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Functional validation of LexDBDGim chimeras in *Saccharomyces cerevisiae*

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GimC/Prefoldin is a hetero-oligomeric complex involved in cytoskeleton biogenesis. It is composed by six different subunits belonging to α (Gim2/Pfd3 and Gim5/Pfd5) and β (Gim1/Pfd6, Gim3/Pfd4, Gim4/Pfd2 and Gim6/Pfd1) classes. This complex interacts with actin and tubulin nascent polypeptides while associated with ribossome and deliver them to chaperonin CCT/TriC. In *Saccharomyces cerevisiae*, the absence of each subunit leads to different phenotypes, for instance, in the presence of osmotic and oxidative stress agents.

In order to identify by two-hybrid system targets that directly interact with Gims and support the stress phenotypes, this work aimed the functional validation of all Gims in *Saccharomyces cerevisiae*. One-hybrid assays with each Lex_{DBD}Gim (Lexgim) chimeras and *LacZ* reporters containing different promoters were performed. The obtained results allow the validation of the Lexgim chimeras in the context of two-hybrid assays. However, since the Gim/target interactions may occur only in stress conditions, the one-hybrid assays are currently being performed upon stress stimuli.

The results also led to the identification of specific promoters in which, under optimal growth conditions, Lexgim chimeras do not operate as activators neither repressors of transcription mediated by RNA polymerase II. In previous work developed in our laboratory with gim-null mutants, no correlation was found between the stress phenotypes and cytoskeleton defects and it was hypothesized that the phenotypic differences could be due to differential expression of specific stress genes. Since literature data does not exclude the presence of Gim subunits in the nucleus, the potential of Lexgims to regulate transcription mediated by RNA polymerase II will be re-evaluated under stress stimuli.