Changes in the ribosomal protein composition and in the ribosome-associated small noncoding RNAs in *Saccharomyces cerevisiae* as a response to environmental stress.

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According to the central dogma of molecular biology, the genetic information encrypted in the DNA molecules is transcribed into RNA and through them to the proteins, which in turn function as enzymes, transport or regulatory molecules. This simple scheme has been extensively complicated and enriched with the discoveries of the 70s, 80s and 90s of the twentieth century. On the basis of these novel discoveries, it was necessary to broaden the knowledge of the RNA new features. Moreover, a novel class of functional transcripts that do not encode proteins emerged. Such RNA molecules are called non-coding RNAs (ncRNAs). ncRNAs play critical roles in the modulation of gene expression at multiple stages, however still for hundreds of thousands of RNAs we only known the sequence. Therefore, studies aiming at determination of the conditions in which ncRNAs are expressed and processes they are involved in, are of crucial importance. Recently, we have described a novel class of ncRNAs, namely ribosome-associated noncoding RNAs (rancRNAs), which directly bind and regulate the ribosome funtion in yeast *Saccharomyces cerevisiae.* It was the first report presenting the possibility of regulation of ribosome function by direct interactions with small noncoding RNAs as a response to stress conditions.

Ribosomes are highly conserved ribonucleoprotein nanomachines that translate information encrypted in the DNA to create the proteins in all cells. All ribosomes are composed of ribosomal RNA and ribosomal proteins. Although their function during protein biosynthesis is evolutionary conserved (is performed in the same way in all organisms), the components of the ribosome differ between organisms, developmental stages or under different environmental changes within one organism. It has been therefore suggested that such reason for heterogeneity of the ribosomes most probably provides means to prepare the translational program of stressed cells for recovery, because proper ribosome functioning is crucial to the health of the cell.

The main aim of the project is to explore in details the hetorogeneity of *Saccharomyces cerevisiae* ribosomes caused by differential environmental conditions as well as to characterize ribosome-associated noncoding RNAs interacing with different subpopulations of heterogenous ribosomes.

By looking at aspects of small RNAs previously not studied, the project will benefit in characterizing a novel class of small RNAs in *S. cerevisiae*, directly interacting with ribosomes and potentially, their contribution to the hetegoregeity of the ribosomes. What is more, the results of the project will allow for evaluation of the knowledge about functions, targets and subcellular localization of rancRNAs.

Eukaryotic cells contain robust mechanisms to respond to and mitigate environmental stress. One important component of stress responses is the regulation of RNA metabolism, which often involves a decrease in general translation and an increase in preferential translation of stress-response genes. This project will reveal an importance of another stress response mechanism, namely the induction of heterogenous ribosomes as well as ribosome-associated small noncoding RNAs. We will therefore reveal a new additional levels of control of gene expression, regulating ribosome heterogeneity during stress in eukaryotic species.