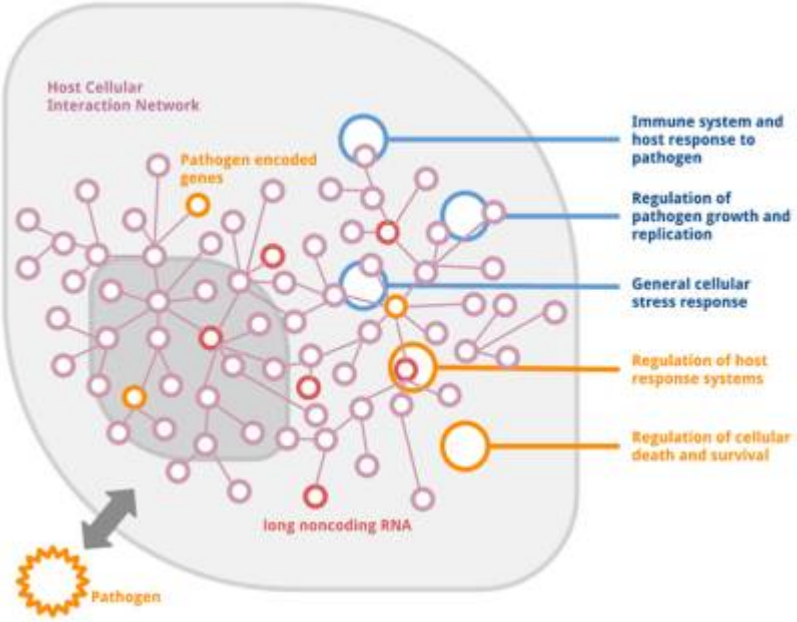
Long non-coding RNA



Long non-coding RNAs are RNA molecules that are longer than 200 nucleotides and do not code for proteins. They have been implicated in various cellular processes, including gene expression regulation at both the transcriptional and the post-transcriptional levels, and increasing evidence indicates that they play vital roles in a variety of disease-related cellular processes.

This somewhat arbitrary limit distinguishes long ncRNAs from small regulatory RNAs such as microRNAs (MicroRNAs), short interfering RNAs (siRNAs), Piwi-interacting RNAs (piRNAs), small nucleolar RNAs (snoRNAs), and other short RNAs.

Functions

Gene Regulation:

Transcriptional Regulation: LncRNAs can interact with DNA, RNA, and proteins to influence the transcriptional activity of genes. They can act as both enhancers and repressors of gene expression. Epigenetic Regulation: LncRNAs are involved in the regulation of chromatin structure and modifications. They can recruit chromatin-modifying complexes to specific genomic loci, influencing the epigenetic landscape. Cellular Processes:

Cell Cycle Regulation: Certain lncRNAs have been implicated in the control of the cell cycle, influencing cell proliferation and differentiation. Apoptosis: LncRNAs can regulate apoptosis by interacting with key molecules involved in apoptotic pathways. Subcellular Structures:

Nuclear Bodies: Some lncRNAs are localized in specific nuclear bodies and contribute to their structure and function. X-Chromosome Inactivation (XCI):

The process of XCI in females involves the upregulation of a lncRNA called XIST, which leads to the inactivation of one X chromosome. Immune Response:

LncRNAs participate in the regulation of immune responses by modulating the expression of genes involved in immune function. Developmental Processes:

LncRNAs are involved in various stages of development, including embryonic development and tissue differentiation. Disease Associations:

Dysregulation of lncRNAs has been implicated in various diseases, including cancer, neurodegenerative disorders, and cardiovascular diseases. RNA Splicing and Translation:

Some lncRNAs play a role in alternative splicing and translation regulation, influencing the final protein products. Cellular Stress Responses:

LncRNAs can be induced in response to various stresses, such as heat shock or DNA damage, and may play a role in cellular stress responses. Interactions with MicroRNAs (miRNAs):

LncRNAs can act as molecular sponges for miRNAs, sequestering them and preventing them from binding to their target mRNAs.

In neurosurgery

- LINC01783 Promotes Glioma Tumorigenesis by Enhancing GATA3 Expression Through CBP-Mediated H3K27 Acetylation to Suppress PTEN Expression
- Delivery of LOXL1-AS1-siRNAs using targeting peptide-engineered extracellular vesicles with focused ultrasound to suppress medulloblastoma metastasis
- LINC00601 promotes the progression of glioma via the p-STAT3 signaling pathway
- Retraction notice to "Current knowledge of antisense long non-coding RNA in the occurrence and prognosis of skull base tumors" [Heliyon 10 (2024) e35960]
- Radio-chemotherapy and metformin selectively modulate the heterogeneous landscape of glioma with ribosome biogenesis, long non coding RNA and immune-escape markers as major player
- NF-YB-driven expression of long non-coding RNA linc01811 inhibiting glioma tumorigenesis by regulating miR-4635/NF-YB axis: A positive feedback loop
- The role of non-coding RNA regulates stem cell programmed death in disease therapy
- Mechanism of LINC01018/miR-182-5p/Rab27B in the immune escape through PD-L1-mediated CD8⁺ T cell suppression in glioma

Long noncoding RNAs (lncRNAs) represent a multidimensional class of regulatory molecules that are involved in many aspects of brain function. Emerging evidence indicates that lncRNAs are localized to the synapse; however, a direct role for their activity in this subcellular compartment in memory formation has yet to be demonstrated. Using lncRNA capture-seq, we identified a specific set of lncRNAs that accumulate in the synaptic compartment within the infralimbic prefrontal cortex of adult male C57/Bl6 mice. Among these was a splice variant related to the stress-associated lncRNA, Gas5. RNA immunoprecipitation followed by mass spectrometry and single-molecule imaging revealed that this Gas5 isoform, in association with the RNA binding proteins G3BP2 and CAPRIN1, regulates the activity-dependent trafficking and clustering of RNA granules. In addition, we found that cell-type-specific, activity-dependent, and synapse-specific knockdown of the Gas5 variant led to impaired fear extinction memory. These findings identify a new mechanism of fear extinction that involves the dynamic interaction between local lncRNA activity and RNA condensates in the synaptic compartment [1)].

Increasing evidence has revealed that lncRNAs will emerge as promising cancer biomarkers or therapeutic targets in cancer treatment. LncRNA-ATB, a Long non-coding RNA activated by TGF-β, was found to be abnormally expressed in certain cancers and participate in the development and progression of tumors. In addition, aberrant lncRNA-ATB expression was also associated with the clinical characteristics of tumors. The purpose of this review is to summarize functions and underlying mechanisms of lncRNA-ATB in tumors and discuss whether lncRNA-ATB can be a biomarker and therapeutic target in cancers [2)].

Genome-wide transcriptional studies have demonstrated that tens of thousands of lncRNA genes are expressed in the CNS and that they exhibit tissue- and cell-type specificity. Their regulated and dynamic expression, and their co-expression with protein-coding gene neighbours, have led to the study of the functions of lncRNAs in CNS development and disorders.

In a review, Cuevas-Diaz Duran et al., from the Vivian L. Smith Department of Neurosurgery, Center for Stem Cell and Regenerative Medicine, UT Brown Foundation Institute of Molecular Medicine, Houston, Tecnologico de Monterrey, describe the general characteristics, localization, and classification of lncRNAs. They also elucidate examples of the molecular mechanisms of nuclear and cytoplasmic lncRNA actions in the CNS and discuss common experimental approaches used to identify and unveil the functions of lncRNAs. Additionally, they provide examples of lncRNA studies of cell differentiation and CNS disorders including CNS injuries and neurodegenerative diseases. Finally, they review novel lncRNA-based therapies. Overall, this review highlights the important biological roles of lncRNAs in CNS functions and disorders [3)].

Importance

see Long non-coding RNA in glioma.

see Long non-coding RNA in meningioma.

see Circular RNAs (circRNAs) are highly stable, circularized Long non-coding RNAs.

see also Long non-coding RNA MALAT1.

Long non-coding RNAs (lncRNAs) have received increased research interest owing to their participation via distinct mechanisms in the biological processes of Clinically Non-Functioning Pituitary Neuroendocrine Tumors. However, changes in the expression of lncRNAs in gonadotrophin adenoma, which is the most common nonfunctional pituitary neuroendocrine tumors, have not yet been reported. In this study, we performed a genome-wide analysis of lncRNAs and mRNAs obtained from gonadotrophin adenoma patients' samples and normal pituitary tissues using RNA-seq. The differentially expressed lncRNAs and mRNAs were identified using fold-change filtering. We identified 839 lncRNAs and 1015 mRNAs as differentially expressed. Gene Ontology analysis indicated that the biological functions of differentially expressed mRNAs were related to transcription regulator activity and basic metabolic processes. Ingenuity Pathway Analysis was performed to identify 64 canonical pathways that were significantly enriched in the tumor samples. Furthermore, to investigate the

potential regulatory roles of the differentially expressed lncRNAs on the mRNAs, we constructed general co-expression networks for 100 coding and 577 non-coding genes that showed significantly correlated expression patterns in tumor cohort. In particular, we built a special sub-network of co-expression involving 186 lncRNAs interacting with 15 key coding genes of the mTOR pathway, which might promote the pathogenesis of gonadotrophin tumor. This is the first study to explore the patterns of genome-wide lncRNAs expression and co-expression with mRNAs, which might contribute to the molecular pathogenesis of gonadotrophin adenoma [4].

References

1)
Liau WS, Zhao Q, Bademosi A, Gormal RS, Gong H, Marshall PR, Periyakaruppiah A, Madugalle SU, Zajaczkowski EL, Leighton LJ, Ren H, Musgrove M, Davies J, Rauch S, He C, Dickinson BC, Li X, Wei W, Meunier FA, Fernández-Moya SM, Kiebler MA, Srinivasan B, Banerjee S, Clark M, Spitale RC, Bredy TW. Fear extinction is regulated by the activity of long noncoding RNAs at the synapse. Nat Commun. 2023 Nov 22;14(1):7616. doi: 10.1038/s41467-023-43535-1. PMID: 37993455.
2)
Tang F, Xu Y, Wang H, Bian E, Zhao B. LncRNA-ATB in cancers: what do we know so far? Mol Biol Rep. 2020 Apr 4. doi: 10.1007/s11033-020-05415-5. [Epub ahead of print] Review. PubMed PMID: 32248383.
3)
Cuevas-Diaz Duran R, Wei H, Kim DH, Wu JQ. Long non-coding RNAs: important regulators in the development, function, and disorders of the central nervous system. Neuropathol Appl Neurobiol. 2019 Jan 13. doi: 10.1111/nan.12541. [Epub ahead of print] PubMed PMID: 30636336.
4)
Li J, Li C, Wang J, Song G, Zhao Z, Wang H, Wang W, Li H, Li Z, Miao Y, Li G, Zhang Y. Genome-wide analysis of differentially expressed lncRNAs and mRNAs in primary gonadotrophin adenomas by RNA-seq. Oncotarget. 2016 Dec 15. doi: 10.18632/oncotarget.13948. [Epub ahead of print] PubMed PMID: 27992366.