Proceedings International
Platinum Open Access Journal (ISSN 2668-6384)

Proceedings, Abstract
Volume 5, Issue 1, 2023, 33
https://doi.org/10.33263/Proceedings51.033

lncRNA Profile in Glioblastoma Samples and Cell Lines †

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† Presented at 2nd Edition of the OncoHub Conference – Connecting Scientists and Physicians for Next Generation Cancer Management, Poiana Brașov, Brașov, 21-23 September 2022

Received: 10.12.2022; Accepted: 20.12.2022; Published: 5.01.2023

Abstract: Glioblastoma is the most frequent and aggressive cancer affecting the central nervous system. Long non-coding RNAs (lncRNAs) aberrant expression correlates with the malignant transformation process, and it could help provide more accessible cellular targets in novel therapeutic approaches, considering the rise of personalized medicine. This study aimed to compare lncRNAs expression profile in U87 cell line to normal human astrocytes (NHA) and further investigate their expression in samples from patients. For this purpose, U87 and NHA were grown according to their specifications, and RNA was extracted from cell lines and patient samples. Due to the eloquence of brain tissue, peritumoral tissue was not available. Further, RNA was revers-transcribed, and cDNA was used for qRT-PCR. NRON, EMX2OS, ZFAS1, HAR1B, and TUG1 were tested using custom-made primers, and their expression was calculated using the $2^{-\Delta\Delta Ct}$ formula. lncRNAs expression revealed statistically significant ($p<0.05$) differences between the cell line and tumor samples, with all lncRNA expression levels, increased in patient samples compared to U87 cell line, although there are differences between samples and glioma line compared to NHA. The sharpest differences were noted in the case of NRON ($p=0.0213$), which had a ~2.5 fold increase in expression in patient samples, whereas in U87 was considerably lower. EMX2OS ($p=0.0234$) has a similar pattern in investigated samples, with a ~1.5-fold increase in lncRNA expression. Among the investigated lncRNAs, TUG1 had the most significant expression modification ($p=0.003$), decreasing both patient samples and the glioma cell line. Similarly, HAR1B ($p=0.429$) and ZFAS1 ($p=0.0377$) levels were decreased in U87 and tumor samples. Extending the sample pool and examining the downstream targets of this lncRNA could help reveal new molecular targets and prognostic/diagnostic markers that may help distinguish between less or more aggressive tumors.

Keywords: cancer; glioblastoma; lncRNA.

Funding

This research received no external funding.

Acknowledgments

This research has no acknowledgment.

Conflicts of Interest

The authors declare no conflict of interest.