

Investigation of the hTERT Amplification as a Prognostic Marker in Patients Effectuated with Breast in Ardabil

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(Received: 08 February 2016; accepted: 16 March 2016)

Breast cancer is the most common cancer among the women and makes up one-third of cancers. Telomerase enzyme is a ribonucleoprotein with reverse transcriptase activity that adds TTAGGG repeated sequences to the ends of the chromosomes. The expression of the catalytic subunit of the enzyme (*hTERT*) in cancer cell lines and different human tumors is shown. So, in this study, the proliferation of copies of the *hTERT* gene in primary breast cancer was studied. Forty five Paraffin tissue samples from breast cancer patients and forty five Paraffin tissue samples from breast non-neoplastic patients was provided from Ardabil Imam Khomeini Hospital's Pathology section and DNA samples were extracted with phenol-chloroform manually, then Real Time PCR was done with *hTERT* Forward, and Reverse primers and *GAPDH* Forward, and Reverse. The tumor sample was compared with the non-tumor one to investigate proliferation of copies of the *hTERT* gene as a prognostic indicator in patients with primary breast cancer. Real time PCR curve analysis for *hTERT* and *GAPDH* genes in tumor samples compared with non-tumor samples showed that, there is no statistical deference's between them ($p=0.322$). The point of the best cut-off value was at >18.1 where sensitivity was 60 and specificity was 58. The area under the ROC curve (AUC) was 0.555. For data analysis Spss statistical software was used. Our current studies on results of amplification *hTERT* gene, in comprising tumors samples with non-tumors is indication of early prognosis in primary breast cancer patients. While, amplification of *hTERT* gene in breast cancer patients compared to the control group indicates that there is no statistical deference's between them and it couldn't be considered as prognosis factor for the primary breast cancer patients. According to conducted research it could be suggested that the *hTERT* gene may be promoted through telomerase activity, but increasing the copy number in various tumor cell line is not always dependent on telomerase activity and it likely could have an independent activity.

Keywords: Breast cancer, Telomerase, *hTERT* gene.

Breast cancer is the most common malignant disease in women all over the world and constitutes one-third of cancers and after lung

cancer is considered the second leading cause of cancer mortality in women^{1,2}.

This disease is increased in Iran and since 1999 has the first country rank among recorded cancers^{3,4}. Due to lack of organized screening and training programs for initial and early detection of breast cancer in Iran, about 70 % of Iranian women

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are diagnosed in dangerous stages of the disease⁵. According to the cancer registration, breast cancer in Ardabil is the most common one, following esophagus and stomach cancers⁶. In human and vertebrates, telomere is composed of double strands with six repeated sequences, which includes G-rich single-stranded overhang at the 3' end. Telomere protects the end of chromosome from breakage of the uncapped DNA, recombination, fusion^{2,7,8}

Due to the existence of a specific structure at the end of the chromosome, DNA polymerase enzyme is unable to complete replication of the (End replication problem) end of the 3' lagging strand. As a result, in every cell division, the human telomere loses 50 to 200 bp.

Telomerase enzyme is a ribonucleoprotein complex of telomere-specific reverse transcriptase activity that uses an RNA template for adding TTAGGG repeated sequences to the ends of the chromosomes, and compensates for the loss of the telomere length. So telomeres are replicated by the telomerase enzyme⁹⁻¹⁵.

Human telomerase enzyme activity is composed of the human telomerase reverse transcriptase (*hTERT*), human telomerase RNA (*hTR*) and Dyskryn¹⁶.

Telomerase enzyme activity does not exist in normal somatic cells, but it is seen in 85% - 90% of human cancers, including more than 95% of breast cancers, which is essential for continued proliferation¹⁷. A limited number of cancers (15%) preserve telomeres through recombination mechanism with an alternative of telomere length (ALT)¹⁸.

hTERT is expressed only in the telomerase cells and is not expressed in differentiated cells^{19,20}. *hTERT* gene will amplify abundantly in human tumors and tumor cell lines. This result implies that an increase in copy numbers of *hTERT* gene, can be involved in the regulation of telomerase expression in the immortalized cells^{21,22}. It is also shown that *hTERT* is a decisive factor for controlling telomerase activity^{20,23,24,25}.

Reproduction of the catalytic subunit of the enzyme (*hTERT*) in cancer cell lines and different human tumors is shown. So, in this study, the proliferation of copies of the *hTERT* gene in primary breast cancer was studied.

MATERIALS AND METHOD

Forty five breast cancer formalin fixed paraffin embedded (FFPE) specimens obtained from the Department of surgery, Imam Hospital, Ardabil, Iran. All patients signed detailed consent forms before the study was conducted. The experimental samples were pre-made on standard slides with 5 micron thick FFPE tissues using the standard method by the Department of Pathology, Imam Hospital.

3-5 slices of 5 micron from selected samples placed in the 1.5 ml micro-tube and DNA samples were extracted with phenol-chloroform manually with using xylol, ethanol, Layzyz buffer, proteinase K, phenol saturated, chloroform - isoamyl alcohol, sodium acetate, isopropanol and the finally 50 micro-liter of distilled water added.

Then the sample for *hTERT* gene put through PCR. For each process, 120 μ l of buffer 10 X, 36 μ l of MgCl₂, 24 μ l of dNTPs, 1 μ l of primers Forward (F) and Reverse (R), 0.1 μ l of the enzyme Taq DNA polymerase and 2 μ l of DNA was used.

Sequences of primers used for F = 5', AGTGGAGACAGGCGCAT3', and R = 5', ATGGTGAGTGCTACATGGTGA3',

Samples that were put through PCR processed in the beginning at 95°C for 30 min, then 35 cycles of 95°C for 30 sec, 35 cycles of 56°C for 30 sec, 35 cycles of 72°C for 30 sec, and finally at 72°C for 7 min. PCR products were electrophoresed at 0.01 agarose gel.

Then all of the samples in addition to *hTERT* gene for GAPDH gene with primer sequences F=5'CTCTCTGCTCCTCCTGTTTCGAC 3' and R=5'TGAGCGATGTGGCTCGGCT 3' were gone through Real Time PCR process. Forty five tumor samples and forty five non-tumor samples were compared to increased amplification of *hTERT* gene are reviewed as a prognostic marker for the Primary breast cancer patients.

Samples were put through Real Time PCR in the beginning at 50°C for 2 min, then at 95°C for 10 min, 60 cycles of 95°C for 15 sec and finally 60 cycles of 60°C 1 min.

RESULTS

In this experiment, Forty five paraffin-embedded tumor samples from breast cancer

patients and 45 paraffin tissue samples from control group was provided and investigations were carried out on them , the results are as follows .

After the DNA tumor and non- tumor samples was extracted, PCR was performed to ensure the absence of primer dimmer. Then the PCR products were analyzed by gel electrophoresis.

To check the purity of the DNA extracted from nano- drop device was used. Absorbance

reading DNA, extracted DNA quality can be achieved. Relative absorbance (Optical Density: OD) DNA at wavelengths 260 to 280 nm was measured. Higher OD at wavelengths 280/260 of 1.8 is an indicator of DNA purity . Different concentrations of DNA samples, using the formula $C1.V1 = C2.V2$ Nanodrop apparatus were identical and were given 20 ng micro liter⁵.

Quantification increased amplification of *hTERT* and *GAPDH* gene in breast cancer patients

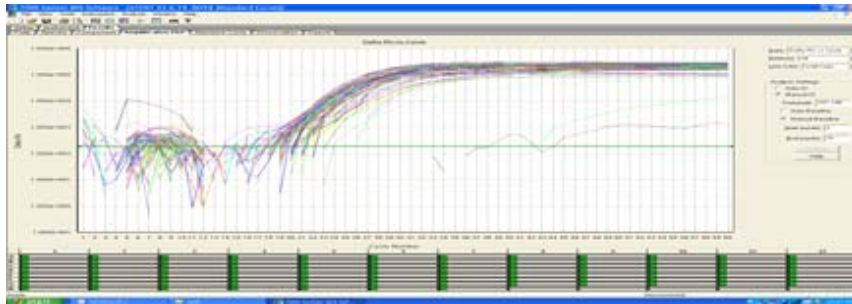


Fig. 1. The curve increased amplification of hTERT gene in samples from patients and control group in the experimental Real time PCR. The amount of fluorescence emitted increased during the cycle of the of increased PCR products amounts

Table 1. hTERT gene amplification in cancer and control group

hTERT	>= 18.2	<18.2	Total
control group	18 (40%)	27 (60%)	45 (100%)
Cancer group	26(57.8%)	19 (42.2%)	45 (100%)
Total	44 (100%)	46 (100%)	90 (100%)

P=0.092

compared with those without tumor was performed. Real time PCR curves amplification of *hTERT* gene in tumor and non- tumor samples, is shown in Figure 1.

hTERT amplification in 19 of Cancer patients is less than 18.2 (%42.2) and in 26 of them it is more than 18.2. (%57.8). hTERT amplification in 27 patient from control group is less than 18.2 (%60) and in 18 of those patients it is more than

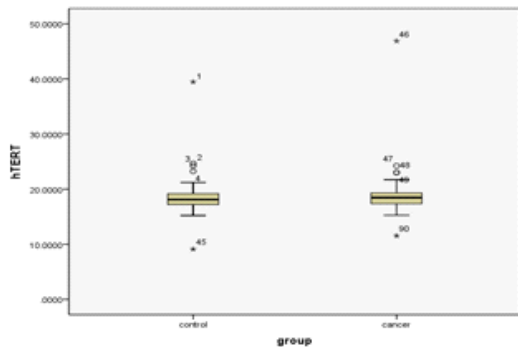


Fig. 2. Amplification of hTERT gene in breast cancer patients compared to the Control group indicates that, there is no statistical association existed between them.

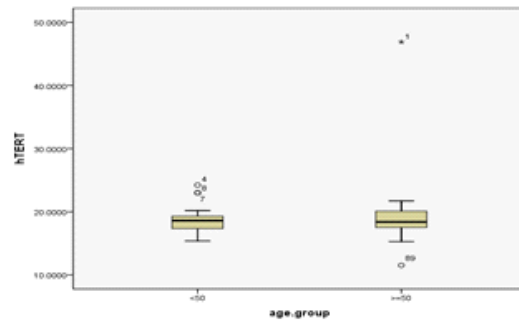


Fig. 3. Boxplot diagram age group indicates that there is no differences between two age groups (P=0.261)

18.2 (%40), which proves that there is no deference with regard to amplification of hTERT between control groups and Cancer Patients. Amplification of hTERT gene in cancer and control group, is shown Table 1.

The average numbers of hTERT on group of Cancer Patient are 19 ± 4.8 and in control group these numbers were 18.6 ± 4 which show that, there is no visible deference in computed average numbers between control group with] group of cancer patients (Figure 2). In cancer patients and control groups the OR=1.4 and the confidence interval (CT) is equal with 0.9 – 2.2 which shows no noticeable deference between two groups.

Average numbers of hTERT in over 50 years old age groups are estimated 20 ± 7.6 and in under 50 years old age groups are 18 ± 3.7 which indicates that there is no deferences between two age groups (P=0.261) (Figure3). Average numbers

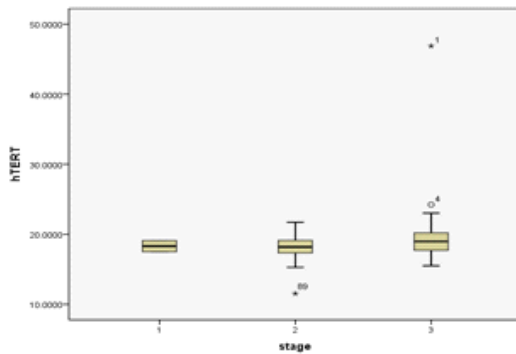


Fig. 4. hTERT boxplot diagram according to stage which indicates that there is no sign of statistical deference (P=0.1)

of GPDH in age group over 50 is 23.3 ± 2.6 and in age group under 50 it is 23.6 ± 2.8 which indicates that there is no sign of statistical deference (P=0.76).

The ratio of existing hTERT , in stage I (18.3 ± 1.1), stage II (17.2 ± 3) and stage III (20.8 ± 6.9), even though there is more hTERT in stageIII, but there is no statistical deferences here (P=0.1) (Figure 4).

Descriptive data of all samples of the Cancer Patients, at stage one, 2 cases (% 4.4), at stage two, 25 cases (% 55.6) at stage three, 18 cases (% 40) are shown (Table2).

A receiver operating characteristic curve (ROC) was developed to evaluate the diagnostic performance of hTERT gene. Each unique hTERT value was used as a cut point to calculate sensitivity and specificity values defining the curve and the area under the curve (AUC) and 95% CI for the area (Table3). The point of the best cut-off value was at >18.2 where sensitivity was 60 and specificity was 57.8 (Figure 5). The area under the ROC curve (AUC) was 0.555(Figure 6).

Table 2. The condition of the stages

	Frequency	Percent	
Valid	1	2	4.4
	2	25	55.6
	3	18	40.0
Total	45	100.0	

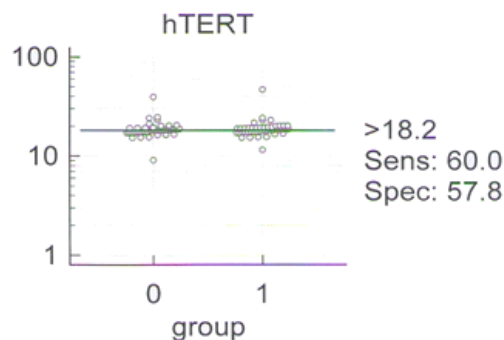


Fig. 5. The point of the best cut-off value was at >18.2 where sensitivity was 60 and specificity was 57.8

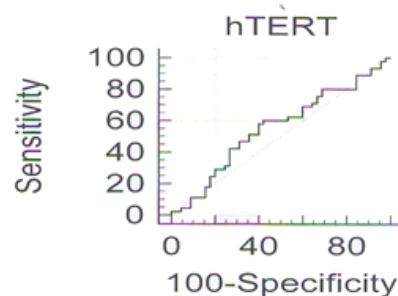


Fig. 6. Amplification of hTERT diagnostic accuracy. ROC curve analysis showing the diagnostic performance of ratio for discriminating patients with breast cancer from controls (AUC=0.555)

Table 3. Area under the ROC curve (AUC)

0.555	Area under the ROC curve (AUC)
0.0616	Standard Error
0.447 to 0.660	95% Confidence interval
0.894	Z statistic
0.3714	Significance level P (Area = 0.5)

Interpretation of results was done using the comparative CT method for quantitation according to this arithmetic formulas:

$$\Delta CT = C_{T \text{ target}} - C_{T \text{ reference}}$$

$$hTERT_{\text{adjusted}} = 2^{-\Delta ct}$$

The mean total in Cancer Groups 20273 ± 135993 and in control group it is 91 ± 601 which shown that there is no deference between two groups. (p=0.322).

The average stage in 2 person is 0.0084 ± 0.0062, in 25person 0.11 ± 0.17 and in 18 person 50681.7 ± 215024 wich shown no statistical deferences among them (P=0.483). The mean age group on 29 person from under 50 is 0.0934 ± 0.16737 and on 16 person from over 50 is 57017 ± 228067.2 which proves that there is no meaningfull diferences between two groups (P=0.181). The average quantity on 11 of patients without 0.12 ± 0.25 and on 34 of the patients have 26831.5 ± 156453 that there is no statistical deferences between two groups (p=0.575).

DISCUSSION

Breast cancer is the most common cancer in women the world. So to reduce mortality from breast cancer, the development of new methods for the treatment, prevention or diagnosis of breast cancer is essential²⁶.

Telomerase is a ribonucleoprotein enzyme consisting of two parts. The first part, subunit active catalytic protein, *hTERT* reverse transcriptase activity that adds telomere repeated sequences to the ends of the chromosomes and that is essential to the continued growth of tumor cells. *hTERT* gene is increasingly amplified in human tumors and tumor cell lines.

The secondary part of the template RNA in humans is called *hTR* and used as a template for telomere synthesis. Telomerase is an therapy target

for ideal anticancer because of its activities in more than 90 % of human cancers, there are including more than 95 % breast cancer, , whereas most somatic cells are indistinguishable²⁷.

Some studies concerning amplification of *hTERT* gene has been associated with cancer cell lines. For example , according to the study U.S. researchers amplification of the *hTERT* gene was observed in 31 % the tumor cell , and 30 % primary tumors , 8 of 21 lung tumors, 3 of 10 cervical tumors, 5 of 19 breast cancer and 1 of 18 neuroblastomas. In addition, 50% cell lines and 22% primary tumors displayed of *hTERT* gene copies with 4-3 copies cell, The present findings suggest that *hTERT* locus may be target for amplification during tumorigenesis and probably, genetic events may help to regulate telomerase activity in human tumors²⁸.

Ying and colleagues studies, amplification of *hTERT* gene was observed in cell lines tumors and various human cancers, as well as a mechanism of telomerase activation is introduced. It is remarkable that telomerase activity increases in both of the primary cells and cancer²⁹.

Thomas and his colleagues, have also concluded the amplification of *hTERT* gene in Lanfobelastic acute leukemia (ALL) and non Lanfobelastic leukemia (ANLL). Quantitative analysis showed that leukemia cells have many numbers of the copies of *hTERT*, *hTERC* are normal PBL. The results indicate that telomerase activity in leukemia cells is associated with amplification of *hTERT* gene, *hTERC*³⁰.

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According to studies conducted by Knvutla and colleagues, amplification in both of the *hTERT* and *TERC* gene occurs in the majority of human cancers³¹.

In various studies, 25-31% of the cell line was examined. Copies of *hTERT* gene were shown in 5 d'' of cell. The observed cell line was derived of the norobelasma, breast cancer carcinoma, cervical cancer and lung cancer. In the bladder cell line and Epidermal carcinoma 3 d'' copies of *hTERT* has been reported³¹.

In primary tumors, increasing of the copies number *hTERT* identified in 12% norobelasma, 42% embryonal tumors (CNS), 22% Hpatocellular carcinoma, 30-63% lung cancer, , 24-30% of cervical cancers, 26% of breast cancers

and 48% of colon cancer. Further analysis of the 2.6 copies number of *hTERT* is shown in leukemia cells³¹.

Zhang and colleagues Saretzki have been reported a link between two *TERT* genes and telomerase activity in multiple cell line and primary tumors, the study Palmqvist primary tumors of samples and other studies of the stability of human breast epithelial cells and human foreskin fibroblasts (Cao et al. unpublished, 2007) no correlation were not observed between the copies number of *hTERT* genes and telomerase activity. No relationship could be observed a complex the telomerase enzyme, consisting of components and multiple evidence, telomerase activity is limited to the level two components (*hTERT* and *hTR*)³².

In a variety of tumors, increasing the copy number of the *TERT* has clinical relevance and prognosis For example, Zhu and his colleagues have shown that Lung Cancer Patients with increased amplification of *hTERT* with reoccurs will not last long. In melanoma, copies of increased amplification of *hTERT* correlated to subunits of melanoma and era of metastasis. Also the research shows that, Amplefication of *hTRET* in different cell line normally is independent of telomerase activities³¹.

Richard and his colleagues in 2005 to increase the hTERT gene copy number in samples from 64 colorectal carcinomas were reviewed and increased copy number (≥ 3 hTERT gene copies/nucleus) were observed in 31(48%) cases. No correlation was found between hTERT gene copy number and hTERT RNA expression or telomerase activity. Data show increase in copy number of the hTERT gene in colorectal carcinoma was the result of unstable telomerase activity levels was not associated³³.

In 2008, based on studies in Russia, the hTERT DNA copy number of the 33 studied tumors compared to normal tissues was unchanged. Similar results was achieved with squamous cell cervical carcinomas (SCC) cell lines in human papillom virus(HPV)genomes. However, the activation of hTERT expression was discovered in 80% of cases (37/46, $p < 0.001$). There was no relationship between the degree of mRNA increase and the tumor size and/or prevalence metastases. No hTERT gene expression was shown in 20% of cases(9/46), while the control GAPDH expression has remained

unchanged. The conclusion was that, the frequent activation of hTERT expression in SCC is not linked with gene amplification³⁴.

Our current studies on results of amplification *hTERT* gene, in comprising tumors samples with non-tumors is indication of early prognosis in primary breast cancer patients. While amplification of *hTERT* gene in breast cancer patients compared to the control group indicates that there is no statistical deference's between them and it couldn't be considered as prognosis factor for the primary breast cancer patients.

According to conducted research it could be suggested that the *hTERT* gene may be promoted through telomerase activity, but increasing the copy number in various tumor cell line is not always dependent on telomerase activity and it likely could have an independent activity.

REFERENCES

1. Alexandra, J, *The genetics of breast cancer, Surgery.*, 2010; **28**: 103-106.
2. Lippman, M, oncology and Hematology, Harrison's principles of internal medicine., 2008: 479-747.
3. Fatemeh A. V., Mireille J.M., Mohsen, M, The effect of demographic and lifestyle changes on the burden of breast cancer in Iranian women, A projection to 2030, *The Breast.*, 2012; 1-5.
4. Garcia, M., Jemal, A and Ward, E, American cancer society, *Cancer facts and figures*, 2007; **63**: 22-26.
5. Harirchi, I., ghaemmaghami, F, Patiner delay in women presenting with advannced breast cancer : an Iranian study, *Public Health.*, 2005; **119**: 885-891.
6. Babaei, M., Jaafarzadeh, H., Sadjadi, A., Samadi, F., Yazdanbod, A., Fallah, M, Cancer Incidence and Mortality in Ardabil : Report of an Ongoing Population-Based Cancer Registry in Iran, *Iranian. J. Publ Health.*, 2009; **38**(4): 35-45.
7. De Lange, T, Shiue, L, Structure and variability of human chromosome ends, *Mol. Cell. Boil*, 1990; **10**: 518-527.
8. Hiyama, E., Hiyama, K, Telomere and Tlomerase n stem cell, *Br. J. Cancer.*, 2007; **96**(7): 1020-1024.
9. Arkhipova, I.R, pyatkov, K.I, Retroelements containing introns in diverse invertebrate taxa, *Net. Genet.*, 2003; **33**: 123-124.
10. Momey, M., Khorramizadeh, MR., Ghaffari, Sh., Yousefi, M., Yekaninejade, MS., Esmaeili, R,

- Effects of silibinin on cell growth and invasive properties of a human hepatocellular carcinoma cell line, HepG-2, Through inhibition of extracellular signal-regulated kinase 1/2 phosphorylation, *Eur. J. pharmacol.*, 2008, **591**(1-3): 13-20.
11. Steven, E., Artandi, A., and Ronald, A., Telomerase and telomerase in cancer, *Carcinogenesis*, 2010; **31**(1): pp. 9-18.
 12. Yang, C., Przyborski, S., A key role for telomerase reverse transcriptase unit in modulating human embryonic stem cell proliferation, *Stem Cells*, 2008; **26**: 850-863.
 13. Bogness, J.F., Zhou, C., Estrogen-receptor-dependent regulation of telomerase activity in human endometrial cancer cell lines, *Gynecol. Oncol.*, 2006; **103**: 417-424.
 14. Chen, J.L., Greider, C.W., Telomerase RNA structure and function: implications for dyskeratosis congenital, *Trends Biochem Sci.*, 2004; **29**: 183-192.
 15. Nosek, I., Kosa, P., On the origin of telomerase: a glimpse at the pre-telomerase world, *BioEssay*, 2006; **28**: 182-190.
 16. Fu, D., Collins, K., Purification of human telomerase complexes identifies factors involved in telomerase biogenesis and telomere length regulation, *Mol. Cell*, 2007; **28**: 773-785.
 17. Sledz, C.A., Holko, M., Veer, M.J., Silverman, R.H., Williams, B.R., Activation of the interferon system by short-interfering RNAs, *Nat cell biol.*, 2003; **5**(9): 834-839.
 18. Kennon, R., Poynter, Patrick, C., Sachs, A., Taylor, B., Genetic inhibition of telomerase results in sensitization and recovery of breast tumor cells, *Mol Cancer Ther.*, 2009; **8**: 1319-1327.
 19. Buseman, C. M., Wright, W. E., Shay, J. W., Is Telomerase a viable target in cancer?, *Mutation Research*, 2011; **730**: 90-97.
 20. Ying, C., Lily, I. H., Amanda S. N., Amplification of Telomerase Reverse Transcriptase Gene in Human Mammary Epithelial Cells with Limiting Telomerase RNA Expression Levels, *Cancer Res.*, 2008; **68**: 3115-3123.
 21. De Lange, T., Protection of mammalian telomeres, *Oncogene*, 2002; **21**: 532-540.
 22. Stewart, S.A., Ben-Porath, I., Erosion of the telomeric single strand overhang at replicative senescence, *Nat. Genet.*, 2003; **33**: 492-496.
 23. Anedchenko, E., Oparina, N., Dmitriev, A., Krasnov, G., Pavlova, L., Alexanderova, N., Kisseljov, F., Senchenko, V., Activation of the *hTERT* expression in squamous cell cervical carcinoma is not associated with gene amplification, *Onco Rep.*, 2008; **20**(2):469-74.
 24. Anju, Z., Chengyun, Z., Charlotta, L., Frequent Amplification of the Telomerase Reverse Transcriptase Gene in Human Tumors, *Cancer Res.*, 2000; **60**: 6230-6235.
 25. Zhu, C.Q., Cut, J.C., Liu, N., Lau, D., Shepherd, F., Squire, J., and Tsao, M.S., Amplification of telomerase (*hTERT*) gene is a poor prognostic marker in non-small-cell lung cancer, *British Journal of Cancer*, 2006; **94**: 1452-1459.
 26. Brunicaudia, F., Andersen, DK, Schwartz's principles of surgery, Mc Graw Hill., 2005: 451-499.
 27. Boyd, N.F., Jensen, A.M., Cooke, G., Mammographic densities and the prevalence and incidence of histological types of benign breast diseases, *Eur. J. cancer. Prev.*, 2000. **9**, 15-28.
 28. Buseman, C. M., Wright, W. E., Shay, J. W., Is Telomerase a viable target in cancer?, *Mutation Research*, 2011; **730**: 90-97.
 29. Anju, Z., Chengyun, Z., Charlotta, L., Frequent Amplification of the Telomerase Reverse Transcriptase Gene in Human Tumors, *Cancer Res.*, 2000; **60**: 6230-6235.
 30. Tomasz, N., Danuta, J., Mariola, Z., Monika, P., Krzysztof, L., Jolanta, R., Karina, N., Przemyslaw, M., and Jerzy, N., Amplification of *hTERT* and *hTERC* genes in leukemic cells with high expression and activity of telomerase, *Oncology Reports*, 2006; **16**: 301-305.
 31. Yi, X., Tesmer, V.M., Both transcriptional and posttranscriptional mechanisms regulate human telomerase template RNA levels, *Mol. Cell. Biol.*, 2000; **19**: 3989-3997.
 32. Ying C., Tracy M., Roger R.R., Increased copy number of the TERT and TERC telomerase subunit genes in cancer cells, *Japanese Cancer Association*, 2008; **99**: 1092-1099.
 33. Richard P., Anju Z., Dawei X., Irina G., Karl-Fredrik N., Astrid G., Ake Ö., Roger S., Göran R., *hTERT* gene copy number is not associated with *hTERT* RNA expression or telomerase activity in colorectal cancer, *Int. J. Cancer*, 2005; **116**: 395-400.
 34. Ekaterina A., Nina O., Alexei D., George K., Larisa P., Natalya A., Fjodor K., Vera S., Activation of the *hTERT* expression in squamous cell cervical carcinoma is not associated with gene amplification, *Oncology Reports*, 2008; **20**: 469-474.