

***In-vivo* Analysis of Galactose Assimilation in Yeast in the context of Genetic Perturbations using “omics” analyses.**

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Galactose assimilation has been extensively studied as an example of a genetic regulatory switch. Besides, however, the importance that unraveling this pathway’s regulation has for basic biological research, its structure and regulation is also of major medical significance. Impairment of galactose assimilation is the cause of galactosemia disease. At present, the molecular mechanisms that lead to the acute toxicity syndrome if galactose concentration in the blood of the patient overpasses a particular threshold, and the chronic complications that accompany a galactosemic individual remain unknown. In this study, using yeast as the model system, two recombinant strains simulating the classic and mild galactosemic genotype were compared to the wild-type strain with respect to their transcriptomic, metabolomic and metabolic output profiles under various experimental conditions. The acquired observations indicated that the galactosemic physiology is different even under conditions of rich glucose media and in the absence of galactose, to extract biologically relevant conclusions regarding GA regulation in the context of the entire yeast physiological network. These results provide the basis for the design of subsequent directed experiments to validate initial formulated hypotheses