Extragenic Supressor Screening of *TIF51A* Mutants Using Genomic Deletions Directed by Transposon

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The translation initiation factor 5A (eIF5A) is an abundant protein and highly conserved in all eukaryotic and archaea organisms. In *Saccharomyces cerevisiae*, eIF5A is encoded by the gene *TIF51A* in aerobic conditions. This protein is essential for cell viability and has been involved in different steps of mRNA metabolism. Although recent studies have suggested a role for eIF5A in translation elongation, its precise function remains unclear. Genetic screens in *Saccharomyces cerevisiae* have been demonstrated to be important tools in the identification of functional relationships in the cell. In order to identify genetic partners of eIF5A, we are using the temperature-sensitive mutant *tif51A-1* and transposon-directed genomic deletions to search for second-site mutations (extragenic suppressors) that allow growth of the mutant strain at the restrictive temperature. For this screening, we generated a start strain harboring knockout alleles of the *TIF51A* and *TIF51B* genes, complemented by the *tif51A-1* allele in a plasmid. This genotype will allow a faster and specific identification of true extragenic suppressors. This strain is being transformed with a transposon-mutagenized genomic yeast library and, out of ~ $3,6x10^4$ transformants, 19 initial candidates were selected so far. The extragenic suppressor screening described here may lead to the identification of factors that positively or negatively regulate eIF5A. The discovery of these functionally related factors may contribute to the understanding of eIF5A role in the cell.

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