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

DOI 10.1074/jbc.L120.012850

Enrique Flores

From the Instituto de Bioquímica Vegetal y Fotosíntesis, CSIC and Universidad de Sevilla, Avda. Américo Vespucio 49, E-41092 Seville, Spain

Edited by Joseph M. Jez

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 CO_2 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.

This work was supported by Grant BFU2017-88202-P from Plan Nacional de Investigación, Spain, co-financed by the European Regional Development Fund. The author declares that he has no conflicts of interest with the contents of this article.

[1] To whom correspondence may be addressed. E-mail: eflores@ibvf.csic.es.

References

1. Zhang, H., Liu, Y., Nie, X., Liu, L., Hua, Q., Zhao, G. P., and Yang, C. (2018) The cyanobacterial ornithine-ammonia cycle involves an arginine dihydrolase. *Nat. Chem. Biol.* **14,** 575–581 CrossRef Medline
2. Burnat, M., Picossi, S., Valladares, A., Herrero, A., and Flores, E. (2019) Catabolic pathway of arginine in *Anabaena* involves a novel bifunctional enzyme that produces proline from arginine. *Mol. Microbiol* **111,** 883–897 CrossRef Medline
3. Zhuang, N., Zhang, H., Li, L., Wu, X., Yang, C., and Zhang, Y. (2019) Crystal structures and biochemical analyses of the bacterial arginine dihydrolase ArgZ suggests a "bond-rotation" catalytic mechanism. *J. Biol. Chem.* **295,** 2113–2124 CrossRef Medline
4. Flores, E., Arévalo, S., and Burnat, M. (2019) Cyanophycin and arginine metabolism in cyanobacteria. *Algal Res.* **42,** 101577 CrossRef