

Abstract

Unicellular organisms such as yeasts are permanently exposed to environmental changes, especially to changes of the concentration of osmotically active substances. Yeast species, which are able to cope with these changes properly, are called osmotolerant (*Zygosaccharomyces rouxii*, *Pichia sorbitophila*, *Debaryomyces hansenii*, etc.). The osmotolerance of yeasts depends on many physiological parameters but the most important is the efficient metabolism of internal osmolytes. This role is played by the small molecule of glycerol in most yeast species. Yeasts have to release the surplus of glycerol during the hypoosmotic shock. On the other hand, the hyperosmotic conditions require synthesis and accumulation of this small compound in a high quantity. The model yeast *Saccharomyces cerevisiae* has two systems transporting glycerol. First of them is the *ScFps1* channel which is important mainly for releasing of glycerol during hypoosmotic shock. The second transporter, called *ScStl1*, is employed in accumulation of glycerol in case of hyperosmotic conditions.

Detailed study of physiological properties of the three above mentioned species was performed within this work. Although they do not differ in basic morphological parameters from *S. cerevisiae*, their difference lies in the ability to survive desiccation, to cope with toxic cations, in potassium homeostasis or in utilization of various carbon sources. According to our data, the genomes of osmotolerant yeast species carry higher amount of genes encoding putative glycerol transporters (homologues of *ScSTL1*). Two sequences (*ZrSTL1* and *ZrSTL2*) were found in the genome of *Z. rouxii* and eight homologues (only one candidate was characterized in detail, *DhSTL2*) in *D. hansenii*. We found that both genes from *Z. rouxii* encode functional plasma-membrane glycerol transporters mediating the uptake of glycerol in symport with protons and that their influence on metabolism is much wider than in *S. cerevisiae*. Both genes are involved in high osmotolerance of *Z. rouxii* and their different level of expression is responsible for the complex regulation of glycerol accumulation. The successful heterologous expression of *ZrSTL1* in *S. cerevisiae* highlighted the ability of this gene to fully complement for *ScSTL1* in its function and to improve the properties of industrial *S. cerevisiae*. The detailed study of *ScSTL1*, *ScFPS1* a *ScHOG1* helped us to find completely new knowledge regarding their involvement in metabolism of *S. cerevisiae*.