MALAT1

The metastases-associated lung adenocarcinoma transcript 1 (MALAT1) is a bona fide Long non-coding RNA (lncRNA). LncRNA MALAT1 was discovered as a prognostic factor for lung cancer metastases but also has been linked to several other human tumor entities.

A study aimed to determine the regulation of long non-coding RNA (lncRNA) MALAT1 on neuronal apoptosis during spinal cord injury (SCI) and to explore its possible mechanisms.

The motor ability of SCI rat models and apoptosis in spinal cord tissue were evaluated. Primary spinal cord neurons (SCNs) were isolated and treated with H2O2 before cell transfection. The apoptosis of SCNs and expression of PRDM5 and MALAT1 were also measured. The interactions among MALAT1, miR-199a-5p, and PRDM5 were detected.

The motor ability of SCI rats decreased significantly. The proportion of apoptotic neurons increased in damaged tissue and SCN, along with an increase in the expression of apoptosis-related proteins c-caspase-3/9, autophagy-related proteins (p62 and LC3 II/I ratio), and proinflammatory factors. Moreover, overexpression of MALAT1 and PRDM5 in damaged SCN resulted in an increased apoptosis rate of neurons, elevated expression of apoptosis-related proteins, and upregulated levels of inflammatory factors. However, miR-199a-5p overexpression/PRDM5 knockdown partially counteracted the effects of MALAT1 overexpression on H2O2-induced SCNs. In addition, MALAT1 negatively regulated miR-199a-5p, which targeted PRDM5.

LncRNA MALAT1 promotes neuronal apoptosis during SCI by regulating the miR-199a-5p/PRDM5 axis [1)].

Ren et al. aimed to investigate the association of long non-coding RNA metastases-associated lung adenocarcinoma transcript 1 (lnc-MALAT1) with acute ischemic stroke (AIS), and its association with disease severity, inflammation, and recurrence-free survival (RFS) in AIS patients. One hundred and twenty AIS patients and 120 controls were recruited. Venous blood samples from AIS patients (within 24 h after symptoms onset) and controls (at the entry to study) were collected to detect plasma lnc-MALAT1 expression by a real-time quantitative polymerase chain reaction. AIS severity was assessed by the National Institutes of Health Stroke Scale (NIHSS) score. Plasma concentrations of inflammation factors (including C-reactive protein (CRP), tumor necrosis factor α (TNF-α), interleukin (IL)-6, IL-8, IL-10, IL-17, and IL-22) were measured and RFS was calculated. lnc-MALAT1 expression was decreased in AIS patients compared to controls, and it had a close correlation with AIS (AUC=0.791, 95% CI: 0.735-0.846). For disease condition, lnc-MALAT1 expression negatively correlated with NIHSS score and pro-inflammatory factor expression (including CRP, TNF-α, IL-6, IL-8, and IL-22), while it positively correlated with anti-inflammatory factor IL-10 expression. Furthermore, lnc-MALAT1 expression was elevated in AIS patients with diabetes. For prognosis, no statistical correlation of lnc-MALAT1 expression with RFS was found, while a trend for longer RFS was observed in patients with lnc-MALAT1 high expression compared to those with lnc-MALAT1 low expression [2)].

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lncRNAs ZFAS1 and MALAT1 were significantly upregulated ($p < 0.05$), whereas lncRNAs LINC00261

and LINC01619 were significantly downregulated in SAH patients with CVS ($p < 0.05$) compared to SAH patients without cerebral vasospasm (CV). Pan et al. applied this lncRNA signature to retrospectively predict CVS in SAH patients (n = 38 for SAH patients without CVS, and n = 27 for SAH patients with CVS). The 4-lncRNA signature was found to be predictive in >40% of samples and the 2-lncRNA comprising MALAT1 and LINC01619 accurately predicted CVS in ~90% cases. These results are initial steps toward personalized management of SAH patients in clinics and provide novel CSF biomarkers that can substantially improve the clinical management of SAH patients [3].

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lncRNA MALAT1 plays an important role on glioma progression and prognosis and may serve as a convictive prognostic biomarker for glioma patients [4] [5].

In a study, Fu et al. found that Malat1 expression and autophagy activity were significantly increased in glioma tissues compared with adjacent normal tissues. Additionally, Malat1 level was positively correlated with the expression of LC3-II (autophagy marker) mRNA in vivo. In vitro assays revealed that Malat1 significantly promoted autophagy activation and cell proliferation in glioma cells. More importantly, inhibition of autophagy by 3-MA relieved Malat1-induced cell proliferation. These data demonstrated that Malat1 activates autophagy and increases cell proliferation in glioma. We further investigated the molecular mechanisms whereby Malat1 functioned on glioma cell autophagy and proliferation. We found that Malat1 served as an endogenous sponge to reduce miR-101 expression by directly binding to miR-101. Moreover, Malat1 abolished the suppression effects of miR-101 on glioma cell autophagy and proliferation, which involved in upregulating the expression of miR-101 targets STMN1, RAB5A and ATG4D. Overall, our study elucidated a novel Malat1-miR-101-STMN1/RAB5A/ATG4D regulatory network that Malat1 activates autophagy and promotes cell proliferation by sponging miR-101 and upregulating STMN1, RAB5A and ATG4D expression in glioma cells [6].

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