Arginine catabolism enzyme AgrE/ArgZ likely involves a cyanobacterial specific factor

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Arginine is a proteinaceous amino acid that is also used in numerous metabolic processes, which is reflected in the presence of numerous different arginine utilization pathways in nature. In cyanobacteria, a novel enzyme showing arginine dihydrolase activity has recently been found and named ArgZ in *Synechocystis* (1) or AgrE in *Anabaena* (2). (AgrE stands for arginine-guanidine–removing enzyme.) Zhuang et al. (3) have reported the crystal structure of *Synechocystis* ArgZ, showing that amino acid residues 1–269 form an α/β propeller domain characteristic of guanidine group–modifying enzymes and describing the catalytic mechanism that removes two ammonia molecules and one CO₂ molecule from arginine, producing ornithine. ArgZ/AgrE consists of ~700 amino acids, and its C-terminal part (amino acid residues 285–700) is homologous to a *Methanococcus maripaludis* protein annotated as lysine-oxoglutarate reductase/saccharopine dehydrogenase. Genetic-biochemical analysis of *Anabaena* AgrE and of *M. maripaludis* protein MMP1218 expressed in *Anabaena* has demonstrated that MMP1218 and the C-terminal part of AgrE show ornithine cyclodeaminase activity (2). Thus, AgrE is a bifunctional enzyme that sequentially transforms arginine → ornithine → proline. This enzyme is essential for full arginine catabolism in cyanobacteria (2, 4) rather than being important only as an arginine dihydrolase (1). Zhuang et al. (3) were unable, however, to ascribe any function to the C-terminal part of ArgZ. Because only the enzyme isolated from *Anabaena* showed ornithine cyclodeaminase activity (2) and Zhuang et al. crystalized the enzyme cloned in *Escherichia coli* (3), I suggest that a cyanobacterial factor is missing from the enzyme that was crystalized.

References


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