Research Paper

Long intergenic non-coding LINC00657 regulates tumorigenesis of glioblastoma by acting as a molecular sponge of miR-190a-3p

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Keywords: LINC00657, glioblastoma, PTEN, miR-190a-3p
Received: December 1, 2018 **Accepted:** February 22, 2019 **Published:** March 5, 2019

ABSTRACT

To detect the aberrantly expressed long non-coding RNAs in glioblastoma, two pairs of glioblastoma and adjacent normal tissues were firstly analyzed by RNA sequencing. Long intergenic non-coding RNA LINC00657 was considered to play a vital role in glioblastoma based on the results of RNA sequencing. Hence, we aimed to investigate the mechanisms by which LINC00657 regulated the tumorigenesis of glioblastoma. The level of LINC00657 in 40 glioblastoma samples and glioblastoma cell lines was detected by RT-qPCR. LINC00657 was significantly decreased in patients with glioblastoma compared with adjacent normal tissues. Overexpression of LINC00657 inhibited proliferation, colony formation, invasion and migration in glioma cells via inducing apoptosis. Dual luciferase report assay indicated LINC00657 was the target of miR-190a-3p. Overexpression of LINC00657 greatly inhibited the relative amount of miR-190a-3p. Besides, miR-190a-3p was found to be a negative regulator of PTEN. Additionally, active-caspase 3 was increased in cells transfected with pcDNA3.1-LINC00657. Finally, *in vitro* results were further confirmed by *in vivo* studies using nude mice bearing with glioblastoma tumors. In conclusion, LINC00657 was effective in inhibiting glioblastoma by acting as a molecular sponge of miR-190a-3p to regulate PTEN expression. Therefore, targeting LINC00657 may serve as a potential strategy for the treatment of patients with glioblastoma.

INTRODUCTION

Glioma is considered to be the most common brain tumor in adults whose occupancy in primary neoplasms of the central nervous system (CNS) is nearly 70% [1]. Based on the definitions of World Health Organization (WHO), glioblastoma (GBM), which is known as WHO grade IV astrocytoma, accounts for about 55% of the adult diffuse glioma patient population [1]. Diagnostic biopsy or surgical is normally used as the first method for therapy. Then, chemotherapy and adjuvant radiation will be performed in the second step [2]. However, there are so many difficulties in complete resection. Furthermore, GBM is not sensitive to chemo-/radio-therapeutic agents [3]. The median survival of primary GBM is consider to be approximately 15 months [1]. Therefore, there is a great need to investigate the molecular mechanisms involved in GBM.

For human beings, the human genome is totally transcribed. Interestingly, the occupancy of protein-coding genes is about 2%. In addition, the rest of transcripts are known as non-coding RNAs containing long non-coding RNAs (lncRNAs) and microRNAs