

# Parts of genome without a known function may play a key role in the birth of new proteins

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Researchers in Biomedical Informatics at IMIM (Hospital del Mar Medical Research Institute) and at the Universitat Politècnica de Catalunya (UPC) have recently published a study in *eLife* showing that RNA called non-coding (lncRNA) plays an important role in the evolution of new proteins, some of which could have important cell functions yet to be discovered.

Ribosomes produce proteins from the instructions found in an RNA molecule. However, only 2% of the human genome is RNA containing information for the synthesis of proteins, meaning it is coding. Other parts of the genome that are transcribed could be "evolutionary noise", parts of the DNA that are copied to RNA randomly but with no concrete biological function. Now, a new sequencing technique has revealed that many of these transcripts (lncRNAs) may also translate into proteins, leading to an intense debate.

"We have confirmed that in all six species that were studied –human beings, mice, fish, flies, yeast and a plant– many of the lncRNAs were associated to ribosomes and seemed to be ready to translate RNA into proteins. This suggests that they could act as a repository for the synthesis of new proteins" explains Mar Albà, a professor at ICREA and the coordinator for the research group on Evolutionary Genomics at IMIM.

The study has found almost 2,500 lncRNAs that had not been studied, besides those identified previously, and has shown that very few lncRNAs are in more than one species. This would suggest that they have evolved recently. This hypothesis is backed by the fact that the properties of the lncRNA molecules show many similarities with the properties of "young" genes that are known to produce proteins.

"The birth of a new functional [protein](#) is a trial and error process that probably requires the production of many transcripts that will not survive the test of time, and lncRNA seems to fit this role. The study of closely related species will allow us to better understand how new coding genes are formed and identify those that can be functional. It will also be interesting to study the link between the alteration of lncRNA expression patterns and certain diseases" concludes Mar Albà.

Provided by Hospital del Mar Medical Research Institute

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