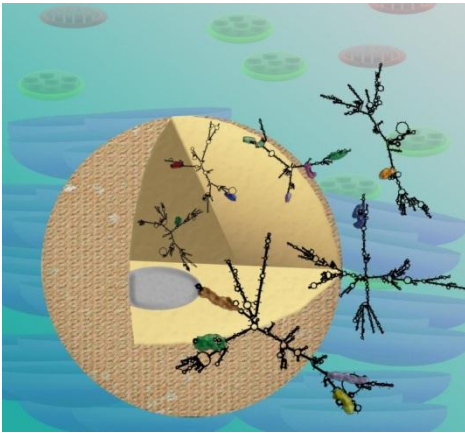


Patterns of RNA regulation in nuclei of plants identified

Biologists in University of Pennsylvania worked in plants in which they cataloged all the interactions that occur between RNA and the proteins that bind to it. Also they studied the interactions in the nuclei, and simultaneously obtained data about the nuclear RNA molecules' structure. Combining these datasets, gives a global view of the patterns that can affect the various RNA regulatory processes that occur before these molecules move into the cytoplasm where translation occurs.



Scientists from Genome Biology, developed a method to obtain a complete catalog of the interactions in live organisms between RNA and RNA-binding proteins, or RBPs, which interact with RNA transcripts to repress, enhance or otherwise alter gene expression in a cell-type specific manner.

The technique is called PIP-seq, for protein interaction profile sequencing. They worked on *Arabidopsis thaliana* to map out all of the RBP interaction sites and also the secondary structure of the RNA transcripts. PIP-seq gives information on the secondary structure of the RNA. Also found out that these sequences have been conserved over evolutionary time and are likely playing an important function in gene regulatory mechanisms.

The scientists observed a relationship between patterns of RBP binding and secondary structure. Two key forms of transcript regulation are alternative splicing, in which pieces of RNA undergo a cut-and-paste process to generate new sequences that can code for various proteins, and alternative polyadenylation, which alters where a transcript ends and an adenine "tail" is added, a process that can enhance either stabilization or degradation of the RNA molecule.

In their analysis, they found that RBP-binding sites and certain patterns of secondary structure were much more common at sites where alternative splicing and alternative polyadenylation occur. Finally, the team zoomed in on one RBP-bound sequence motif that was particularly abundant and found that it interacted with an RBP called CP29A. Eventually scientists would like to go into humans and other organisms to see similar patterns.

Source: <http://www.sciencedaily.com/releases/2014/12/141231140431.htm>