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Biomarkers in colorectal cancer

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Chapter 1

General introduction and thesis outline

COLORECTAL CANCER INCIDENCE, TREATMENT AND PROGNOSIS

Colorectal cancer (CRC) is the second most common diagnosed cancer in females and the third most common cancer in males and accounts for the second cause of cancer death in Europe with an estimated incidence of 447.000 new CRC cases and 215.000 deaths, in 2012¹. As shown in figure 1, the estimation of the prognosis is mainly determined by conventional staging such as, tumour, node and metastasis (TNM) classification. Despite a continuous improvement of the TNM classification, outcome among patients with the same tumour stage varies significantly². Consequently, it could be stated that adequate individualized assessment could not be accomplished with conventional classification. Furthermore, evidence is accumulating that rectal tumours differ from colon tumours^{3,4}, resulting in a separation of colon and rectal cancer regarding biology and treatment.

In general, treatment of CRC employs a multidisciplinary approach, though surgery remains the cornerstone of curative treatment for non-metastasized CRC in most cases. Prior to surgery, clinical staging is performed by a combination of endoscopy, CT (Computerized Tomography) and in rectal cancer also MRI (Magnetic Resonance Imaging). For colon cancer stage III and high risk stage II, surgery is followed by adjuvant chemotherapy⁵⁻⁷. Still, approximately 20% of the patients with stage I-III colon cancer, develop metastatic disease within 5 years⁸. For rectal cancer, important advances have been made in treatment with the implementation of total mesorectal excision (TME)⁹, combined with preoperative (chemo)radiotherapy and the ability to more accurately stage rectal cancer with MRI. However, approximately 30% of the patients with rectal cancer treated with a curative intent will develop distant metastasis¹⁰⁻¹². Adjuvant chemotherapy was thought to prevent distant metastasis by eliminating micrometastases and circulating tumour cells. However, the advantageous effect of adjuvant chemotherapy for patients with stage II/III rectal cancer, treated with preoperative (chemo)radiotherapy and TME surgery, is not accepted as a standard in according to ESMO guidelines¹³. In the PROCTOR-SCRIPT trial, a multicentre randomized phase III trial, patients were randomized between adjuvant chemotherapy or observation in patients with (y)pTNM stage II-III rectal cancer treated with preoperative (chemo)radiotherapy and TME surgery. This study showed no survival benefit for patients with (y)pTNM stage II-III rectal cancer treated with adjuvant chemotherapy compared to observation¹⁴. In order to provide robust and stable evidence¹⁴ for the use of adjuvant chemotherapy in patients with locally advanced rectal cancer, a meta-analysis based on individual patient data was performed in this thesis. Furthermore, accumulating evidence suggests a more important role for preoperative chemo radiation therapy (CRT) compared with postoperative CRT in rectal cancer patients^{11,15}. Trials with intensified preoperative treatment, such as the RAPIDO trial, are in progress, and results

are awaited ¹⁶. Furthermore, in patients with locally advanced rectal cancer receiving preoperative chemo radiation a complete pathological response has been observed in 20-30%, consequently there is an emerging role for watch-and-wait strategies as introduced by Habr-Gama ¹⁷. However, more data and long term outcomes are needed before this organ-preservation strategy could be incorporated safely. Therefore, The European Registration of Cancer Care, and the Cahmpalimaud foundation has initiated the International Watch and Wait Database to collect uniform data ¹⁸.

Currently, in contrast to colon cancer for rectal cancer, there are no molecular markers for rectal cancer that evaluate, whether a patient benefit from preoperative treatment, predict response to (chemo)radiotherapy or whether a tumour will metastasize.

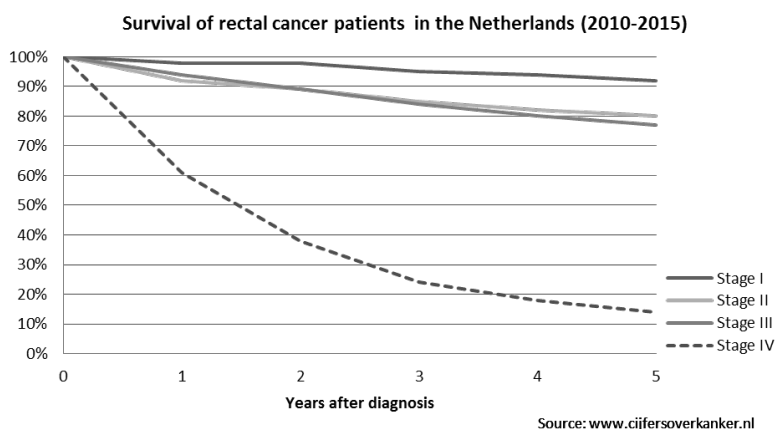
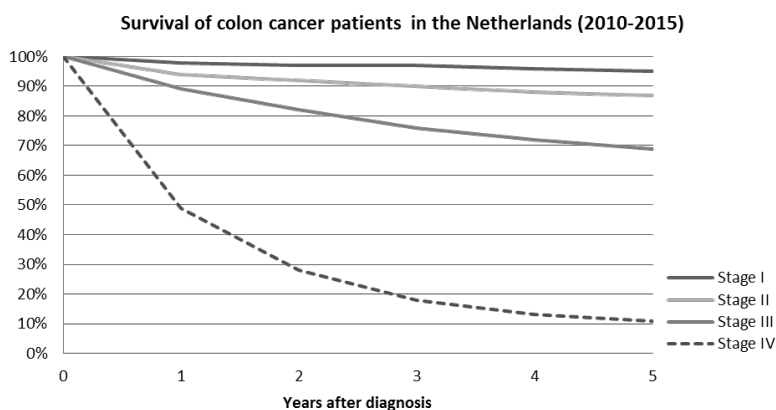


Figure 1: Survival curves. Upper panel shows survival of colon cancer patients stratified by disease stage. Lower panel shows survival of rectal cancer patients stratified by disease stage.

PROGNOSTIC AND PREDICTIVE BIOMARKERS IN CRC

Treatment choices are mainly influenced by the TNM classification, which provides an estimation of the clinical prognosis and creates uniformity in the diagnosis of oncologic diseases^{19,20}. Although, outcome among patients with the same tumour stage differs². Insight into the biological diversity of CRCs in relation to clinical features is needed, to ultimately find the right equilibrium in the treatment to avoid mortality and morbidity and prevent over- and under treatment.

Biomarkers are biological entities that can be measured, for example in blood or tumour tissue, to be used as indicators of pathological processes. Investigating biomarkers that reflect tumour growth and metastatic potential can provide information on the clinical outcome, based on the underlying biological mechanism. The detection of prognostic and predictive biomarkers has become a crucial part of CRC research. Despite encouraging preliminary data, so far the use of biomarkers in clinical practice is very limited. In CRC, only a few biomarkers are used in daily clinical practice, such as *RAS/RAF* and microsatellite status. For example, it has been demonstrated that *RAS* mutations were found in patients who were resistant to monoclonal antibodies targeting the epidermal growth factor receptor²¹. A second well known example is microsatellite instability (MSI), which is without doubt the single most informative genetic characteristic in early stage colon cancer. In contrast to colon cancer, the implications of a MSI tumour located in the rectum remain undefined. Besides the fact that MSI is a hallmark of hereditary non-polyposis colorectal cancer (HNPCC), MSI is found in approximately 15% of the sporadic CRC tumours²². In addition, accumulating evidence advocates that deficient mismatch repair mechanism, especially in early-stage colon cancer, is associated with a clinical prognostic advantage²³⁻²⁵, in comparison with microsatellite stable (MSS) colon tumours. In contrast, an adverse prognostic effect of MSI was observed in metastatic CRC²⁶. On the predictive value of MSI regarding the response to 5-fluorouracil (5-FU), although with conflicting results,^{25,27-29} accumulating preclinical and clinical evidence reports a resistance to 5-fluorouracil (5-FU), in patients with deficient MMR tumours^{24,25,30,31}.

SOURCES OF BIOMARKERS IN CRC

Tumour-immune interactions

Molecular mechanisms responsible for tumour genesis are likely to influence clinical outcome. In 2000, it has been proposed that six biological alterations must be acquired during the multistep development of cancer³². These well-known six hallmarks of cancer consist of: sustaining proliferative signalling, activating tissue invasion, evading growth

suppression and metastasis, enabling replicative immortality, inducing angiogenesis, and resisting apoptosis. After the recognition of the importance of tumour microenvironment, additional hallmarks were added in 2011 of which evasion of the immune recognition was one of these emerging hallmarks³³. The concept of tumour immune-editing, in order to escape the host defence immunity is currently widely accepted³⁴. A well described mechanism, in the escape from the host immune recognition and destruction is complete loss or downregulation of classical HLA class I molecules. Downregulation or complete loss of HLA class I diminishes tumour-associated antigen presentation on the cell membrane. Consequently, cytotoxic T-cells recognition and destruction of tumour cells is minimized^{35,36}. Another mechanism in escaping the anti-tumour immune response, could be *de novo* expression of non-classical HLA class I proteins on the cell surface, such as HLA-G a molecule with important immunomodulatory properties. HLA-G is rarely expressed in non-pathological conditions, other than in immune privileged sites, such as placenta tissue, where it is involved in fetal immune tolerance towards the maternal immune system^{37,38}. Alternative splicing of the primary HLA-G transcript has been described in literature, resulting in seven HLA-G isoforms: four membrane bound (HLA-G1, G2, G3 and G4) and three soluble isoforms (HLA-G5, G6 and G7)³⁹. Furthermore, HLA-G expression in a *de novo* matter has been reported in human tumour cells, including CRC⁴⁰⁻⁴². The influence of the tumour-driven *de novo* expression of HLA-G in escaping immune surveillance is by interaction with inhibitory receptors on T lymphocytes and natural killer (NK) cells⁴⁰, in other words HLA-G functions as an immune checkpoint inhibiting antitumor responses. This could explain why expression of the HLA-G protein on tumour cells might be associated with higher tumour grade and adverse prognosis⁴³. Therefore, HLA-G has been proposed as a potential target for immunotherapy strategies⁴⁴. However, it should be noted that discrepancies among and within different tumour types were reported. For, CRC, HLA-G expression, detected with immunohistochemistry (IHC), varies from 20-72%^{44,45}. IHC is a widely accepted technique, although remains controversial in detecting HLA-G protein expression^{46,47}. To firmly evaluate HLA-G protein expression additional molecular and biochemical analysis are essential. Thereby, HLA-G protein expression should be investigated in patient derived samples, rather than (cancer) cell lines. In this thesis, HLA-G expression was intensively investigated in both CRC cell lines and patient derived samples. Moreover, different biochemical techniques to detect HLA-G were used and results will be compared in order to firmly evaluate whether or not results obtained by IHC will be reliable and if HLA-G indeed plays an important role in CRC.

Tumour genetics and epigenetics

Currently, the first genetic biomarkers are used clinically, such as *RAS/RAF* and MSI status. In the current guidelines it has been recommended to determine *RAS* and *BRAF*

mutation status in patients with irresistible CRC metastasis. Since patient with *BRAF* mutated tumours do not benefit from anti-epidermal growth factor receptor (EGFR) treatment⁴⁸. In addition, in patients with wild-type *RAS/BRAF* metastasized colon cancer, anti-EGFR therapy is only recommended in colon cancer patients with left-sided primary tumours^{49,50}.

As earlier mentioned, approximately 15% of the sporadic stage II-III CRC has MSI²² and in addition MSI tumours have distinct features such as a more proximal localization, higher grade, a mucinous histology with tumour infiltrating lymphocytes and the presence of a *BRAF* mutation. Furthermore, a prognostic advantage has been observed for MSI tumours²³⁻²⁵. Currently, accumulating evidence illustrates the significance of determining MSI in colon cancer. Besides a prognostic effect, MSI status is predictive of response to adjuvant chemotherapy. For example, in patients with high-risk stage II colon cancer with MSI tumours, no beneficial effect of adjuvant chemotherapy has been observed, indicating that these patients should not be treated with 5-FU-based adjuvant chemotherapy^{25,51,52}. Therefore, the routine screening for deficient mismatch repair (MMR) mechanisms in patients with newly diagnosed CRC has been supported by the guidelines from American Society of Clinical oncology (ASCO), the European Society for Medical Oncology (ESMO) and has been implemented in the most recent edition of the TNM staging classification (eight edition, 2017)⁵³⁻⁵⁵. In contrast to colon cancer, the role of a MSI in rectal cancer remains undefined. The long-term prognosis of MSI in sporadic rectal cancers has not been well-established in large patient cohorts, although it may be highly relevant to enable the implementation of personalized treatment strategies driven by biomarkers. Furthermore, an increased radio-sensitivity in MSI tumours has been suggested based on *in vitro* experiments and in small patient series^{56,57}. Accordingly, the clinical significance of MSI in rectal cancer needs to be evaluated in a large rectal cancer cohort.

Interestingly, MMR germline mutations are found in patients with HNPCC, although in sporadic CRC MSI results most frequently from inactivation of the *MLH1* gene by hypermethylation of CpG islands in the promoter region^{58,59}. This example illustrates the important role of epigenetics in carcinogenesis. Epigenetics has become a recent focus in cancer research. Besides hypermethylation, genome-wide DNA hypomethylation is an crucial epigenetic alteration in cancer too. In CRC, hypomethylation is considered as an early event in the carcinogenesis and thereby contributing to genomic instability^{60,61}. To indirectly measure global hypomethylation, the methylation status of long interspersed nucleotide element (LINE-1) repeats can be used as surrogate marker⁶². LINE-1 repeats make-up approximately 17% of the human genome and are present on most of the chromosomes⁶³. Tumour LINE-1 methylation status is intensively

studied and a decrease of LINE-1 methylation has been observed in almost all human malignancies^{64,65}. LINE-1 hypomethylation in CRC is thought to be associated with an adverse prognosis, which suggests a role for LINE-1 as prognostic biomarker⁶⁶. In the current available literature tumour LINE-1 methylation status has been related to clinical outcome in CRC. However, LINE-1 methylation status was predominantly investigated in study cohorts consisting of rectal and colon cancer patients together. Compelling evidence illustrates that rectal cancers biologically differ significantly from colon cancer^{3,4}. For rectal cancer it has been demonstrated by Benard *et al.* that LINE-1 hypomethylation was associated with an unfavourable survival and higher tumour recurrence rates, in early stage⁶⁷. Large patient studies on exclusively patients with early stage colon cancer are not available in the current literature. Therefore, studies investigating the prognostic role of tumour LINE-1 methylation level in stage II colon cancer specifically are needed. In this thesis we aimed to investigate the prognostic role of tumour LINE-1 methylation level in stage II colon cancer, in order to identify high-risk patient to ultimately avoid over-, or under treatment.

OUTLINE OF THE THESIS

Potential relevant biomarkers can be found at different levels in tumour development and disease progression. This thesis is divided into three overarching parts. Colorectal cancer was studied from a population-based perspective (part I) to a molecular level, detailed as protein expression (part II) and (epi)genetics (part III), as indicated in Figure 2. In part I the use of adjuvant chemotherapy in patients with locally advanced rectal cancer, who underwent resection after preoperative (chemo)radiotherapy, was evaluated in a meta-analysis based on individual patient data. Since four randomized controlled trials individually did not end the ongoing debate about the role of adjuvant chemotherapy^{14,68-70}. In part II the ability by tumour cells to evade the immune recognition was studied, especially the role of the non-classical HLA class I molecule HLA-G was studied in detail. In part III, an epigenetic biomarker, LINE-1 methylation level, was studied in a dedicated stage II colon cohort. In addition, an established genetic biomarker for colon cancer, MSI, was studied in a large rectal cancer cohort.

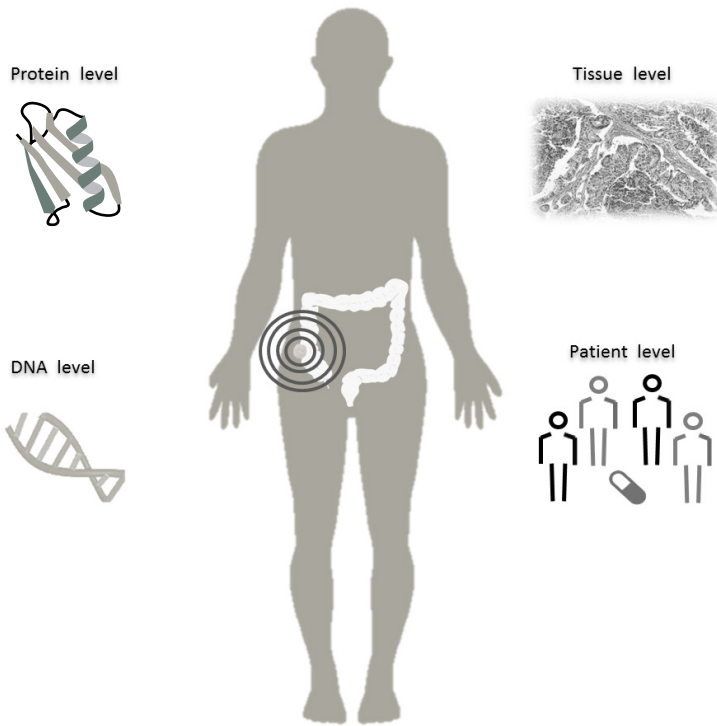


Figure 2: Global overview of different levels involved in colorectal cancer formation and disease progression investigated in this thesis.

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