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Evolutionary Diversification of Paralogous Genes in the yeast *Saccharomyces cerevisiae*: Its Physiological Role

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For many years, it was accepted that the *Saccharomyces cerevisiae* (*S. cerevisiae*) lineage arose from a Whole Genome Duplication (WGD), making this yeast an interesting model to study diversification of paralogous genes. Recently, a phylogenetic study found compelling evidence indicating that *S. cerevisiae* lineage arose from an interspecies hybridization between one strain related to the Kluyveromyces, Lachancea and Eremothecium (KLE) clade and another one related to Z*ygosaccharomyces rouxii and Torulaspora delbrueckii* (ZT). Although whether the hybrid was the result of the fusion of two diploid cells or two haploid cells that underwent a WGD, is still an open question, both scenarios result in the formation of an allotetraploid with two copies of every gene. After the allotetraploid was formed, intragenic recombinations, full gene conversion, differential gene loss and selection pressures shaped *S. cerevisiae* genome to the one we observe today, harboring conserved blocks of duplicated genes. Retained duplicate genes (paralogs) can simply provide increased dosage of the same protein, or may go through a process of subfunctionalization or neofunctionalization, in which both copies of the gene lose a subset of their ancestral functions, while acquiring new properties. *S. cerevisiae* has been used as a model organism to analyze gene duplication dynamics and the functional fates of duplicated genes. In this conference I will present and discuss functional diversification pathways of three paralogous gene pairs, whose products are involved in amino acid metabolism and whose sub-subfunctionalization led to the separation and specialization of the ancestral function between the two duplicated genes. Examples of the subfunctionalization of paralogous pairs which was been achieved through: i) modifications of the coding sequence leading to paralogous proteins with particular kinetic properties *(GDH1/GDH3)*, ii) modifications of the regulatory region determining differential expression of each gene copy BAT1/BAT2 leading to the specialized functions of Bat1 and Bat2 encoded transaminases, and iii) selective organization of homo or hetero-oligomeric isozymes with peculiar biochemical properties (*LEU4/LEU9)*, will be presented and the functional repercussion of diversification will be amply discussed.

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