F802 Suppressor analysis of the *ydr1-7* gene in yeast

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The human Drl gene represses transcription by sequestering and by preventing formation of transcription preinitiation complex. The *YDR1* gene is the counter part of the human Drl 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* mutaenesis. 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℃ 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℃. 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 $mapA^{1.2.3}P^{0.0}$ and $mapA^{1.2.3}P^{1.2}$ among fifteen haplotypes were found to be higher frequencies, and *mapA* appeared to have higher activity than *mapP* in the lavae and adult flies reared with standard medium.