**The interconnection of molecular evolution, gene network, and cellular aging**   
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Pleiotropic traits, such as cellular aging, are shaped by gene networks which channeled the molecular evolution of individual genes into phenotypic manifestations. We recently proposed a mathematical model and demonstrated that cellular aging is an emergent property of gene networks and the characteristics of the aging process are linked to network robustness and gene interaction patterns. In this study, we aim to dissect the interconnection of molecular evolution, interaction pattern, robustness, and life-history traits in *Saccharomyces* *cerevisiae*. We evaluated the causal relationship of these factors with life span using partial regressions and extracted principal components from interacting factors. We found that molecular evolution influence life span through growth fitness.