FER1L4

Novel Long non-coding RNA Fer-1-like protein 4 (FER1L4) has been reported to play crucial regulatory roles in tumor progression.

FER1L4 (Fer-1 Like Family Member 4, Pseudogene) is a Pseudogene. Diseases associated with FER1L4 include Endometrial Cancer and Gastric Cancer.

Its clinical significance and biological role in osteosarcoma (OS) is completely unknown.

Fei et al. analyzed the expression levels of FER1L4 in tissues of OS patients and cell lines via quantitative RT-PCR (qRT-PCR). The effect of FER1L4 on cell proliferation, colony formation, migration and invasion was analyzed by cell counting kit-8 (CCK-8), colony formation, wound healing and transwell invasion assay, respectively. Novel targets of FER1L4 were selected through a bioinformatics soft and confirmed using a dual-luciferase reporter system and qRT-PCR. To detect the role of FER1L4 in vivo tumorigenesis, tumor xenografts were created.

They found that the expression of FER1L4 was significantly downregulated in OS tissues and cell lines; moreover, low expression of FER1L4 was associated with advanced tumor-nude-metastasis (TNM) stage, lymph node metastases, and poor overall survival. Functional assays showed that upregulation of FER1L4 significantly inhibited OS cell proliferation, colony formation, migration, and invasion in vitro, as well as suppressed tumor growth in vivo. Assays performed to determine the underlying mechanism, indicated that FER1L4 interacted directly with miR-18a-5p. Subsequently, they found that FER1L4 significantly increased PTEN expression, a known target of miR-18a-5p, in OS cells. Furthermore, PTEN was found to be down-regulated, and positively correlated with FER1L4 in OS tissues.

These findings suggest that FER1L4, acting as a competing endogenous RNA (ceRNA) of miR-18a-5p, exerts its anti-cancer role by modulating the expression of PTEN. Thus, FER1L4 may be a novel target for the prevention and treatment of OS [1].

In a study, data from The Cancer Genome Atlas was mined in order to investigate the association between FER1L4 expression and prognosis in patients with glioma. A short interfering (si)RNA targeting FER1L4 was transfected into U373-MG and U251 glioma cell lines, and cell viability, invasion and apoptosis were examined using CCK-8, Transwell and Annexin V-fluorescein isothiocyanate/propidium iodide assays, respectively. FER1L4 was significantly upregulated in high-grade glioma compared with low-grade glioma. Additionally, high expression of FER1L4 significantly predicted poor prognosis in patients with glioma. The expression of FER1L4 in glioma cell lines was significantly higher compared with that in normal astrocytes. Furthermore, by downregulating FER1L4 using siRNA, the invasiveness and viability of the glioma cells significantly decreased, while apoptosis significantly increased. The findings from the present study indicate that FER1L4 serves a role in the occurrence and progression of glioma, and could be used as a prognostic biomarker for this disease [2].

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2)
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