Significance of Cytoplasmic Expression of Telomerase Reverse Transcriptase in Patients with Hepatocellular Carcinoma Undergoing Liver Resection

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Abstract

Telomerase reverse transcriptase (TERT) is reportedly expressed in various types of cancer. However, the significance of TERT expression in hepatocellular carcinoma (HCC) has not been fully evaluated. Herein, we evaluated TERT expression in resected HCC tumor tissues using immunohistochemistry. TERT expression was assessed in both the cytoplasm and the nucleus of HCC cells. The relationships between TERT expression and clinical characteristics were investigated. Among the 135 HCCs, TERT expression was positive only in the cytoplasm in 86 tumors (63.7%), was positive only in the nucleus in 3 tumors (2.2%), was positive in both the cytoplasm and the nucleus in 5 tumors (3.7%) and was negative in 41 tumors (30.4%). Cytoplasmic TERT expression was significantly associated with HBs antigen, poor tumor differentiation, and DNA-dependent protein kinase catalytic unit (DNA-PKcs) expression. However, TERT expression in the cytoplasm or in the nucleus was not significantly correlated with the overall or the recurrence-free survival periods. In conclusion, TERT was mainly expressed in the cytoplasm of HCC tissues. Cytoplasmic TERT expression is closely associated with HBV-related HCC and DNA-PKcs expression. The overexpression of TERT and DNA-PKcs arise from cccDNA and may be related to liver carcinogenesis in the presence of HBV infection.

1. Introduction

Hepatocellular carcinoma (HCC) is the most common primary liver cancer and the third leading cause of cancer-related death worldwide.[1] The incidence and mortality of HCC are reportedly increasing in North America and several European regions and decreasing in traditionally high-risk regions, including Asian countries.[2] Nevertheless, the prevalence of HCC remains a critical global health issue. The major risk factors for HCC are chronic hepatitis B virus (HBV) or hepatitis C virus (HCV) infection, heavy alcohol drinking, diabetes, and nonalcoholic fatty liver disease.[3]

Telomerase reverse transcriptase (TERT) is the catalytic protein subunit of telomerase and is responsible for maintaining chromosomal integrity and genomic stability through the addition of telomeres to the ends of chromosomes.[4] The expression of telomerase is enhanced in germ cell lines and stem cells, but is suppressed in most somatic human cells.[5] In somatic cells, telomere loss occurs during each round of cell division, resulting in cellular aging.[5] In contrast, telomerase is reactivated to prevent critical telomere shortening in cancer cells, thereby enabling cancer cells to acquire replicative immortality.[6] Promoter mutations lead to an enhancement of TERT transcription and the acquisition of immortality in cancer cells.

Telomere shortening and reactivation of telomerase are described in a broad range of human cancers, including liver cancer.[7,8] Telomerase reactivation is associated with the alteration of transcriptional regulators of the TERT promotor in cancer, TERT promotor mutations or rearrangements and DNA copy number amplifications.[9] It has been reported that reactivation of the telomerase enzymes was shown in more than 80% of HCCs, and TERT promotor somatic mutations was found in 59% of the HCCs.[8, 9]

Regarding the relationship between liver disease and TERT promoter mutation of HCC, the mechanisms of the mutation have been reported in HBV- and HCV-related HCC.[9] In HBV related HCC, HBV directly integrates to TERT promoter region and activated TERT transcription.[10] On the other hand, TERT promoter mutation of HCV-related HCC is more frequent compared as that of HBV.[10] Although HCV is not able to integrate into host genome unlike HBV, it is considered that the core proteins of HCV directly affect TERT promoter.[11] However, the intensity of TERT expression in HCC was not differed by TERT promoter mutation.[12] It is skeptical whether TERT expression is associated with the outcome of HCC patients.

Actually, there are a few reports which show the relationship between the outcome of HCC patients and the intercellular distribution of TERT protein expression. The TERT protein has been reported to be mainly distributed in the nuclei of glioblastoma cells, renal cell carcinoma cells, and lung cancer, oral cancer, colorectal cancer, and thyroid cancer cells.[13–18] Conversely, two previous studies have shown that TERT protein is mainly distributed in the cytoplasm of HCC tumor cells.[12, 19] Since telomeres are present in the nucleus, the predominant distribution of TERT in the cytoplasm of HCC tumor cells is difficult to understand. The intracellular distribution of TERT in HCC tumor cells remains to be validated, since only the two above-mentioned reports have assessed this finding. Additionally, the means by which the intracellular TERT distribution affects the clinical characteristics and outcomes of HCC patients undergoing surgery remains unknown.

In this study, we performed immunohistochemistry using two types of antibodies for TERT and evaluated TERT expression in resected HCC tumor tissues. We confirmed the significant of cytoplasmic expression of TERT in HCC cells from patients who had undergone liver resection. Additionally, we investigated the relationship between the intracellular distribution of TERT in HCC tumor tissues and the expression of DNA-protein kinase catalytic subunit (DNA-PKcs), which our group previously reported as a novel predictor in HCC patients.[20]

2. Results

2.1. TERT expression in HCC

First, 135 HCCs were stained using a rabbit monoclonal TERT antibody. TERT expression was positive only in the cytoplasm in 86 tumors (63.7%), was positive only in the nucleus in 3 tumors (2.2%), was positive in both the cytoplasm and the nucleus in 5 tumors (3.7%), and was negative in 41 tumors (30.4%), respectively (Fig. 1). In total, TERT expression in the HCC tissues was positive in the cytoplasm in 91 tumors (67.4%) and was positive in the nucleus in 8 tumors (5.9%).

2.2. Results of repeated IHC using another primary antibody for TERT

Because the intracellular distribution of TERT in HCC tissues apparently differed from that found in other malignancies, repeated immunohistochemistry using a mouse monoclonal antibody was performed for

85 HCCs. As shown in Table 1, the results of the two immunohistochemical series were consistent for 69 of the HCC tumors (81.1%, 69/85, expression shown by gray-colored cells). The results of the two types of TERT antibodies were shown to be significantly consistent ($P < 0.001$).

2.3. Correlation between TERT expression in the cytoplasm and clinical and pathological characteristics

Table 2 shows the clinical and pathological characteristics of the patients stratified according to TERT expression in the cytoplasm of the HCC tissues. The analyses revealed significant intergroup differences in the HBsAg (positive/negative), poor tumor differentiation (yes/no), and DNA-PKcs expression (positive/negative).

2.4. Correlation between tumor TERT expression in the nucleus and clinical and pathological characteristics

Table 3 shows the clinical and pathological characteristics of the patients stratified according to TERT expression in the nucleus of the HCC tissues. Analyses revealed no significant intergroup differences in the clinical and pathological characteristics.

2.5. Relationship between intracellular distribution of TERT expression and postoperative outcomes

The median follow-up period was 1089 days (range, 12-2562 days). During the observation period, 54 patients died; the cause of death was cancer recurrence in 35 patients; liver failure in 9 patients; pneumonia in 4 patients; renal failure, sepsis, ureteral cancer, gastrointestinal perforation in one patient each; and unknown in 2 patients. TERT expression in the cytoplasm or in the nucleus was not significantly associated with the overall and recurrence-free survival periods (Fig. 2).

3. Discussion

The present results showed that TERT was mainly expressed in the cytoplasm of HCC tumor tissues, as reported previously.[12, 19] The present results were confirmed using another TERT antibody (Table 3). These findings suggest that TERT protein might be transferred from the nucleus to the cytoplasm of HCC tumor cells, since TERT protein is originally expressed in the nucleus.[13–18] Overall, 67.4% (91/135) of the HCC tumors had positive TERT expression in the cytoplasm, and TERT expression in the nuclei was negative in most of the cases. The reason for this irregular intercellular distribution of TERT in HCC tumor cells remains uncertain.

Interestingly, oxidative stress reportedly induces TERT translocation from the nucleus to the cytoplasm in human embryonic kidney cells.[21] Previously, we reported that NRF2, a transcription factor that responds to oxidative stress, frequently accumulates in the nucleus in approximately 70% of HCC tumors.[22] This finding suggests that most HCC tumors are subjected to oxidative stress because of a good oxygen

supply from the liver, which is a hyper vascular organ. These observations support the hypothesis that TERT is transferred from the nucleus to the cytoplasm in HCC tumor cells as a result of oxidative stress.

Our results showed that cytoplasmic TERT expression was significantly associated with HBsAg. Previous studies have revealed a relationship between HBV infection and TERT expression.[10, 12, 19] TERT overexpression in HBV-associated HCC tumors has been ascribed to TERT promoter mutations or HBV integration into the genetic locus of TERT. [10, 12, 19] However, the relationship between HBV infection and cytoplasmic TERT expression remains unclear. Our results support the hypothesis that the overexpression of cytoplasmic TERT may be caused by a TERT promoter mutation or HBV genomic integration into the human genome.

Our results showed that cytoplasmic TERT expression was significantly associated with DNA-PKcs expression. DNA-PKcs is reportedly a host protein of HBV-RNA and is significantly associated with HBV infection and the postoperative outcome of HCC patients undergoing surgery.[20, 23] Because HBsAg and HBV-RNA are transcribed by covalently closed circular DNA (cccDNA), TERT and DNA-PKcs expression in HBV-related HCC would arise from cccDNA. However, the current anti-viral drugs for HBV are unable to treat cccDNA; consequently, the development of treatments for cccDNA is needed to improve the outcomes of patients with HBV infection.

Although our results showed that cytoplasmic TERT expression was significantly associated with poor tumor differentiation, a previous study reported that higher cytoplasmic TERT expression was associated with well-differentiated HCC tumors.[19] On the other hand, another report showed that telomerase activation was significantly related to the poor tumor differentiation of HCC tumors.[24] In thyroid cancer, TERT promoter mutation was frequently observed in poorly differentiated tumors.[25] The role of TERT is not only the acquisition of tumor immortality, but also interactions with several oncogenic pathways such as the Wnt/beta-catenin signal pathway and p53 suppression.[26, 27] Although the relationship between cytoplasmic TERT expression and tumor differentiation remains unclear, the present evidence suggests that cytoplasmic TERT expression might affect the tumor dedifferentiation of malignancies, including HCC.

Previous studies have reported that TERT promoter mutation and TERT expression are associated with unfavorable outcomes in HCC patients.[10, 12, 19] On the other hand, our results showed that TERT expression in the cytoplasm or in the nucleus was not closely associated with the postoperative outcomes of HCC patients. Our results suggested that TERT expression is associated with neither tumor progression nor metastasis (Tables 2 and 3). Because the TERT mutation already occurs in premalignant liver tumor cells,[9, 12] the role of TERT in HCC probably does not involve tumor progression, but rather involves liver carcinogenesis and tumor dedifferentiation.

A potential limitation of the present study was that this was a retrospective study performed at a single institution and with a small cohort of patients. Therefore, we could not exclude the influence of bias

provided by the retrospective design of the study, and this may explain the inconsistencies with previous reports.

In conclusion, unlike its expression in other malignancies, TERT is mainly expressed in the cytoplasm of HCC tumor tissues. Cytoplasmic TERT expression was significantly associated with HBsAg, poor tumor differentiation, and DNA-PKcs expression. The overexpression of TERT and DNA-PKcs arise from cccDNA and may be related to liver carcinogenesis in the presence of HBV infection. Further studies examining the treatment of cccDNA in HBV infection are required.

4. Methods

4.1. Patients

This study was conducted with the approval of the Ethical Review Board of the Dokkyo Medical University Hospital (ID number: 28110), in compliance with the Ethical Guidelines for Clinical Research published by the Ministry of Health, Labor and Welfare, Japan. A written informed consent was obtained from each patient enrolled in this study.

From January 2012 to October 2019, 455 liver resections were performed for HCC at the Second Department of Surgery, Dokkyo Medical University Hospital. Among these, 135 HCC patients with good-quality pathological samples were retrospectively enrolled in this study. The 135 patients included 103 males and 32 females, with a mean age ± standard deviation (S. D.) of 68.6 ± 9.0 years (range, 33–91 years). Thirty-seven patients were positive for hepatitis B surface antigen (HBsAg), 37 were positive for anti-hepatitis C virus antibody (HCVAb), 2 were positive for both HBsAg and HCVAb, and 59 were negative for both.

Routine postoperative surveillance was usually performed every 3 months for patients who had undergone surgery. To detect HCC recurrences, the levels of tumor markers, including alpha-fetoprotein (AFP) and protein induced by vitamin K antagonist II (PIVKA-II), were measured every 3 months after surgery. In addition, helical dynamic computed tomography was also performed every 3 months or when the tumor marker levels exceeded the normal range. Beginning at 3 years after the surgery, the HDCT interval was extended from 6 to 12 months. HDCT was performed whenever an elevation in the tumor marker levels was observed.

4.2. Primary antibody and immunohistochemistry

The methods of immunohistochemistry have been described previously.[20] In brief, resected liver specimens were fixed in 10% v/v formalin, cut into blocks, and embedded in paraffin. The blocks were sliced into 4 μm-thick sections and stained with hematoxylin and eosin or used for immunohistochemical analysis. The TERT antibodies used for the analysis were a rabbit monoclonal antibody (Y182, ab32020, Abcam, UK) and a mouse monoclonal antibody (A-6, sc-393013, Santa Cruz, USA). The antibody for DNA-PKcs used was a mouse monoclonal antibody (#12311, Cell Signaling Technology, USA). The sections

were subjected to dewaxing, heat-induced epitope retrieval with citrate buffer, antibody incubation (TERT: dilution 1:50, 15 minutes; DNA-PKcs: dilution 1:30, 45minutes) and counterstaining on a BOND Max immunostainer using Bond Epitope Retrieval Solution 2 (pH-9.0, 20 minutes) and the Bond Polymer Refine Detection kit (Menarini, Berlin, Germany). The TERT expression was judged as positive when staining of the cytoplasm or the nucleus was observed in more than 30% of the tumor cells.

4.3. Statistical analysis

The correlation between the intercellular distribution of TERT expression and various clinical and pathological characteristics were analyzed using the chi-square or Mann-Whitney *U* test, as appropriate. The following clinical and pathological characteristics were examined: patient age (years), sex (male/female), HBsAg (positive/negative), HCVAb (positive/negative), Child-Pugh class (B/A), liver cirrhosis (yes/no), poor tumor differentiation (yes/no), serum levels of AFP (ng/mL) and PIVKA-II (mAU/mL), size of the largest tumor nodule (cm), tumor number (≥2/1), portal vein invasion (yes/no), tumor-node-metastasis (TNM) stage in accordance with the Union for International Cancer Control (UICC) classification, 8th edition,[28] and DNA-PKcs expression (positive/negative). The Kaplan-Meier method and the log-rank test were performed to investigate the relationship between TERT expression and the postoperative outcomes of HCC patients. All the statistical analyses were performed using IBM SPSS statistics version 25.0 software for Windows (IBM Co., New York, NY, USA), and differences with *P* values of < 0.05 were considered as being statistically significant.

Declarations

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Authors contributors

T.A. conceived the study. Y.N., T.S. and T.A. searched the published works. Y.N., T.S., T.A., S.S., T.M., T.S., Y.S., S.M., Y.I., and K.K. performed the operations. Y.N., T.S. and T.A. performed the data analyses and interpreted the data. T.S. and M.I. performed the statistical analyses. Y.N. wrote the first draft of the report; T.A. and K.K. made critical reviews of the manuscript. All the authors have approved the final version of the report.

Competing interests

The authors declare no competing interests.

Data Availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Ethics declarations

This study was conducted with the approval of the Ethical Review Board of the Dokkyo Medical University Hospital (ID number: 28110), in compliance with the Ethical Guidelines for Clinical Research published by the Ministry of Health, Labor and Welfare, Japan.

Consent to participate

We provided the enrolled patients with the opportunity to opt out on our website (www2.dokkyomed.ac.jp/dep-m/surg2/pg334.html).

References

1. Altekruse SF, Henley SJ, Cucinelli JE, McGlynn KA. Changing hepatocellular carcinoma incidence and liver cancer mortality rates in the United States. Am J Gastroenterol 2014; 109: 542-553. doi:10.1038/ajg.2014.11.
2. Kulik L, El-Serag HB. Epidemiology and Management of Hepatocellular Carcinoma. Gastroenterology 2019; 156, 477-491 e471. doi:10.1053/j.gastro.2018.08.065.
3. Singal AG, El-Serag HB. Hepatocellular Carcinoma From Epidemiology to Prevention: Translating Knowledge into Practice. Clin Gastroenterol Hepatol 2015; 13: 2140-2151. doi:10.1016/j.cgh.2015.08.014.
4. Moyzis RK, et al. A highly conserved repetitive DNA sequence, (TTAGGG)n, present at the telomeres of human chromosomes. Proc Natl Acad Sci U S A 1988; 85: 6622-6626. doi:10.1073/pnas.85.18.6622.
5. Blasco MA. Telomeres and human disease: ageing, cancer and beyond. Nat Rev Genet 2005; 6: 611-622. doi:10.1038/nrg1656.
6. Hanahan D,Weinberg RA. Hallmarks of cancer: the next generation. Cell 2011; 144: 646-674. doi:10.1016/j.cell.2011.02.013.
7. Killela PJ,et al. TERT promoter mutations occur frequently in gliomas and a subset of tumors derived from cells with low rates of self-renewal. Proc Natl Acad Sci U S A 2013; 110: 6021-6026. doi:10.1073/pnas.1303607110.
8. In der Stroth L, Tharehalli U, Günes C, Lechel A. Telomeres and telomerase in the development of liver cancer. Cancers 2020; 12: E2048. Doi: 10.3390/cancers12082048.
9. Nault JC, et al. High frequency of telomerase reverse-transcriptase promoter somatic mutations in hepatocellular carcinoma and preneoplastic lesions. Nat Commun 2013; 4:2218. doi:10.1038/ncomms3218.

10. Kawai-Kitahata F, et al. Comprehensive analyses of mutations and hepatitis B virus integration in hepatocellular carcinoma with clinicopathological features. J Gastroenterol 2016; 51: 473-486. doi:10.1007/s00535-015-1126-4.
11. Donaires FS, Scatena NF, Alves-Paiva RM, Podlevsky JD, Logeswaran D, Santana BA, Teixeira AC, Chen JJL, Calado RT, Martinelli ALC. Telomere biology and telomerase mutations in cirrhotic patients with hepatocellular carcinoma. *PLoS One* 2017; 12, e0183287, doi:10.1371/journal.pone.0183287.
12. Yang X, et al.Telomerase reverse transcriptase promoter mutations in hepatitis B virus-associated hepatocellular carcinoma. *Oncotarget* 2016; 7, 27838-27847, doi:10.18632/oncotarget.8539.
13. Schjolberg AR, Clausen OP, Burum-Auensen E, De Angelis PM. Aneuploidy is associated with TP53 expression but not with BRCA1 or TERT expression in sporadic colorectal cancer. Anticancer Res 2009; 29: 4381-4387.
14. Palani J, Lakshminarayanan V, Kannan R. Immunohistochemical detection of human telomerase reverse transcriptase in oral cancer and pre-cancer. Indian J Dent Res 2011; 22: 362. doi:10.4103/0970-9290.84281.
15. Qin Y, et al. RFPL3 and CBP synergistically upregulate hTERT activity and promote Lung cancer growth. Oncotarget 2015; 6: 27130-27145. doi:10.18632/oncotarget.4825.
16. Insilla AC, et al. TERT promoter mutations and their correlation with BRAF and RAS mutations in a consecutive cohort of 145 thyroid cancer cases. Oncol Lett 2018; 15: 2763-2770. doi:10.3892/ol.2017.7675.
17. Trifunovic J, et al.. Immunohistochemical expression of proliferative markers in renal cell carcinoma. J BUON 2018; 23: 1103-1110.
18. Potharaju M, et al. Clinicopathological Analysis of HIF-1alpha and TERT on Survival Outcome in Glioblastoma Patients: A Prospective, Single Institution Study. J Cancer 2019; 10: 2397-2406. doi:10.7150/jca.32909.
19. Huang W, et al. Promoter mutations and cellular distribution of telomerase in non-clear cell and clear cell hepatocellular carcinoma. Oncotarget 2017; 8: 26288-26297. doi:10.18632/oncotarget.15458.
20. Shimizu T, et al. Tumor DNA-dependent protein kinase catalytic subunit expression is associated with hepatitis B surface antigen status and tumor progression in patients with hepatocellular carcinoma. Sci Rep 2018; 8: 15019. doi:10.1038/s41598-018-33427-6.
21. Haendeler J, Hoffmann J, Brandes RP, Zeiher AM, Dimmeler S. Hydrogen peroxide triggers nuclear export of telomerase reverse transcriptase via Src kinase family-dependent phosphorylation of tyrosine 707. Mol Cell Biol 2003; 23: 4598-4610. doi:10.1128/mcb.23.13.4598-4610.2003.
22. Shimizu T, et al. Frequent alteration of the protein synthesis of enzymes for glucose metabolism in hepatocellular carcinomas. J Gastroenterol 2014; 49: 1324-1332. doi:10.1007/s00535-013-0895-x.
23. Sekiba K, et al. DHX9 regulates production of hepatitis B virus-derived circular RNA and viral protein levels. Oncotarget 2018; 9: 20953-20964. doi:10.18632/oncotarget.25104.
24. Piao YF, He M, Shi Y, Tang TY. Relationship between microvessel density and telomerase activity in hepatocellular carcinoma. World J Gastroenterol 2004; 10: 2147-

2149. doi:10.3748/wjg.v10.i14.2147.

25. Siraj AK, et al. Telomerase reverse transcriptase promoter mutations in cancers derived from multiple organ sites among middle eastern population. Genomics 2020; 112: 1746-1753. doi:10.1016/j.ygeno.2019.09.017.
26. Jin X, et al. Human telomerase catalytic subunit (hTERT) suppresses p53-mediated anti-apoptotic response via induction of basic fibroblast growth factor. Exp Mol Med 2010; 42: 574-582. doi:10.3858/emm.2010.42.8.058.
27. Zhang Y, Toh L, Lau P, Wang X. Human telomerase reverse transcriptase (hTERT) is a novel target of the Wnt/beta-catenin pathway in human cancer. J Biol Chem 2012; 287: 32494-32511. doi:10.1074/jbc.M112.368282.
28. James DB, Mary KG, Christian W, eds. TNM Classification of MALIGNANT TUMORS Eighth Edition. WILEY Blackwell 2017; 80-81.

Tables

Table 1

Results of immunohistochemistry using two types of primary antibodies for TERT

Mouse mAb **Rabbit mAb**	**Cytoplasm (-)** **Nucleus (-)**	**Cytoplasm (+)** **Nucleus (-)**	**Cytoplasm (-)** **Nucleus (+)**	**Cytoplasm (+)** **Nucleus (+)**
Cytoplasm (-) **Nucleus (-)**	17	10	1	4
Cytoplasm (+) **Nucleus (-)**	3	39	1	4
Cytoplasm (-) **Nucleus (+)**	0	1	0	1
Cytoplasm (+) **Nucleus (+)**	0	1	0	3

Mouse mAb; mouse monoclonal primary TERT antibody

Rabbit mAb; rabbit monoclonal primary TERT antibody

Table 2

Relationships between clinical characteristics and TERT expression in the cytoplasm in patients with hepatocellular carcinoma undergoing surgery.

Variable	TERT (−) (n = 44)	TERT (+) (n = 91)	*P*-value
Age (years)	71 (67-75)	69 (63-75)	0.279
Gender (male/female)	33/11	70/21	0.805
HBsAg (positive/negative)	6/38	33/58	0.007
HCVAb (positive/negative)	15/29	24/67	0.354
Child-Pugh class (B/A/NA)	8/36/0	13/77/1	0.576
Liver cirrhosis (yes/no/NA)	12/31/1	38/51/2	0.101
Poor tumor differentiation (yes/no/NA)	3/40/1	19/72/0	0.043
AFP (ng/mL)	4 (3-58)	10 (4-92)	0.849
PIVKA-II (mAU/mL)	38 (18-146)	79 (27-587)	0.239
Size of largest tumor nodule (cm)	3.2 (2.2-5.3)	3.0 (2.0-5.6)	0.135
Tumor Number (≧2/1)	11/33	23/67	0.973
Portal vein invasion (yes/no)	13/31	21/70	0.417
TNM Stage (I/II/III)	21/13/10	42/23/26	0.741
DNA-PKcs (positive/negative/NA)	16/14/14	37/12/42	0.042

Chi-squared and Mann-Whitney *U* test, median (IQR).

AFP: alpha-fetoprotein; PIVKA-II: protein induced by Vitamin K antagonist II; HBsAg: hepatitis B surface antigen; HCVAb: anti-hepatitis C virus antibody;

NA: not available; TNM: tumor-node-metastasis;

DNA-PKcs: DNA-dependent protein kinase catalytic subunit

Table 3

Relationships between clinical characteristics and TERT expression in the nucleus in patients with hepatocellular carcinoma undergoing surgery.

Variable	TERT (−) (n = 127)	TERT (+) (n = 8)	*P*-value
Age (years)	70 (65-75)	70 (66-72)	0.733
Gender (male/female)	96/31	7/1	0.442
HBsAg (positive/negative)	37/90	2/6	0.802
HCVAb (positive/negative)	38/89	1/7	0.292
Child-Pugh class (B/A/NA)	20/106/1	1/7/0	0.799
Liver cirrhosis (yes/no/NA)	46/79/2	4/3/1	0.280
Poor tumor differentiation (yes/no/NA)	20/106/1	2/6/0	0.499
AFP (ng/mL)	7 (3-74)	3 (2-18)	0.103
PIVKA-II (mAU/mL)	71 (23-444)	41 (22-80)	0.187
Size of largest tumor nodule (cm)	3.1 (2.1-5.9)	2.9 (1.9-4.2)	0.363
Tumor Number (≧2/1)	33/94	1/7	0.394
Portal vein invasion (yes/no)	33/94	1/7	0.394
TNM Stage (I/II/III)	58/33/36	5/3/0	0.212
DNA-PKcs (positive/negative/NA)	50/25/52	3/1/4	0.251

Chi-squared and Mann-Whitney *U* test, median (IQR).

AFP: alpha-fetoprotein; PIVKA-II: protein induced by Vitamin K antagonist II;

HBsAg: hepatitis B surface antigen; HCVAb: anti-hepatitis C virus antibody;

NA: not available; TNM: tumor-node-metastasis;

DNA-PKcs: DNA-dependent protein kinase catalytic subunit

Figures

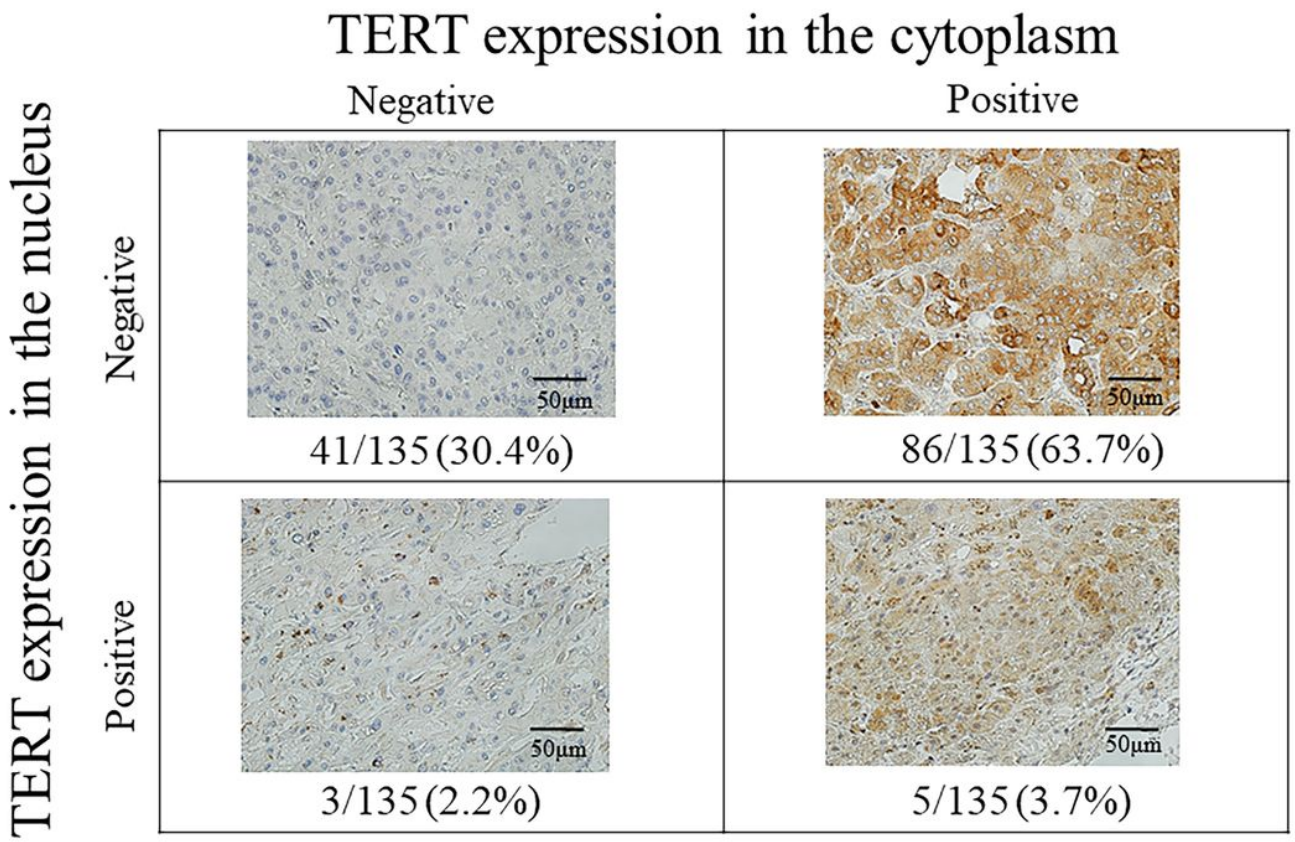

Figure 1

Immunohistochemistry of HCC tumors: TERT expression in the cytoplasm and in the nucleus of HCC tissues.

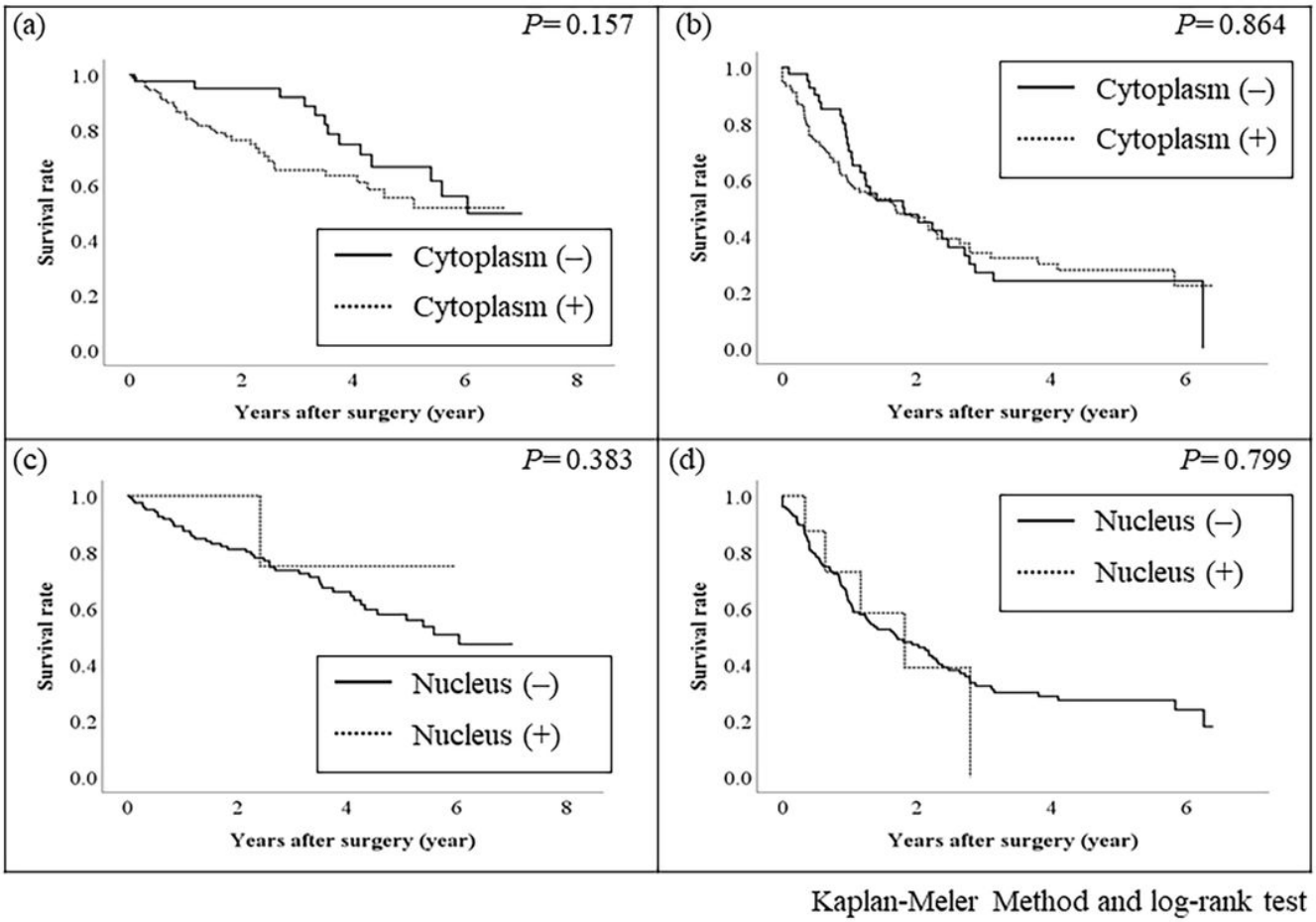

Figure 2

Relationship between TERT expression in the cytoplasm or in the nucleus and postoperative survival in HCC patients undergoing liver resection. (a) TERT expression in the cytoplasm and OS, (b) TERT expression in the cytoplasm and RFS, (c) TERT expression in the nucleus and OS, and (d) TERT expression in the nucleus TERT and RFS.