

F802

Suppressor analysis of the *ydr1-7* gene in yeast

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The human Dr1 gene represses transcription by sequestering and by preventing formation of transcription preinitiation complex. The *YDR1* gene is the counter part of the human Dr1 and is essential gene for viability in the yeast *Saccharomyces cerevisiae*. Overexpression of the *YDR1* gene is toxic to the cells. We generated *ydr1* conditional mutants by *in vitro* mutagenesis. Using *ydr1* conditional mutants suppression analysis was performed to isolate more genes involved in transcription in yeast. The *ydr1-3* allele is a conditional ts mutant at 37°C and resulted from E35K. 12 revertants of the *ydr1-3* allele were isolated using DEB (dimethyl ethyl butane). Genetic analysis such as dominance/recessiveness, complementation test, linkage analysis and pleiotropic phenotype determination revealed that there are 4 different recessive suppressor genes designated *syd1*, *syd2*, *syd3* and *syd4*, respectively. Both the *syd1* and *syd3* mutants showed cs phenotype at 16°C. Using the cs phenotype associated with the *syd1* and *syd3* mutation we are cloning the wildtype *SYD* genes.

F803

Studies on Alpha-amylase Gene Expression in Natural Populations of *Drosophila melanogaster* : *Amy* Variants and *map* Distribution

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The frequency distribution of electrophoretic variants of alpha-amylase (*Amy* strains) was analyzed from Korean natural populations of *Drosophila melanogaster* during the period 1997 to 1998. It was revealed that the populations analyzed in this study consisted of nine *Amy* strains from a total 1,430 of isofemale lines. Among these strains, the *Amy*¹ was found to be the most frequent allele with the frequency of 76.43% (1,093 lines). The frequencies of *Amy*^{1.3} and *Amy*^{1.2} appeared to be 13.62% and 6.15%, respectively, whereas the other six *Amy* strains (*Amy*^{1.2.3}, 1.4, 1.5, 1.6, 4.5, 1.3.6) were distributed under 1% from the total flies. Midgut amylase-activity patterns of larvae and adult flies showed three different regions; anterior (AMG), middle (MMG) and posterior (PMG). Amylase activity of AMG and PMG was characterized by strain-specific differences, and MMG was completely lacked the activity. Midgut amylase-activity patterns (*map*) indicated that the *mapA*^{1.2.3P^{0.0} and *mapA*^{1.2.3P^{1.2} among fifteen haplotypes were found to be higher frequencies, and *mapA* appeared to have higher activity than *mapP* in the larvae and adult flies reared with standard medium.}}