NEAT1, a long non-coding RNA, controls cell survival and is up-regulated in breast cancer

Z.A. Almnaseer1, M. Mourtada-Maarabouni1.

1Keele University, School of Life Sciences, Newcastle-Under-Lyme, United Kingdom.

Background:

Nuclear Enriched Abundant Transcript 1 (NEAT1) is a nuclear long-non coding RNA transcribed from the familial tumour syndrome multiple endocrine neoplasia (MEN) type 1 locus on chromosome 11. NEAT1 is reported to be overexpressed in prostate cancer and a direct transcriptional target of hypoxia-inducible factor in breast cancer cells. The aims of this study were to determine: i) the effects of silencing NEAT1 on breast cancer cell survival, ii) the effects of NEAT1 silencing on the expression of two genes located on the same chromosome, iii) the levels of NEAT1 in breast cancer samples.

Materials and Methods:

MCF7 and MDA-MB 231 cells were transfected with NEAT1 antisense oligonucleotides (ASO), controls received scrambled oligonucleotide. In some experiments, cells were exposed to ultraviolet-C (UV-C) light post-transfection to induce apoptosis, and then culture viability and apoptosis were assessed. Commercial Breast Cancer cDNA Arrays were used to evaluate the levels of NEAT1 in breast cancer samples. NEAT1 expression was evaluated by qRT-PCR TaqMan® analysis, using relative standard curve method.

Results:

In MCF7 and MDA-MB-231 cells, siRNA-mediated silencing of NEAT1 reduced basal survival. NEAT1 silencing enhanced UV- induced cell death and this response was associated with a significant increase in the expression levels of Estrogen-Related Receptor Alpha (ESRRA) and BAD (BCL2-Associated Agonist of Cell Death). NEAT1 levels were found to be significantly increased in breast cancer samples.

Conclusion:

Overall, the results suggest that NEAT1 regulates cell survival and the expression of neighbouring genes in ER+ and TNBC cells. The substantial increase in NEAT1 expression levels in breast cancer tissues suggests that NEAT1 may function as an oncogene