Journal of Pharmaceutical Research International

34(2A): 10-19, 2022; Article no.JPRI.81664
ISSN: 2456-9119
(Past name: British Journal of Pharmaceutical Research, Past ISSN: 2231-2919, NLM ID: 101631759)

Gene Expression Analysis of Specific Genes Related to Genomic Stability in Colon Cancer Cell Lines - A Resource for Cancer Research

Ghadah Alamro [a], Norah Almousa [a], Jamilah Almusallam [a], Maram Bin Watyan [a], Sara Alghamdi [a], Sadeem Al- Jabr [a], Nada Alqahtani [a], Abeer Aldbass [a], Ramesa Shafi Bhat [a*] and Sooad Al Daihan [a]

[a] Department of Biochemistry, College of Science, King Saud University, Saudi Arabia.

Authors' contributions

This work was carried out in collaboration among all authors. Authors GA and JA Performed the experimental work and revised the manuscript. Authors NA, MBW, SA, and SJA Performed the experimental work. Authors RSB and AAD Acquisition of the data and Author RSB Drafted the manuscript. Author SAD Supervise the overall. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/JPRI/2022/v34i2A35355

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/81664

Original Research Article

Received 05 November 2021
Accepted 10 January 2022
Published 13 January 2022

ABSTRACT

Appropriate cell models are the foundation of cancer research as all the cell lines are not the same in their ability to mimic primary tumor tissue. Molecular characteristics of various cell lines can help in selecting the right cell model for biomedical studies. This study describes the gene expression profile of nine genes, include the six-protein shelterin complex, tankyrases1and 2, and *CTNNB1* in three different models of human colon cancer cell lines. Also, the relative telomere length in each cell line was evaluated. All genes' expression levels were analyzed using a real-time polymerase chain reaction. Nearly all test genes were significantly highly expressed in HT-29 as compared to HCT-116 and SW-620. SW-620 record a significantly increased expression of the *CTNNB1* gene (P-value < 0.01) while most genes were poorly expressed in HCT-116. A positive correlation between *CTNNB1* and *hTERT* expression was found in HCT-116 and SW-620 but not in HT-29. Telomere was found to be of the same length in all cell. Gene expression data presented in our results can assist in selecting appropriate cell lines in colon cancer research. Unique molecular properties of various cancer cell lines should be evaluated before selecting a cell line mmodelfor research purposes.

**Corresponding author: E-mail: rbhat@ksu.edu.sa;*

Keywords: β-catenin; colon cancer cell lines; gene expression; shelterin complex; telomere; tankyrases.

1. INTRODUCTION

Colorectal cancer (CRC) is one of the most occurring types of cancer worldwide. According to GLOBOCAN 2018, CRC is the third most commonly diagnosed cancer with nearly 1.8 million new cases, and the second leading cause of cancer death, accounting for 9.2% of all cancer deaths [1].CRC is a heterogeneous disease with diverse molecular pathways typically due to loss of genomic stability either by genetic or epigenetic alterations. Telomeres play a significant role in maintaining genomic stability and their dysfunction can modulate many cell signals like the Wnt/β-catenin pathway leading to cancer [2].

The involvement of deregulated Wnt/β-catenin cascade with colorectal cancer has been well documented [3]. One of the most studied and critical Wnt pathways is canonical Wnt signaling, which functions by regulating the amount of the transcriptional co-activator β-catenin that controls the central developmental gene expression program [4]. Telomere dysfunction can occur due to impaired telomere length or by disruption of the shelterin complex. Many human diseases especially cancer are linked with mutations in shelterin. Shelterin complex is composed of six key individual proteins, the telomere repeat-binding factor 1 and 2 (TRF1 and TRF2), protection of telomeres 1 (POT1), repressor/activator protein 1 (RAP1), TRF1 and TRF2 interacting protein 1 (TIN2), and TIN2-interacting protein 1 (TPP1) [5,6]. Telomere is also regulated by tankyrase which is involved in many cellular and molecular processes related to tumor suppressors.

Human cell lines obtained from malignant tumors are being used as a valuable in vitro model in cancer research for decades [7]. Cell line-based studies are being promoted all over the world to understand the genetic and epigenetic mechanisms involved in many kinds of malignancy [8]. Although cell lines are inexpensive and easy to handle in the laboratory, appropriate selection of proper cell line for a particular study need to be evaluated for best results [9]. Cell lines have their origin from tumor tissue samples of a patient [10,11]. Sorting the cell for a particular study is a very crucial step as cells in the experiment should truly represent the type of cancer they are supposed to represent. Usually, cell lines represent gene expression patterns the same as their cellular origin [11]. Cell lines have their unique genetic characteristics like HCT116 has a mutation in codon 13 of the KRAS proto-oncogene and is mainly used for biomedical studies involving colon cancer proliferation and corresponding inhibitors [12,13]. These cells are most suitable for therapeutic research and drug screenings [14]. HT-29 has a mutation in the p53 gene [15]. These cells are mostly used to study the structural and molecular events involved in cell differentiation and are best fit for studies focusing on the anticancer effect of different food compounds [16,17]. SW-620 is used to study metastasis processes [18]. Physiological properties like cell proliferation rate, drug sensitivities, and metabolism depend on the gene expression patterns of particular cell lines [19]. HCT-116, HT-29, and SW-620 cell lines are the most commonly used cell lines in colorectal cancer studied but literature reporting the gene expression patterns of some specific genes related to genomic stability in these cells is not available. Therefore, different colorectal cancer cell line models were used, HCT-116, HT-29 and SW-620 to evaluate the telomere length and the expression of the telomere-associated proteins; telomerase, TRF1, TRF2, POT1, TPP1, TIN2, TNKL1, and TNKS2 and how they correlate with the transcriptional factor β-catenin expression level.

2. MATERIALS AND METHODS

2.1 Cell Culture

Three human colon cancer cell lines HCT-116, HT-29, and SW-620 were used in the present study and were kindly provided by Stem Cell Unit, Department of Anatomy at King Khalid University Hospital, Riyadh, KSA. All cell lines were cultured in DMEM medium supplemented with 10% (v/v) fetal bovine serum and 1% (v/v) penicillin-streptomycin (Invitrogen, Carlsbad, CA, USA) at 37˚C in a humidified atmosphere containing 5% CO2.

2.2 Nucleic Acid Isolation

The DNA and total RNA were isolated from each cell line using RNeasy Mini Kit and QIAamp DNA Mini Kit, respectively, according to the manufacturer's instructions (Qiagen). The

isolated nucleic acids were quantified spectrophotometrically (NanoDrop 8000, Thermo Fisher Scientific).

2.3 Assessment of Gene Expression via RT-qPCR

Total RNA was reverse-transcribed to cDNA using the High Capacity cDNA Reverse Transcription Kit (Applied Biosystems), according to the manufacturer's instruction. The expression of each gene was assessed by quantitative PCR using SYBR® Green-based assay (Bio-Rad). Each reaction was carried out in triplicates with a final volume of 10 µl containing 1X SYBR® Green Master Mix, 200 nM forward and reverse primers, and 19.5 ng of cDNA. The Primer sequences and annealing temperature are listed in Table 1. The reactions were performed in ViiA™ 7 Real-Time PCR System (Applied Biosystems) using the following cycling parameters: 1 cycle at 95°C for 5min followed by 45 cycles of amplification (denaturation at 95°C for 15 sec, annealing at 60°C for 30 sec, and extension at 60°C for 30 sec). The relative gene expression was normalized using glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*) expression. A non-template negative control was included in each run to check the background signal.

2.4 Measurement of Relative Telomere Lengths

Telomere length was determined by a previously described qPCR protocol (42) .In brief, two PCR master mixes were prepared, one for telomere reaction with telomere (TEL) primer pair, and the other for single-copy gene reaction with human beta-globin gene (*HBG*) primer pair. The Primer sequences and annealing temperature are listed in Table 1. Each reaction contained 1X SYBR® Green Master-mix (Applied Biosystems, UK), 20 ng of DNA sample, *Tel-1* (300 nM), *Tel-2* (900 nM), *HBG-1*, and *HBG-2* (400 nM). All reactions were performed by Light Cycler 480 II system (Roche Applied Science) using the following PCR cycling condition: initial denaturation at 95°C for 15 minutes followed by 45 cycles of (denaturation at 95°C for 15 sec, indicated annealing temperature for 2 min, and extension at 72°C for 30 sec).

2.5 Statistical Analysis

All statistical analyses were performed using GraphPad Prism® software (version 8.2.0 GraphPad Inc, USA). The relative gene expression was calculated using the copy number method. Nevertheless, the relative telomere length was calculated using $2^{-\Delta\Delta Ct}$ method (where ΔCt= Ct single copy gene-Ct telomere). Unpaired Student's t-test was used to estimate the difference in the gene expression and telomere length between colon cancer cell lines Pearson's correlation and Linear regression were used to test the association between the different variables. All data are presented as the mean ± standard error of the mean, and the P-value of less than 0.05 was considered statistically significant.

3. RESULTS

3.1 Assessment of β-catenin and Telomere Related Proteins Expression

The gene expression profile of telomere related proteins *(hTERT, TERF1, TERF2, POT1, TIN2, TPP1, TNKS1,* and *TNKS2*) and *CTNNB1* of all cancer cell lines are presented in Fig. 1. SW-620 expressed a significantly higher level of β-catenin as compared to the other two cell lines. Comparing SW-620 and HT-29m there was a significant difference in the expression in all studied genes except *hTERT* and its negative regulator *POT1*. HT-29 showed a significantly high expression of *TRF1, TRF2, TPP1,* and *TNKS2* as compared to SW-620 and HCT-116, where HCT-116 showed the least expression of almost all test genes. The expression level of *hTERT* in all cell lines was found to be the same (Fig. 1). Interestingly, *POT1* which functions in telomere length regulation through controlling telomerase access to the overhang did not show any significant difference in its expression between the selected colon cancer cell lines, as the case in *hTERT*. One notable finding is that the expression pattern of *TERF1, TERF2*, *TPP1*, and *TNKS2* was almost identical in all studied cell lines. Furthermore, the level of the previously mentioned genes was significantly low in HCT-116 and high in HT-29, the native and mutated *TP53* models. Person correlation between all the genes of three cell lines is summarized and presented in Figure 3. *CTNNB1* was positively correlated with all studied genes of all cell lines except *POT1* in SW-620 and *TERF1* and *POT1* in HCT-116 it was found to be negatively correlated with its expression. A negative correlation between *hTERT* and *POT1* was found in all three cell lines. In SW-620 and HCT-116,

POT1 was negatively correlated with almost all the genes. Further, genes that were mainly involved in telomere structure regulation (*TERF1, TERF2, TIN2 TPP1* and *TNKS1*) were found to be correlated in HT-29. Fig. 2 summarizes the correlation findings.

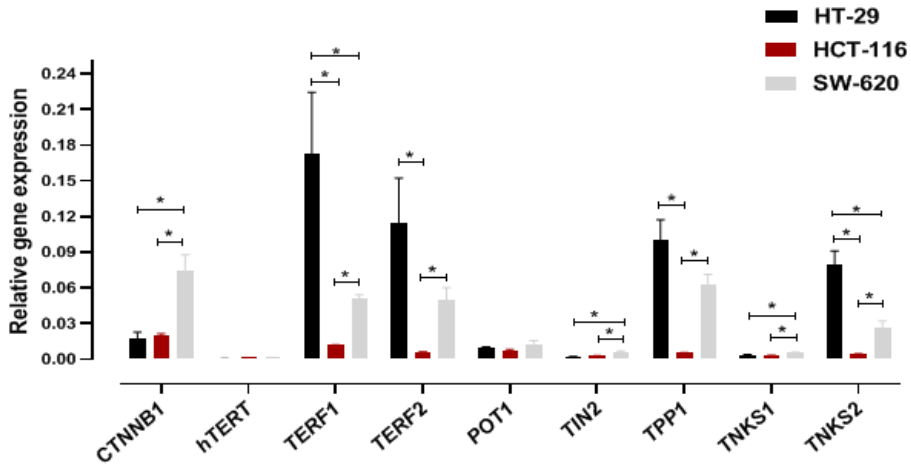

Fig. 1. Expression of *CTNNB1* and telomere-related proteins in three types of human colon cancer

** for P-value < 0.05*

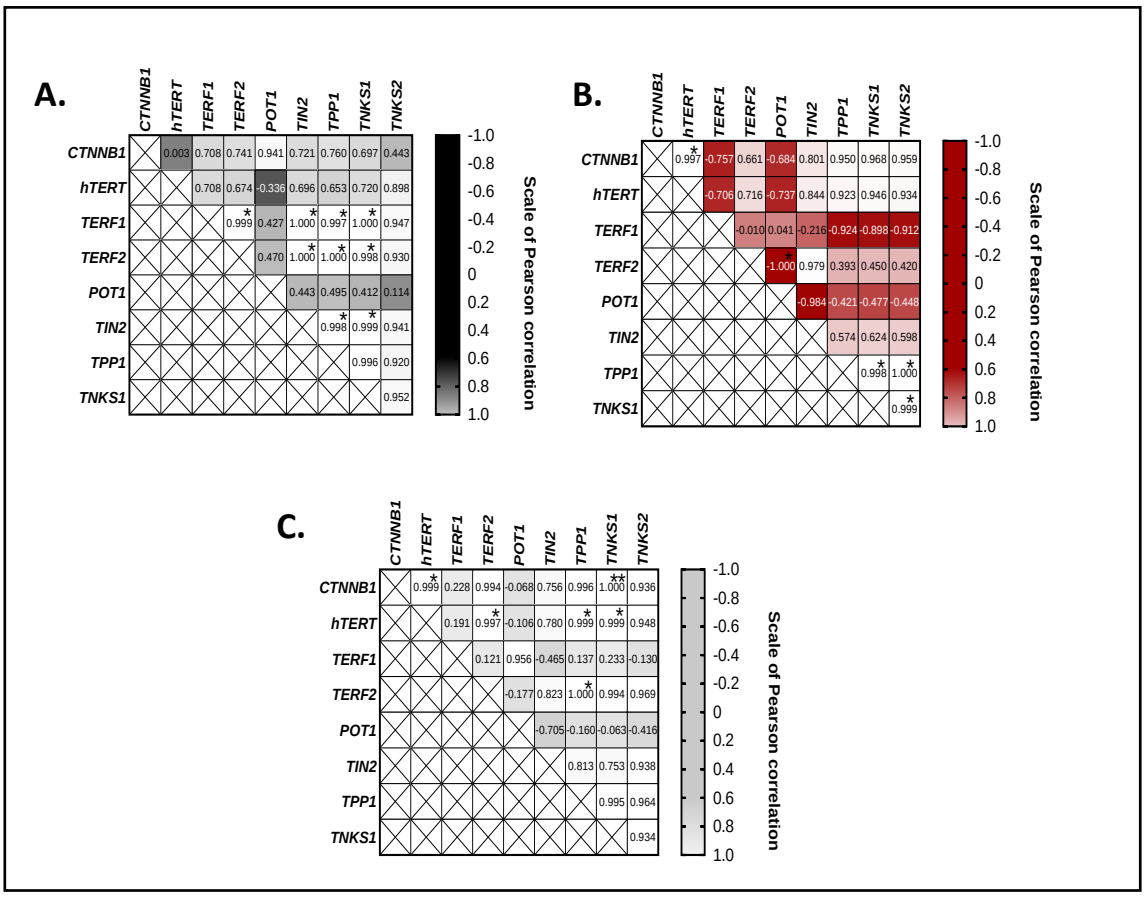

Fig. 2. Correlation between the expression of the interest genes in different model of human colorectal cancer, A. HT-29, B. HCT-116, C. SW-620

** for P-value < 0.05, ** for P-value < 0.01*

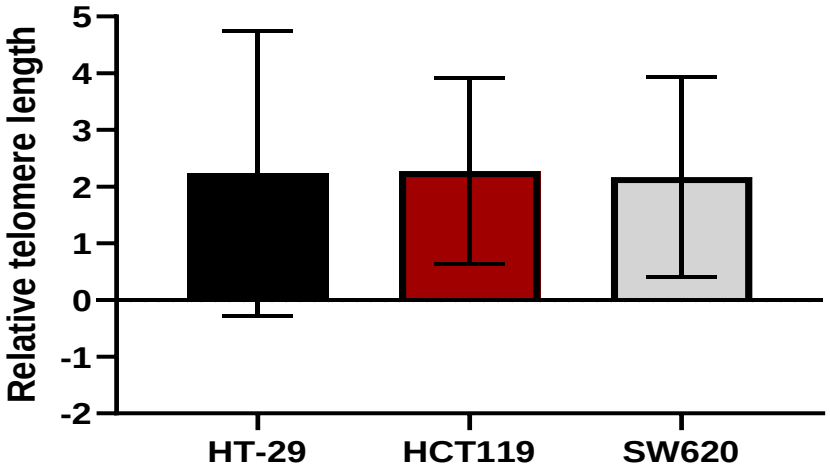

Fig. 3. Relative telomere length (RTL) in three different colorectal cancer cell lines, all three models show almost the same telomere length

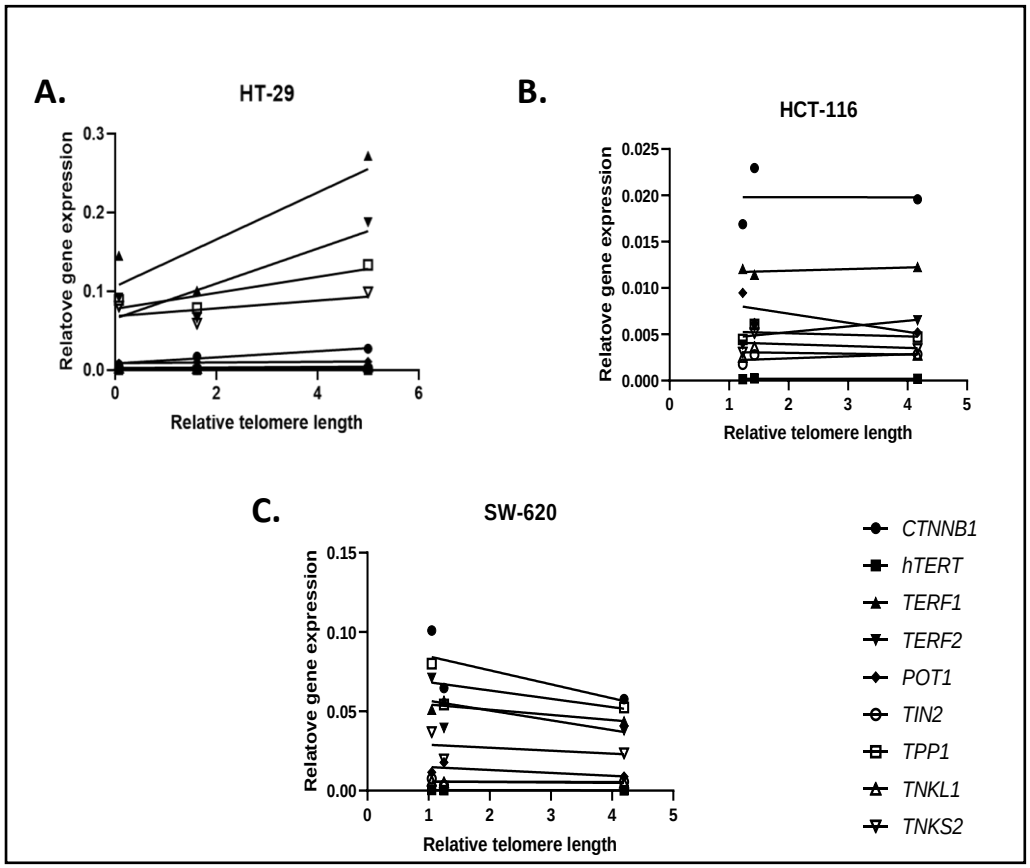

Fig. 4. Pearson's correlation between gene expression of telomere related proteins and relative telomere length in the studied colorectal cancer cell lines, A. in HT-29 telomere length is positively associated with the expression of all interests genes, B. no notable results were recorded and C. SW-620 shows a negative correlation between the telomere length and the expression of all genes

3.2 Relative Telomere Length (RTL) Measurement and Correlation with Gene Expression

Telomere was found to be of the same length in all cell lines as shown in Fig. 3. The correlation analysis was performed with Pearson's correlation test to demonstrate the association between the gene expression of the telomere related proteins and *CTNNB1* with telomere length (Fig. 4). Interestingly, HT-29 and SW-620 show a counter result. While the telomere length in HT-29 shows a positive correlation with the expression of all studied genes, the telomere length of SW-620 on other hand was negatively correlated with the expression of all genes. In the case of HCT-116, no notable correlation or pattern was found between telomere length and the expression of all genes. Overall, the analysis showed that among the studied genes, no significant correlation was determined between telomere length and their expression.

4. DISCUSSION

Studies have found that telomere dysfunction is associated with chromosomal instability, a hallmark of cancer and causative of the acquisition of genetic lesions that are involved in the stepwise progression of cells into malignancy. Indeed, different factors and pathways may play a role in the regulation of telomere-related proteins and thus telomere biology. Previous studies have been documenting that Wnt/ β-catenin pathway is involved [20]. The present work aims to estimate the relative telomere length and the expression level of the telomere related proteins (*hTERT, TERF1, TERF2, POT1, TIN2, TPP1, TNKS1* and *TNKS2*) using q-PCR in most commonly used colon cancer cell lines and how they correlate with the transcriptional factor β-catenin expression level. The mRNA level of β-catenin and *TNKS1* was significantly higher in SW-620 as compared to the other two cells. SW620 is metastatic and poorly differentiated as compared to HT-29 and HCT116 which suggests that β-catenin may play an important role in metastasis. Lai *et al* explored the molecular marker for metastasis in human cancer tissue. He reported an elevated level of β-catenin expression in a poorly differentiated tissue. Similar results are reported in human hepatoma cell line HA22T which has high proliferation activity [21]. Many human cancers are reported with mutations and abnormal expression of β-catenin which is correlated with tumor invasion and metastasis [22]. Remarkably, it has been found that SW-620 owns a mutated *APC* [23,24] and wildtype *CTNNB1*status [24]. Previous studies have reported that both *TNKS1* and *TNKS2* reducing β-catenin degradation by destabilizing the levels of Axin [25]; a key effector in the Wnt pathway and has been identified as a tumor suppressor and therefore hyperactivation Wnt/β-catenin signaling [26,27]. This finding is compatible with a previous study which found that the Wnt/β-catenin pathway is activated during CRC progression and accompanied by enhanced cell invasive behavior [28]. This makes the Wnt/β-catenin pathway become a potential therapeutic target for inhibiting CRC metastasis. Therefore, due to the role of tankyrase in Wnt/β-catenin signaling, Tankyrase 1 inhibitors may become a promising therapeutic target for CRC through suppressing Wnt signaling and tumor growth.

hTERT is one of the main catalytic subunits of the telomerase enzyme and is expressed in almost 90 % of human cancers. The expression level of *hTERT* in all cell lines was found to be the same in the presented data. Our results are well supported by Kawanishi-Tabata et.al (2002) results where he proved that the expression level of *hTERT* was not correlated with cancer progression in colon carcinoma [29]. Furthermore, copy number gain of the *hTERT* gene is highly correlated with *hTERT* expression found in neuroblastomas and lung cancer, but no such correlation has been found in colorectal carcinomas [30].

On examining the expression level of the six protein components of the shelterin complex we found that HT-29 showed significantly high expression of *TRF1, TRF2*, and *TPP1* as compared to SW-620 and HCT-116, where HCT-116 showed the least expression of almost all components of shelterin complex. Many reports have shown overexpression of *TRF1* and *TRF2* in many kinds of cancer tissues [31]. HT-29 is a mutant for the p53 gene. Shelterins protect the chromosomes and prevent their ends but any kind of genotoxic stress or mutation can induce tumor [32]. The p53 protein is known for its tumor suppressor properties and plays a major role in the maintenance of genome integrity [33]. Mutation in p53 in HT-29 can be related to the high expression of these shelterin proteins as p53 protein-enhanced telomere stability even in presence of DNA damage. Some studies have also reported the inhibition of *TRF2* in the induction of apoptosis in a p53 dependent manner. Impressively, there was a significant

correlation between the expression of *TERF1* and *TERF2*, *TPP1* and *TNKS1.* Likewise, *TERF2* expression was significantly correlated with the three previously mentioned genes. However, *TPP1* has correlated with *TERF1* and *TERF2* expression but not tankyrases. These findings suggest that these telomeric proteins may play a role in cancer by enhancing the genomic instability through controlling DNA damage response (DDR) and manipulating the telomere structure but not length since we found that all the three colon cancer cell lines were almost having the same length. The suggestion is consistent with published data that found a significant correlation between *TERF1* and *TERF2* expression and demonstrates an inverse relation between *TERF1* and *TERF2* level with DDR activation [34].

Tankyrase proteins having poly(ADP-ribose) polymerase activity are the main components of the human telomeric complex among which Tankyrase-1 and 2 are most important. Change of expression level of these two proteins is identified in many cancers tissues. The expression level of the Tankyrase-1 and Tankyrase 2 were found to be significantly high in HT-29 followed by SW-620 whereas HCT-116 showed the least expression. The expression level of the Tankyrase protein depends on the tumor stage [35]. Cell lines used in the study were different in their ability to differentiate as HT-29 has an intermediate capacity to differentiate while SW-620 and HCT-116 are highly aggressive cell lines with the least differentiation. Our results agree with Abdulaziz, et al (35), who found high expression of *TNKS1* in the early stages than late stages of CRC development. Also, Gelmini et al. (2006) [36], reported an inverse relation of TNKS with colon cancer stages.

As shown in Fig 2.C, *CTNNB1* was significantly positively correlated with *hTERT,* while the last one was significantly correlated with *TERF2*. This finding is compatible with a study that found that the *hTERT* is a target of the Wnt/β-catenin pathway, and induction of β-catenin expression leads to increased *hTERT* expression while silencing endogenous β-catenin expression by β-catenin gene-specific shRNA effectively decreased *hTERT* expression [37]. Altered expression of β-catenin is found to be correlated with poor prognosis, aggressive phenotype and metastasis [38–40]. as clearly shown in our results of SW-620 cell lines where we found a strong correlation of *CTNNB1* and with other genes as compared to the other two cells. Our results showed a strong correlation between β-catenin and *hTERT* concerning the different capacities of differentiation among the cell lines. The expression status of β-catenin significantly correlates with the de-differentiation process and prognosis in many human cancers tissues [41].

Table 1. Primers sequence used to evaluate gene expression using real-time q-PCR and relative telomere length

Gene	Primer sequence (5′ - 3′)	Ta (°C)	Reference
GAPDH	For: GGT ATC GTG GAA GGA CTC ATG AC Rev: ATG CCA GTG AGC TTC CGT TCA GC	60	[43]
CTNNB1	For: TCT GAG GAC AAG CCA CAA GAT TAC A Rev: TGG GCA CCA ATA TCA AGT CCA A		[44]
hTERT	For: CGT CCA GAC TCC GCT TCA TC Rev: GAG ACG CTC GGC CCT CTT		[45]
TERF1	For: CCA CA TGA TGG AGA AAA TTA AGA GTT AT Rev: TGC CGC TGC CTT CAT TAG A		[46]
TERF2	For: TCA ATC GCT GGG TGC TCA A Rev: GTA CCG GCT ACC CCG AAA G		[47]
POT1	For: GAA GTG GAC GGA GCA TCA TT Rev: TTT GTA GCC GAT GGA TGT GA		[48]
TPP1	For: GCG TGA CGT CTC ACA TCG Rev: ATC GTG ATG GTT CTG CCT TC		[49]
TIN2	For: GGC CTA AAG GCC AAG GTG GTG Rev: GGC CAA ATC CAC AGG AGC CTC		[50]
TNKS1	For: GTC CCT GAC AGC CTA GAA ATA AG Rev: GGG AAC AGT AGC AGT TGA GTA TG		[51]
TNKS2	For: TCC GGA CAA CAA GGT CTT AAC Rev: CTC TTC CTC CAC AGA CTG AAA C		[51]

Gene	Primer sequence (5′ - 3′)	Ta (°C)	Reference
TEL-1	GGT TTT TGA GGG TGA GGG TGA GGG TGA GGG TGA	55	[52]
TEL-2	GGG T TCC CGA CTA TCC CTA TCC CTA TCC CTA TCC CTA TCC CTA		
HBG-1	GCT TCT GAC ACA ACT GTG TTC ACT AGC	60	[52]
HGB-2	CAC CAA CTT CAT CCA CGT TCA CC		

**For: forward, Rev: reverse, Ta: annealing temperature.*

5. CONCLUSION

The selection of appropriate cell lines for molecular-based cancer studies is a very critical step to interpret and understand cancer biology. The gene expression patterns of some specific genes of HCT-116, HT-29, and SW-620 cell is reported to help researchers to choose the most appropriate cell line models for cancer studies.

CONSENT

It is not applicable.

ETHICAL APPROVAL

It is not applicable.

ACKNOWLEDGMENTS

This project was funded by King Abdulaziz City for Science and Technology (KACST) under project (1-17-00-001-0011) and (1-17-01-001-0049).

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Bray F, Ferlay J, Soerjomataram I, Siegel RL, Torre LA, Jemal A. Global cancer statistics 2018: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. CA: A Cancer Journal for Clinicians. 2018;68(6).
2. MSP, DCC. The Chromosomal Instability Pathway in Colon Cancer. Gastroenterology. 2010;138(6).
3. Bernstein C, R. A, Nfonsam V, Bernstei H. DNA Damage, DNA Repair and Cancer. In: New Research Directions in DNA Repair; 2013.
4. Kim MK. Novel insight into the function of Tankyrase (Review). Oncology Letters. 2018;16.
5. MacDonald BT, Tamai K, He X. Wnt/beta-catenin signaling: componentMacDonald BT, Tamai K & He X (2009) Wnt/beta-catenin signaling: components, mechanisms, and diseases. Dev. Cell 17: 9–26s, mechanisms, and diseases. Developmental Cell. 2009;17(1).
6. Polakis P. The many ways of Wnt in cancer. Current Opinion in Genetics and Development. 2007:17.
7. Mirabelli P, Coppola L, Salvatore M. Cancer cell lines are useful model systems for medical research. Cancers. 2019:11.
8. Masters JRW. Human cancer cell lines: Fact and fantasy. Nature Reviews Molecular Cell Biology. 2000:1.
9. Geraghty RJ, Capes-Davis A, Davis JM, Downward J, Freshney RI, Knezevic I, et al. Guidelines for the use of cell lines in biomedical research. British journal of cancer. 2014;111(6).
10. Kodack DP, Farago AF, Dastur A, Held MA, Dardaei L, Friboulet L, et al. Primary Patient-Derived Cancer Cells and Their Potential for Personalized Cancer Patient Care. Cell Reports. 2017;21(11).
11. Salvadores M, Fuster-Tormo F, Supek F. Matching cell lines with cancer type and subtype of origin via mutational, epigenomic, and transcriptomic patterns. Science Advances. 2020;6(27).
12. Rajput A, Dominguez San Martin I, Rose R, Beko A, LeVea C, Sharratt E, et al. Characterization of HCT116 Human Colon Cancer Cells in an Orthotopic Model. Journal of Surgical Research. 2008;147(2).
13. 116 (HCT116) ATCC CCL-247TM.
14. Pellegrini P, Serviss JT, Lundbäck T, Bancaro N, Mazurkiewicz M, Kolosenko I, et al. A drug screening assay on cancer cells chronically adapted to acidosis. Cancer Cell International. 2018;18(1).
15. He X, Liao J, Liu F, Yan J, Yan J, Shang H, et al. Functional repair of p53 mutation

in colorectal cancer cells using trans-splicing. Oncotarget. 2015;6(4).
16. Martínez-Maqueda D, Miralles B, Recio I. HT29 cell line. In: The Impact of Food Bioactives on Health: In Vitro and Ex Vivo Models. 2015.
17. Baricault L, Denariaz G, Houri JJ, Bouley C, Sapin C, Trugnan G. Use of ht-29, a cultured human colon cancer cell line, to study the effect of fermented milks on colon cancer cell growth and differentiation. Carcinogenesis. 1995;16(2).
18. Xu Y, Zhang L, Wang Q, Zheng M. Comparison of Different Colorectal Cancer With Liver Metastases Models Using Six Colorectal Cancer Cell Lines. Pathology and Oncology Research. 2020;26(4).
19. Ji J, Chen X, Yi Leung S, A Chi JT, Man Chu K, Tsan Yuen S, et al. Comprehensive analysis of the gene expression profiles in human gastric cancer cell lines. Oncogene. 2002;21(42).
20. Park J il, Venteicher AS, Hong JY, Choi J, Jun S, Shkreli M, et al. Telomerase modulates Wnt signalling by association with target gene chromatin. Nature. 2009:460.
21. Lai TY, Su CC, Kuo WW, Yeh YL, Kuo WH, Tsai FJ, et al. β-Catenin plays a key role in metastasis of human hepatocellular carcinoma. Oncology Reports. 2011;26(2).
22. Li YJ, Wei ZM, Meng YXYX, Ji XR. β-catenin up-regulates the expression of cyclinD1, c-myc and MMP-7 in human pancreatic cancer: Relationships with carcinogenesis and metastasis. World Journal of Gastroenterology. 2005;11(14).
23. Ilyas M, Tomlinson IPM, Rowan A, Pignatelli M, Bodmer WF. β-Catenin mutations in cell lines established from human colorectal cancers. Proceedings of the National Academy of Sciences of the United States of America. 1997;94(19).
24. El-Bahrawy M, Poulsom SR, Rowan AJ, Tomlinson IT, Alison MR. Characterization of the E-cadherin/catenin complex in colorectal carcinoma cell lines. International Journal of Experimental Pathology. 2004;85(2).
25. Bao R, Christova T, Song S, Angers S, Yan X, Attisano L. Inhibition of Tankyrases Induces Axin Stabilization and Blocks Wnt Signalling in Breast Cancer Cells. PLoS ONE. 2012;7(11).
26. Clevers H. Wnt/β-Catenin Signaling in Development and Disease. Vol. 127, Cell. 2006.
27. Rubinfeld B, Albert I, Porfiri E, Fiol C, Munemitsu S, Polakis P. Binding of GSK3beta to the APC-beta-catenin complex and regulation of complex assembly [see comments]. Science. 1996;272(5264).
28. Bahrami A, Amerizadeh F, ShahidSales S, Khazaei M, Ghayour-Mobarhan M, Sadeghnia HR, et al. Therapeutic Potential of Targeting Wnt/β-Catenin Pathway in Treatment of Colorectal Cancer: Rational and Progress. Journal of Cellular Biochemistry. 2017;118(8).
29. Kawanishi-Tabata R, Lopez F, Fratantonio S, Kim N, Goldblum J, Tubbs R, et al. Telomerase activity in Stage II colorectal carcinoma. Cancer. 2002;95(9).
30. Cao Y, Bryan TM, Reddel RR. Increased copy number of the TERT and TERC telomerase subunit genes in cancer cells. Vol. 99, Cancer Science. 2008.
31. Smogorzewska A, van Steensel B, Bianchi A, Oelmann S, Schaefer MR, Schnapp G, et al. Control of Human Telomere Length by TRF1 and TRF2. Molecular and Cellular Biology. 2000;20(5).
32. Mir SM, Tehrani SS, Goodarzi G, Jamalpoor Z, Asadi J, Khelghati N, et al. Shelterin complex at telomeres: Implications in ageing. Vol. 15, Clinical Interventions in Aging. 2020.
33. Muñoz-Fontela C, Mandinova A, Aaronson SA, Lee SW. Emerging roles of p53 and other tumour-suppressor genes in immune regulation. Vol. 16, Nature Reviews Immunology. 2016.
34. Raynaud CM, Jang SJ, Nuciforo P, Lantuejoul S, Brambilla E, Mounier N, et al. Telomere shortening is correlated with the DNA damage response and telomeric protein down-regulation in colorectal preneoplastic lesions. Annals of Oncology. 2008;19(11).
35. Alwarthan HAM, Anazi MSAL, Parine NR, Bhat RS, Alamro G, Aljarbou F, et al. The expressional level of tankyrase-1 gene and its regulation in colorectal cancer in a Saudi population. Biocell. 2019;43(2).
36. Gelmini S, Poggesi M, Pinzani P, Mannurita SC, Cianchi F, Valanzano R, et al. Distribution of Tankyrase-1 mRNA expression in colon cancer and its prospective correlation with progression stage. Oncology Reports. 2006;16(6).
37. Zhang Y, Toh LL, Lau P, Wang X. Human telomerase reverse transcriptase (hTERT) is a novel target of the Wnt/β-catenin

pathway in human cancer. Journal of Biological Chemistry. 2012;287(39).
38. Tuominen VJ, Ruotoistenmäki S, Viitanen A, Jumppanen M, Isola J. ImmunoRatio: A publicly available web application for quantitative image analysis of estrogen receptor (ER), progesterone receptor (PR), and Ki-67. Breast Cancer Research. 2010;12(4).
39. Jung CK, Jung JH, Lee A, Lee YS, Choi YJ, Yoon SK, et al. Diagnostic use of nuclear β-catenin expression for the assessment of endometrial stromal tumors. Modern Pathology. 2008;21(6).
40. Yu Z, Weinberger PM, Provost E, Haffty BG, Sasaki C, Joe J, et al. β-Catenin functions mainly as an adhesion molecule in patients with squamous cell cancer of the head and neck. Clinical Cancer Research. 2005;11(7).
41. Padhi S, Saha A, Kar M, Ghosh C, Adhya A, Baisakh M, et al. Clinico-Pathological Correlation of β-Catenin and Telomere Dysfunction in Head and Neck Squamous Cell Carcinoma Patients. Journal of Cancer. 2015;6(2).
42. Cawthon RM. Telomere measurement by quantitative PCR. Nucleic acids research. 2002;30(10).
43. Chao A, Tsai CL, Jung SM, Chuang WC, Kao C, Hsu A, et al. BAI1-Associated Protein 2-Like 1 (BAIAP2L1) Is a potential biomarker in ovarian cancer. PLoS ONE. 2015;10(7).
44. Zhang M, Shi J, Huang Y, Lai L. Expression of canonical WNT/β-CATENIN signaling components in the developing human lung. BMC Developmental Biology. 2012;12.
45. Zhao X, Zhang C, Le Z, Zeng S, Pan C, Shi J, et al. Telomerase reverse transcriptase interference synergistically promotes tumor necrosis factor-related apoptosis-inducing ligand-induced oral squamous cell carcinoma apoptosis and suppresses proliferation in vitro and in vivo. International Journal of Molecular Medicine. 2018;42(3).
46. Pal D, Sharma U, Singh SK, Kakkar N, Prasad R. Over-expression of telomere binding factors (TRF1 & TRF2) in renal cell carcinoma and their inhibition by using SiRNA induce apoptosis, reduce cell proliferation and migration invitro. PLoS ONE. 2015;10(3).
47. Butler KS, Hines WC, Heaphy CM, Griffith JK. Coordinate regulation between expression levels of telomere-binding proteins and telomere length in breast carcinomas. Cancer Medicine. 2012;1(2).
48. Izgi A, Gunal A, Yalcin S, Gunduz U. Telomere 1 (POT1) gene expression and its association with telomerase activity in colorectal tumor samples with different pathological features. Biomedicine and Pharmacotherapy. 2014;68(7).
49. Wang T, Mei SC, Fu R, Wang HQ, Shao ZH. Expression of shelterin component POT1 is associated with decreased telomere length and immunity condition in humans with severe aplastic anemia. Journal of Immunology Research. 2014;2014.
50. Bellon M, Datta A, Brown M, Pouliquen JF, Couppie P, Kazanji M, et al. Increased expression of telomere length regulating factors TRF1, TRF2 and TIN2 in patients with adult T-cell leukemia. International Journal of Cancer. 2006;119(9).
51. Roy S, Liu F, Arav-Boger R. Human cytomegalovirus inhibits the PARsylation activity of tankyrase—a potential strategy for suppression of the wnt pathway. Viruses. 2015;8(1).
52. Grabowski P, Hultdin M, Karlsson K, Tobin G, Åleskog A, Thunberg U, et al. Telomere length as a prognostic parameter in chronic lymphocytic leukemia with special reference to VH gene mutation status. Blood. 2005;105(12).

Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/81664