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 Moulière1,2,3,4, Stanislas Du Manoir1,2,3,4, Caroline Bascoul-Mollevi1,2,3,4,5, Brigitte Gillet6, Michelle Nouaille7, Catherine Fiess5, Evelyne Crapez1,2,3, 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.

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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 therapeutic 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 multilocal 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 guideline 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.

Sample set

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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

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noninvasive, quantitative, and qualitative analysis of the tumor genome. Tumor cells release ccfDNA, which exhibits the genetic and epigenetic alterations of the tumor of origin (4). The clinical significance of tumor-derived ccfDNA released in the blood of patients with colorectal cancer has already been investigated as a prognostic tool in previous studies using various technologic approaches (5–9). In a recent large meta-analysis, a high correlation between ccfDNA concentration and mCRC patient survival was observed, revealing that the presence of mutations (5). The ccfDNA fragmentation level has been described, including advanced breast cancer (10), lung cancer (11, 12), prostate cancer (13), pancreatic cancer (14), and other cancer types (15).

However, the majority of these studies have focused on the total ccfDNA concentration in the blood or on the detection of genetic or epigenetic alterations (16–20). Moreover, the relationship between total ccfDNA concentration and outcome may be biased because an increase in the level of total ccfDNA might also be indicative of non-cancerous disease, such as inflammation or trauma (16). Thus, recent studies on the clinical application of ccfDNA have mainly focused on qualitative analysis such as the presence of mutations (5). The ccfDNA fragmentation level has been also investigated as a predictive tool for cancer progression (21–23).

On the basis of our observations on their structures and origins, we designed Intplex, an allele-specific, Q-PCR–based system specifically adapted for ccfDNA analysis (24). With using this method, we reported the first clinical validation in oncology by testing the presence of KRAS/BRAF point mutations in a cohort of 106 mCRC patients (25). The Intplex method enables simultaneous determination of the total ccfDNA concentration, point mutation detection, mutant ccfDNA concentration, mutation load (% of mutant ccfDNA among total ccfDNA), and ccfDNA integrity.

Here, we examined overall survival (OS) of 97 mCRC patients; this is the largest cohort of mCRC patients studied for potential prognostic interest of ccfDNA analysis. The five Intplex parameters were simultaneously determined for the first time in all patients. We investigated the value of these parameters according to OS by univariate and multivariate analysis. The results were compared with the prognostic value of the CEA.
(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 plasma 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 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 ±10 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>
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<tr>
<th>Patient’s characteristics</th>
<th>N = 97</th>
<th>(%)</th>
</tr>
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<tr>
<td>Centre</td>
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<td></td>
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<tr>
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</tr>
<tr>
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<td>CHU Limoges</td>
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<tr>
<td>Age</td>
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<tr>
<td>Median (min–max)</td>
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</tr>
<tr>
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<td>58</td>
<td>59.8</td>
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<tr>
<td>Female</td>
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<td>40.2</td>
</tr>
<tr>
<td>Localization tumor primitive</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Right Colon</td>
<td>22</td>
<td>22.7</td>
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<tr>
<td>Left Colon</td>
<td>41</td>
<td>42.2</td>
</tr>
<tr>
<td>Rectum</td>
<td>34</td>
<td>35.1</td>
</tr>
<tr>
<td>Primary tumor in place</td>
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<td></td>
</tr>
<tr>
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<td>45.4</td>
</tr>
<tr>
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<td>53</td>
<td>54.6</td>
</tr>
<tr>
<td>Synchronous metastasis</td>
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<td></td>
</tr>
<tr>
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<td>82.5</td>
</tr>
<tr>
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<td>17</td>
<td>17.5</td>
</tr>
<tr>
<td>No. of metastatic sites</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>51</td>
<td>54.3</td>
</tr>
<tr>
<td>&gt;1</td>
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<td>45.7</td>
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</tr>
<tr>
<td>Chemotherapy</td>
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<td></td>
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<tr>
<td>Naive</td>
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<td>63.9</td>
</tr>
<tr>
<td>Neoadjuvant/adjuvant</td>
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<td>71.4</td>
</tr>
<tr>
<td>Palliative (N = 13)</td>
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<td></td>
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<tr>
<td>1 line metastatic</td>
<td>5</td>
<td>38.5</td>
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<tr>
<td>&gt;2 lines metastatic</td>
<td>8</td>
<td>61.5</td>
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Univariate analysis of clinical variables. Relation between OS and number of metastatic sites was evaluated in 94 mCRC patients. Categories were 1 metastatic site or more than 1 site. Univariate analysis revealed that there was no significant relation between number of metastasis and OS ($P = 0.489$; HR, 1.071; 95% confidence interval (CI), 0.73–1.96). When dichotomizing patients around 65 years, there was no statistical significant relation with OS (log-rank test: $P = 0.058$; HR, 1.65; 95% CI, 0.98–2.76; $N = 93$). Regarding the gender, there was no statistical difference between men and women (log-rank test: $P = 0.77$; HR, 0.93; 95% CI, 0.56–1.54; $N = 97$). Tumor localization seemed to be of prognostic value because there was a statistical relation with OS. Median OS for right colon cancer patients was of 15.2 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 statistical differences in OS was found between the WT patients (Table 3; Kaplan–Meier survival curves were not shown due to the high survival rates). 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 statistical differences in OS was found between the WT patients (Table 3; Kaplan–Meier survival curves were not shown due to the high survival rates). 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).

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 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 sets): Patients with Ref A BRAF below 26.7 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. If ccfDNA fragmentation was evaluated in 97 mCRC patients on both KRAS and BRAF using the DII, Patients showing higher DII KRAS (DII determined with KRAS primer set) than the median value (0.12) had a higher median total concentration (16.2 μg/L (0.57–1,999.7) of plasma) than those below the median (Ref A KRAS or BRAF (total ccfDNA concentrations determined with Ref A KRAS or Ref A BRAF, mA and CEA (Supplementary Information: relation with tumor burden).

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).

CcfDNA 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.

Figure 1. Study flowchart. 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 WT BRAF sequence; DII KRAS, DNA integrity index determined using KRAS primer set; DII BRAF, DII determined using BRAF primer set; mA, total ccfDNA concentration; mA%, mutation load (% of mutant ccfDNA among total ccfDNA).
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.

**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...
Patients with high mutation load have statistically reduced OS. Mutant mCRC patients with mutation loads (mA%) lower than 10.72% (median mA% of the full cohort) had a median OS of 31.6 months compared with 11.4 months in patients with a higher mA (P = 0.0089; HR, 2.72; Supplementary Fig. S3).

Patients with high mutation load have statistically reduced OS. Mutant mCRC patients with mutation loads (mA%) lower than 10.72% (median mA% of the full cohort) had a median OS of 31.6 months compared with 11.4 months for patients with higher levels (P = 0.15; HR, 2.8; 95% CI, 0.82–3.62). Although the median OS of the latter group was less than half than that of the former group, there was no statistical difference. This tendency was confirmed with different thresholds: When studying the first tertile (4.14%), the median OS of patients with low mA% was 34.6 months compared with 13.9 months for patients with higher levels (P = 0.05; HR, 2.29; 95% CI, 0.97–5.44; Fig. 3B). When analyzing the second tertile (15.9%), patients with low mA% presented a median OS of 22.1 months compared with 11.3 months for patients with higher levels (P = 0.08; HR, 1.93; 95% CI, 0.9–4.21; Table 3). When the 5 patients exhibiting a BRAF V600E mutation were removed from the evaluated cohort, we observed that there was a trend showing a difference in OS for patients with low mA% with a median OS of 31.6 months compared with patients showing higher levels as the median OS decreased to 17.3 months (P = 0.11; HR, 1.827; Supplementary Fig. S4).

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 unprecedentedly 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 BRAF V600E (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).
Table 3. OS analysis on the entire cohort

<table>
<thead>
<tr>
<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>
</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>
</tr>
<tr>
<td>&gt; Median: 16.2 μg/L</td>
<td>30/41</td>
<td>17.8</td>
<td>1.50</td>
</tr>
<tr>
<td>≤ 5 μg/L</td>
<td>15/23</td>
<td>27.2</td>
<td>1.00 (0.68-2.25)</td>
</tr>
<tr>
<td>&gt; 5 μg/L</td>
<td>38/60</td>
<td>21.7</td>
<td>1.24</td>
</tr>
<tr>
<td>K Ras mutant status</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>
</tr>
<tr>
<td>Mutant</td>
<td>24/38</td>
<td>20.9</td>
<td>1.11</td>
</tr>
<tr>
<td>BRAF mutant status</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>WT</td>
<td>59/92</td>
<td>21.9</td>
<td>1.00 (1.13-25.4)</td>
</tr>
<tr>
<td>Mutant</td>
<td>5/5</td>
<td>3.4</td>
<td></td>
</tr>
<tr>
<td>K Ras or BRAF mutant</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>K Ras mutant</td>
<td>24/38</td>
<td>20.9</td>
<td>1.00 (3.72-6.487)</td>
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<tr>
<td>BRAF mutant</td>
<td>5/5</td>
<td>3.4</td>
<td>6.106</td>
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<tr>
<td>Ref A K Ras (ng/mL)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤ 1st tertile: 15.6 μg/L</td>
<td>19/32</td>
<td>22.23</td>
<td>1.00 (0.465-1.635)</td>
</tr>
<tr>
<td>&gt; 1st tertile: 15.6 μg/L</td>
<td>45/65</td>
<td>21.17</td>
<td>1.05</td>
</tr>
<tr>
<td>≤ Median: 26.0</td>
<td>26/49</td>
<td>28.5</td>
<td>1.00 (0.17-3.20)</td>
</tr>
<tr>
<td>&gt; Median: 26.0</td>
<td>38/48</td>
<td>18.07</td>
<td>1.94</td>
</tr>
<tr>
<td>≤ 2nd tertile: 47.5 μg/L</td>
<td>39/64</td>
<td>23.17</td>
<td>1.00 (0.14-3.15)</td>
</tr>
<tr>
<td>&gt; 2nd tertile: 47.5 μg/L</td>
<td>25/33</td>
<td>13.9</td>
<td>1.89</td>
</tr>
<tr>
<td>Ref A BRAF (ng/mL)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤ 1st tertile: 13.6 μg/L</td>
<td>19/32</td>
<td>22.23</td>
<td>1.00 (0.465-1.635)</td>
</tr>
<tr>
<td>&gt; 1st tertile: 13.6 μg/L</td>
<td>45/65</td>
<td>21.17</td>
<td>1.05</td>
</tr>
<tr>
<td>≤ Median: 27.6</td>
<td>28/49</td>
<td>24.5</td>
<td>1.00 (0.13-3.11)</td>
</tr>
<tr>
<td>&gt; Median: 27.6</td>
<td>36/48</td>
<td>20.5</td>
<td>1.88</td>
</tr>
<tr>
<td>≤ 2nd tertile: 48 μg/L</td>
<td>39/64</td>
<td>24.9</td>
<td>1.00 (0.15-3.19)</td>
</tr>
<tr>
<td>&gt; 2nd tertile: 48 μg/L</td>
<td>25/33</td>
<td>13.9</td>
<td>1.92</td>
</tr>
<tr>
<td>DII K Ras</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤ 1st tertile: 0.07 μg/L</td>
<td>20/31</td>
<td>20.8</td>
<td>1.00 (0.65-1.94)</td>
</tr>
<tr>
<td>&gt; 1st tertile: 0.07 μg/L</td>
<td>44/66</td>
<td>22.2</td>
<td>1.1</td>
</tr>
<tr>
<td>≤ Median: 0.12</td>
<td>30/47</td>
<td>19.2</td>
<td>1.00 (0.66-1.76)</td>
</tr>
<tr>
<td>&gt; Median: 0.12</td>
<td>34/50</td>
<td>23.07</td>
<td>1.09</td>
</tr>
<tr>
<td>≤ 2nd tertile: 0.23 μg/L</td>
<td>44/66</td>
<td>22.03</td>
<td>1.00 (0.77-1.98)</td>
</tr>
<tr>
<td>&gt; 2nd tertile: 0.23 μg/L</td>
<td>25/33</td>
<td>22.23</td>
<td>1.18</td>
</tr>
<tr>
<td>DII BRAF</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤ 1st tertile: 0.07 μg/L</td>
<td>25/34</td>
<td>20.6</td>
<td>1.00 (0.95-2.78)</td>
</tr>
<tr>
<td>&gt; 1st tertile: 0.07 μg/L</td>
<td>39/63</td>
<td>23.07</td>
<td>1.62</td>
</tr>
<tr>
<td>≤ Median: 0.19</td>
<td>34/49</td>
<td>17.7</td>
<td>1.00 (0.81-2.25)</td>
</tr>
<tr>
<td>&gt; Median: 0.19</td>
<td>30/48</td>
<td>26.90</td>
<td>1.44</td>
</tr>
<tr>
<td>≤ 2nd tertile: 0.20 μg/L</td>
<td>41/64</td>
<td>20.8</td>
<td>1.00 (0.60-1.7)</td>
</tr>
<tr>
<td>&gt; 2nd tertile: 0.20 μg/L</td>
<td>23/33</td>
<td>22.23</td>
<td>1.03</td>
</tr>
<tr>
<td>Mutant ccfDNA concentration (ng/mL)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤ 1st tertile: 1.06 μg/L</td>
<td>10/14</td>
<td>22.1</td>
<td>1.00 (125-2.055)</td>
</tr>
<tr>
<td>&gt; 1st tertile: 1.06 μg/L</td>
<td>19/29</td>
<td>13.9</td>
<td>1.59</td>
</tr>
<tr>
<td>≤ Median: 3.06</td>
<td>13/22</td>
<td>31.6</td>
<td>1.00 (1.25-5.93)</td>
</tr>
<tr>
<td>&gt; Median: 3.06</td>
<td>16/21</td>
<td>36.0</td>
<td>2.72</td>
</tr>
<tr>
<td>≤ 2nd tertile: 7.53 μg/L</td>
<td>16/28</td>
<td>21.1</td>
<td>1.00 (128-5.78)</td>
</tr>
<tr>
<td>&gt; 2nd tertile: 7.53 μg/L</td>
<td>13/15</td>
<td>6.83</td>
<td>2.72</td>
</tr>
<tr>
<td>Mutation load (%)</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>
</tr>
<tr>
<td>&gt; 1st tertile: 4.14 %</td>
<td>22/29</td>
<td>13.9</td>
<td>2.29</td>
</tr>
<tr>
<td>≤ Median: 10.72</td>
<td>13/22</td>
<td>31.6</td>
<td>1.00 (0.82-3.62)</td>
</tr>
<tr>
<td>&gt; Median: 10.72</td>
<td>16/21</td>
<td>11.4</td>
<td>1.72</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>
</tr>
<tr>
<td>&gt; 2nd tertile: 15.9 %</td>
<td>12/15</td>
<td>11.3</td>
<td>1.93</td>
</tr>
</tbody>
</table>

NOTE: Ref A K Ras, Ref A BRAF, DII K Ras, 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 K Ras/BRAF–mutant cohort around the first tertile, the median and the second tertile.

Abbreviations: DII K Ras, DII determined using K Ras primer set; DII BRAF, DII determined using BRAF primer set; mA, mutant ccfDNA concentration; mA%, mutation load (% of mutant ccfDNA among total ccfDNA); mo, months; Ref A K Ras, total ccfDNA concentration as determined by targeting a WT K Ras sequence; Ref A BRAF, total ccfDNA concentration as determined by targeting a BRAF WT sequence; WT, wild-type for the K Ras and BRAF mutations tested.

Strong Prognostic Value of Multiparametric ccfDNA Analysis

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

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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, DII determined using KRAS primer set.
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 (more than 2,000-fold) among the mCRC patients (35), an observation later confirmed by Bettegowda and colleagues (6). We believe that quantitative analysis of ccfDNA may be of prognostic value in regard to determination of the minimal residual disease, especially post-surgery when deciding on adjuvant therapy. It could be a biologic tool to decipher the prognosis difference between the 5 and 6 colorectal cancer subtypes recently revealed (38). Other approaches involving ccfDNA analysis were taken into consideration in regard to prognosis, such as presence of methylated DNA as independent prognostic factors in mCRC (18).

We analyzed sex, age, metastasis number, tumor differentiation, and tumor localization in respect to the evaluation of the ccfDNA parameters on prognosis. Our data only highlight statistical difference between of right- and left-sided origin of the primary tumor. Although differences varied with stages, meta-analysis on early-stage colon cancer reported a worse prognosis for right-sided tumors (41, 42). More investigation is needed to better decipher the molecular differences such as RAS or BRAF mutational status between right- and left-sided colon cancers and their association with prognosis, prediction of PFS benefit, and interaction with anti-EGFR therapy.

Although the cohort size of the mutant cohort (N = 43) in our study is somewhat a limiting factor, its analysis revealed original observations in respect the prognosis value of mA or mA%. However, work on a larger cohort of patients with mutation should be initiated to assess those observations as well as the ccfDNA fragmentation-based prognostic value in this population. Moreover, we need to be cautious about the values of ccfDNA concentration or fragmentation because those two parameters can vary under specific physiopathologic conditions such as inflammation. In addition, multiparametric analysis on stage II/III patients should be evaluated.

Altogether, the data revealed that ccfDNA analysis should not be limited to the qualitative determination of the presence of genetic alteration, but rather be implemented in the course of patient follow-up by the quantitative determination of other parameters. For instance, we showed the high-diagnostic capacity of total ccfDNA concentration for discriminating healthy individuals and mCRC patients with a statistical significance of \(P < 0.001\) (AUC = 0.92; refs. 24, 35). The various qualitative and quantitative parameters could directly be compared in respect to their diagnostic power by this single-run multiparametric method and potentially could synergistically be associated in an algorithm. Furthermore, the observations made in this report benefited from the ultra-sensitivity of the method in quantifying a specific sequence based on published and ongoing clinical studies (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 cfDNA, 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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Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): S. El Messaoudi, F. Mouliere, C. Bascoul-Mollevi, B. Gillet, M. Nouaille, C. Fiess, E. Crapez, F. Bibeau, T. Mazard, D. Perzet, M. Mathonnet, M. Ychou, A.R. Thierry
Study supervision: C. Theillet, A.R. Thierry

References


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

Safia El Messaoudi, Florent Mouliere, Stanislas Du Manoir, et al.


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