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# Unique amino acid metabolism in hyperthermophilic archaea

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Archaea represent the third domain of life and exhibit a wealth of unique biological functions and mechanisms, providing valuable insight into the diversity of mechanisms in biology. Understanding the common and distinct properties among the three domains of life is necessary to envision the origin of life and how it evolved. Additionally, the variety of novel biological systems identified in the Archaea, such as metabolic and regulatory mechanisms, provide a vast resource of biomolecules that can be applied in various fields of biotechnology.

Here we will present our recent research on the metabolism of the hyperthermophilic archaeon, *Thermococcus kodakarensis*. The organism is an obligate heterotroph and anaerobe, and grows on a variety of organic compounds including peptides/amino acids, oligo- and poly-saccharides, and organic acids such as pyruvate. The genome consists of 2,088,737 bp with 2,306 predicted coding regions. Among the 2,306 genes, function based on primary structure can only be predicted on approximately half of the genes. Consequently, our understanding on many of the metabolic pathways in *T. kodakarensis* remains incomplete. The presentation here will focus on enzymes and pathways related to amino acids including proline, ornithine, arginine and aspartic acid. The biosynthesis of proline in *T. kodakarensis* utilizes ornithine as a precursor[1]. In search of the source of ornithine, we focused on the arginine deiminase pathway. Although two downstream gene homologs were found on the genome, we were unable to identify a gene corresponding to arginine deiminase. Bioinformatic analyses led to the identification of a novel enzyme, which we designated arginine synthetase[2]. In terms of aspartic acid, *T. kodakarensis* possesses an incomplete tricarboxylic cycle, and the biosynthesis pathway of aspartic acid is unknown. Here, four Class I aminotransferases[3,4] from *T. kodakarensis* were examined to identify the enzyme responsible for the conversion of oxaloacetate to aspartate.

1) R. Zheng, *J. Biol. Chem.* **2018**, *293*, 3625. 2) Y. Michimori, *Proc. Natl. Acad. Sci. USA*. **2024**, *121*, e2401313121. 3) Y. Su, *Front. Microbiol.* **2023**, *14*, 1126218. 4) Y. Michimori, *Proc. Natl. Acad. Sci. USA*. **2024**, *121*, e2311390121.