

[Evolutionary hypothesis of telomere length in primary breast cancer- and brain tumor- patients: A tracer for Genomic-tumor heterogeneity and instability](#) 2011 Mar 8. [Epub ahead of print]Cell Biol Int.

Abstract . [Atri M](#) , [Kamalian N](#) , [Mehrazin M](#) , [Kheirollahi M](#) , [Mehdipour P](#)

It was previously reported that tumor samples had shorter telomeres than the surrounding normal tissue. Hereby, the initial sign of correlation between malignant tissue and telomere behavior could be noticed. Bridging knowledge between germ- and somatic- cells could facilitate understanding cellular evolution. The aim of our investigation was to provide evidence for the evolutionary hypothesis of telomere length in primary breast cancer and brain tumors which might be applied as a prognostic and/or predictive marker. DNA extraction from the frozen tissues was performed using high pure PCR template preparation kit. Standard protocol of Telo TTAGGG Telomere Length Assay kit, a non-radioactive chemiluminescent assay, was used. The protein expression in extracted cells was analyzed by immuno-Fluorescence. We also detected telomerase activity. The genomic/ tumor ratio (G/T) for telomere length in two group of patients affected with primary breast cancer (BC) and primary brain tumor (BT) revealed significant differences in both BC patients (G/T ratio: