

Sample Abstract - *Developmental Biology & Genetics*

Abstract Title: Loss of Elongation-Like Factor 1 Spontaneously Induces Diverse, RNase H-Related Suppressor Mutations in *Schizosaccharomyces pombe*

A healthy individual may carry a detrimental genetic trait that is masked by another genetic mutation. Such suppressive genetic interactions, in which a mutant allele either partially or completely restores the fitness defect of a particular mutant, tend to occur between genes that have a confined functional connection. Here we investigate a self-recovery phenotype in *Schizosaccharomyces pombe*, mediated by suppressive genetic interactions that can be amplified during cell culture. We performed a survival competition assay, followed by calculating the frequency of phenotypic recovery and RNA-fluorescence in situ hybridization (RNA-FISH). Cells without Elf1, an AAA+ family ATPase, have severe growth defects initially, but quickly recover growth rates near to those of wild-type strains by acquiring suppressor mutations. *elf1Δ* cells accumulate RNAs within the nucleus and display effects of genome instability such as sensitivity to DNA damage, increased incidence of lagging chromosomes, and mini-chromosome loss. Notably, the rate of phenotypic recovery was further enhanced in *elf1Δ* cells when RNase H activities were abolished and significantly reduced upon overexpression of RNase H1, suggesting that loss of Elf1-related genome instability can be resolved by RNase H activities, likely through eliminating the potentially mutagenic DNA–RNA hybrids caused by RNA nuclear accumulation. Using whole genome sequencing, we mapped a few consistent suppressors of *elf1Δ* including mutated Cue2, Rpl2702, and SPBPJ4664.02, suggesting previously unknown functional connections between Elf1 and these proteins. Our findings describe a mechanism by which cells bearing mutations that cause fitness defects and genome instability may accelerate the fitness recovery of their population through quickly acquiring suppressors. We propose that this mechanism may be universally applicable to all microorganisms in large-population cultures.

KEY

Abstract contains sufficient background to understand the problem under investigation

Abstract must contain a hypothesis, objective or statement about the problem under investigation

Abstract must contain a brief statement of the experimental methods/methodology used

Essential results must be present in summary form (even if preliminary)

Abstract must contain a conclusion that explains how the work contributes to the hypothesis, objective or statement of problem

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