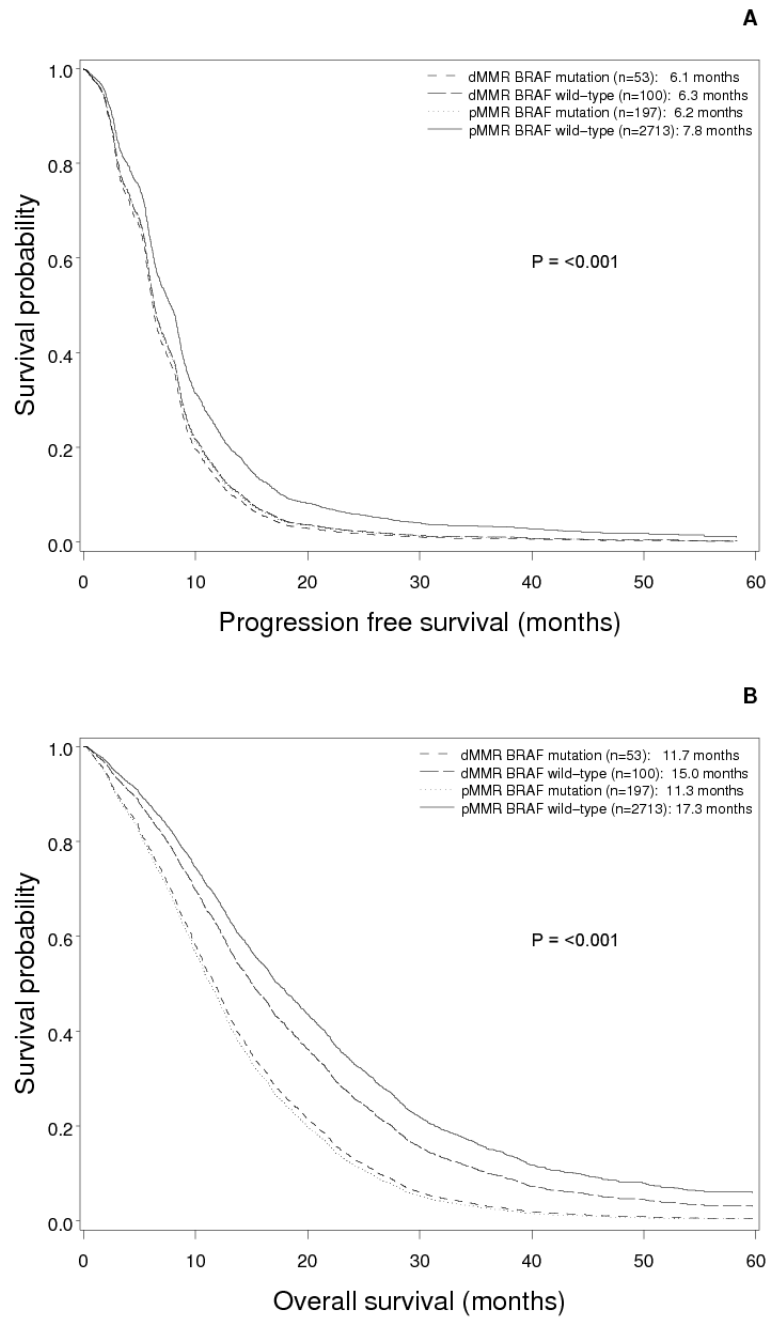


Figure 1. Progression-free (A) and overall survival (B) curves of all patients included in the pooled data set comparing patients with dMMR / $BRAF^{MT}$ tumors, dMMR / $BRAF^{WT}$ tumors, pMMR / $BRAF^{MT}$ tumors and pMMR / $BRAF^{WT}$ tumors

Table 1
Prevalence of MMR and *BRAF* mutation status in patients with mCRC subdivided by study

	dMMR	pMMR	total	<i>BRAF</i> ^{MT}	<i>BRAF</i> ^{WT}	total
CAIRO	18 (5.6%)	304 (94.4%)	322	25 (7.8%)	297 (92.2%)	322
CAIRO2	29 (5.6%)	487 (94.4%)	516	45 (8.7%)	471 (91.3%)	516
COIN	65 (4.4%)	1396 (95.6%)	1461	120 (8.2%)	1341 (91.8%)	1461
FOCUS	41 (5.4%)	723 (94.6%)	764	60 (7.9%)	704 (92.1%)	764
<i>Pooled data set</i>	153 (5.0%)	2910 (95.0%)	3063	250 (8.2%)	2813 (91.8%)	3063
<i>p</i> value			0.614			0.943

NOTE: Statistically significant results are set in bold

p values represent heterogeneity between the four studies

Abbreviations: dMMR = deficient mismatch repair, pMMR = proficient mismatch repair, mt = mutant tumors, wt = wild-type tumors

Table 2
Prevalence of *BRAF* mutation status stratified for MMR status, and MMR status stratified for *BRAF* status in mCRC patients subdivided by study

	<i>BRAF</i> ^{MT}			<i>BRAF</i> ^{WT}			dMMR			pMMR		
	dMMR	pMMR	total	dMMR	pMMR	total	<i>BRAF</i> ^{MT}	<i>BRAF</i> ^{WT}	total	<i>BRAF</i> ^{MT}	<i>BRAF</i> ^{WT}	total
CAIRO	12 (48.0%)	13 (52.0%)	25	6 (2.0%)	291 (98.0%)	297	12 (66.7%)	6 (33.3%)	18	13 (4.3%)	291 (95.7%)	304
CAIRO2	12 (26.7%)	33 (73.3%)	45	17 (3.6%)	454 (96.4%)	471	12 (41.4%)	17 (58.6%)	29	33 (6.8%)	454 (93.2%)	487
COIN	20 (16.7%)	100 (83.3%)	120	45 (3.4%)	1296 (96.6%)	1341	20 (30.8%)	45 (69.2%)	65	100 (7.2%)	1296 (92.8%)	1396
FOCUS	9 (15.0%)	51 (85.0%)	60	32 (4.5%)	672 (95.5%)	704	9 (22.0%)	32 (78.0%)	41	51 (7.1%)	672 (92.9%)	723
<i>Pooled data set</i>	53 (21.2%)	197 (78.8%)	250	100 (3.6%)	2713 (96.4%)	2813	53 (34.6%)	100 (65.4%)	153	197 (6.8%)	2713 (93.2%)	2910
<i>p</i> value			0.002			0.239			0.007			0.330

NOTE: Statistically significant results are set in bold

p values represent heterogeneity between the four studies

Abbreviations: dMMR = deficient mismatch repair, pMMR = proficient mismatch repair, mt = mutant tumors, wt = wild-type tumors

Table 3
Individual study data, pooled data set and pooled analysis of survival data in relation to MMR and BRAF mutation status

		dMMR	pMMR	BRAF MT	BRAF WT	
	number of patients	18	304	25	297	
CAIRO	PFS	mo. (95% CI)	5.7 (4.2-8.8)	6.9 (6.2-7.9)	5.1 (4.1-7.7)	7.0 (6.3-8.2)
		HR (95% CI)	1.34 (0.81-2.22)		1.57 (1.03-2.38)	
CAIRO	OS	mo. (95% CI)	14.8 (12.0-26.0)	17.9 (16.1-19.2)	11.3 (8.3-15.0)	18.1 (16.2-19.4)
		HR (95% CI)	1.26 (0.74-2.16)		2.20 (1.43-3.38)	
CAIRO2	PFS	number of patients	29	487	45	471
		mo. (95% CI)	7.5 (6.4-10.5)	10.5 (9.6-11.4)	6.9 (6.2-8.5)	10.6 (9.7-11.8)
CAIRO2	OS	HR (95% CI)	1.66 (1.13-2.45)		2.03 (1.48-2.79)	
		mo. (95% CI)	15.6 (12.9-22.3)	22.0 (20.3-24.1)	13.1 (10.7-16.5)	22.4 (21.0-24.9)
COIN	PFS	HR (95% CI)	1.60 (1.07-2.40)		2.30 (1.65-3.20)	
		number of patients	65	1396	120	1341
COIN	OS	mo. (95% CI)	5.7 (5.4-6.1)	6.5 (6.2-6.8)	5.8 (5.6-6.2)	6.5 (6.3-6.9)
		HR (95% CI)	1.56 (1.20-2.02)		1.38 (1.14-1.68)	
FOCUS	PFS	mo. (95% CI)	10.7 (9.3-13.0)	16.0 (15.0-16.9)	10.2 (9.0-11.7)	16.5 (15.3-17.1)
		HR (95% CI)	1.80 (1.37-2.37)		2.02 (1.65-2.48)	
FOCUS	OS	number of patients	41	723	60	704
		mo. (95% CI)	8.1 (6.5-9.1)	8.0 (7.4-8.3)	8.1 (6.8-8.9)	8.0 (7.4-8.3)
Pooled data set	PFS	HR (95% CI)	0.98 (0.71-1.35)		0.98 (0.74-1.28)	
		mo. (95% CI)	16.6 (13.6-21.7)	15.5 (14.5-16.6)	12.3 (10.5-14.8)	15.7 (14.8-17.0)
Pooled data set	OS	HR (95% CI)	0.90 (0.64-1.27)		1.52 (1.15-2.00)	
		number of patients	153	2910	250	2813
Pooled data set	PFS	mo. (95% CI)	6.2 (5.9-7.0)	7.6 (7.3-8.0)	6.2 (6.0-6.8)	7.7 (7.4-8.0)
		HR (95% CI)	1.33 (1.12-1.57)		1.34 (1.17-1.54)	
Pooled data set	OS	mo. (95% CI)	13.6 (12.4-15.6)	16.8 (16.3-17.5)	11.4 (10.5-12.4)	17.2 (16.7-18.0)
		HR (95% CI)	1.35 (1.13-1.61)		1.91 (1.66-2.19)	

NOTE: Statistically significant results are set in bold

Abbreviations: PFS = progression-free survival, OS = overall survival, mo. = median PFS and OS time in months, HR = hazard ratio, CI = confidence interval, dMMR = deficient mismatch repair, pMMR = proficient mismatch repair, mt = mutant tumor, wt = wild-type tumor

Table 4
Individual study data, pooled data set and pooled analysis of survival data and association between MMR and BRAF mutation status

		BRAF ^{MT}			BRAF ^{WT}			dMMR			pMMR		
		dMMR	pMMR	dMMR	dMMR	pMMR	dMMR	pMMR	dMMR	pMMR	dMMR	pMMR	
CAIRO	number of patients	12	13	6	6	291	12	12	6	6	13	291	
	mo. (95% CI)	6.6 (4.6-12.6)	4.1 (2.4-6.4)	3.6 (2.0-16.4)	3.6 (2.0-16.4)	7.1 (6.4-8.2)	6.6 (4.6-12.6)	6.6 (4.6-12.6)	3.6 (2.0-16.4)	3.6 (2.0-16.4)	4.1 (2.4-6.4)	7.1 (6.4-8.2)	
CAIRO	HR (95% CI)	2.38 (0.80-7.09)		3.19 (0.96-10.63)			0.34 (0.08-1.44)				2.60 (1.21-5.55)		
	mo. (95% CI)	13.2 (10.1-28.6)	8.3 (5.9-13.6)	18.6 (12.4-53.5)	18.6 (12.4-53.5)	18.2 (16.2-19.4)	13.2 (10.1-28.6)	18.6 (12.4-53.5)	18.6 (12.4-53.5)	8.3 (5.9-13.6)	18.2 (16.2-19.4)		
CAIRO2	HR (95% CI)	2.14 (0.70-6.54)		0.97 (0.25-3.57)			1.63 (0.34-7.77)				3.29 (1.53-7.04)		
	number of patients	12	33	17	17	454	12	12	17	17	33	454	
CAIRO2	mo. (95% CI)	5.7 (4.4-8.5)	7.5 (6.4-9.7)	9.3 (7.2-14.8)	9.3 (7.2-14.8)	10.7 (9.9-12.1)	5.7 (4.4-8.5)	9.3 (7.2-14.8)	9.3 (7.2-14.8)	7.5 (6.4-9.7)	10.7 (9.9-12.1)		
	HR (95% CI)	0.54 (0.22-1.34)		1.25 (0.62-2.49)			2.65 (0.95-7.41)				1.79 (1.09-2.93)		
COIN	mo. (95% CI)	10.4 (7.8-17.2)	14.1 (11.5-19.4)	21.0 (15.2-36.4)	22.4 (21.1-25.0)	10.4 (7.8-17.2)	10.4 (7.8-17.2)	21.0 (15.2-36.4)	21.0 (15.2-36.4)	14.1 (11.5-19.4)	22.4 (21.1-25.0)		
	HR (95% CI)	0.61 (0.25-1.52)		1.14 (0.54-2.40)			2.94 (1.02-8.52)				2.04 (1.21-3.44)		
FOCUS	number of patients	20	100	45	45	1296	20	20	45	45	100	1296	
	mo. (95% CI)	5.9 (5.4-8.5)	5.8 (5.6-6.2)	5.6 (5.1-6.1)	6.6 (6.3-7.0)	5.9 (5.4-8.5)	5.9 (5.4-8.5)	5.6 (5.1-6.1)	5.6 (5.1-6.1)	5.8 (5.6-6.2)	6.6 (6.3-7.0)		
FOCUS	HR (95% CI)	1.05 (0.53-2.11)		1.72 (1.14-2.60)			0.78 (0.37-1.66)				1.42 (1.07-1.88)		
	mo. (95% CI)	10.5 (8.2-16.3)	10.2 (8.9-11.8)	10.8 (9.2-14.0)	16.7 (15.6-17.5)	10.5 (8.2-16.3)	10.5 (8.2-16.3)	10.8 (9.2-14.0)	10.8 (9.2-14.0)	10.2 (8.9-11.8)	16.7 (15.6-17.5)		
FOCUS	HR (95% CI)	1.04 (0.52-2.10)		1.85 (1.19-2.88)			1.08 (0.50-2.34)				2.07 (1.54-2.79)		
	number of patients	9	51	32	32	672	9	9	32	32	51	672	
FOCUS	mo. (95% CI)	6.8 (4.9-12.0)	8.3 (6.8-9.1)	8.3 (6.8-9.6)	8.0 (7.4-8.3)	6.8 (4.9-12.0)	6.8 (4.9-12.0)	8.3 (6.8-9.6)	8.3 (6.8-9.6)	8.3 (6.8-9.1)	8.0 (7.4-8.3)		
	HR (95% CI)	0.75 (0.28-2.00)		0.91 (0.56-1.49)			1.37 (0.49-3.79)				0.93 (0.63-1.39)		
FOCUS	mo. (95% CI)	13.5 (9.8-28.7)	12.2 (10.2-14.8)	17.5 (14.0-24.0)	15.6 (14.7-16.9)	13.5 (9.8-28.7)	13.5 (9.8-28.7)	17.5 (14.0-24.0)	17.5 (14.0-24.0)	12.2 (10.2-14.8)	15.6 (14.7-16.9)		
	HR (95% CI)	1.21 (0.44-3.36)		0.85 (0.50-1.44)			1.51 (0.52-4.42)				1.55 (1.03-2.33)		
Pooled data set	number of patients	53	197	100	100	2713	53	53	100	100	197	2713	
	mo. (95% CI)	6.1 (5.6-7.7)	6.2 (6.0-6.9)	6.3 (5.8-7.4)	6.3 (5.8-7.4)	7.8 (7.4-8.1)	6.1 (5.6-7.7)	6.1 (5.6-7.7)	6.3 (5.8-7.4)	6.3 (5.8-7.4)	6.2 (6.0-6.9)	7.8 (7.4-8.1)	
Pooled data set	HR (95% CI)	0.95 (0.62-1.46)		1.32 (1.00-1.75)			1.07 (0.67-1.70)				1.34 (1.10-1.64)		
	mo. (95% CI)	11.7 (9.9-14.4)	11.3 (10.3-12.5)	15.0 (13.1-18.0)	17.3 (16.7-18.1)	11.7 (9.9-14.4)	11.7 (9.9-14.4)	15.0 (13.1-18.0)	15.0 (13.1-18.0)	11.3 (10.3-12.5)	17.3 (16.7-18.1)		
Pooled data set	HR (95% CI)	1.05 (0.68-1.63)		1.22 (0.91-1.65)			1.51 (0.93-2.46)				1.94 (1.57-2.40)		
	number of patients	53	197	100	100	2713	53	53	100	100	197	2713	

NOTE: Statistically significant results are set in bold

Abbreviations: PFS = progression-free survival, OS = overall survival, mo. = median PFS or OS time in months, HR = Hazard ratio, CI = confidence interval, dMMR = deficient mismatch repair, pMMR = proficient mismatch repair, mt = mutant tumor, wt = wild-type tumor