Studying the Role of Robustness in Cellular Aging

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Aging is a complex trait and likely to involve many genes. We hypothesize that cellular aging are influenced by the configuration of gene/protein interaction network, and network robustness is a key factor in shaping the aging characteristics. We chose to test our hypothesis in the budding yeast *Saccharomyce cerevisiae,* an effective model for the study of cellular aging. We chose several proxies to estimate robustness, including connectivity, expression robustness, morphological robustness, and growth fitness. Moreover, we investigated the evolutionary patterns of genes with different deleterious effect on lifespan. Our study can give new sights on the intricate gene interaction network underlying the cellular aging process.