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**Telomeres, telomerase and colorectal cancer**

Bertorelle R *et al*.Telomeres, telomerase and colorectal cancer

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**Abstract**

Colorectal cancer (CRC) is the third most common cancer worldwide and, despite improved treatments, is still an important cause of cancer-related deaths. CRC encompasses a complex of diseases arising from a multi-step process of genetic and epigenetic events. Besides heterogenei**ty** in the molecular and biological features of CRC, chromosomal instability is a hallmark of cancer and cancer cells may also circumvent replicative senescence and acquire the ability to sustain unlimited proliferation. Telomere/telomerase interplay is an important mechanism involved in both genomic stability and cellular replicative potential, and its dysfunction plays a key role in the oncogenetic process. The erosion of telomeres, mainly because of cell proliferation, may be accelerated by specific alterations in the genes involved in CRC, such as *APC* and *MSH2*. Although there is general agreement that the shortening of telomeres plays a role in the early steps of CRC carcinogenesis by promoting chromosomal instability, the prognostic role of telomere length in CRC is still under debate. The activation of telomerase reverse transcriptase (TERT), the catalytic component of the telomerase complex, allows cancer cells to grow indefinitely by maintaining the length of the telomeres, thus favouring tumour formation/progression. Several studies indicate that TERT increases with disease progression, and most studies suggest that telomerase is a useful prognostic factor. Plasma TERT microRNA may also be a promising marker for the minimally invasive monitoring of disease progression and response to therapy.

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**Key words:** Telomere; Telomerase; Telomerase reverse transcriptase; Colorectal cancer; Prognostic marker

**Core tip:** Telomere/telomerase interplay is an important mechanism involved in both genomic stability and cellular replicative potential. Telomere shortening is an early event that contributes to genetic instability, which plays a key role in the early steps of carcinogenesis. The activation of telomerase, which preserves replicative potential by maintaining the length of telomeres, occurs during the adenoma-carcinoma sequence and increases during tumour progression. While the prognostic value of telomere length is controversial, most studies agree that the level of telomerase in tumours represents a useful prognostic marker. Circulating telomerase reverse transcriptase is a promising marker for the minimally invasive monitoring of disease and response to therapy.

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**INTRODUCTION**

Colorectal cancer (CRC) is the third most common cancer worldwide; over 1.2 million new cancer cases and nearly 600000 deaths are estimated to have occurred in 2008[1]. Despite improved treatments, increased awareness and early detection, which have all contributed to prolonged survival, CRC is still an important cause of cancer-related deaths[1]. CRCs encompass a complex of diseases with different molecular pathways and biological characteristics arising from a multi-step process that involves several genetic and epigenetic events[2,3]. The stepwise change in morphology from normal epithelium to carcinoma occurs through a multi-step genetic model with the loss of the functions of tumour suppressor genes, such as adenomatous polyposis coli (*APC*) and TP53, and the gain of the function of oncogenes, such as *KRAS*. Recent genome-wide sequencing analyses have estimated as many as 80 mutated genes in CRC. Although a smaller number of mutations are considered drivers of tumourigenesis, multiple genetic hits are required for tumour onset and progression[4]. Many efforts have been made to identify molecular markers that predict the outcome of CRC patients, and several genetic and epigenetic alterations that are involved in the development of CRC have been proposed as prognostic markers of disease progression; however, no agreement has been reached[5,6]. Besides great heterogeneity of the molecular and biological features, chromosomal instability may play a key role in the early steps of carcinogenesis[7]. Cancer cells may also circumvent replicative senescence and acquire the ability to sustain unlimited proliferation[8]. Telomere/telomerase interplay is an important mechanism involved in the genomic stability and cellular replicative potential, and telomere/telomerase dysfunction has emerged as playing a key role in carcinogenesis. Here, we review the role of telomeres and telomerase in the genesis and progression of CRC.

**TELOMERES AND TELOMERASE**

Telomeres are specialised DNA structures located at the end of chromosomes; they are essential for stabilising chromosomes by protecting them from end-to-end fusion and DNA degradation[9]. In human cells, telomeres are composed of (TTAGGG)n tandem repeats that are associated with the capping proteins TTAGGG repeat binding factor (TRF)1, TRF2, repressor and activator protein 1, TRF1-interacting nuclear protein 2, protection of telomeres 1 (POT1), which constitute the shelterin complex[10]. Telomeres are progressively shortened during each cell division by replication-dependent loss of sequences at the DNA termini, caused by the failure of DNA polymerase to completely replicate the 3' end of chromosomes[11]. When telomeres become critically short (*i.e.*, the Hayflick limit), they are no longer protected by the shelterin complex; at that point they are recognised as DNA double-strand breaks that trigger a DNA damage response (DDR), and the cells undergo replicative senescence and apoptosis[10]*.* If protective mechanisms, such as that of the TP53 protein, are inactive, cells continue to proliferate; the further erosion of telomeres impairs their role in protecting chromosome ends and ultimately causes chromosomal instability[12]. Thus, telomere erosion may play two conflicting roles: tumour suppression by inducing cell death, and tumour promotion by causing genetic instability, a key event in the initiation of carcinogenesis. It has been recently advanced that short telomeres may also affect genome-wide DNA methylation, which may modulate oncogene and oncosuppressor gene expression[13]. However, cell division-associated telomere shortening prevents unlimited cell proliferation and thus tumour development/progression. To escape this proliferation barrier, cells must stabilise their telomeres. Most tumours maintain their ability to grow indefinitely through the inappropriate expression of telomerase, a ribonucleoprotein complex containing an internal RNA component [telomerase RNA (TR), or telomerase RNA component (TERC)] and a catalytic protein with telomere-specific reverse transcriptase activity [telomerase reverse trancriptase (TERT)][14]. TERT which synthesises *de novo* telomere sequences by using TR as a template, is the rate-limiting component of the telomerase complex, and its expression is correlated with telomerase activity[15]. While TR has broad tissue distribution and is constitutively present in normal and tumour cells, expression of TERT, which is usually repressed in normal somatic cells, occurs in germ-line cells and most cancer cells. TERT is essential for unlimited cell growth and thus plays a critical role in tumour formation and progression[16]*.*

Regulation of telomerase operates at several biological levels: transcription, mRNA splicing, subcellular localisation of each component and the assembly of TR and TERT in an active ribonucleoprotein. Transcription of the *TERT* gene is most likely the key determinant in the regulation of telomerase activity; notably, TERT transcriptional activity is specifically up-regulated in cancer cells, but is silent in most normal cells. The *TERT* gene consists of approximately 35 kb DNA and comprises 16 exons and 15 introns. At the transcriptional level, more than 20 transcription factor-binding sites that act as activators or repressors have been identified within the TERT promoter. The cooperation of MYC and SP1 is required for the full activation of the *TERT* promoter, while TP53, through its interaction with SP1, down-regulates TERT. *TERT* is also directly activated by nuclear factor-kB, hypoxia-inducible factor (HIF)-1, and the ETS/MYC complex. The histone methyltransferase SMYD3 also directly contributes to inducible and constitutive TERT expression in normal and malignant human cells. TERT expression is suppressed by the oncosuppressor genes *WT127* and *MEN1,* and through the MAD/MYC and TGF-β/SMAD pathways. The cell cycle inhibitors p16INK4a and p27KIP1 have also been shown to down-regulate TERT expression in cancer cells[17]. Regulation of *TERT* transcription may also involve DNA methylation, because the *TERT* promoter contains a cluster of CpG sites. At the post-transcriptional level, modulation of telomerase may occur by alternative splicings that may be tissue-specific; at least 10 different variants of TERT mRNA have been described, and some of these splicing products may exert a dominant negative function by competitive interaction with components of the telomerase complex[18,19]. Telomerase activity is also controlled through post-translational modifications of the TERT protein. Phosphorylation of the protein at critical sites by the PI3K/AKT kinase pathway seems to be crucial for telomerase activity[20]. Telomere-associated shelterin plays a role in the activity of telomerase; TPP1 is heterodimerised with POT1 and the POT1-TPP1 complex can recruit and stimulate telomerase activity, thereby regulating telomere length through the TPP1-telomerase interaction[21]. Notably, recent studies have suggested that, in addition to maintaining telomere length, TERT is involved in several other cell functions. The expression of TERT increases replicative kinetics[22,23], promotes cell growth under adverse conditions and may also act as an anti-apoptotic agent[24-26]. High levels of telomerase confer resistance to several antineoplastic drugs [27,28].

We direct our attention here to the questions listed in Table 1. The answers to these questions are important in defining the role of telomere/telomerase interplay in the CRC carcinogenesis.

**TELOMERES AND GENETIC INSTABILITY IN THE GENESIS OF COLORECTAL CANCERS**

There are at least two major pathways by which molecular events can lead to CRC; most CRCs (approximately 85% of cases) are characterised by chromosomal instability (CIN), while the other CRCs have a microsatellite instability (MSI) phenotype. CIN is a dynamic process of allelic imbalance at several chromosomal loci, with chromosome amplification and translocation, and it is an efficient mechanism for causing the loss of oncosuppressor genes, such as *APC, TP53,* and *SMAD* family member 2 and 4 involved in the TGF-β signaling pathway, and the activation of oncogenes, such as *KRAS* and *BRAF,* which activate the mitogen-activated protein kinase signalling pathway[29]. The MSI phenotype is generated by a deficient DNA mismatch repair (MMR) system. Alterations to one of the seven known *MMR* genes (*MSH2, MLH1, MSH6, PMS1, PMS2, MSH3*, and *MLH3*) cause unrepaired errors in the nucleotide repeat sequences, known as microsatellites. Methylation of promoters of *MMR* genes, particularly *MLH1*, is the most frequent mechanism for silencing *MMR* genes in sporadic CRCs, which in fact is frequently associated with the GpG island methylator phenotype[4,30]. While the significance of telomere alterations in MSI is unclear, telomere dysfunction may be considered a major driving force in the generation of CIN.

Several studies have demonstrated that telomeres are shorter in CRCs than in the adjacent mucosa(Table 2). While telomere length in somatic cells primarily reflects cellular proliferation, in tumour cells it reflects the balance between cellular proliferation with telomere loss and telomerase activity with *de novo* synthesis of telomeric sequences. Evidence that telomeres are shorter in CRCs than in adjacent mucosa, even in well-differentiated tumours, strongly supports the concept that telomere erosion is a critical initial event in colorectal carcinogenesis. TRF1 is a main negative regulator of telomere length; over-expression of TRF1 in colorectal cells is correlated with shorter telomeres[38]. Telomere shortening in colorectal polyps was recently correlated with large-scale genomic rearrangements[43]. Notably, telomere shortening in adenomas is not correlated with polyp size. In addition, the great differences in telomere length (differences of up to 4.6 kb between normal mucosa and polyps) are too large to be explained by replicative telomere erosion alone. Thus, the telomere length in CRC may reflect the short telomere length in the cells that originated the tumours, and telomere erosion may even precede the colorectal adenomagenesis[43]. Because this pattern has been observed in colorectal adenomas from patients with familial adenomatous polyposis, it remains to be established whether it also occurs in sporadic CRCs.

Approximately 15% of CRCs present MSI, whereas the *TP53* gene is the known major genetic alteration in CRCs with chromosomal instability and stable microsatellites (MSS)[5,44]. A study performed on a large number of CRCs demonstrated that both MSI and MSS tumours have shorter telomeres compared with adjacent mucosa, but MSI cancers have shorter telomeres than MSS cancers[41]. This result matches another study[44]*.* The MSI pathway involves the failure of the MMR system[46], which maintains genetic stability by repairing DNA replication errors and preventing chromosomal recombinations; a deficiency in MMR helps cells overcome cellular crises caused by the critical shortening of telomeres[47]. Thus, cells from MSI cancers may undergo more replicative cycles and more pronounced shortening of telomeres before stabilising compared with cells from MSS cancers. The difference is particularly great and significant when MSI tumours are compared with MSS tumours carrying the wild-type *TP53* gene. Notably, MSS tumours with a mutated *TP53* gene have slightly shorter telomeres than MSS tumours with the wild-type *TP53* gene do. In cells with mutated *TP53*, telomeres may protract their shortening with cell proliferation. However, TP53 is a well-known negative regulator of the *TERT* promoter, and mutated TP53 protein may also result in TERT activation, so telomere stabilisation may occur earlier than it does in MSI tumours[41].

The down-regulation of MSH2 is associated with greater telomere shortening than in control cells; thus MSH2 deficiency may accelerate telomere shortening[48]. It is worth noting that the leukocyte telomeres of patients with Lynch syndrome, a hereditary CRC syndrome caused by germline mutations in *MMR* genes are shorter than those of age-matched controls[49]. Whether a shorter telomere length in leukocytes is a risk factor for CRC or a consequence of either disease treatment or disease burden is a controversial question[50-52], but there is general agreement that telomere shortening is an early event in colorectal carcinogenesis, even in sporadic CRC (Figure 1). Activation of the DDR is almost universal during the earliest stages of carcinogenesis[53,54]. A recent study suggested that telomere length is inversely correlated with activation of the DDR pathway, and telomere fusion may leads to general genomic instability[40].

While there is general agreement that telomere shortening, which is mainly caused by high proliferation of preneoplastic lesions and most likely accelerated by alterations in genes such as *APC* and *MSH2*, is an early event in the CRC carcinogenesis, there is no agreement concerning the role of telomere length as a marker of disease progression. Only a few studies report that telomeres are longer in late stage cancer than in preneoplastic lesions and/or early neoplastic stages; the activation of telomerase and/or high levels of telomerase expression may explain the increase in telomere length with disease progression[37,38]. However, other studies have not indicated any correlation between telomere length and tumour stage or grade (Table 2). Telomere lengths may stabilise with tumour progression because of increased telomerase activity that compensates for replicative telomere loss[41,55].

**TELOMERASE AS A MARKER OF DISEASE PROGRESSION IN COLORECTAL CANCER**

Two main strategies are used to estimate telomerase levels: quantification of TERT mRNA and quantification of telomerase activity. The telomerase level, even in telomerase-positive tumour cells, is estimated to be relatively low (approximately 100 molecules per cell), so its detection, either as mRNA or activity, requires methods based on polymerase chain reaction (PCR) amplification. In general, all quantitative data acquired with real-time PCR must be normalised by a housekeeping gene. The ideal housekeeping gene should not vary with disease progression. The glyceraldehyde 3-phosphate dehydrogenase gene, which is often employed as housekeeping gene, is activated by HIF and is thus expressed at higher levels in advanced disease than in tumours at early stages. Other genes, such as thehypoxanthine-guanine phosphoribosyltransferase 1 (*HPRT1*) gene, which does not vary with tumour stage[56], allow a more reliable estimation of TERT levels. In CRC, a study by real-time PCR with *HPRT1* as a housekeeping gene demonstrated that there is a good relationship between the levels of all TERT transcripts and the full-length TERT transcript; in addition, levels of TERT mRNA correlated with telomerase activity, as estimated with a telomere repeat amplification protocol (TRAP) assay[54]. Although there are no clinically approved telomerase assays, several promising approaches have recently been published[57].

There is general agreement that TERT levels and telomerase activity increase with the adenoma-carcinoma sequence[60,64, 70], and are higher in CRCs than in adjacent non-cancerous mucosa (Table 3). Normal adjacent mucosa may have some detectable TERT mRNA and telomerase activity, mainly because of intestinal crypt basal cells[55,58]. These findings strongly support the hypothesis that telomerase activation is subsequent to telomere erosion (Figure 1).

Most studies have demonstrated that TERT expression and/or telomerase activity increase with tumour progression (Table 3 and Figure 2A). Well-differentiated and moderately differentiated tumours have significantly lower TERT levels than poorly differentiated tumours do, and late-stage tumours (Dukes C and D) show higher telomerase activity than early-stage tumours[63,67].Only a few studies have found no correlation between levels of telomerase activity, as assessed by the semi-quantitative TRAP assay, and tumor progressio[38,58,61]*.* Unlike telomere length, levels of telomerase expression/activity do not correlate with MSI status and increase with disease progression in both MSI and MSS tumours[68,73]. The finding that TERT mRNA is higher in tumours bearing *TP53* mutations[66] may support the hypothesis that high TERT expression is a marker of poor outcome and poor response to therapy[27,73].

**TELOMERASE, BUT NOT TELOMERES, MAY ACT AS A PROGNOSTIC FACTOR IN COLORECTAL CANCERS**

Pathologic tumour staging remains a key determinant of CRC prognosis and treatment. Invasive cancers are confined within the wall of the colon (stages I and II), but if untreated they spread to regional lymph nodes (stage III) and then metastasise to distant sites (stage IV). Although radical resection and adjuvant therapy are effective curative treatments, the risk of disease recurrence cannot be foreseen, even among patients at the same tumour stage. Although 5-fluorouracil-based adjuvant chemotherapy is the standard care for stage III patients, the role of adjuvant therapy for stage II is still debated. The controversial results obtained in various studies[74-78] may reflect the molecular and biological heterogeneity of CRC and highlight the need for definitive prognostic markers able to stratify patients.

While most studies do not confirm the prognostic role of telomere length (Table 2), there is general agreement that high levels of TERT and /or telomerase activity are associated with poor prognosis (Table 3) Only two studies do not confirm the prognostic value of TERT[72] or telomerase activity[62]. High levels of TERT mRNA and/or telomerase activity have been associated with worse overall survival (OS) and this negative prognostic effect is independent of pathologic stage. In particular, over a median follow-up of 70 mo, patients with high levels of TERT mRNA (above the median) had approximately double the risk of death compared with patients with low levels of TERT (below the median) did[73].Only two studies analysed stage II patients in detail. In one study, in which telomerase activity was determined with TRAP assay, patients with telomerase-positive CRCs had longer disease-free survival (DFS) than did patients with telomerase-negative tumours[62]. In the second study, TERT levels estimated using real-time PCR significantly stratified stage II patients; stage II patients with high TERT levels showed significantly worse median OS and DFS than patients with low TERT levels did[73]*.*

In recent years, great efforts have been made to identify markers for minimally invasive early diagnosis and/or monitoring of disease. The expression of epithelial cell adhesion molecules has been used primarily to detect CRC cells in the hematopoietic milieu, and the detection of circulating cancer cells is a promising approach, although its diagnostic/prognostic role needs to be established[79].The detection of cancer-related RNA molecules in plasma has recently been proposed as a marker of cancer onset and outcome, and ongoing studies indicate that circulating microRNAs may be biomarkers for the early detection of CRC[80,81]*.* Within this framework, recent studies suggest that cell-free circulating TERT mRNA is also a potential marker of disease.

Transcripts of TERT have been detected in the plasma of patients with different tumours, including CRC[82,83]. In a series of CRCs (stage I to stage IV), the TERT mRNA levels in plasma were related to those in tumours[55] (Figure 2B). In addition, while 95% of patients with tumours had detectable cell-free circulating TERT, aged-matched controls were negative in almost all cases[55]. This finding suggests that TERT levels in plasma reflect those in tumours. Very promising findings have been reported in patients with rectal cancer who underwent chemoradiotherapy (CRT) prior to surgery; plasma TERT was significantly decreased in patients who underwent a complete pathologic response, but remained unchanged or increased in patients who did not respond to CRT[84] (Figure 2C). These findings also suggest that circulating TERT is a useful marker for monitoring the response to therapy. However, further studies with a prospective design and with a large sample sizes are required to clearly define the prognostic role of telomerase in CRC patients and to ascertain the cut-off values and reliability of circulating TERT as a marker for monitoring disease outcome and response to therapy.

**CONCLUSION**

Besides extensive heterogeneity in the molecular and biological features of CRC, chromosomal instability plays a key role in the early steps of carcinogenesis. The majority of studies agree that telomere shortening is an early event in the oncogenetic process and that telomere erosion leads to genetic instability. Telomerase, which maintains telomere length and preserves the cell's replicative potential, is activated during the adenoma-carcinoma sequence and its activity increases during tumour progression.

While most studies do not confirm the prognostic role of telomere length, there is general agreement that high levels of TERT and/or telomerase activity are associated with poor prognosis. Emerging data also suggest that circulating TERT levels reflects tumour TERT levels. Overall, there is sufficient evidence to indicate that telomerase is a useful marker for monitoring and predicting disease outcome. A caveat to the use of telomerase as a marker is the availability of simple and reliable assays to quantify telomerase expression and/or activity. The use of reliable assays will allow researchers to compare data and to define useful cut-off values to discriminate between patients at low and high risk of disease progression.Further studies with a prospective design and large sample sizes are required to clearly define the prognostic role of telomerase and to acertain its reliability as a circulating biomarker for the minimally invasive monitoring of disease and the response to therapy.

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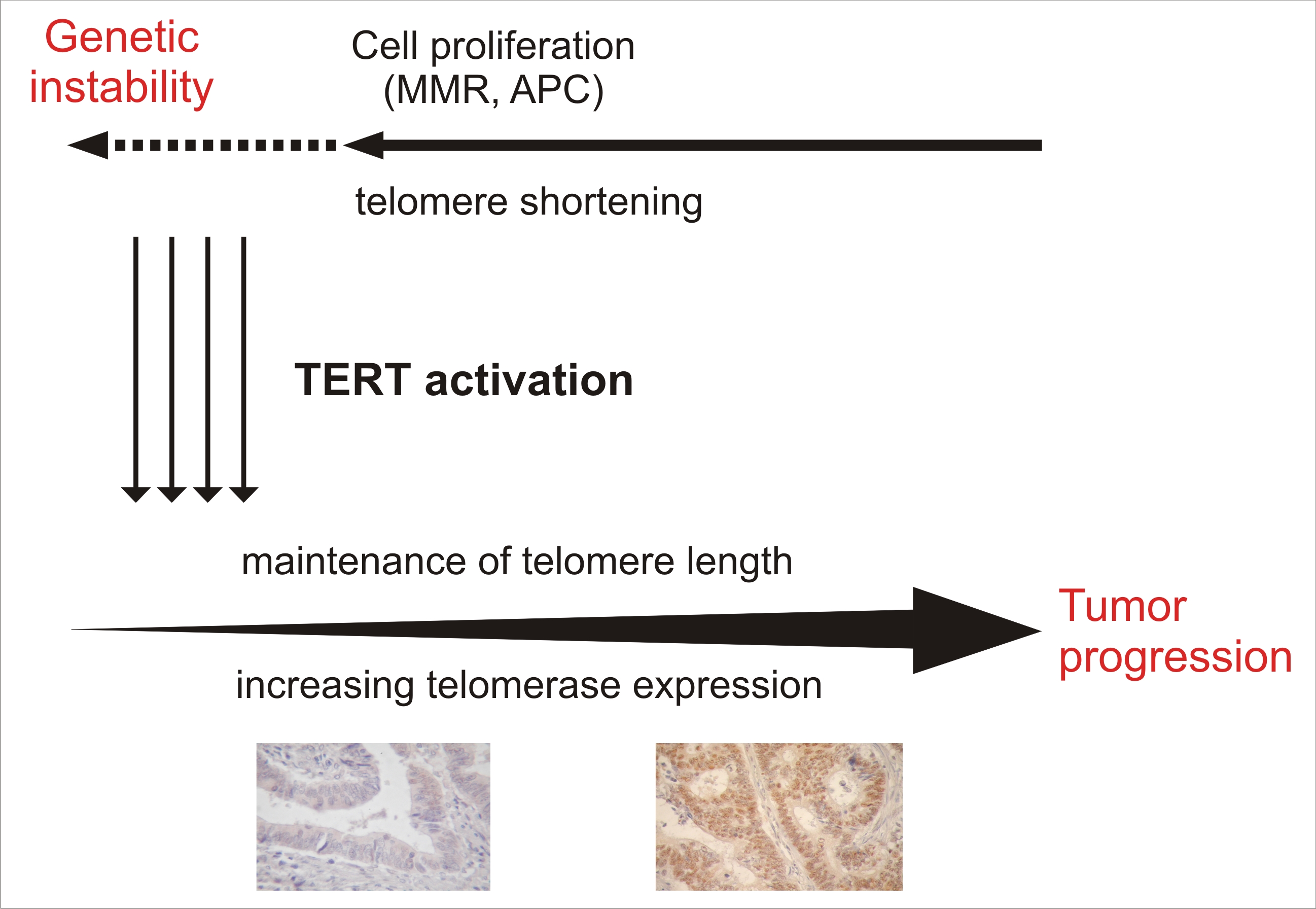
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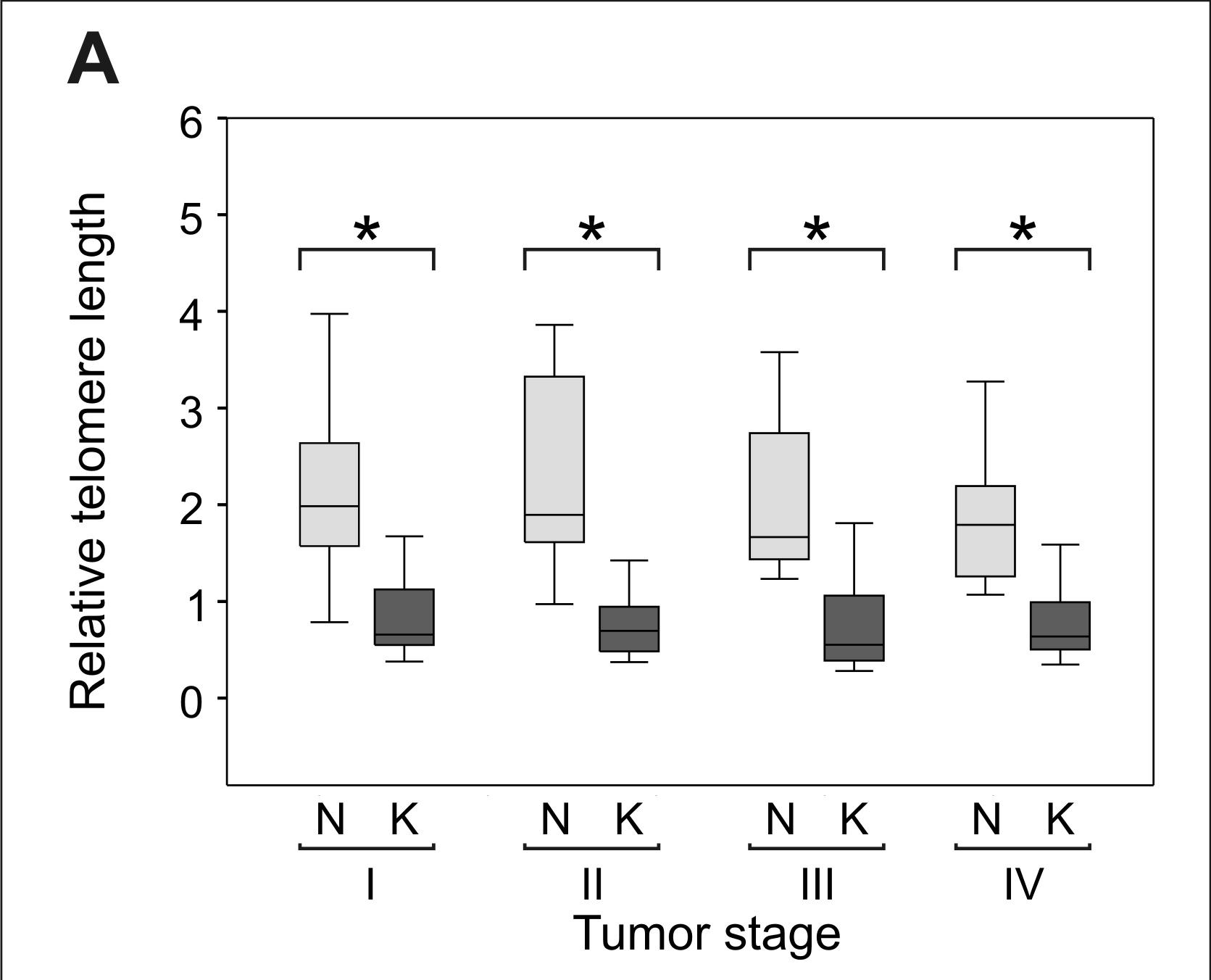
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**Legends to Figures**



**Figure 1 Model of telomere/telomerase interplay in the carcinogenesis of colorectal cancer.** Telomere shortening is mainly caused by cell proliferation in preneoplastic lesions. Erosion of telomeres may be accelerated by mutations in specific genes, such as the adenomatous polyposis coli (*APC*) gene or DNA mismatch repair (*MMR*) system genes. The activation of telomerase reverse transcriptase (TERT), the catalytic unit of the telomerase, occurs during the adenoma-carcinoma sequence; TERT and telomerase activity levels increase with tumour progression. Inserts: Immunohistochemical analysis of TERT expression in stage I (left) and stage IV (right) tumours. Mayer's haematoxylin counterstaining; original magnification × 20.

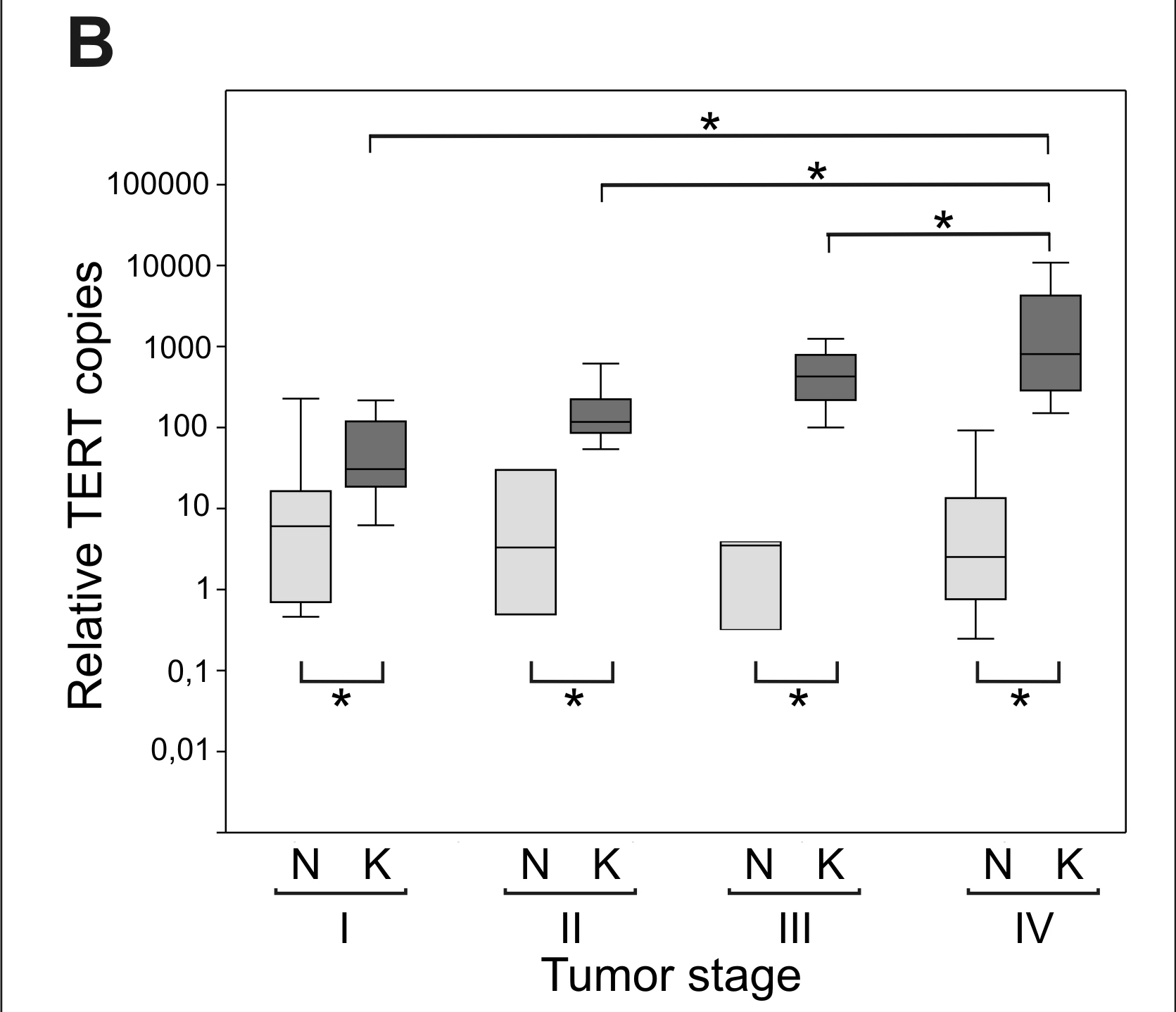


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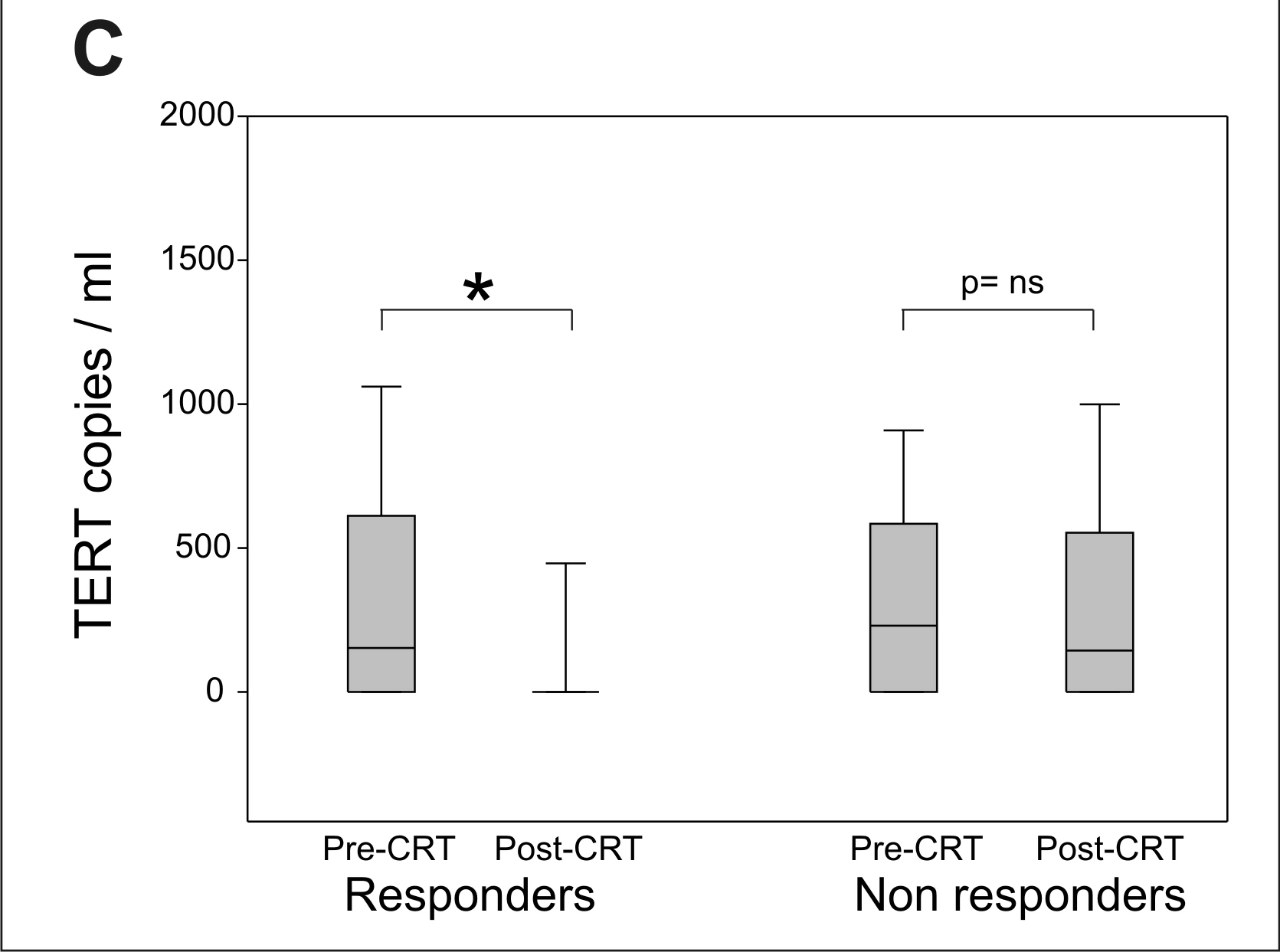
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**Figure 2 Representative panels of telomere length and** **telomerase reverse transcriptase levels.** A: Relative telomere length in tumours (K) and adjacent mucosa (N) according to tumour stages I (30 samples), II (45 samples), III (29 samples), and IV (29 samples). The cases included those reported in Rampazzo *et al*[41]. Telomere length was significant shorter in tumours than in adjacent mucosa (b*P* < 0.01 *vs* tumours in adjacent mucosa) at all tumour stages, but telomere lengths did not significantly differ with tumour stage. Relative telomere length was estimated using real-time polymerase chain reaction (PCR)[41]; B: Telomerase reverse transcriptase (TERT) levels in tumours (K) and adjacent mucosa (N) according to tumour stages I (K: 25 samples, N: 17 samples), II (K: 35 samples; N: 10 samples), III (K: 15 samples; N: 5 samples), and IV (K: 30 samples; N: 22 samples). The cases included those reported in Terrin *et al*[55]. TERT levels were significantly higher in tumours than in adjacent mucosa and significantly increased (b*P* < 0.01 *vs* tumours in adjacent mucosa) with tumour stage. TERT levels were estimated using real-time PCR [41,55]; C: Plasma TERT levels before and after the chemoradiotherapy prior to surgery in responders (35 samples) and non-responders (42 samples) with rectal cancer. The cases included those reported in Pucciarelli *et al*[85]. TERT levels in plasma were estimated using real-time PCR[85]. Boxes and whiskers: 25th to 75th and 10th to 90th percentiles, respectively; the median is the central line in each box.

**Table 1 Telomeres and telomerase: outstanding questions regarding their role in the genesis and progression of colorectal cancer**

Is the shortening of telomeres an early or late event in colorectal carcinogenesis?

Does telomere shortening play a role in genomic instability?

Do telomere lengths correlate with telomerase expression/activity?

Do telomere lengths correlate with disease progression?

Do levels of telomerase expression/activity increase with disease progression?

Do telomere and/or telomerase act as prognostic markers for disease outcome?

**Table 2 Telomere lengths and colorectal cancer**

|  |  |  |
| --- | --- | --- |
| **Reference** | **Cases** | **Main findings** |
| Hastie *et al*[31]*,* 1990 | 23 (20 CRCs, 3 adenomas)  and patient-matched non-cancerous mucosa  (frozen samples) | TL  Decrease with age in noncancerous cells (33bp per year)  Shorter in CRCS and adenomas than in normal mucosa |
| Engelhardt *et al* [32] , 1997 | 80 (50 CRCs, 20 polyps, 10 colitis) and CRC patientmatched noncancerous mucosa  (frozen samples) | TL  Shorter in CRCS than in normal mucosa  Shorter in CRCS than in polyps and colitis  Longer in latestage cancer with higher telomerase activity  Do not differ between colon and rectum cancer |
| Takagi *et al*[33]*,* 1999 | 61 CRC (including 12 nonulcerating and 39 ulcerating tumours, according to Borrmann's classification) and patientmatched noncancerous mucosa  (frozen samples) | TL  Shorter in nonulcerating CRCS than in normal mucosa  Shorter in nonulcerating than in ulcerating tumours  Not correlated with tumour stage or grade  Not correlated with telomerase activity |
| Katayama *et al*[34]*,* 1999 | 35 (26 CRCs, 9 polyps)  (frozen samples) | TL  Do not differ between CRCS and polyps |
| Nakamura *et al*[35]*,* 2000 | 124 CRC and patientmatched noncancerous mucosa  (frozen samples) | TL  Shorter in CRCS than in normal mucosa  Decrease with age in both cancer and noncancerous cells (44 and 50 bp/year) |
| Plentz *et al*[36]*,* 2003 | 10 (adenomacarcinoma transition)  (paraffinembedded samples) | TL  Shorter in highgrade dysplastic areas than in the surrounding adenoma |
| Gertler *et a*l[37], 2004 | 57 CRC and patientmatched noncancerous mucosa  (frozen samples) | TL  Shorter in CRCS than in adjacent mucosa  Decrease with age only in noncancer cells (19 bp per year)  Correlate with tumour stage, being longer in advanced tumours  Correlate with tert mrna levels  Lead to a poor prognosis if TL cancer/ TL noncancer > 0.9  Do not differ between colon and rectum cancer |
| GarciaAranda *et al*[38]*,* 2006 | 91 CRC (23 rightcolon, 13 leftcolon, 55 rectum) and patientmatched noncancerous mucosa  (frozen samples) | TL  Shorter in crc than in adjacent mucosa  Shorter in rightcolon cancers than in tumours located in other sites  Shorter in poorly differentiated tumours  Tend to be longer in telomerasepositive CRCS  Have prognostic value (longer telomeres: poor clinical outcome)  Correlated with the expression of TRF1 protein |
| O’Sullivan *et al*[39]*,* 2006 | 38 (26 adenomas, 12 CRCs)  (paraffinembedded samples) | TL  Shorter in adenomas than in adjacent and distant mucosa  Similar in CRCS and adjacent and distant mucosa |
| Raynaud *et al*[40]*,* 2008 | 15, each case with normal mucosa, lowgrade dysplasia, highgrade dysplasia and carcinoma  (paraffinembedded samples) | TL  Shorter in lowgrade and highgrade dysplasia than in carcinoma  Inversely correlated with activation of the DDR pathway |
| Rampazzo *et al*[41]*,* 2010 | 118 CRC (53 rightcolon, 30 leftcolon, 35 rectum) and patientmatched noncancerous mucosa  (frozen samples) | TL  Shorter in CRCS than in adjacent mucosa  Shorter in rightcolon cancers than in tumours located in other sites  Shorter in MSI than in mss tumours  Decrease with age only in noncancer cells  Not correlated with tumour stage or grade  Not correlated with tert mRNA levels |
| Valls *et al*[42]*,* 2011 | 147 CRC and patientmatched noncancerous mucosa  (frozen samples) | TL  Shorter in CRCS than in adjacent mucosa  In cancer correlate with TL in normal mucosa  Do not differ between colon and rectum cancer  Not correlated with tumor stage  Have prognostic value (TL cancer/ TL noncancer ≤ 1: higher OS) |
| Roger *et al*[43]*,* 2013 | 135 (85 polyps from 10 patients with FAP, 50 CRCs)  (frozen samples) | TL  Shorter in polyps than in normal mucosa  Correlated with genomic rearrangement in polyps  Independent of adenoma size  In polyps may reflect the TL of the originating cells |

TL: Telomere lengths; CRC: Colorectal cancer; DDR: DNA damage response; OS: Overall survival; FAP: Familial adenomatous polyposis.

**Table 3 Telomerase as a marker of disease in colorectal cancer**

|  |  |  |
| --- | --- | --- |
| **Reference** | **Cases** | **Main findings** |
| Engelhardt *et al*[32]*,* 1997 | 80 (50 CRCs, 20 polyps, 10 colitis) cancerous and 50 CRC patientmatched noncancerous mucosa specimens | Telomerase activity  Absent in normal tissues  Higher in CRCS than in nonneoplastic lesions  Higher in latestage than in earlystage tumours |
| Tatsumoto *et al*[58]*,* 2000 | 100 CRC and patientmatched noncancerous mucosa specimens | Telomerase activity  Higher in CRC than in adjacent noncancerous mucosa  detectable in adjacent noncancerous mucosa derived from intestinal crypt basal cells  Not correlated with CRC stage or grade has prognostic value for OS and DFS (high telomerase activity: poor prognosis) |
| Niiyama *et al*[59], 2001 | 140 CRC and patientmatched noncancerous mucosa specimens;  20 adenomas | TERT mRNA and telomerase activity  Higher in CRCs than in adenomas  Higher in adenomas than in normal mucosa |
| Naito *et al*[60]*,* 2001 | 66 (50 adenomas, 6 mucosal carcinomas, 10 invasive carcinomas) specimens | Positive correlation between TERT mRNA and telomerase activity  TERT levels increase with adenomacarcinoma sequence |
| Gertler *et al*[61]*,* 2002 | 57 CRC and patientmatched noncancerous mucosa specimens | Both CRC and adjacent noncancerous mucosa are positive for TERT  TERT levels lower in tumours than in noncancerous mucosa in most cases  TERT levels not correlated with tumour stage  TERT has prognostic value for OD and DFS (high telomerase activity: poor prognosis) |
| Kawanishi-Tabata *et al*[62]*,* 2002 | 122 CRCs, stage II  (52 colon, 70 rectum) | 80% of CRC are telomerasepositive  Higher percentage of telomerasepositive tumours in the colon than in the rectum  High telomerase activity: Good prognosis |
| Ghori *et al*[63]*,* 2002 | 30 CRCs and 20 patientmatched noncancerous mucosa specimens | Telomerase activity  Higher in CRCs than in adjacent noncancerous mucosa  Correlated with Duke's stage |
| Boldrini *et al*[64]*,* 2002 | 36 CRC and patientmatched noncancerous mucosa specimens,  8 adenomatous polyps,  9 dysplastic polyps | Telomerase activity  Absent in normal mucosa and adenomas  Higher in CRCs than in dysplastic polyps  Higher in latestage than in earlystage tumours |
| Malasaka *et al*[65]*,* 2004 | 41 CRC and patientmatched noncancerous mucosa specimens | Telomerase activity  Present in 83% of CRCs  Absent or at very low level in normal mucosa  Higher in metastatic tumours |
| Boldrini *et al*[66]*,* 2004 | 43 CRCs | TERT levels and telomerase activity higher in tumours with mutated *TP53* |
| Sanz-Casla *et al*[67]*,* 2005 | 103 CRCs | Telomerase activity increases with tumour progression (Duke's stage)  Higher percentage of telomerasepositive tumours in the colon than in the rectum  Telomerase activity has prognostic value for DFS (high telomerase activity: poor prognosis) |
| Garcia-Aranda *et al*[38]*,* 2006 | 91 CRC and patientmatched noncancerous mucosa specimens | Telomerase activity  Present in 81% of CRCs  Present at very low levels in 15% of normal samples  Not correlated with tumour progression  No prognostic value |
| Vidaurreta *et al*[68]*,* 2007 | 97 CRCs | Telomerase activity  present both in MSI and MSS tumours  has prognostic value for OS ( high telomere activity: poor prognosis ) |
| Bautista *et* *al*[69]*,* 2007 | 108 rectal cancer and patientmatched noncancerous mucosa specimens | Telomerase activity  Higher in rectal cancer than in normal mucosa  Not correlated with tumour stage and grade  Has prognostic value for DFS and OS |
| Terrin *et al*[55]*,* 2008 | 85 CRC and 42 patientmatched noncancerous mucosa specimens,  49 plasma samples | TERT levels  Higher in CRCs than in adjacent noncancerous mucosa  Increase with tumour stage and grade  Not correlated with MSI status  Not correlated with tumour location  Plasma TERT levels correlated with tumour TERT levels |
| Valls Bautista *et al*[70], 2009 | 6 cases, each with cancer, polyps and normal mucosa; 8 polyps and normal mucosa | Telomerase activity  Increases with adenomacarcinoma sequence |
| Kojima *et al*[71]*,* 2011 | 106 CRC and paired adjacent noncancerous mucosa specimens | Elongation of the 3’OH of telomere by telomerase may increase Malignant potential of cancer cells  Telomerase activity has prognostic values for OS (telomeraseactivated without 3'OH shortened telomeres: poor prognosis) |
| Safont *et al*[72]*,* 2011 | 48 CRC and adjacent noncancerous mucosa specimens and 48 plasma samples | Plasma TERT levels correlated with tumour TERT levels  Higher circulating TERT levels in stage IV tumours  No correlation between telomerase expression and prognosis |
| Bertorelle *et al*[73]*,* 2013 | 137 CRCs | TERT levels:  Increase with tumour stage and grade  Not correlated with MSI status  Not correlated with tumour location  Have prognostic value for OS and for both OS and DFS for stage II patients (high TERT levels: poor prognosis) |

CRC: Colorectal cancer; DFS: Disease free survival; OS: Overall survival.