Mismatch repair status and \( \text{BRAF} \) 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 \( \text{BRAF} \) mutation (\( \text{BRAF}^{\text{MT}} \)) 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 \( \text{BRAF} \). 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 \( \text{BRAF}^{\text{MT}} \). \( \text{BRAF}^{\text{MT}} \) 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 1.16-1.57).

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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 NCT00312000), CAIRO2 (ClinicalTrials.gov 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 BRAFMT (Table 1). There was no evidence of heterogeneity for the prevalence of dMMR and BRAFMT in the four studies; p=0.614 and p=0.943, respectively (Table 1). A BRAFMT 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 BRAFMT status between the four studies. In the CAIRO study, there were significantly more patients with a combined dMMR and BRAFMT (dMMR / BRAFMT) 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 BRAFMT (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, BRAFMT and BRAFWT 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 BRAFMT compared to BRAFWT
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<sup>MT</sup> and BRAF<sup>WT</sup> 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<sup>MT</sup> 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<sup>WT</sup> 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<sup>MT</sup> compared to BRAF<sup>WT</sup> 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<sup>MT</sup> compared to BRAF<sup>WT</sup> 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<sup>MT</sup> 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<sup>MT</sup> 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<sup>MT</sup> and dMMR, our data suggest that the poor prognostic value of dMMR is driven by the BRAF<sup>MT</sup> 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 BRAFMT 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 BRAFMT in dMMR tumors are scarce, but in line with our results.(32, 33) The strong inter-relationship between BRAFMT 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 BRAFMT 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 BRAFMT tumors have a worse prognosis.(35) Subsequently, this may lead to a shift in the dMMR / BRAFMT ratio in mCRC patients.

There is increasing evidence identifying BRAFMT 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 BRAFMT 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 BRAFWT 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 \textit{BRAF}\textsuperscript{MT} in mCRC could not be addressed.

In conclusion, dMMR and \textit{BRAF}\textsuperscript{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 \textit{BRAF}\textsuperscript{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**

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

**REFERENCES**


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 BRAFMT 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

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

*p 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

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

\(p\) 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

<table>
<thead>
<tr>
<th></th>
<th>dMMR</th>
<th>pMMR</th>
<th><em>BRAF</em></th>
<th><em>BRAF</em></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>no. (95% CI)</td>
<td>mo. (95% CI)</td>
<td>HR (95% CI)</td>
<td>mo. (95% CI)</td>
</tr>
<tr>
<td>CAIRO</td>
<td>18</td>
<td>304</td>
<td>25</td>
<td>297</td>
</tr>
<tr>
<td>PFS</td>
<td>5.7 (4.2-8.8)</td>
<td>6.9 (6.2-7.9)</td>
<td>5.1 (4.1-7.7)</td>
<td>7.0 (6.3-8.2)</td>
</tr>
<tr>
<td>OS</td>
<td>14.8 (12.0-26.0)</td>
<td>17.9 (16.1-19.2)</td>
<td>11.3 (8.3-15.0)</td>
<td>18.1 (16.2-19.4)</td>
</tr>
<tr>
<td>CAIRO2</td>
<td>29</td>
<td>487</td>
<td>45</td>
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<td>6.9 (6.2-8.5)</td>
<td>10.6 (9.7-11.8)</td>
</tr>
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<td>22.0 (20.3-24.1)</td>
<td>13.1 (10.7-16.5)</td>
<td>22.4 (21.0-24.9)</td>
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<td>5.8 (5.6-6.2)</td>
<td>6.5 (6.3-6.9)</td>
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<td>16.5 (15.3-17.1)</td>
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<td>704</td>
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</tr>
<tr>
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<td>15.5 (14.5-16.6)</td>
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<td>15.7 (14.8-17.0)</td>
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<td>2813</td>
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<tr>
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<td>17.2 (16.7-18.0)</td>
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</tbody>
</table>

**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

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<td>pMMR</td>
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<td>14.1 (11.5-19.4)</td>
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<tr>
<td>OS</td>
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</tr>
</tbody>
</table>

**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