Circulating DNA as a Strong Multimarker Prognostic Tool for Metastatic Colorectal Cancer Patient Management Care

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Circulating DNA as a Strong Multimarker Prognostic Tool for Metastatic Colorectal Cancer Patient Management Care

Safia El Messaoudi1,2,3,4, Florent Mouliere1,2,3,4, Stanislas Du Manoir1,2,3,4, Caroline Bascoul-Mollevi1,2,3,4,5, Brigitte Gillet6, Michelle Nouaille7, Catherine Fiess5, Evelyne Crapez1,2,3,4, Frederic Bibeau1,2,3,4,9, Charles Theillet1,2,3,4, Thibault Mazard1,2,3,4,10, Denis Pezet6, Muriel Mathonnet7, Marc Ychou1,2,3,4,10, and Alain R. Thierry1,2,3,4

Abstract

Purpose: Circulating cell-free DNA (ccfDNA) is a valuable source of tumor material obtained from a simple blood sampling that enables noninvasive analysis of the tumor genome. Our goal was to carry out a multiparametric analysis of ccfDNA and evaluate its prognostic value by investigating the overall survival (OS) of 97 metastatic colorectal cancer patients (mCRC).

Experimental Design: Qualitative parameters (determination of the main KRAS exon2 and BRAF V600E mutations) and quantitative parameters (total ccfDNA concentration, mutant ccfDNA concentration, the proportion of mutant ccfDNA, and ccfDNA integrity index) were determined simultaneously in a single run using a unique Q-PCR multimarker approach (100% success rate).

Results: The median follow-up time was 36 months and median OS was 22 months. Patients showing high ccfDNA levels had significantly shorter OS (18.07 months vs. 28.5 months, P = 0.0087). Moreover, multivariate analysis revealed that a high ccfDNA level is an independent prognostic factor (P = 0.034). All ccfDNA parameters were of prognostic interest: patients with higher levels of mutant ccfDNA and higher mutation loads for the detected mutations had shorter OS (P = 0.0089 and P = 0.05, respectively). In addition, the level of ccfDNA fragmentation correlated positively with decreased OS in the exclusive KRAS/BRAF-mutant cohort of patients (P = 0.0052) and appeared as a strong independent prognostic factor (P = 0.0072), whereas it was not significant in the exclusive KRAS/BRAF WT cohort of patients (P = 0.67).

Conclusions: Our data provide for the first time qualitative and quantitative evidence in favor of multiparametric ccfDNA analysis in mCRC patients for prognostic assessment. Clin Cancer Res, 22(12): 3067–77. ©2016 AACR.

Introduction

A strong need exists for a noninvasive tool to improve the prognosis evaluation of colorectal cancer patients, particularly for patients in the early stage as well as for stratifying stage IV patients. The current prognostic gold standard for colorectal cancer patient classification remains the TNM classification (1). Metastatic colorectal cancer patients (mCRC) show a broad range of outcomes. No prognosis-validated biomarker is currently available for mCRC management (2). Several prognostic factors have been reported in the literature as predictors of mCRC patient survival: number of hepatic metastases, node-positive compared with node-negative primary, poorly differentiated compared with well or moderately primary, extra-hepatic disease compared with liver-only disease, tumor diameter, positive compared with negative resection margins, MSI versus MSS status and the carcinoembryonic antigen (CEA) level (3). Nonetheless, the CEA level is measured in current clinical practice at the time of diagnosis to establish disease prognosis and constitutes a tool for disease follow-up. However, CEA is not specific to colorectal tumors or to the tumor process. Hence, there is an urgent need for a colorectal tumor-specific noninvasive biomarker.

Circulating cell-free DNA (ccfDNA) is a potential source of tumor material, obtained by simple blood sampling, enabling
Translational Relevance

There is an urgent need for a colorectal tumor-specific biomarker beside the TNM classification. Here, we study the prognostic potential of circulating cell-free DNA (ccfDNA) analysis according to a multiparametric approach by a sensitive and specific analytic system we previously validated for its diagnostic and theragnostic capacities. This noninvasive analysis simultaneously provided qualitative (determination of the main KRAS and BRAF mutations) and quantitative (total ccfDNA concentration, mutant ccfDNA concentration, the proportion of mutant ccfDNA, and ccfDNA integrity) information from a simple blood sampling. Each of this parameter significantly correlated with overall survival and showed much higher prognostic value than CEA, revealing that multimarker ccfDNA analysis could bring new insights in the management care of colorectal cancer patients.

Materials and Methods

Patients

Ninety-seven mCRC patients recruited from 3 clinical centers were analyzed to investigate the prognostic value of qualitative and quantitative parameters determined from ccfDNA analysis. Specific characteristics of this patient cohort were described previously under the STARD criteria (25). Eligible patients were male or female, age ≥ 18 years, with histologically confirmed mCRC. Patients had measurable disease as defined by the Response Evaluation Criteria in Solid Tumors version 1.1 (RECIST v1.1) and were not treated by chemotherapy or radiotherapy in the 4 weeks before the enrollment. Written, informed consent was obtained from all participants before the onset of this noninterventional study. According to the French Public Health Code Article L1131-1 and the following articles, no specific ethical approval is required for this type of study.

Specimen characteristics and preparation

Samples were handled accordingly with a pre-analytic guide-line previously established by our group (26). Briefly, 4 mL blood samples were collected in K3 EDTA tubes. Plasma was isolated within 1 hour after drawing blood. The isolation process consisted in a two-step centrifugation. First, blood tubes were centrifuged for 10 minutes in a Heraeus Multifuge LR centrifuge with a speed spin of 1,200 × g and a temperature of 4°C. Supernatant was collected, and the buffy coat was avoided with precaution. The collected supernatant was centrifuged a second time to remove any possible remaining cells. This second centrifugation step was performed for 10 minutes at 4°C and with a spin speed of 16,000 × g. Plasma supernatant was then transferred in a 1.5 mL tube, extracted immediately after or stored at −20°C. CcfDNA extraction was performed with the Qiagen Blood Mini Kit, and by following the main steps of the "Blood and body fluid protocol." However, we modified two elements: during the extraction, 1 mL of plasma was processed sequentially in one column. Then, ccfDNA was eluted in 130 μL of elution buffer. Eluted ccfDNA was stored at −20°C before Q-PCR analysis. Freeze-thawing was avoided to reduce fragmentation of the eluted ccfDNA, and no extracts were conserved for more than three months at −20°C.

Assay methods

Intplex is a Q-PCR-based method specifically aimed at analyzing ccfDNA. Intplex is based on a nested design, where two short amplicons (60–100 bp ± 10 bp) are implemented among a larger amplicon (300 ± 10 bp). One of the short amplicons targets a specific locus hotspot of interest (KRAS codon 12, 13 or BRAF codon 600 in our experiments, but it is applicable to other point mutations). The other short amplicon is designed for amplifying a wild-type (WT) sequence. This amplicon quantification provides an estimation of the total concentration of ccfDNA fragment sequences either when targeting KRAS or BRAF sequence (Ref A KRAS and RefB BRAF). Intplex methodology, primer design and validation have been described previously (24, 25).

In all plasma samples, total ccfDNA concentration (ref A), positivity for a mutation, mutant fragments concentration (mA), mutated allele frequency (mA%), and the DNA integrity index...
(DII) were determined with an analysis flowchart detailed in a previous study by our team (24, 25). Quality control was one of the assets of the method used. First, a stringent pre-analytic guideline ensured the integrity of DNA and potentially excluded samples due to non-proper blood or plasma handling (26). Numeric traceability guaranteed proper sample archiving in a specific blood collection bank for colorectal cancer plasma samples at Dr. Thierry’s Laboratory (no. DC-2013-1931). Quality control of the ccfDNA concentration benefited from the determination of two values by targeting two different WT sequences in two different genes (BRAF and KRAS). Samples with concentration values below our quality threshold (concentration below minimal value obtained from plasma samples from healthy donors) revealing sample mishandling following blood collection or for unknown reason were excluded. The coefficient of variation of the ccfDNA concentration from a blood sample was determined as 24% (24). In each single run, negative and positive controls were quantified for each mutations and one standard curve was prepared. Q-PCR amplification was controlled by melt curve differentiation. RT-PCR assay were carried out in duplicate.

The concentration obtained when targeting the mutant sequence corresponded to the concentration of the alleles bearing the mutation (mA). The proportion of mutant allele (mutation load, mA%) was determined by quantifying the relative ratio between mA and Ref A.

The degree of ccfDNA fragmentation was assessed simultaneously by targeting KRAS and BRAF sequences from each plasma DNA sample by calculating the DII (DII KRAS and DII BRAF). The DII was determined by calculating the ratio of the concentration determined using the primer set amplifying a large target (300 bp) to the concentration determined using the primer set amplifying a short target (<100 bp; ref. 24). Details of the Q-PCR program, the ccfDNA quantification system, the Q-PCR reaction and the primer designs are described in the supporting information.

Study design and statistics

Sample size justification of the cohort is described in Supplementary Methods. The study was performed according to the REMARK criteria. Blood for ccfDNA analysis was collected around the date of first metastatic diagnosis [median: 1.3 months (0–39)] of delay after first metastatic diagnosis. CEA measurements were taken in the 2 months preceding or following the blood sampling for ccfDNA analysis. None of the patients included in the cohort have been treated by chemotherapy or radiotherapy before CEA analysis and blood drawing for ccfDNA analysis. Data were summarized by frequency for categorical variables, and by median and range values for continuous variables. OS was calculated from the date of first metastatic diagnosis to the date of death. Survival rates were estimated using the Kaplan–Meier method and the log-rank test was used to identify the prognostic variables. Univariate analysis was performed for each ccfDNA parameter, CEA, and clinical parameters. One univariate analysis has been realized on the entire cohort (N = 97) and another has been studied in the exclusive KRAS/BRAF–mutant cohort (N = 43).

Age, localization of the tumor, CEA, Ref A KRAS, RefA BRAF, and mutant status were implemented in a multivariate COX proportional hazards model for analysis on the entire cohort. mA, mA%, mutant status, CEA, Ref A KRAS, DII KRAS, and DII BRAF were included for the multivariate analysis model on the mutant cohort. Statistical analysis was performed using the STATA 11.0 software (StataCorp LP).

Results

Patient characteristics and study design

Patient baseline characteristics, number and localization of metastasis, and number of previous lines of therapy are listed in Table 1. Of note, 106 mCRC patients were initially included in this study in the period between July 2010 and December 2012. Eight patients were excluded from the study because of irrespective inclusion criteria (volume of plasma at least of 2 ml and ccfDNA concentration at least of 5 ng/ml of plasma) and one was lost from sight. Qualitative parameters (determination of the main KRAS exon2 and BRAF V600E mutations) and quantitative parameters (total ccfDNA concentration, mutant ccfDNA concentration, the proportion of mutant ccfDNA, and ccfDNA integrity index) were determined simultaneously in a single run using a unique Q-PCR multimarker approach (100% success rate). Total ccfDNA concentration and DII determined both by targeting KRAS and BRAF WT sequences were available for 97 mCRC patients. We could obtain CEA values in the conditions of delay between CEA analysis and ccfDNA analysis for 83 mCRC patients. Forty-three patients harbored a KRAS or BRAF mutation and mA and mA% were determined for each of these mutations. The study flowchart is described in Fig. 1. The median follow-up time was 36 months (0–104 months). Median OS was 22 months, which is consistent with current data on OS of mCRC patients (from 18 to 24 months). OS data are described in Supplementary Fig. S1.

Table 1. Patient’s baseline characteristics

<table>
<thead>
<tr>
<th>Patient’s characteristics</th>
<th>N = 97 (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Centre</td>
<td></td>
</tr>
<tr>
<td>ICIM Montpellier</td>
<td>25 (25.8)</td>
</tr>
<tr>
<td>CHU Clermont-Ferrand</td>
<td>22 (22.7)</td>
</tr>
<tr>
<td>CHU Limoges</td>
<td>50 (51.5)</td>
</tr>
<tr>
<td>Age</td>
<td></td>
</tr>
<tr>
<td>Median (min–max)</td>
<td>66.6 (36–87)</td>
</tr>
<tr>
<td>Missing data</td>
<td>4 (4.1)</td>
</tr>
<tr>
<td>Gender</td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>58 (59.8)</td>
</tr>
<tr>
<td>Female</td>
<td>39 (40.2)</td>
</tr>
<tr>
<td>Localization tumor primitive</td>
<td></td>
</tr>
<tr>
<td>Right colon</td>
<td>22 (22.7)</td>
</tr>
<tr>
<td>Left colon</td>
<td>41 (42.2)</td>
</tr>
<tr>
<td>Rectum</td>
<td>34 (35.1)</td>
</tr>
<tr>
<td>Primary tumor in place</td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>44 (45.4)</td>
</tr>
<tr>
<td>Yes</td>
<td>53 (54.6)</td>
</tr>
<tr>
<td>Synchronous metastasis</td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>80 (82.5)</td>
</tr>
<tr>
<td>Yes</td>
<td>17 (17.5)</td>
</tr>
<tr>
<td>No. of metastatic sites</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>51 (53.2)</td>
</tr>
<tr>
<td>&gt;1</td>
<td>45 (47.8)</td>
</tr>
<tr>
<td>Missing data</td>
<td>3 (3.1)</td>
</tr>
<tr>
<td>Chemotherapy</td>
<td></td>
</tr>
<tr>
<td>Naive</td>
<td>62 (63.9)</td>
</tr>
<tr>
<td>Neoadjuvant/adjuvant</td>
<td>25 (26.1)</td>
</tr>
<tr>
<td>Palliative (N = 13)</td>
<td></td>
</tr>
<tr>
<td>1 line metastatic</td>
<td>5 (38.5)</td>
</tr>
<tr>
<td>&gt;2 lines metastatic</td>
<td>8 (61.5)</td>
</tr>
</tbody>
</table>
metastatic sites, presence of the primary tumor at time of blood sampling, and differentiation of the tumor. Detailed data and figures are presented in Supplementary Fig. S2 and Supplementary Table S2. Note, as illustrated and detailed in Supplementary Data, there is a significant correlation between tumor burden with Ref A KRAS, Ref A BRAF, mA and CEA (Supplementary Information: relation with tumor burden).

**CEA value**

Median CEA concentration determined from the 83 mCRC patients whom we obtained CEA values in the conditions of delay between CEA analysis and ccfDNA analysis was 16.2 µg/L (0.57–1,999.7) of plasma.

**OS analysis on the entire cohort**

**Relation between CEA and OS.** Patients with lower CEA levels than the median concentration (16.2 µg/L) presented a median OS of 28.1 months compared with 17.8 months for patients with higher levels (P = 0.088; HR, 1.60; 95% CI, 0.99–2.16). N = 83; Table 3). Nevertheless, patients with lower CEA levels than the current clinical threshold of significance (5 µg/L) had a median OS of 27.2 months compared with patients with higher levels with a median OS of 21.7 months (P = 0.48; HR, 1.24; 95% CI, 0.68–2.25; Fig. 2A and Table 3).

**Correlation of mutant status with OS.** Patients WT for KRAS exon 2 and BRAFV600E showed a median OS of 21.9 months compared with 20.9 months for KRAS-mutant mCRC patients and 3.4 months for BRAF-mutant mCRC patients (Table 3). Kaplan–Meier survival curves were established (Fig. 2B) for each mutant status. No statistic differences in OS was found between the WT (N = 54) and KRAS-mutant mCRC patients (N = 38; P = 0.675; HR, 1.11; 95% CI, 0.67–1.95). However, there was a statistically high significant difference between the median OS of BRAF-mutant patients (N = 5) and KRAS-mutant patients (N = 38; P < 0.0001; HR, 6.106; 95% CI, 5.72–6.45). Median OS of WT patients showed a statistically high significant difference when compared with BRAF-mutant patients (P < 0.0001; HR, 8.93; 95% CI, 3.13–25.4; Fig. 2B and Table 3).

**Higher total ccfDNA concentration is statistically correlated with a decrease in OS.** Patients with Ref A KRAS (total ccfDNA concentration determined with KRAS primer set) below the median of 26 ng/mL of plasma had a median OS of 28.5 months compared with 18.07 months for patients with Ref A KRAS higher than the median (P = 0.0087; HR, 1.94; 95% CI, 1.17–3.20; Fig. 2C). We observed also a significant statistical difference when analyzing Ref A BRAF (total ccfDNA concentrations determined with BRAF primers set): Patients with Ref A BRAF below 27.6 ng/mL of plasma had a median OS of 24.5 months compared with 20.5 months for patients with higher levels (P = 0.013; HR, 1.55; 95% CI, 1.13–3.11; Fig. 2D). Statistically significant differences were also determined when comparing with the second tertile value of Ref A KRAS or BRAF (P = 0.013 and 0.011; HR, 1.89 and 1.92; 95% CI, 1.14–3.15 and 1.15–3.19, respectively; Table 3).

**CcfDNA fragmentation and OS.** ccfDNA fragmentation was evaluated in 97 mCRC patients on both KRAS and BRAF using the DIIL. Patients showing higher DIIL KRAS (DIIL determined with KRAS primer set) than the median value (0.12) had a higher...
median OS than patients with lower levels (23.07 months vs. 19.2 months; Table 3). This observation was the same when analyzing DII BRAF (DII determined with BRAF primer set): patients with a DII higher than the median (0.119) had a median OS of 23.07 months compared with 17.17 months for patients with highly fragmented DNA. When analyzing the first tertile of DII BRAF (0.07), a significant difference was shown, although not statistically, between the two groups of patients ($P = 0.08$; HR, 1.62; 95% CI, 0.95–2.78; Table 3). It seemed that a higher level of fragmentation had a tendency to be correlated with worse prognosis.

**Figure 2.** OS analysis on the entire cohort. A, Kaplan–Meier survival curve and log-rank test according to CEA dichotomized around the standard threshold of 5 μg/L ($N = 83$). B, Kaplan–Meier survival curve and log-rank test according to the mutant status determined by ccfDNA analysis ($N = 97$). C, Kaplan–Meier survival curve and log-rank test according to Ref A KRAS determined by ccfDNA analysis dichotomized around the median (26 ng/mL, $N = 97$). D, Kaplan–Meier survival curve and log-rank test according to Ref A BRAF determined by ccfDNA analysis dichotomized around the median (27.6 ng/mL, $N = 97$). Abbreviations: WT, wild-type for the KRAS and BRAF mutations tested; Ref A KRAS, total ccfDNA concentration as determined by targeting a WT KRAS sequence; Ref A BRAF, total ccfDNA concentration as determined by targeting a BRAF WT sequence.

**Multivariate analysis on the entire cohort.** CcfDNA parameters that were found to be highly significant in univariate analysis, BRAF mutant, Ref A KRAS, and Ref A BRAF (total ccfDNA concentration), CEA, tumor localization, and age were included in a multivariate Cox proportional hazards model on the entire cohort. Results showed that total ccfDNA concentration appeared
Higher total ccfDNA concentration and fragmentation are correlated with decreased OS. Ref A KRAS and DII KRAS (total ccfDNA concentration and DII determined with KRAS primer sets) were highly significant in univariate analysis in the mutant cohort (P = 0.016 and 0.0052; HR, 2.58 and 0.26; 95% CI, 1.16–5.78 and 0.1–0.71, respectively, N = 43; Fig. 3C and D) whereas CEA was not significant (P = 0.81; HR, 0.89; 95% CI, 0.35–2.28, Fig. 3E).

Multivariate analysis Implementation in a multivariate Cox proportional hazards model revealed that Ref A KRAS appeared as an independent prognostic factor (P = 0.057; HR, 3.67; N = 43) and that DII KRAS appeared as a strong independent prognostic factor (P = 0.0072; HR, 3.57; N = 43). Note that when studying DII KRAS in the exclusive WT patients cohort, it did not appear of prognostic value (P = 0.67, N = 54, data not shown).

Discussion

Several reports have already described the potential impact of ccfDNA on the prognosis of patient outcome in terms of either OS or progression-free survival (6, 9, 28, 29). Most of these previous publications were oriented to analyze the correlation between an increase in the total level of ccfDNA with a decrease in PFS and OS. Other analytic parameters exhibited by ccfDNA, such as fragmentation levels, epigenetic alterations, or allelic frequencies for a particular mutation have not been studied extensively. In this study, simultaneous determination of five parameters by ccfDNA analysis on a cohort of 97 mCRC patients allowed us unprecedently to assess the strong prognostic significance of multivariate ccfDNA analysis. Analysis of the prognostic significance of each parameter was studied by dichotomizing the population to the median value in univariate analysis. Multivariate analysis was realized by assessing each parameter found statistically significant in univariate analysis.

First of all, we confirm the usefulness of point mutation detection by ccfDNA analysis as a prognostic tool. Our data showed the previously established prognosis influence of BRAFV600E (P < 0.0001; HR, 8.93; 95% CI, 3.13–25.4; ref. 30). However, there was no difference, in our cohort, in OS between WT and KRAS-mutant patients (P = 0.675; HR, 1.11; 95% CI, 0.67–1.85), although some authors have reported that the presence of KRAS mutation is indicative of poor outcome (31). Nevertheless, literature analysis tends to show that there is sometimes confusion around the terms prognostic and prediction of therapeutic response. Indeed, KRAS point mutations are more correlated to anti-EGFR resistance than to outcome (32).

Next, we showed that high levels of total ccfDNA concentration were strongly correlated with poor outcome in mCRC patients. This observation has already been reported (6). Nevertheless, it is the first time, to our knowledge, that this parameter has been studied simultaneously on two different genes by targeting either a KRAS or a BRAFWT sequence highlighting the robustness of our

Table 2. Median value and range of the five studied parameters as determined by ccfDNA analysis

<table>
<thead>
<tr>
<th>Parameter</th>
<th>KRAS</th>
<th>BRAF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Median total ccfDNA concentration (ng/mL of plasma)</td>
<td>26.0 (25.8–131.55)</td>
<td>27.6 (12.1–1227.15)</td>
</tr>
<tr>
<td>Mutation frequency in cohort (%)</td>
<td>38</td>
<td>5</td>
</tr>
<tr>
<td>Median DII</td>
<td>0.12 (0.0006–0.93)</td>
<td>0.11 (0.003–0.85)</td>
</tr>
<tr>
<td>Median mutant ccfDNA concentration (ng/mL of plasma)</td>
<td>3.06 (0.04–507.6)</td>
<td>3.6 (0.5–64.5)</td>
</tr>
<tr>
<td>Median mutation load (mA%)</td>
<td>10.72 (0.51–64.4)</td>
<td>10.72 (0.51–64.4)</td>
</tr>
<tr>
<td>Median CEA concentration (μg/L of plasma)</td>
<td>16.2 (0.57–19.997)</td>
<td>16.2 (0.57–19.997)</td>
</tr>
</tbody>
</table>

Abbreviations: mA%, mutation load (% of mutant ccfDNA among total ccfDNA).
The analytic process and the robustness of the prognostic significance of total cfDNA concentration. Previous observations of our group on xenografted mice have shown the strong correlation between tumor volume and cfDNA concentration (33), and other works have showed that cfDNA concentration is positively correlated to tumor burden (7, 28, 34). Spindler and colleagues (8) revealed the correlation between the concentration of mutant cfDNA (mA) and OS. Our study

<table>
<thead>
<tr>
<th>Table 3. OS analysis on the entire cohort</th>
<th>Death occurrence</th>
<th>Median OS (Mo)</th>
<th>HR (95% CI)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>CEA (µg/L)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤Median: 16.2 µg/L</td>
<td>23/42</td>
<td>28.1</td>
<td>1.00 (0.99–2.16)</td>
<td>0.088</td>
</tr>
<tr>
<td>&gt;Median: 16.2 µg/L</td>
<td>30/41</td>
<td>17.8</td>
<td>1.50</td>
<td></td>
</tr>
<tr>
<td>≤5 µg/L</td>
<td>15/23</td>
<td>27.2</td>
<td>1.00 (0.68–2.25)</td>
<td>0.48</td>
</tr>
<tr>
<td>&gt;5 µg/L</td>
<td>38/60</td>
<td>21.7</td>
<td>1.24</td>
<td></td>
</tr>
<tr>
<td>KRAS mutant status</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>WT</td>
<td>40/59</td>
<td>21.9</td>
<td>1.00 (0.67–1.85)</td>
<td>0.675</td>
</tr>
<tr>
<td>Mutant</td>
<td>24/38</td>
<td>20.9</td>
<td>1.11</td>
<td></td>
</tr>
<tr>
<td>BRAF mutant status</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>WT</td>
<td>59/92</td>
<td>21.9</td>
<td>1.00 (3.13–25.4)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Mutant</td>
<td>5/5</td>
<td>3.4</td>
<td>8.93</td>
<td></td>
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<tr>
<td>KRAS or BRAF mutant</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>KRAS mutant</td>
<td>24/38</td>
<td>20.9</td>
<td>1.00 (5.72–6.487)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>BRAF mutant</td>
<td>5/5</td>
<td>3.4</td>
<td>6.06</td>
<td></td>
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<tr>
<td>Ref A KRAS (ng/mL)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤1st tertile: 15.6&gt;</td>
<td>19/32</td>
<td>22.23</td>
<td>1.00 (0.465–1.635)</td>
<td>0.23</td>
</tr>
<tr>
<td>&gt;1st tertile: 15.6</td>
<td>45/65</td>
<td>21.17</td>
<td>1.05</td>
<td></td>
</tr>
<tr>
<td>≤Median: 26.0</td>
<td>26/49</td>
<td>28.5</td>
<td>1.00 (1.17–3.20)</td>
<td>0.0087</td>
</tr>
<tr>
<td>&gt;Median: 26.0</td>
<td>38/48</td>
<td>18.07</td>
<td>1.94</td>
<td></td>
</tr>
<tr>
<td>≤2nd tertile: 47.5</td>
<td>39/64</td>
<td>23.17</td>
<td>1.00 (1.14–3.15)</td>
<td>0.013</td>
</tr>
<tr>
<td>&gt;2nd tertile: 47.5</td>
<td>25/33</td>
<td>13.9</td>
<td>1.89</td>
<td></td>
</tr>
<tr>
<td>Ref A BRAF (ng/mL)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤1st tertile: 13.6</td>
<td>19/32</td>
<td>22.23</td>
<td>1.00 (0.465–1.635)</td>
<td>0.23</td>
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<tr>
<td>&gt;1st tertile: 13.6</td>
<td>45/65</td>
<td>21.17</td>
<td>1.05</td>
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</tr>
<tr>
<td>≤Median: 27.6</td>
<td>28/49</td>
<td>24.5</td>
<td>1.00 (1.13–3.11)</td>
<td>0.013</td>
</tr>
<tr>
<td>&gt;Median: 27.6</td>
<td>36/48</td>
<td>20.5</td>
<td>1.88</td>
<td></td>
</tr>
<tr>
<td>≤2nd tertile: 48</td>
<td>39/64</td>
<td>24.9</td>
<td>1.00 (1.15–3.19)</td>
<td>0.011</td>
</tr>
<tr>
<td>&gt;2nd tertile: 48</td>
<td>25/33</td>
<td>13.9</td>
<td>1.92</td>
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</tr>
<tr>
<td>DII KRAS</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤1st tertile: 0.07</td>
<td>20/31</td>
<td>20.8</td>
<td>1.00 (0.65–1.94)</td>
<td>0.72</td>
</tr>
<tr>
<td>&gt;1st tertile: 0.07</td>
<td>44/66</td>
<td>22.2</td>
<td>1.1</td>
<td></td>
</tr>
<tr>
<td>≤Median: 0.12</td>
<td>30/47</td>
<td>19.2</td>
<td>1.00 (0.66–1.76)</td>
<td>0.73</td>
</tr>
<tr>
<td>&gt;Median: 0.12</td>
<td>34/50</td>
<td>23.07</td>
<td>1.09</td>
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</tr>
<tr>
<td>≤2nd tertile: 0.23</td>
<td>44/66</td>
<td>22.03</td>
<td>1.00 (0.77–1.98)</td>
<td>0.52</td>
</tr>
<tr>
<td>&gt;2nd tertile: 0.23</td>
<td>25/33</td>
<td>22.23</td>
<td>1.18</td>
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<tr>
<td>DII BRAF</td>
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<td></td>
<td></td>
<td></td>
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<tr>
<td>≤1st tertile: 0.07</td>
<td>25/34</td>
<td>20.6</td>
<td>1.00 (0.95–2.78)</td>
<td>0.08</td>
</tr>
<tr>
<td>&gt;1st tertile: 0.07</td>
<td>39/63</td>
<td>23.07</td>
<td>1.62</td>
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</tr>
<tr>
<td>≤Median: 0.19</td>
<td>34/49</td>
<td>17.77</td>
<td>1.00 (0.81–2.25)</td>
<td>0.15</td>
</tr>
<tr>
<td>&gt;Median: 0.19</td>
<td>30/48</td>
<td>26.90</td>
<td>1.44</td>
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<tr>
<td>≤2nd tertile: 0.20</td>
<td>41/64</td>
<td>20.8</td>
<td>1.00 (0.60–1.7)</td>
<td>0.9</td>
</tr>
<tr>
<td>&gt;2nd tertile: 0.20</td>
<td>23/33</td>
<td>22.23</td>
<td>1.05</td>
<td></td>
</tr>
<tr>
<td>Mutant cfDNA concentration (ng/mL)</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>≤1st tertile: 1.06</td>
<td>10/14</td>
<td>22.1</td>
<td>1.00 (125–2.055)</td>
<td>0.57</td>
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<tr>
<td>&gt;1st tertile: 1.06</td>
<td>19/29</td>
<td>13.9</td>
<td>1.59</td>
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<tr>
<td>≤Median: 3.06</td>
<td>13/22</td>
<td>31.6</td>
<td>1.00 (1.25–5.93)</td>
<td>0.0089</td>
</tr>
<tr>
<td>&gt;Median: 3.06</td>
<td>16/21</td>
<td>11.3</td>
<td>2.72</td>
<td></td>
</tr>
<tr>
<td>≤2nd tertile: 7.53</td>
<td>16/28</td>
<td>22.1</td>
<td>1.00 (1.28–5.78)</td>
<td>0.0071</td>
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<tr>
<td>&gt;2nd tertile: 7.53</td>
<td>15/15</td>
<td>6.83</td>
<td>2.72</td>
<td></td>
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<tr>
<td>Mutation load (%)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤1st tertile: 4.14</td>
<td>7/14</td>
<td>34.53</td>
<td>1.00 (0.97–5.44)</td>
<td>0.053</td>
</tr>
<tr>
<td>&gt;1st tertile: 4.14</td>
<td>22/29</td>
<td>13.9</td>
<td>2.29</td>
<td></td>
</tr>
<tr>
<td>≤Median: 10.72</td>
<td>13/22</td>
<td>31.6</td>
<td>1.00 (0.82–3.62)</td>
<td>0.15</td>
</tr>
<tr>
<td>&gt;Median: 10.72</td>
<td>16/21</td>
<td>11.4</td>
<td>1.72</td>
<td></td>
</tr>
<tr>
<td>≤2nd tertile: 15.9</td>
<td>17/28</td>
<td>22.1</td>
<td>1.00 (0.9–4.12)</td>
<td>0.08</td>
</tr>
<tr>
<td>&gt;2nd tertile: 15.9</td>
<td>12/15</td>
<td>11.3</td>
<td>1.93</td>
<td></td>
</tr>
</tbody>
</table>

NOTE: Ref A KRAS, Ref A BRAF, DII KRAS, DII BRAF, and CEA are tested by dichotomization of the entire cohort on the first tertile, the median, and the second tertile. CEA is dichotomized around the median and the standard threshold of 5 µg/L. mA and mA% are tested by dichotomization of the exclusive KRAS/BRAF–mutant cohort around the first tertile, the median and the second tertile.

Abbreviations: DII KRAS, DII determined using KRAS primer set; DII BRAF, DII determined using BRAF primer set; mA, mutant cfDNA concentration; mA%, mutation load (% of mutant cfDNA among total cfDNA); mo, months; Ref A KRAS, total cfDNA concentration as determined by targeting a WT KRAS sequence; Ref A BRAF, total cfDNA concentration as determined by targeting a BRAF WT sequence; WT, wild-type for the KRAS and BRAF mutations tested.
Figure 3.
OS analysis on the KRAS or BRAF mutant cohort. A, Kaplan–Meier survival curve and log-rank test according to mA determined by ccfDNA analysis dichotomized around the median (3.06 ng/mL, \( N = 43 \)). B, Kaplan–Meier survival curve and log-rank test according to mA% dichotomized to the first (1st) tertile (4.14%) determined by ccfDNA analysis (\( N = 43 \)). C, Kaplan–Meier survival curve and log-rank test according to Ref A KRAS dichotomized around the second tertile (2nd tertile; 107.0 ng/mL, \( N = 43 \)). D, Kaplan–Meier survival curve and log-rank test according to DII KRAS determined by ccfDNA analysis dichotomized around the second tertile (2nd tertile; 0.20, \( N = 43 \)). E, Kaplan–Meier survival curve and log-rank test according to CEA dichotomized around the standard threshold of 5 μg/L (\( N = 36 \)). Abbreviations: mA, mutant ccfDNA concentration; mA%, mutation load (% of mutant ccfDNA among total ccfDNA); Ref A KRAS, total ccfDNA concentration as determined by targeting a WT KRAS sequence; DII KRAS, Dil determined using KRAS primer set.
Strong Prognostic Value of Multiparametric ccfDNA Analysis

confirms this observation, as there was a strong statistical decrease in OS for KRAS- or BRAF-mutant patients with mA higher than the median value (3.06 ng/mL). This was consolidated by the high statistical significance of the mutation load (percentage of mutant alleles among total ccfDNA amount, mA%) on prognosis: Patients with lower mutation load than the median value of 10.72% exhibited a median OS of 31.6 months compared with 11.2 months for patients with a higher mutation load. There was a clear trend showing that high mutation load indicated poor prognosis. As for the mutation load, prognosis of patients with high mA is worse whatever the total ccfDNA concentration. However, it has to be considered that mA% and mA in a mutant sample, while being related, do not represent the same meaning: mA% is rather linked to the proportion of malignant cells versus tumor microenvironment cells and could be altered by tumor cloning, whereas mA is rather linked to the total concentration of ccfDNA. We hypothesize that this biomarker might be of great diagnostic potential in regard to individualizing management care. The prognostic value of mutant ccfDNA concentration seems to be stronger than the prognostic value of total ccfDNA concentration (P = 0.0089 and 0.016; HR, 2.72 and 2.58; 95% CI, 1.25–5.93 and 1.16–5.73, respectively). We could explain this phenomenon by the fact that mA determination is derived from the quantification of ccfDNA exclusively deriving from malignant cells whereas total ccfDNA concentration is determined from quantifying malignant as well as nonmalignant-derived ccfDNA.

We observed a higher ccfDNA fragmentation level from colorectal cancer patients as compared with healthy individuals butressing the notion that fragmentation could be an interesting parameter for diagnosis (35, 36). In regard to prognosis, patients with a higher fragmentation level showed, in this study, a lower median OS of 17 months as compared with 23 months for patients with a lower fragmentation level. Note, ccfDNA fragmentation index as well as total ccfDNA concentration showed similar values by using either KRAS or BRAF primer sets, confirming the accuracy of our method. Interestingly, univariate analysis as well as multivariate analysis in the exclusive KRAS/BRAF-mutant cohort revealed that DII KRAS (DII determined with KRAS primer set) was highly significant in univariate and multivariate analysis (P = 0.0052 and 0.0072 respectively, N = 43) whereas it was not significant in the exclusive WT cohort (P = 0.67; N = 54). This raises questions about possible biologic and/or physiopathologic association between mutant status and ccfDNA fragmentation and their link to tumor progression.

Each of the parameters, point mutation detection, total ccfDNA concentration, mutant ccfDNA concentration, mutation load, and ccfDNA fragmentation, shows individually their prognostic potential and promise better prognostic potential than CEA (single-copy detection of variant alleles down to a sensitivity of 0.005% mutant to WT ratio, being the lowest level found in the literature). The success rate of our method for detecting ccfDNA in plasma is 100% in more than 400 stage I to IV colorectal cancer and 120 healthy individual plasma samples and the mean data turnaround time is 2 days for multiplex analysis (24, 25, 35).
Achievement of personalized medicine and targeted therapies require further information about the residual risk and the potential benefit of additional treatments. Overcoming the limitation of a restricted number of molecular analyses in tumor tissue by a noninvasive and repetitive blood test, in particular the qualitative and quantitative multimarker analysis of ccfDNA, would be an approach necessary for the early identification of high-risk cancer patients, monitoring disease course, and therapy response.

Disclosure of Potential Conflicts of Interest

F. Bibeau reports receiving speakers bureau honoraria from and is a consultant/advisory board member for Amgen and Merck. No potential conflicts of interest were disclosed by the other authors.

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Study supervision: C. Theillet, A.R. Thierry

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References

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