

**GENETIC AND ENVIRONMENTAL FACTORS OF FITNESS VARIATION IN YEAST GENE-DELETION STRAINS**

Ryszard Korona<sup>1</sup>

<sup>1</sup>*Jagiellonian University, Institute of Environmental Sciences, Krakow, Poland*

ryszard.korona@uj.edu.pl

Quantification and comprehension of phenotypic variation in terms of an interplay between genetic and environmental factors has been pursued for decades. This goal is no less important in the (post)genomics era because any analysis of genetic systems needs to take into account that they were shaped by natural selection evaluating fitness, an overall performance of phenotypes. We use a collection of yeast gene-deletions to determine distribution of fitness effects caused by single and multiple deletions in different laboratory environments. Our results show that beneficial mutations are much rarer and smaller in effect than deleterious ones confirming observations made previously with mutations of spontaneous origin and unknown nature. Deleterious mutations form bimodal distribution in which lethal and slightly negative effects greatly outnumber those of intermediate strength. The bimodality applies not only to an entire organism but also to particular cellular components and thus should be counted among basic features of genetic systems. Considering multiple factors, there is no evidence that environmental stress enlarges negative effects of mutations. Neither interactions between mutations aggravate fitness losses. On the contrary, interactions between genes and between genes and environment have a general alleviating effect. This is because an impairment inflicted upon the metabolism of a growing cell appears most harmful when growth is fastest irrespective whether the insult originates from a decline in quality of the external environment or from the deregulation of the internal environment. Theoretical models and empirical tests are needed to explain how this pattern is produced.