Gene acquisition, duplication and metabolic specification: the evolution of fungal methylisocitrate lyases.

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Abstract

Gene duplication represents an evolutionary mechanism for expanding metabolic potential. Here we analysed the evolutionary relatedness of isocitrate and methylisocitrate lyases, which are key enzymes of the glyoxylate and methylcitrate cycle respectively. Phylogenetic analyses imply that ancient eukaryotes acquired an isocitrate lyase gene from a prokaryotic source, but it was lost in some eukaryotic lineages. However, protists, oomycetes and most fungi maintained this gene and successfully integrated the corresponding enzyme into the glyoxylate cycle. A second gene, encoding a highly related enzyme, is present in fungi, but absent from other eukaryotes. This methylisocitrate lyase is specifically involved in propionyl-CoA degradation via the methylcitrate cycle. Although bacteria possess methylisocitrate lyases with a structural fold similar to that of isocitrate lyases, their sequence identity to fungal methylisocitrate lyases is low. Phylogenetic analyses imply that fungal methylisocitrate lyases arose from gene duplication of an ancient isocitrate lyase gene from the basidiomycete lineage. Mutagenesis of active-site residues of a bacterial and fungal isocitrate lyase, which have been predicted to direct the substrate specificity

of iso- and methylisocitrate lyases, experimentally confirmed the possibility of direct evolution of methylisocitrate lyases from isocitrate lyases. Thus, gene duplication has increased the metabolic capacity of fungi.

Beteiligte Forschungseinheiten

Mikrobielle Pathogenitätsmechanismen Bernhard Hube Mehr erfahren

Microbiome Dynamics Gianni Panagiotou Mehr erfahren

International Leibniz Research School Peter F. Zipfel Mehr erfahren

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