

## New Functions For New Genes, Non-coding RNAs Get Into The Action

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Research at the Centre for Genomic Regulation (CRG) in Barcelona, Spain and the Wistar Institute in Philadelphia, USA has revealed a novel mechanism for the control of human genes.

The work, published in Cell, present an anticipated mode of regulation of some processes such as differentiation and development or oncogenesis.

Thanks to the new technological advances in genome sequencing, we know that a major portion of the genome is being transcribed but only a small portion of this transcriptome contains the protein-coding sequences. So, even the long non-coding RNAs constitute a large portion of the mammalian transcriptome, their cellular functions remain elusive.

Scientists have already described the role of some small RNAs in gene regulation but they still know a few about the long ones. Long non-coding RNAs are transcripts longer than 100 nucleotides. For a number of these non-coding RNAs, the authors show that their presence increase the synthesis of nearby proteins involved in crucial processes in development and disease.

"Positive regulation of proteins mediated through RNA is a completely new finding" exclaims Ulf Anderson Ørom, first author of the paper. DNA regions have been known for many years to confer both negative and positive regulation of protein synthesis. "The fact that RNA is much easier to manipulate than DNA could mean that this discovery has a vast therapeutic potential" explains Ørom.

The work has been led by Ramin Shiekhattar, group leader at the Centre for Genomic Regulation (CRG) in Barcelona and now at the Wistar Institute and co-authored by Cedric Notredame and Roderic Guigo from the Bioinformatics and Genomics Programme at the Centre for Genomic Regulation (CRG).

Shiekhattar and collaborators have seen a new role for a class of long non-coding RNAs in positive regulation of protein-coding genes. "This seriously challenges our understanding of genes and how the human genetic network is regulated" says Dr. Shiekhattar and adds, "we are happy to contribute another important piece to the puzzle".

Research has through a combination of computational analysis and laboratory experiments lead to these intriguing findings. "10 years after the Human Genome Project this work illustrates how new databases like ENCODE and Havana, established with high throughput sequencing techniques, can be used to address key biological questions. It is also a showcase of how these new technologies bring together wet lab and in-silico biologists." states Cedric Notredame, group leader at the CRG Comparative Bioinformatics group.

Sources: Centre for Genomic Regulation, [AlphaGalileo Foundation](#).

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