The versatility of *Escherichia coli* enolase: from glycolysis to RNA degradation and its possible association by Sue Lin-Chao, Institute of Molecular Biology, Academia Sinica

*E. coli* is present in the gut of warm-blooded mammals and can grow aerobic and anaerobic conditions. Under anaerobiosis, *E. coli* is able to convert glucose into pyruvate through the glycolytic pathway, in which enolase catalyzes the penultimate step, the reversible conversion of 2-phosphoglycerate into phosphoenolpyruvate. Enolase is essential for the carbohydrate metabolism via glycolysis. Besides its glycolytic function, enolase is a component of RNA degradosomes, a multi-component ribonucleolytic complex located at the cytoplasmic membrane and involved in the RNA processing and degradation (1-4). Besides the enolase, the RNA degradosomes consist of other three major components: RNase E endoribonuclease (an essential RNase for cell viability), PNPase 3’→5’ exoribonuclease, and RhlB RNA helicase. Each component binds to a specific micro-domain within the C-terminal half of RNase E. Global analysis of *E. coli* RNA degradosome function using DNA microarrays demonstrated that the integrity of a functioning degradosome is necessary for normal function of mRNA turnover for post-transcriptional control of gene expression (5), indicating that individual protein components that are not ribonucleases also have an important role in regulating mRNA degradation. It has been well recognized that there is a tight coupling of ribonuclease and RNA helicases in RNA degradation machines. However, why *E. coli* degradosome requires the enolase has been a long-standing mystery. Until recently, my laboratory has elucidated a mechanism by which *E. coli* uses enolase-bound degradosomes in the stabilization of a small RNA to switch from rod-shaped to filamentous form in response to anaerobiosis (6). In this talk, I will present insights of the possible association of enolase in glycolytic function and RNA degradation.

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*Proc. Natl. Acad. Sci. U. S. A.* 114(38), E8025-E8034.doi: 10.1073/pnas, 2017