

Abstract

Yeasts are unicellular eukaryotic microorganisms, capable of forming of organised multicellular communities, the colonies. Many yeast strains possess a characteristic colony morphology under defined living conditions. Another feature typical for many feral and pathogenic yeast strains is the ability to switch their morphotype. This phenomenon, called the phenotypic switching, contributes to a rapid adaptation to the changing harmful environment and is often connected with changes of the stress resistance or with the changes of virulence of pathogenic yeasts. Phenotypic switching can be observed even in non-pathogenic yeast *Saccharomyces cerevisiae*. The strain BR-F, isolated from nature, switches under laboratory conditions from fluffy to smooth morphology of the strain BR-S. This phenotypic switch is accompanied by broad changes in the phenotype. Transcriptome analyses of the strains BR-F and BR-S have shown, among others, changes in expression of the subtelomeric genes that are under control of the histone acetylases and deacetylases.

My work was aimed to the histone deacetylase Sir2p, which could influence the phenotypic switching in *Saccharomyces cerevisiae*. The *sir2* deletion mutant of the strain BR-S, prepared in our laboratory, was used for my studies. The results show, that the strain BR-S with the deletion of *SIR2* gene, possesses some characteristics similar to the feral strain BR-F, along with properties similar to the smooth strain BR-S. Moreover, the *sir2* deletion mutant of the strain BR-S has increased frequency of the phenotypic switching when compared to the strain BR-S. A new hyper fluffy morphotype of the *sir2* deletion mutant of the strain BR-S was isolated during the switching experiments, showing morphology and other features similar to the strain BR-F. A new strain, derived from the *sir2* deletion mutant of the strain BR-S, expressing GFP under the control of an inducible galactose promoter was prepared in this study. The new strain will be used in future for the studies of the differentiation of the cells within the yeast colony.

This pilot study contributed to our knowledge of the phenotypic switching in the yeast *Saccharomyces cerevisiae*, however, more investigation will be required to uncover the role of the Sir2 histone deacetylase in the phenotypic switching.