Abstract (*English*)

In response to environmental stresses, cells try to adapt to changed living conditions. Regulation of translation process provides fast-responding and versatile system enabling execution of stress-induced expression program. Messenger ribonucleoprotein complexes (mRNPs) engaged in translation and mRNA turnover are remodelled and may accumulate into higher-order assemblies, in connection to stress-induced translational changes. Stress granules (SGs) and processing bodies (PBs) are examples of such assemblies. Through them, further fate of mRNA molecules and certain translation machinery components is determined. In an effort to better understand the entire role of SGs in cellular metabolism, we performed the analysis of heat-induced SGs in model organism *Saccharomyces cerevisiae*. We contributed to the finding that SGs phenomenon is evolutionary conserved in eukaryotic kingdom proving that SGs are formed also in unicellular yeast *S. cerevisiae* under robust heat stress. The SGs reassemble their counterparts from higher eukaryotes in core composition and proposed functions. However, they possess also unique nature, which seems to be specific to the yeast. We further extended the data about heat-induced SGs, with a focus on additional composition, dynamics, associated proteins and a relation to other cellular structures. One of SGs-associated protein, Mmi1, was characterized in detail. This multifunctional protein was found to be engaged in heat stress response of the yeast, most probably, by its association with both SGs and protein degradation machinery. Taken together, we established model of heat-induced SGs in yeast *S. cerevisiae* and further contributed to the knowledge about SGs phenomenon, which participates in cellular metabolism and stress response. Moreover, in an effort to analyse connection of *Reactive Species*-producers to heat-induced SGs and to cell physiology in general, we extended data about functioning of NOX (NADPH oxidase) enzymes in cell physiology identifying and further characterizing a member of this protein family in yeast *S. cerevisiae*, Yno1 protein. Our evidence about this extramitochondrial *Reactive Species*-producer brings new data about the protein role in the yeast physiology.