

## Comparative transcriptomics of the effects of prionization and inactivation of the Swi1 protein in *Saccharomyces cerevisiae*

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**Motivation and Aims:** Prions are infectious, self-perpetuating conformational states of proteins. Most part of known prions were found in yeast *Saccharomyces cerevisiae*. Usually, prion state is associated with the formation of protein fibrils (amyloids) and considered to be equal to functional inactivation of the protein. Swi1 is a component of the key chromatin remodeling complex SWI/SNF of yeast and was found to form prion [SWI<sup>+</sup>]. Inactivation of Swi1 affects many different processes in yeast cells and has the nonsense-suppression phenotype (growth on the media without adenine) in strains with the mutant variants of the *SUP35* gene. The goal of this study was to compare the effects of prionization and deletional inactivation of the Swi1 protein on the transcription of different genes.

**Methods:** The next-generation RNA sequencing (RNA-seq) of the yeast transcriptomes of the [SWI<sup>+</sup>], [swi<sup>-</sup>], and *swi1*Δ strains was performed using Illumina HiSeq 2500 platform. The expression levels of several genes were analyzed using quantitative real-time PCR.

**Results:** Using RNA-seq we compared transcriptome-wide effects of prionization and deletional inactivation of Swi1 and found significant differences. In particular, about 20 yeast genes that are downregulated in the *swi1*Δ strain, are upregulated in the [SWI<sup>+</sup>] strain. In addition, we found that nonsense-suppression phenotype had also different mechanisms in the [SWI<sup>+</sup>] and *swi1*Δ strains [1]. The deletion of *SWI1* leads to increased expression of the *ade1-14* mutant allele, while in the [SWI<sup>+</sup>] strains nonsense-suppression is caused by downregulation of the *SUP45* gene encoding eRF1 release factor.

**Conclusion:** Prionization of Swi1 protein and deletion of *SWI1* have different effects on transcription of yeast genes and, in some cases, the consequences of prion formation are similar to “gain-of-function” mutation.

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### References

1. Antonets K.S. et al. (2017) Distinct mechanisms of phenotypic effects of inactivation and prionization of Swi1 protein in *Saccharomyces cerevisiae*. *Biochemistry (Mosk.)*. 82(10):1147-1157.