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Komagataella phaffii yeast as a model organism in biotechnology and fundamental research

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The choice of a model organism in biology is based on various factors, such as practical significance and ease of manipulation. *Saccharomyces cerevisiae* yeast is one of the most widely used and well-studied eukaryotic models. However, developments in NGS, proteomics, metabolomics and gene editing methods allow other species to become the object of fundamental research. A good example of such emerging model organisms is the yeast *Komagataella phaffii*.

K. phaffii belongs to a unique group of eukaryotic methylotrophs that can use methanol as the sole source of carbon and energy. On the other hand, *K. phaffii* seems to be more characteristic of the common ancient yeast ancestors than the rapidly evolving *S. cerevisiae*. Comparative studies between *S. cerevisiae* and *K. phaffii* will shed light on the mechanisms of evolution of metabolic pathways and regulatory systems. Such studies are accelerated by the practical importance of *K. phaffii* as a common microbial production host in biotechnology.

In our studies, we demonstrate that some amino acids greatly affect gene expression in *K. phaffii* [1]. Transcriptome analysis revealed drastic changes in gene expression when proline was present in the media. About 18.9% of total protein-coding genes were differentially expressed, including genes involved in methanol utilization [2]. Our results show that the unique methanol metabolism pathway is regulated not only by methanol, but also by other carbon sources. Therefore, our findings suggest that the regulation of methanol metabolism pathway is integrated into other cellular regulatory networks. Methanol metabolism, acquired by *K. phaffii* during evolution, is tightly associated with nitrogen an amino acid metabolism.

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