Genomic MAL locus of a methylo trophic yeast Hansenula polymorpha: disclosing the role of two MAL-activator genes

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Genomic clustering of functionally related genes is not very common in yeasts. Mostly these genes are scattered over the genome. Still, there are several gene clusters in Saccharomyces cerevisiae for example the MAL cluster with genes of maltose metabolism. We have studied the expression and regulation of HpMAL11 (maltase) and HpMAL2 (α-glucoside transporter) genes in H. polymorpha MAL locus. These genes are adjacent and divergently transcribed from a shared bidirectional promoter region (1-3). Further sequencing of the H. polymorpha MAL-locus revealed next to HpMAL2 two potential MAL-activator genes - HpMALAKT1 and HpMALAKT2. The gene adjacent to potential MAL-activator genes has similarity to nuclear porin genes and so we suggest that H. polymorpha MAL-locus consists of four genes. We plan to specify requirement of these putative MAL-activator genes for maltose utilization by deleting respective genes in yku80 strain of H. polymorpha which has highly decreased non-homologous recombination (Saraya et al., 2012). Phenotype of respective deletion mutants will be studied and required complementation tests will be performed.

In S. cerevisiae five MAL clusters, MAL1-MAL4 and MAL6, are found in subtelomeric regions of different chromosomes each containing at least three genes encoding a maltose permease, a maltase and an activator of these genes. The maltose permease and maltase genes are coordinately transcribed from a bidirectional promoter region as in H. polymorpha. In some MAL-loci of S. cerevisiae contain additional copy of the activator gene. In S. cerevisiae, intracellular maltose is predicted to act as inducer of MAL genes. Most interestingly, we have shown that in H. polymorpha, not maltose, but rather its hydrolysis product (glucose in unphosphorylated state) acts as transcriptional activator of MAL genes. However, when the amount of glucose-6P increases in the cell, MAL promoters become repressed (Suppi et al., 2013). The role of MAL activators in this process has yet to be revealed.

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References: