EPIGENETICS OF IncRNAs:

HOTAIR AND ITS RELATIONSHIP WITH CANCER



Marta Urtizberea Merino

Faculty of Biosciences, Biochemestry degree, Universitat Autònoma de Barcelona, June 2015

Introducction

Epigenetics is the study of alterations in gene expression that are not caused by changes in the DNA sequence. The epigenetic that establish different patterns of gene expression includes: methylation of cytosine, posttranslational modification of histone proteins and chromatin remodeling proteins and RNA-based mechanisms. These processes that regulate gene expression patterns, are run by the non-codifying material of the genome. Without being translated into protein can function as RNA. They are referred to, as non-coding RNAs (ncRNA) and are divided into several large groups. This work will focus on IncRNA. IncRNAs are transcripts produced by RNA polymerase II longer than 200 nucleotides. They are processed by splicing and may or may not be polyadenylated [1] [2].

Structure and function

IncRNAs are typically formed by random RNA sequences. They have structural motifs in triplet over the gene body critical for their funcción, evolutionarily conserved. However, the 5 'and 3' are fully destructured.

Biological functions:

- -Regulation of gene expression. IncRNA remodel chromatin to make genes more or less accessible. It aims to increase or decrease the expression of theme.
- -Maintenance of pluripotency. IncRNA maintain the pluripotency of stem cells. They Suppress or activate cell differentiation related genes.
- -Nuclear-organization. IncRNA organize the nucleus with the formation of paraspeckles. IcnRNA retain the mature mRNA in paraspeckles and prevent translation.
- -Alternative splicing. IncRNAs play a critical role in the alternative splicing of the mRNA maturation. [2]

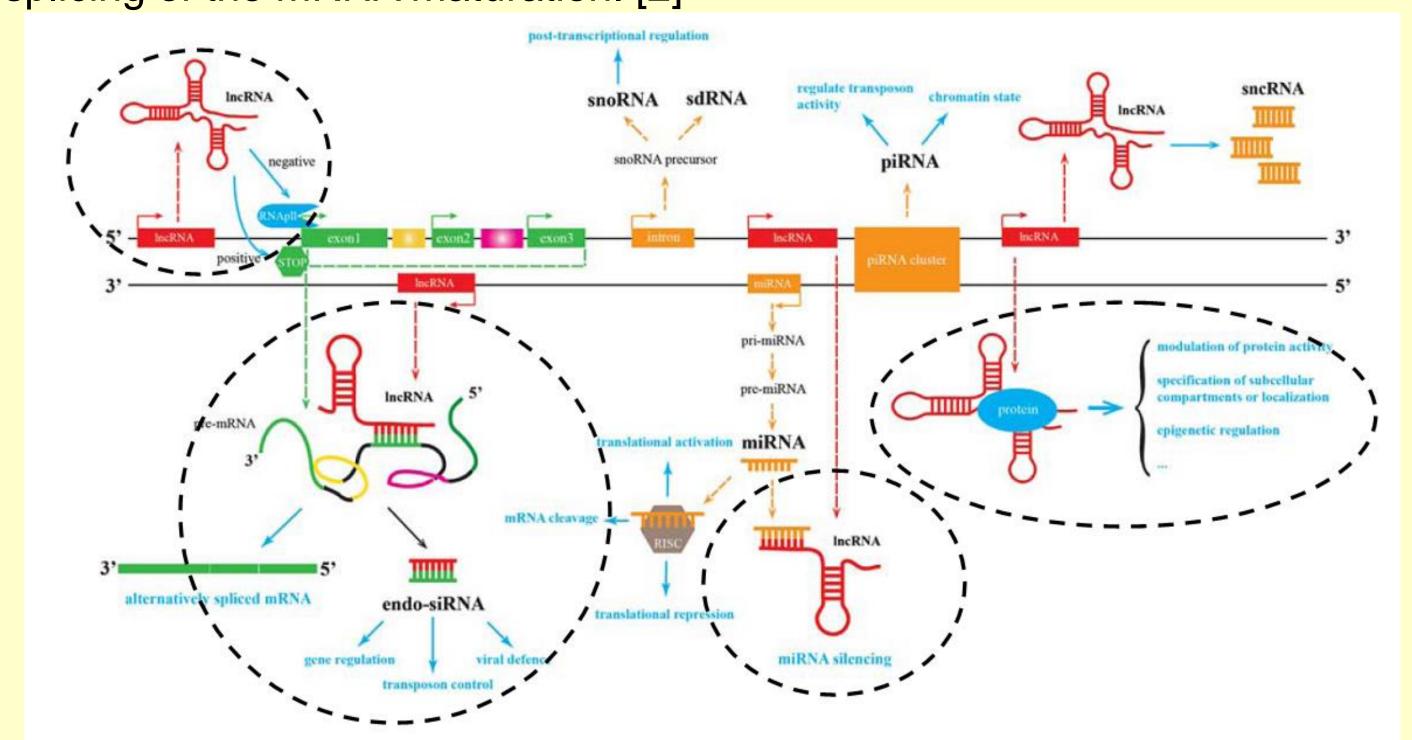


Figure 1: major ncRNA. Highlights IncRNAs where appears their structure and their most important functions. Figure comes from [3]

Classification of IncRNA15 Class Promoter-associated (pRNA) Gen body-associated (sense) (gsRNA) Gen body-associated (antisense) (gaRNA) Enhancer-associated (eRNA) Intergenic (lincRNA)

Mechanisms of action

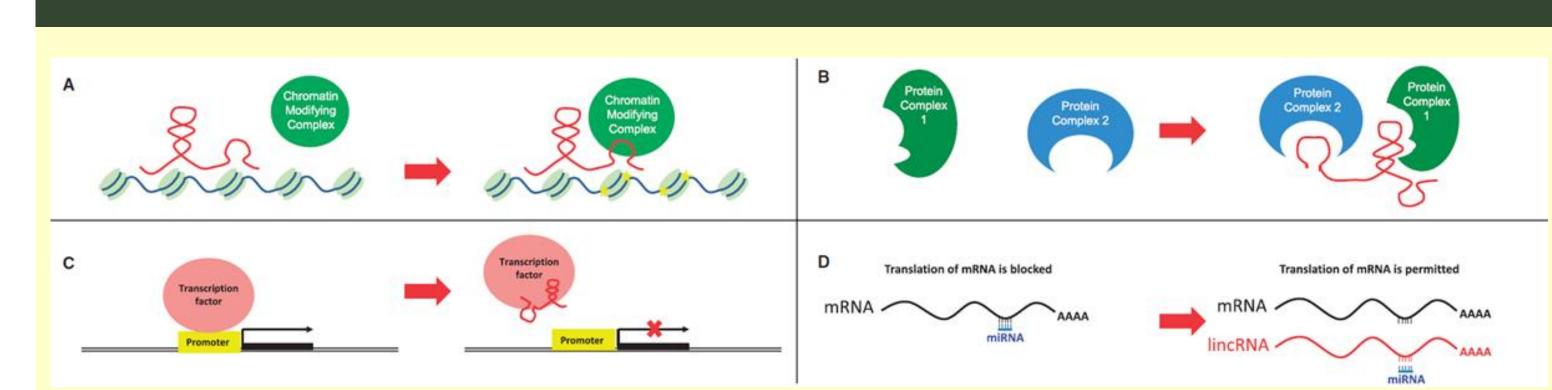


Figure 3: Mechanisms of action by which IncRNA can exert their function. A) IncRNAs can act as guides of chromatin-modifying complexes to regulate gene expression. B) IncRNAs can be scaffolds and bring two proteins in space to perform their role. C) IncRNAs can bind to transcription factors and prevent them of binding to their target genes. D) IncRNAs can inhibit the action of a miRNA joining them by homology. Figure comes from [2]

IncRNA in cancer: HOTAIR

IncRNAs are closely related to cancer. They regulate the expression of genes involved in cellular proliferation. When they deregulated, the cell cycle is disturbed.

HOTAIR (HOX Antisense Intergenic RNA) is a IncRNA found in the cluster HOXC, in the chromosome 12q13.13, it is transcribed in antisense and represses in trans the HOXC cluster of chromosome 2 along 40kb. HOTAIR recruits the protein complexes PRC2 and LSD1 so as to modify the chromatin and suppress the expression of their target genes. In cancer, HOTAIR is overexpressed and alters the expression pattern of genes involved in epithelial mesenchymal transition, dedifferentiate the cell and promote ability proliferation, invasiveness and metastasize [2].

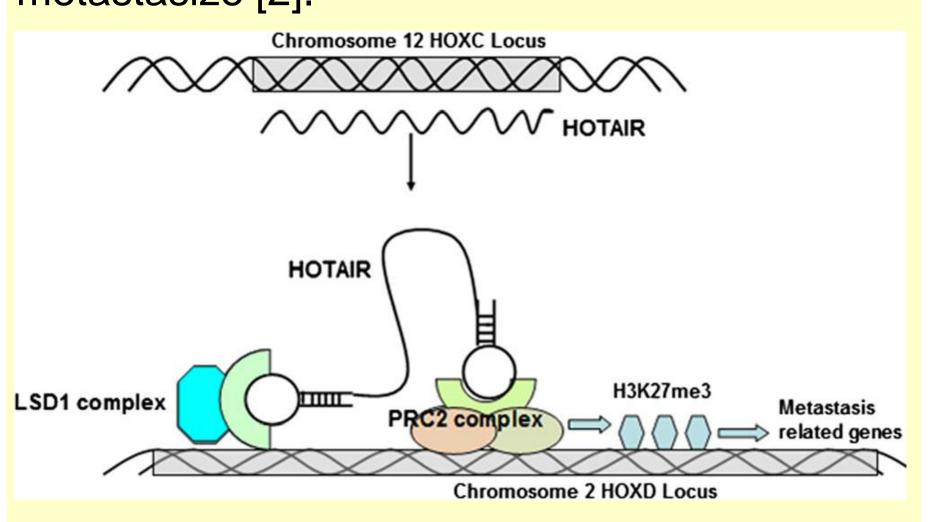


Figure 4. Figure comes from [5]

Regulation

• HOTAIR is induced by estradiol (E2) in a dose dependant manner, because of its estrogen response elements (EREs) [5].

Mechanisms of action

- HOTAIR recruits de chromatin modifying complexes PRCS and LSD1. It brings them to the promoter of their target genes.
 - PRC2 → H3K27me3 → gain of a repressive mark
 - LSD1

 → demethylation H3K4

 → loss of an activating mark

Breast cancer

 HOTAIR incresses its expression in primary breast cancer tissue 2000 folds, and metastasizes to the lung. The retargeting of PRC2 alters the expression of 854 genes, although, is not clearly if HOTAIR levels can serve as diagnostic or prognosis.

Biomarker and therapy

- HOTAIR can be a good biomarker because:
- It has tissue specific expression
- It's the effector molecule
- Can be easily accessible (body fluids)
- It is easily quantifiable [2]

- Possible therapy
 - Interference RNA
 - Inhibitors of IncRNA target proteins

Conclusions

- ✓ IncRNAs are very important in cell function, because of their role regulating gene expression.
- ✓ IncRNAs aberrant functions can cause diseases like cancer.
- ✓ In a high percentage of breast cancers, HOTAIR is overexpressed. Although its correlation with the severity and prognosis of the disease is unclear.
- ✓ Further studies are needed to better understand of the mechanism of action of IncRNA and to use them as therapy.

Gibney, E. R. & Nolan, C. M. Epigenetics and gene expression. *Heredity (Edinb)*. **105**, 4–13 (2010). Qi, P. & Du, X. The long non-coding RNAs, a new cancer diagnostic and therapeutic gold mine. *Mod. Pathol.* **26,** 155–65 (2013).

Moran, V. a, Perera, R. J. & Khalil, A. M. Emerging functional and mechanistic paradigms of mammalian long non-coding RNAs. Nucleic Acids Res. 40, 6391–400 (2012). Bonasio, R. & Shiekhattar, R. Regulation of Transcription by Long Noncoding RNAs. Annu. Rev. Genet. (2014). doi:10.1146/annurev-genet-120213-092323 Wu, Y. et al. Long noncoding RNA HOTAIR involvement in cancer. Tumour Biol. 35, 9531-8 (2014). Bhan, A. et al. Antisense Transcript Long Noncoding RNA (IncRNA) HOTAIR is Transcriptionally Induced by Estradiol. 27, 3707–3722 (2013).