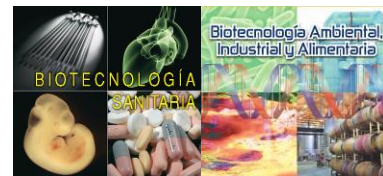


Talk

Proteasome dynamics during quiescence in *Schizosaccharomyces pombe*



Odriozola Gil, Yosú; Ruiz Romero, Gabriel; Rodríguez Daga, Rafael

Department of cellular biology and biotechnology, Centro Andaluz de Biología del Desarrollo (CABD),
Universidad Pablo de Olavide, Carretera de Utrera km. 1 41013 Sevilla

Tutor académico: Silvia Salas Pino

Keywords: proteasome complex; ubiquitin-proteasome-system; quiescence.

ABSTRACT

The Proteasome is one of the largest protein complexes present in eukaryotic cells and it is responsible for 90% of total protein degradation. Thus, proteasome availability and correct function are key elements in eukaryotic cells from yeast to human to deal with unfolded or unwanted proteins.

When the concentration of cells in culture increases, cells initiate a metabolic reprogramming in order to become quiescent. During this developmental state of no proliferation, the proteasome is sequestered in cytoplasmic granules, so they are readily available when those cells resume growth. However, the mechanisms involved in proteasome storage and recycling are poorly understood.

Here, we use the fission yeast as eukaryotic model to study proteasome dynamics. Previous work done in our laboratory have shown that the existence of two separate proteasome pools: one cytoplasmic and one nuclear.

The objective of this work is to study the formation, composition and dissolution of the proteasome storage granules (PSGs), and to analyze consequences for cell survival in conditions in which PSGs are not formed during quiescence.

To accomplish this, we are using a collection of deletion of kinases to try to interfere with proteasome storage signalling, and a mutant required for the synthesis of ubiquitin, the molecule that target proteins for degradation via proteasome. All these mutants were expressing the proteasome subunits tagged with either GFP or tomato as proteasome marker. We used confocal imaging, fluorescence recovery after photobleaching (FRAP) experiments and cell survival assays in cells exposed to low glucose concentration to promote quiescence to induce PSGs and study their localization and dynamics.

Our result show that whereas none of the kinases assayed so far present significant defects in PSG formation, a mutant defective in the polyubiquitin gene (*ubi4*), shows a severe reduction in the number of cells capable of generating these PSGs in low glucose. This result suggests an important role of the ubiquitin in the formation and/or composition of PSGs. We are currently checking deletion of additional kinases, analyzing the rate of PSGs dissolution upon refeeding with rich media, as well as setting up assays to determine the rate of cell survival in conditions of defective PSG formation.

REFERENCES

Gu, Z. C., Wu, E., Sailer, C., Jando, J., Styles, E., Eisenkolb, I., ... Enenkel, C. (2017). Ubiquitin orchestrates proteasome dynamics between proliferation and quiescence in yeast. *Molecular Biology of the Cell*, 28(19), 2479–2491. <https://doi.org/10.1091/mbc.E17-03-0162>

Enenkel, C. (2018). The paradox of proteasome granules. *Current Genetics*, 64(1), 137–140. <https://doi.org/10.1007/s00294-017-0739-y>

Yedidi, R. S., Fatehi, A. K., & Enenkel, C. (2016). Proteasome dynamics between proliferation and quiescence stages of *Saccharomyces cerevisiae*. *Critical Reviews in Biochemistry and Molecular Biology*, 51(6), 497–512. <https://doi.org/10.1080/10409238.2016.1230087>