

Evolution of amino acids biosynthetic systems—Diversity of serine biosynthetic enzymes

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Amino acids are the building blocks of proteins and fundamental for life on Earth. Therefore, amino acid biosynthetic pathways are essential systems. Exploring ancestral amino acid biosynthetic pathways is important for understanding the evolution of early life on Earth. Ancestral serine biosynthetic systems were investigated by analyzing their conservation and diversity in modern organisms, resulting in the discovery of more diversity among serine producing enzymes than previously known. Here, I present on the newly discovered diversity of serine biosynthetic enzymes and consider what this means for the evolution of life.

A variety of organisms are known to synthesize serine from 3-phosphoglycerate, an intermediate of glycolysis/gluconeogenesis, by a three-step enzymatic reaction (Fig). Each respective enzyme had been thought to arise from a common origin. However, detailed genomic analysis using the MGD database revealed that a variety of organisms lack a gene for phosphoserine phosphate (PSP), an enzyme catalyzing the last step of the reaction, while possessing the first two enzymatic genes. One representative is a thermophilic and hydrogen-oxidizing autotrophic bacterium belonging to the phylum Aquificae. Detailed biochemical analyses revealed that Aquificae possess a novel protein that shares the same function which has no homology to the classical PSP. Furthermore, genomic analyses revealed that the novel PSP exists not only in Aquificae but is also distributed among diverse bacterial phyla which lack the classical PSP. The distribution of classical and novel PSPs suggests that both PSPs arose independently before the division of existing bacterial phyla.

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