

## **ENERGY BIOGENESIS: HOW TO COORDINATE TWO GENOMES**

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### *Mitochondrion, regulation*

Mitochondria are considered to be the powerhouse of the cell. In mitochondria the degradation of the carbohydrates is coupled with the synthesis of high-energy molecules such as ATP, which powers up the vast majority of chemical reactions of the cell.

The biogenesis and function of mitochondria is the result of coordination between the nuclear genome, where there is more than 95% of mitochondrial genes, and the mitochondrial genome.

This coordination is particularly rigorous also because the protein complexes both of respiratory chain (OXPHOS) and mitochondrial ribosomes are assembled according to well-established stoichiometric relationships.

In higher eukaryotes has been reported that this type of coordination is achieved mainly at the transcriptional level. Various experimental observations suggest the presence of a fine-tuned communication between mitochondrial and nuclear genomes that results in the interdependent expression of OXPHOS genes and ribosomal genes encoded by mtDNA and nuclear genome.

Having previously identified, by using a series of bioinformatics analysis, a group of five DNA motifs that, for the distribution and frequency in putative regulatory regions of OXPHOS, TCA, and ribosomal genes, could be regarded as excellent regulatory sequences, we decided to validate this analysis by means of the One-Hybrid Assay.

The One-hybrid assay was performed using two different DNA motifs as bait, the Site II motif (ref) and the Ac/tTGT motif. This analysis showed that some proteins are able to interact "in vivo" with those motifs. We have identified a transcription factor belonging of the family AP2/ERF/B3 (AtERF#115) that binds Site II motif. The transcription factor is part of the regulative cascade of ethylene, this finding could help explain the mechanisms by which ethylene is able to influence the respiration (e.g. climacteric).

We have also identified two transcription factors belonging to the family of bZIP (AtbZIP18 and AtbZIP52), when we used the Ac/tTGT motif as a DNA-bait. The transcription factors are involved in the process of growth and development of the plant.

The family of bZIP transcription factors is required in the process of growth and development of the plant and therefore it can be possible that AtbZIP18 and AtbZIP52 may be involved in response to those processes.