#### Manuscript Draft

Manuscript Number:

Title: Liquid biopsy for rectal cancer: a systematic review

Article Type: Review Article

Section/Category: Systematic or Meta-analysis Studies

Keywords: rectal cancer; liquid biopsy; ctDNA; non-operative management.

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Abstract: Background: The management of locally advanced rectal cancer (RC) is an evolving clinical field where the multidisciplinary approach can reach its best and liquid biopsy for obtaining tumor-derived component such as circulating tumor DNA (ctDNA) might provide complementary informations.

Methods: A systematic review of studies available in literature of liquid biopsy in non-metastatic RC has been performed according to PRISMA criteria to assess the role of ctDNA as a diagnostic, predictive and prognostic biomarker in this setting.

Results: Twenty-five publications have been retrieved, of which 8 full-text articles, 7 abstracts and 10 clinical trials. Results have been categorized into three groups: diagnostic, predictive and prognostic. Few but promising data are available about the use of liquid biopsy for early diagnosis of RC, with the main limitation of sensitivity due to low concentrations of ctDNA in this setting. In terms of prediction of response to chemoradiation, still inconclusive data are available about the utility of a pre-treatment liquid biopsy, whereas some studies report a positive correlation with a dynamic (pre/post-treatment) monitoring. The presence of minimal residual disease by ctDNA was consistently associated with worse prognosis across studies.

Conclusions: The use of liquid biopsy for monitoring response to chemoradiation and assess the risk of disease recurrence are the most advanced potential applications for liquid biopsy in RC, with implications also in the context of non-operative management strategies.

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August 19th, 2019

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Editors-in-Chief, Cancer Treatment Reviews

Dear Professors Pavlidis and Stahel,

We would like to submit to your attention the manuscript entitled "Liquid biopsy for rectal cancer: a systematic review" for publication in Cancer Treatment Reviews.

The management of locally advanced rectal cancer is an evolving clinical field where the multidisciplinary approach can reach its best and liquid biopsy for obtaining tumor-derived component such as circulating tumor DNA (ctDNA) might provide important complementary pieces of information. While there are many reviews available in the literature concerning the broad applications of liquid biopsy in cancer treatment, including a few about colorectal cancer as a whole, no systematic review has been performed with the focus of this specific tumor type, that has distinctive clinical features and different treatment modalities as compared to colon cancer.

We performed a systematic review categorizing results into three groups: diagnostic, predictive and prognostic applications of liquid biopsy for rectal cancer. We found interesting potential application of this diagnostic tool with implications also in the context of the emerging approach of non-operative management strategies, making overall the topic of very up to date according to the latest developments in this type of cancer. We therefore would like to submit our systematic review to the Journal for consideration since we feel that Cancer Treatment Reviews can offer proper dissemination to pathologists and oncologists.

Thank You very much indeed for your attention and collaboration. Kindest regards,

#### Prof. Andrea Sartore-Bianchi, M.D.

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# \*Conflict of Interest Statement

# CONFLICT OF INTEREST

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Liquid biopsy for rectal cancer: a systematic review

### Abstract

complementary informations.

Background: The management of locally advanced rectal cancer (RC) is an evolving clinical field where the multidisciplinary approach can reach its best and liquid biopsy for obtaining tumor-derived component such as circulating tumor DNA (ctDNA) might provide

Methods: A systematic review of studies available in literature of liquid biopsy in nonmetastatic RC has been performed according to PRISMA criteria to assess the role of ctDNA as a diagnostic, predictive and prognostic biomarker in this setting.

Results: Twenty-five publications have been retrieved, of which 8 full-text articles, 7 abstracts and 10 clinical trials. Results have been categorized into three groups: diagnostic, predictive and prognostic. Few but promising data are available about the use of liquid biopsy for early diagnosis of RC, with the main limitation of sensitivity due to low concentrations of ctDNA in this setting. In terms of prediction of response to chemoradiation, still inconclusive data are available about the utility of a pre-treatment liquid biopsy, whereas some studies report a positive correlation with a dynamic (pre/post-treatment) monitoring. The presence of minimal residual disease by ctDNA was consistently associated with worse prognosis across studies.

Conclusions: The use of liquid biopsy for monitoring response to chemoradiation and assess the risk of disease recurrence are the most advanced potential applications for liquid biopsy in RC, with implications also in the context of non-operative management strategies.

**Key Words**: rectal cancer, liquid biopsy, ctDNA, non-operative management

### **BACKGROUND**

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47 Colorectal cancer (CRC) is one of the most diagnosed cancers worldwide, with 1.84 million estimated new cases in 2018 [1]. About 25-30% of all colorectal cancer diagnoses 48 49 accounts for rectal cancer (RC) [2]. In the European Union, the incidence of RC is ~125000 per year, i.e. ~35% of the total colorectal cancer incidence, reflecting 15–25 50 cases/100 000 population per year and is predicted to further increase in both genders. 51 52 The mortality is 4–10/100 000 population per year, with a median age at diagnosis of ~70 53 years [3]. The rectum and colon have a different embryological origin, anatomy and function [4]. RC 54 55 has thus distinctive clinical features as compared to colon cancer, with an increased risk of local spread and recurrence. As a consequence, the treatments for primary rectal and 56 57 colon cancer are different [5]. The incidence of RC has been decreasing as the 58 increasingly spread use of screening allows for identification and endoscopic removal of 59 premalignant lesions [6]; however, several recent studies have shown an increase in 60 incidence of rectal cancers among young people [7]. 61 The treatment landscape in RC paralleled that of colon cancer and has evolved over the 62 last decade following the approval of several targeted therapies for the advanced disease, 63 leading to improvements in tumor response rates and patient survival [8,9]. However, 64 progresses in medical treatment in the metastatic setting have been mainly incremental despite considerable advances in the knowledge of tumor biology [10]. In this regard, 65 primary tumor location (right-sided or left-sided of the colorectum) has been identified as a 66 surrogate marker for underlying molecular classification, with differences in a continuum 67 spectrum between colon and rectal carcinomas [11]. 68 69 In the non-metastatic setting, operative approaches such as transanal endoscopic 70 microsurgery, open and laparoscopic proctectomy [12] are effective in earlier stages, while 71 a trimodality treatment (pre-operative chemoradiation therapy (CRT), surgery with total

mesorectal excision (TME) followed by adjuvant chemotherapy) is the standard of care for locally advanced RC patients. A significant risk of distal recurrence is present in rectal tumors radically operated in particular within the first 5 years for stages II and III of Dukes at around 30% and 50%. respectively. probably caused by the presence of micrometastatic spread [6]. A pooled analysis of five European randomized controlled trials demonstrated that the 5-year distant metastasis rate was 30.8% in 2.759 recruited patients [3]. An increasing number of reports suggested that a non-operative management (NOM), consisting of close surveillance of patients with clinical complete response (cCR) after chemoradiotherapy, could be an acceptable alternative to rectal surgery (proctectomy). Led by small prospective series published since the late 90's by Habr-Gama and colleagues [13,14], several international series have reported similar oncologic outcomes in cCR patients followed by close active surveillance (the so-called watch-andwait (W&W) or NOM approach) compared to those treated with radical surgery [15,16]. More recently, the International Watch & Wait Database (IWWD) described the outcome of the W&W strategy in a large-scale registry of more than 1000 patients, reporting excellent survival and small risk of local unsalvageable disease recurrence [17]. Despite the body of retrospective literature is greatly increasing, key knowledge gaps limiting widespread use of W&W/NOM remain, and clinical studies aimed at identifying patients who are good candidates for this approach are ongoing [18]. Follow-up supported by clinical examinations, imaging and endoscopies aims to improve prognosis by early detection of local or distant recurrence. Isolated carcinoembryonic antigen (CEA) monitoring is insufficiently sensitive. The analysis of serum protein levels, such as CEA, allows a fast and cost-effective method to quantify cancer progress, but it's distorted by limited sensitivity and specificity, in particular during treatment courses due to inflammation and discharge of protein in the bloodstream. Moreover, a portion of patients

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with metastatic RC does not show visible plasmatic CEA levels during the disease[19,20].

The management of RC is an evolving clinical field where the multidisciplinary approach can reach its best and the ability to discern patients at low risk from those at high risk of recurrence is the prerequisite for the most appropriate treatment choice. With this regard, liquid biopsy for obtaining tumor-derived component such as circulating tumor DNA (ctDNA) or circulating tumor cells (CTCs) might provide crucial complementary information at the diagnosis of RC and in different moments during its treatment. Liquid biopsies may indeed represent a precious basin of new generation biomarkers [21,22] and are being evaluated also in RC for diagnosis, treatment choice, monitoring disease response, tracking acquired mutations linked to targeted therapy resistance, and detecting minimal residual disease.

The aim of this systematic review is to assess the role of ctDNA as a diagnostic, predictive and prognostic biomarker in non-metastatic RC.

### **METHODS**

# **Definition of the Outcome**

The purpose is to evaluate the current clinical potential of liquid biopsy, in particular cell-free DNA (cfDNA)/ circulating tumor DNA (ctDNA), in non-metastatic RC patients.

# Data Source and Search Strategy

A systematic literature review was performed according to PRISMA Statement Criteria [23,24] in June 2019. The PubMed database was systematically reviewed as of June 11<sup>th</sup>, 2019 and all retrieved studies were manually screened for relevant references missed in the primary search. Unpublished data presented as abstract in relevant international

congresses [American Society of Clinical Oncology (ASCO), European Society of Medical Oncology (ESMO)] were also systematically searched for. Furthermore, ongoing clinical trial exploring the value of liquid biopsy in non-metastatic rectal cancer were searched on clinicaltrial.gov. The decision to include a study for review was made by consensus between two authors (EGP and DM). The research criteria were limited to human studies published only in English language. The Medical Subject Heading terms used for the search were ("rectal" or "rectum" or "LARC") and ("liquid biopsy" or "ctDNA" or "cfDNA" or "circulating tumor DNA" or "circulating free DNA" or "methylated DNA" or "DNA methylation").

132 Main study inclusion criteria:

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- Involved the measurement of cfDNA/ctDNA in plasma/serum in patients with RC;
- Diagnosis, treatment response and/or survival data collected and correlated with
   cf/ctDNA.
- 136 Study exclusion criteria:
  - Involved patients with metastatic RC;
  - Involved patients with CRC without mention about the tumor location.

#### RESULTS

- 141 A total of 838 records were screened to be included in the systematic review (**Figure 1**).
- We identified 8 records found through database searching (PUBMED) and 17 additional
- records identified through other sources (ESMO, ASCO, Clinicaltrial.gov).
- 144 As a result, 26 records were eligible and included in the systematic review: 8 full-text
- articles studies, 7 abstracts presented at international congresses, and 10 ongoing ctDNA
- 146 clinical trials.
- 147 We subdivided our results into 3 categories according to the investigated role of
- 148 ctDNA/cfDNA or methylated DNA: diagnostic, predictive of treatment response and

prognostic (in terms of disease recurrence or survival) (**Figure 2**). Finally, we provide a summary of published or presented works (**Table 1**) and of ongoing trials (**Table 2**).

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# cfDNA and ctDNA as diagnostic tool

In 2011 an Italian group evaluated the ability of cfDNA to discriminate healthy patients (plasma samples collected after a negative colonoscopy) from patients with RC. Through guantitative PCR (using Alu 115, Alu 147 and β-globin gene), they found that the baseline level of cfDNA was significantly higher in RC patients than in healthy individuals [25]. A Chinese group also observed higher concentration of cfDNA in RC than in healthy individuals, where mutated KRAS and methylated MGMT were not detected. Moreover, the ratio of 400-/100-bp DNA fragments (an index of cfDNA integrity) was higher in RC patients than in healthy controls, in which cfDNA is considered to originate mainly from apoptotic process of normal cells [26]. Shalaby et al. highlighted the capacity of MGMT and ERCC1 methylation status to distinguish benign and malignant rectal tumors. The study was performed in blood and tissue of 43 benign and 50 malignant rectal tumors patients. They observed a significant higher frequency of MGMT and ERCC1 methylation in RC patients than in cases with benign tumors, both in tissue and blood samples (sensitivity around 60% and specificity of 93-95% for each gene on plasma). The combination of MGMT and ERCC1 methylation reached a specificity for differentiation between benign and malignant rectum tumor of 100% in blood samples, with a sensitivity of 32% [27]. More recently, Zhang et al. observed that both colon and RC could be detected by ctDNA, with the latter having lower median plasma cfDNA concentrations in plasma than colon cancer patients (14.2 ng/ml vs. 8.94 ng/ml). The study was conducted on 29 patients, including 10 with RC. For each patient, a freshly frozen tissue sample was collected during

surgery and the plasma obtained was analyzed using an 85-gene panel, with a mutation concordance rate between ctDNA and tissue of 70% in all patients, lower in the subgroup of RC patients (5/10, 50%) [28].

At the present time, one clinical trial is exploring the feasibility of ctDNA as a detection index for RC (**Table 2**).

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# cfDNA and ctDNA as tool to predict treatment response

Different groups analyzed the role of cf/ctDNA as a tool to monitor treatment response after CRT in locally-advanced rectal cancer (LARC). In 2008, Zitt and colleagues [29] observed for the first time a correlation between the concentration of cfDNA and clinical response after surgery (not after neoadjuvant CRT) in 26 patients: responders exhibited a reduction in cfDNA level, while non-responders showed an incremented cfDNA [29]. Agostini et al. analyzed cfDNA on 67 LARC patients before and after neoadjuvant CRT, before surgery. Levels of longer fragments of cfDNA were reduced in responsive patients (tumor regression grade (TRG) 1-2, according to the Mandard score) compared to nonresponsive (TRG 3-5). In particular the post-CRT cfDNA integrity (the ratio of 400-/100-bp DNA fragments) was associated with response (P = 0.0009), confirming that cfDNA long fragments are more tumor-specific than short fragments. Baseline levels of cfDNA were not correlated with tumor response [25]. The relationship between cfDNA concentration and TRG score was also observed by a Chinese group who focused also on different aspects of cfDNA: the 400-/100-bp ratio of DNA fragments, the methylation status of *MGMT* and the mutational status of *KRAS*. They treated 34 LARC patients with CRT followed by surgery. The good response group of patients had a significantly higher baseline 400-bp plasma cfDNA levels and showed a significant decrease of these fragments in plasma after CRT. On the contrary, no difference was observed regard the level of 100-bp fragments before and after CRT both

200 in responders and non-responders. In addition, the rate of MGMT promoter methylation at 201 baseline was higher in responders, with no reduction after treatment, while the rate of 202 KRAS mutation decreased in both groups after CRT [26]. 203 Shalaby et al. described the same correlation between methylated status of the promoter 204 of MGMT and ERCC1 genes with response to CRT. A higher methylation status was 205 associated with a better tumor response after preoperative CRT [27]. A Danish group quantified the total level of cfDNA by fluorescence assay, using 40 µL of 206 207 plasma of 123 LARC patients. They observed no differences either between baseline and post-treatment (CRT preceded by induction chemotherapy in 42% of cases) levels of 208 209 cfDNA or between patients achieved a pathological complete response (pCR) and poor responders [30]. 210 211 Carpinetti et al. firstly observed a decrease in ctDNA (detected due to tumor-specific 212 chromosomal rearrangements) in 4 patients that achieved a response to CRT. By the way, 213 cfDNA was negative both in patients with partial and complete pathological response [31]. 214 Tie et al. analyzed tissue and multiple plasma samples of 159 LARC patients treated with 215 neoadjuvant CRT through next generation sequencing (NGS). ctDNA was detectable in 77% of plasma samples before treatment, 8% during CRT and 12% at a postoperative 216 stage. Detectable ctDNA after surgery was associated with known high risk pathological 217 218 features (i.e. ypT3-4, node positive), but there was no statistically meaningful association 219 between reduction or negativization of ctDNA after CRT and pCR [32]. 220 Li et al. observed in a small study of 30 patients that ctDNA level variations (somatic 221 mutations identified by NGS of 61-gene panels) can predict pathological response to neoadjuvant CRT, better than classic markers as CEA or CA 19.9 [33]. 222 223 McDuff et al. reported a higher rate of R0-node negative resections after CRT among 17 224 patients with undetectable preoperative ctDNA, compared to 10 patients with detectable

ctDNA. The former group had a higher pCR rate (24% vs. 10%) [34].

226 Chen et al. identified ctDNA analyzing the methylation status of *BCAT1* or *IKZF1* gene 227 through qPCR assay in 9 LARC patients. Five patients showed positivity for one or both of 228 methylated genes before CRT, four of them exhibited a decrease in detection after 229 treatment, consistent with partial or complete responses [35]. 230 Two Chinese prospective cohort studies, presented at 2019 ASCO meeting, recruited 180 231 LARC patients, overall, with serial plasma collection analyzed through NGS gene panels to

detect mutations in ctDNA [36,37]. Yang et al. reported a negative correlation between presence of *TP53* and *APC* gene in pre-treatment samples and response to nCRT, and detectability of pre-treatment mutations during nCRT significantly decreased from TRG3 to TRG0 group [37]. Zhou et al. observed a significant predictive role of pre-surgery ctDNA

levels, where its persistency was linked with pathological N+, while an undetectable

preoperative ctDNA correlated with pathological downstaging [36].

At the present time, six clinical trials are exploring the possibility to use ctDNA as a predictive tool (**Table 2**).

# cfDNA and ctDNA as a prognostic tool for disease recurrence or survival

In a Danish study of 123 LARC patients, a solid association of baseline cfDNA level (measured through a fluorescence assay) with disease free survival (DFS) was found. High levels of cfDNA were correlated with higher risk of local or distant recurrence and with shorter time to recurrence. A non-statistically significative trend for overall survival (OS) was also observed [30].

At a median follow up of 24 months, Tie and colleagues noticed an increased risk of recurrence in patients with ctDNA persistence after CRT or surgery. This risk of recurrence was irrespective either of pathological risk level (ypT3-4N+ vs ypT1-2N0 vs pCR) or of adjuvant therapy, with an estimate 3y RFS of 33% vs 87%. Post-operative ctDNA

251 detection was a stronger prognostic biomarker than CEA levels. Moreover, 74% of patients 252 recurred within 12 months after surgery, 9/19 had persistent ctDNA in plasma [38]. As already said, Carpinetti et al, analysed in 4 LARC patients the use of ctDNA to monitor 253 254 disease response and recurrence. Two patients with persistent positive level of ctDNA, during their follow up, developed liver metastasis concomitantly with an incremental in 255 ctDNA level. Other 2 patients showed a drop in ctDNA levels after CRT, with negative 256 follow up for recurrence and no more evidence of ctDNA in plasma [31]. 257 258 Four studies, presented at last ASCO and ESMO congresses, have explored the use of ctDNA as a tool to assess response and predict surgical outcome in LARC [34,35,39,40]. 259 260 McDuff et al., among 22 patients treated with preoperative CRT, reported a shorter recurrence free survival in cases with detectable post-operative ctDNA [34]. Khakoo 261 showed that persistence of ctDNA at mid CRT or detection of ctDNA at the end of CRT 262 263 were associated with development of metastasis [40]. In the work presented by Chen, one 264 patient that showed persistent high level of methylated genes after CRT, recurred in two 265 months after surgery [35]. 266 Conversely, in a study performed on 97 LARC patients receiving induction chemotherapy with CAPOX followed by CRT and then adjuvant CAPOX with or without cetuximab 267 268 (EXPERT-C trial), Sclafani et al. did not found a significant association between ctDNA 269 positivity/negativity and progression free survival (PFS) or OS using gPCR [41]. 270 At the 2019 ASCO meeting, Yang et al. described a significant association between 271 persistence of pre-treatment mutations in ctDNA after completion of CRT and worse DFS 272 [37]. 273 Eight clinical trials are exploring the possibility to use cf/ctDNA as a prognostic tool (Table 274 **2**).

# DISCUSSION

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In present review several studies supported the use of liquid biopsy in RC as an innovative, minimally invasive procedure that could assist either the diagnostic-staging process and the assessment of treatment response. The limitations of data retrieved are mostly related to the relatively small sample size of the studies, heterogeneity of techniques used for liquid biopsy and timing of plasma samples (eg. after CRT or after surgery), and differences in treatment courses (e.g. induction chemotherapy or not) for patients with different stages of non-metastatic RC. We found 4 studies (overall 204 patients) which explored the role of liquid biopsy as a diagnostic tool in RC. Measurement of cfDNA levels was performed with different techniques: ALU-based quantitative-PCR, tracking mutations of KRAS, or, more recently, tracking of several gene with NGS and assessing the methylation status of MGMT and ERCC1 in ctDNA. These reports, although heterogeneous, suggest that measuring cfDNA levels or detecting ctDNA might discriminate RC patients from healthy controls and from individuals harbouring rectal adenoma. In particular, a high specificity in discriminating RC was reported for MGMT and ERCC1 methylation or KRAS mutation detection. These data are consistent with results obtained in colorectal cancer patients [42-44]. However, it should be taken into account that in this setting of early detection of cancer, the sensibility of liquid biopsy is limited by low concentrations of circulating DNA in this setting, that have been reported to be even lower in RC [28]. Contrasting data have been retrieved about the reliability of circulant DNA as a tool to predict treatment response in RC. The clinical value of baseline levels of cf/ctDNA is not clear. Only one small study showed a correlation between higher levels of longer cfDNA fragments (index of DNA integrity) and response [26], but these data were not consistent with results of a previous wider study [25]. Nevertheless, a strong methylation of MGMT or ERCC1 genes at baseline might better predict a tumor response after preoperative CRT [26,27]; on the contrary, detection of TP53 and APC gene in ctDNA of pre-treatment

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samples has been negatively associated with response to CRT [37]. Notably, in a previous 303 304 presentation of the same study, Yang et al. reported no difference in baseline ctDNA levels between responders and non-responders [39]. 305 306 A noteworthy evidence, observed by most groups with different assays, consists in the reduction in cf/ctDNA levels in responders, while non-responders can show an 307 308 incremented circulant DNA [25,26,29,31-33,35-37,45]. The timing of plasma collection 309 represents a crucial aspect in this setting: at baseline, after induction chemotherapy, after 310 neoadjuvant CRT, after surgery. Zitt et al. observed a reduction of DNA levels after CRT in 311 all 26 patients but it was not predictive of pathological downstaging. A significant difference 312 between responders and non-responders was found only in plasma samples collected 313 after surgery [29]. 314 In this same setting, a DNA integrity index (a ratio between long and short DNA fragments) 315 has been proposed to be a useful guide to discriminate responding and non-responding 316 patients even with plasma analysis conducted after neoadjuvant CRT [25,26]. 317 More recent studies, adopting NGS assays, have demonstrated the potential of post-CRT 318 ctDNA samples to predict tumor response, enhancing the confidence in ctDNA as a tool to guide patient selection for watch and wait strategy. Different groups observed a correlation 319 320 between undetectable preoperative ctDNA status and pathological downstage [33,36-321 38,45]. A weaker methylation of BCAT1 or IKZF1 has been observed after CRT in good responders by Chen et al. [35]. 322 Finally, we found inconclusive data about the association between reduction or total 323 324 clearance of circulant DNA after CRT and pCR. Likely, circulant DNA has no sufficient sensitivity to rule out the presence of minimal residual disease [38]. 325 326 In terms of survival and disease recurrence, almost all studies have shown a correlation 327 between persistence of ctDNA after treatment and disease recurrence during follow up

328 [30,32,35-37,40,45]. One group also observed an association between high baseline cfDNA level and local or distant recurrence, with a trend for shorter OS [30]. 329 Tie et al., in a recent prospective study of LARC patient, detected ctDNA in 77%, 8,3% and 330 331 12% of pretreatment, postchemoradiotherapy and post-surgery plasma samples, respectively. On the basis of ctDNA levels, they were able to stratify patients at very high 332 risk of recurrence (ctDNA detectable after CRT (HR 6.6) or after surgery (HR 13.0)). 333 estimating a 3-year recurrence-free survival of 33% vs 87% in positive/negative ctDNA 334 335 patients. Postoperative ctDNA status remained an independent predictor of RFS irrespective of clinicopathological risk factor or adjuvant chemotherapy [38] 336 337 These results are in line with the conclusions of studies conducted in the setting of resected colorectal cancer, where evidence of ctDNA after surgery or after adjuvant 338 339 chemotherapy were linked with shorter recurrence-free survival [46,47]. 340 In contrast, among patients treated in the EXPERT-C trial (induction CAPOX, CRT, 341 surgery, adjuvant CAPOX +/- cetuximab) a significant association between ctDNA 342 positivity/negativity and PFS or OS was not observed. However, the plasma sample in this 343 study was collected before surgery and all patients received both neoadjuvant and adjuvant chemotherapy [48]. 344 The potential role of liquid biopsy in RC is also currently being explored as translational 345 346 endpoints in numerous clinical trials and can find an important application in the setting of NOM. The ongoing No-Cut study, a phase 2 clinical trial, will assess whether an 347 oxaliplatin-enhanced neoadjuvant CRT, followed by an imaging-intensive, liquid biopsy-348 349 enriched surveillance, can spare stage II-III rectal cancers from undergoing up-front 350 demolitive radical surgery with a clinically acceptable rate of distant relapse. The 351 translational component of the study could establish, by retrospective correlative analysis 352 of contextual imaging and blood molecular findings, whether circulating mutated and/or methylated tumoral DNA is a predictive marker for residual disease, and whether there is a correlation between ctDNA and cancer relapse (NCT03565029) (**Figure 3**).

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# Ethical approval and consent to participate

Not applicable because the article is a review.

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# Contributors

- Daniela Massihnia: conception and design of the review, acquisition, analysis and interpretation of data, drafting of the article.
- Elio Gregory Pizzutilo: conception and design of the review, acquisition, analysis and interpretation of data, drafting of the article.
- Alessio Amatu: acquisition and interpretation of data, critical revision of the draft.
- Federica Tosi: acquisition and interpretation of data, critical revision of the draft.
- Silvia Ghezzi: acquisition and interpretation of data, critical revision of the draft.
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- Pietro Di Masi: acquisition and interpretation of data, critical revision of the draft.
- Elena Righetti: acquisition and interpretation of data, critical revision of the draft.
- Giorgio Patelli: acquisition and interpretation of data, critical revision of the draft.
- Francesco Scaglione: interpretation of data, critical revision of the draft.
- Angelo Vanzulli: interpretation of data, critical revision of the draft.
- Salvatore Siena: conception and design of the review, analysis and interpretation of data,
- 374 critical revision of the draft, final approval of the version to be submitted.
- Andrea Sartore-Bianchi: conception and design of the review, analysis and interpretation
- of data, drafting of the article, critical revision of the draft, final approval of the version to be
- 377 submitted.

# Acknowledgement

Authors are supported by grants from Associazione Italiana Ricerca Cancro grant AIRC 5 x mille [Project ID 51000] Special Program Molecular Clinical Oncology, AIRC Investigator Grant [Project ID 20685 and 16788], and AIRC Special Program 5 per mille metastases [Project ID 21091]; IANG-CRC grant from Fondazione Regionale Ricerca Biomedica (FRRB) of Regione Lombardia; CORDIS Community Research and Development Information Service, Horizon 2020 [Project ID 635342] grant Molecularly Guided Trials with Specific Treatment Strategies in Patients with Advanced Newly Molecular Defined Subtypes of Colorectal Cancer (MoTriColor); Fondazione Oncologia Niguarda Onlus, grant Terapia Molecolare dei Tumori and grant Studies to Develop Therapies Against Colorectal Cancer in Young Adults.

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# **Funding**

No one for this paper

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### **Declaration of interests**

- 395 A.S-B. has acted as a consultant/advisory member for Amgen, Bayer, Lilly and Merck-
- 396 Serono. S.S is advisory board member for Amgen, Bayer, BMS, Celgene, Incyte, Merck,
- Novartis, Roche, Seattle Genetics. A.A. is advisory board member for Amgen and Bayer.

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   Sci Rep 2018;8:1445. doi:10.1038/s41598-018-19212-5.

- 558 Figure Legends
- 559 **Figure 1:** Flow diagram representing the systematic review process performed according
- to PRISMA Statement.
- Figure 2: Euler-Venn diagram representing the results of our systematical research
- 562 divided according to the role of ct/cf DNA
- 563 Figure 3: Study design of NO-CUT trial and the potential role of liquid biopsy in non-
- operative management of rectal cancer.

**Table 1:** Studies exploring the role of liquid biopsy in non-metastatic rectal cancer \* Only as an abstract

Reference	Year	N. patients	Country	Assay	Main findings					
Diagnostic										
Agostini et al.	2011	67	Italy	qPCR	cfDNA levels (using Alu 115, 247 and $\beta$ globin gene) were higher in RC than in healthy group (P < 0.0001).					
Sun et al.	2014	34	China	qPCR	Concentrations of 100 bp and 400 bp fragments and the ratio of 400-/100-bp DNA were higher in RC than in healthy group (p<0.01).  Mutated <i>KRAS</i> and methylated <i>MGMT</i> were not found in cfDNA of healthy controls.					
Shalaby et al.	2017	93	Egypt	PCR	MGMT or ERCC1 were methylated for 4.7% and 7% in the blood of patients with benign lesions and for 58% and 60% in RC patients (p < 0.001).					
Zhang et al.*	2019	10	China/USA	NGS	Mutation concordance rate among ctDNA and tissue was 50% in RC patients.					
Predict/Monitor Treatment Response										
Zitt. et al.	2008	26	Austria	qPCR	Post surgery cfDNA responders: 2.2 ng/ml; cfDNA non responders: 5.1 ng/ml (p = 0.006).					
Agostini et al.	2011	67	Italy	qPCR	Baseline cfDNA levels not correlated with tumor response. In responders, the median levels of Alu 247 and the cfDNA integrity index (the ratio of 400-/100-bp DNA fragments) were significantly lower after CRT compared to baseline (p = 0.0048 and 0.0005, respectively).					
Sun et al.	2014	34	China	PCR	The good response group had significantly higher baseline 400-bp DNA levels and DNA integrity index. Good response group had lower cfDNA integrity after CRT compared before CRT.  MGMT promoter methylation at baseline was higher in responders, with no reduction after treatment, while the rate of KRAS mutation decreased in both groups after CRT.					
Shalaby et al.	2017	93	Egypt	PCR	Significant correlation between baseline MGMT and ERCC1 methylation and response to CRT.					
Schou et al.	2018	123	Denmark	Fluorescence	No differences in cfDNA levels between before and after CRT.					
Carpinetti et al.	2015	4	Brazil	Whole genome sequencing	ctDNA levels decreased in RC achieving response to CRT.					
Tie et al.	2018	159	Australia	NGS	No association between post-CRT ctDNA status and pCR. Postoperative ctDNA detection was associated with high-risk pathological factors such as ypT3-4 and ypN1-2 stage.					

Li et al.* 1	2017	30	China	NGS	ctDNA predicts change in tumor burden better than CEA.				
McDuff et al.* 1	2019	31	USA	NGS	The rate of R0-NN resection was higher among pts with undetectable preoperative ctDNA compared to pts with a detectable ctDNA.				
Chen et al.* 1	2019	9	USA	qPCR	Methylated <i>BCAT1</i> or <i>IKZF1</i> genes were found in 5/9 patients. Correlation between decrease of methylation and partial/complete response.				
Zhou et al.* 1	2019	61	China	NGS	Correlation between undetectable preoperative ctDNA status and pathological downstage (p=0.02). Correlation between preoperative ctDNA positivity and the persistently involved lymph node (p = 0.02).				
Yang et al.* 1	2019	119	China	NGS	TP53 and APC gene in pre-treatment samples negatively correlated with response to nCRT.  Detection of pre-treatment mutations in any time points during nCRT was significantly (P = 0.03) decreased from TRG3 to TRG0 group.				
Predicting disease recurrence									
Tie et al. 1	2018	159	Australia	NGS	Worse RFS if ctDNA was detectable after CRT or after surgery (estimated 3-year recurrence-free survival was 33% for postoperative ctDNA-positive patients vs 87% for ctDNA-negative).				
Schou et al. 1	2018	123	Denmark	Fluorescence	High risk of recurrence pts with baseline cfDNA levels above 75 <sup>th</sup> quartile (HR=2.48, 95% P=0.007).				
Carpinetti et al. 1	2015	4	Brazil	Whole genome sequencing	Changes of ctDNA levels after surgery predict tumour recurrence.				
McDuff et al* 1	2019	31	USA	NGS	Patients with detectable postoperative ctDNA had worse RFS.				
Khakoo et al.* 1	2018	47	UK	Sequencing	ctDNA level was higher in pts who showed metastases (64%) related to pts that did not (8.3% P = 0.0005).				
Chen et al.* 1	2019	9	USA	qPCR	Patients with high levels of methylated <i>IKZF1</i> and <i>BCAT1</i> in post-treatment ctDNA recurred 2 months after surgery.				
Sclafani et al. 0	2018	97	UK	ddPCR	No difference in outcome between patients with or without detectable ctDNA after CRT.				
Yang et al.* 1	2019	119	China	NGS	Detection of pre-treatment mutations in ctDNA after completion of nCRT was significantly associated with worse DFS.				

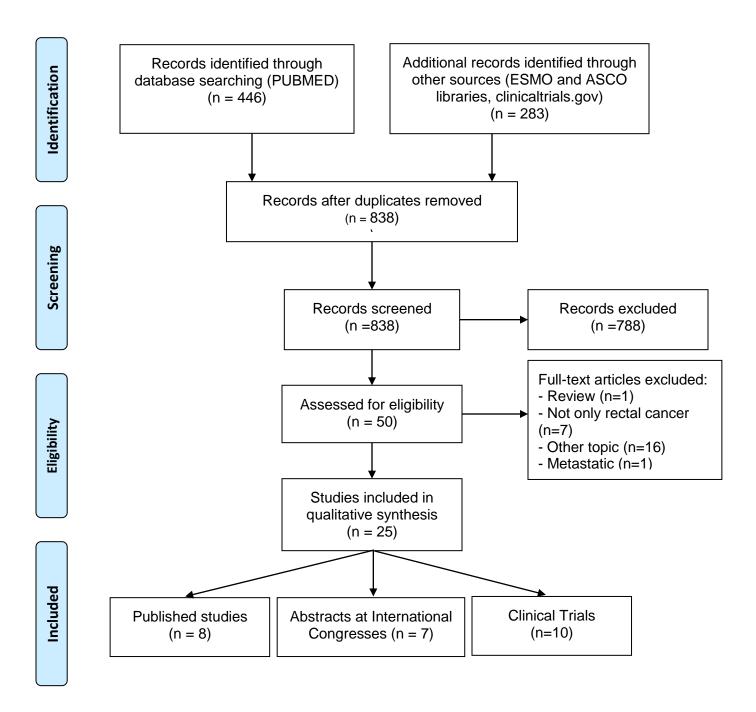
cfDNA: circulating free DNA; RC: rectal cancer; ctDNA: circulating tumor DNA; CRT: chemoradiotherapy; pCR: pathologic complete response; NN: node negative; TRG: tumor regression grade; RFS: relapse-free survival; DFS: disease-free survival.

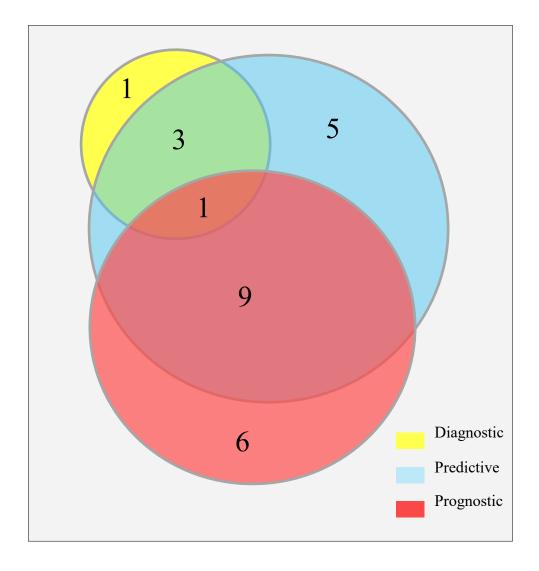
**Table 2.** Ongoing studies investigating the role of cf/ct-DNA in non-metastatic rectal cancer.

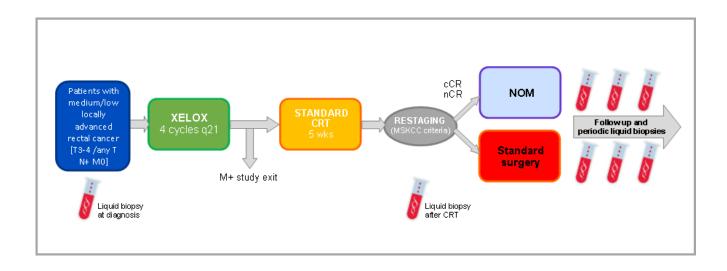
Study (Study ID) STATUS	Location	Phase	Pts	cf/ct DNA related outcomes
Total Neoadjuvant Treatment Without Surgery For Locally Advanced Rectal Cancer: Prospective Clinical Trial To Assess Tumor Complete Response, Circulating Tumor Genetic And Epigenetic Biomarkers, And Stromal Transcriptome To Interpret Clinical Outcome (NO-CUT) (NCT03565029)	Italy	II	180	PROGNOSTIC: local a/o relapse free survival
Circulating Tumour DNA (ctDNA) Rectal Cancer and the Relationship to Extramural Venous Invasion (NCT02579278)	UK	Observational, Prospective	40	<b>PREDICTIVE</b> : presence or absence of ctDNA post CRT in EMVI-positive rectal cancer
Application of Circulating Tumor DNA Test in the Diagnosis and Treatment of Patients With Advanced Rectal Cancer (NCT03615170)	China	Observational, Prospective	200	DIAGNOSTIC: explore the feasibility of ctDNA as a detection index for rectal cancer PREDICTIVE: evaluation of preoperative concurrent chemoradiotherapy, so as to provide guidance for subsequent treatment PROGNOSTIC: search for possible recurrence related mutations
Observational Study on Rectal Cancer to Verify if Response After Chemo-radiotherapy Can be Predicted With a Particular Blood Test. (LiBReCa) (NCT03699410)	Switzerlan d	Observational, Prospective	35	PREDICTIVE: negative prognostic value of ctDNA drawn from the mesenteric and peripheral blood to investigate if can predict the response after chemo-radiotherapy and before surgery
A Study of the Role of Circulating Tumor DNA in Predicting the Likelihood of Organ Preservation After Clinical Complete Response to Neoadjuvant Therapy for Rectal Cancer (NCT03749083)	USA	Observational, Prospective	55	PROGNOSTIC: local recurrence rate
Investigation of the Value of ctDNA in Diagnosis, Treatment, and Surveillance of Surgically Resectable Colorectal Cancer – Cohorts for T1-2N0 rectal cancer who undergo local or radical resection (NCT03038217)	China	Observational, Prospective	300	PROGNOSTIC: disease free survival, local recurrence rate, overall survival
MRI Simulation-guided Boost in Short-course Preoperative Radiotherapy for Unresectable Rectal Cancer (SUNRISE) (NCT03714490)	China	Phase II	200	PREDICTIVE: predicting of treatment response PROGNOSTIC: survival
Multicenter, Prospective, RCT : Investigation of Combined Modality Therapy for Locally Advanced Mid/Low Rect (NCT03042000)	China	Prospective, observational	1200	PREDICTIVE: predicting the therapeutic effects of NCRT PROGNOSTIC: disease free survival
Totally Neoadjuvant FOLFOXIRI + Short-course Radiation + XELOX in Patients With Locally Advanced Rectal Cancer (NCT03484221)	China	Phase II	30	PROGNOSTIC: survival
Preoperative Chemoradiotherapy With Raltitrexed for Intermediate or Locally Advanced Rectal Cancer in the Fit Elderly (NCT02992886)	China	Phase II	68	PREDICTIVE: predictive treatment response PROGNOSTIC: disease free survival

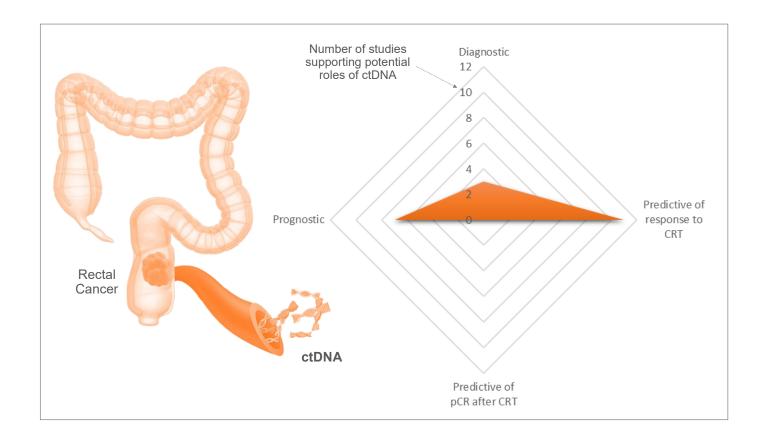


# **PRISMA 2009 Flow Diagram**









# \*Highlights (for review)

- Liquid biopsy for obtaining tumor-derived component such as circulating tumor DNA (ctDNA) might be used as a biomarker for improving rectal cancer management
- ctDNA is under study in rectal cancer as for diagnostic, predictive and prognostic utility
- Monitoring response to chemoradiation and assessing the risk of disease recurrence are the most advanced potential applications for liquid biopsy in rectal cancer