

Interaction of D-cycloserine with a D-amino acid transaminase from *Haliscomenobacter hydrossis*

Bakunova A. *, Matyuta I., Nikolaeva A., Boyko K., Popov V., Bezsudnova E.

Bach Institute of Biochemistry, Research Centre of Biotechnology, RAS, Moscow, Russia

* albakunova@mail.ru

Key words: D-amino acid transaminase, enzyme inhibition, D-cycloserine, substrate recognition

Motivation and Aim: Studying the structures of enzyme complexes with inhibitors is a great way to explore the substrate recognition mode of the enzyme. Recently, we characterized pyridoxal-5'-phosphate (PLP)-dependent D-amino acid transaminase (DAAT) from bacterium *Haliscomenobacter hydrossis* (Halhy) with a new type of the recognition site for the substrate α -carboxyl group [1]. D-cycloserine (D-CS) is a cyclic analog of serine. Various PLP-dependent enzymes, including transaminases (TA), are able to accommodate D-CS in their active sites. D-CS is proposed to react with TA through the canonical sequence of reaction steps and finally forms irreversibly a stable aromatic compound with PLP or dissociates from the active site [2–5]. Determination of the structure of the Halhy complex with D-CS can shed light on both the mechanism of D-CS interaction with Halhy and the mode of substrate binding in the active site of the new type of DAAT.

Methods and Algorithms: We explored the interaction of D-CS with Halhy by the combination of UV-Vis spectroscopy, enzyme kinetics and X-ray crystallography.

Results: D-CS is a strong inhibitor of Halhy with IC_{50} value of 3 μ M. The inhibited enzyme shows an absorbance maximum near 330–340 nm, indicative of a completed catalytic half-reaction. In the crystal structure D-CS is covalently attached to the cofactor and presents in two different states: an intermediate product, external aldimine, and a stable aromatic compound. Contrary to expectations, D-CS is not held by numerous noncovalent interactions in the active site. The only hydrogen bond was found between the oxygen of D-CS carbonyl group and the ϵ -amino group of the catalytic lysine.

Conclusion: D-CS binds PLP irreversibly; however, the excess of PLP restores the activity of Halhy. In the active site of Halhy D-CS interacts specifically with PLP, however, no specific interaction with the residues of the recognition site is observed. The modes of the natural substrates binding and D-CS coordination are different.

Acknowledgements: This work was funded by the Russian Science Foundation, grant No. 19-14-00164.

References

1. Bakunova A.K., Nikolaeva A.Y. et al. The Uncommon Active Site of D-Amino Acid Transaminase from *Haliscomenobacter hydrossis*: Biochemical and Structural Insights into the New Enzyme. *Molecules*. 2021;26(16):5053. doi: 10.3390/molecules26165053.
2. Peisach D. et al. D-cycloserine inactivation of D-amino acid aminotransferase leads to a stable noncovalent protein complex with an aromatic cycloserine-PLP derivative. *J Am Chem Soc*. 1998;120:2268–2274. doi: 10.1021/ja973353f.
3. Amorim Franco T.M., Favrot L., Vergnolle O., Blanchard J.S. Mechanism-based inhibition of the mycobacterium tuberculosis branched-chain aminotransferase by D- and L-cycloserine. *ACS Chem Biol*. 2017;12:1235–1244. doi: 10.1021/acschembio.7b00142.
4. de Chiara C., Homšak M. et al. D-Cycloserine destruction by alanine racemase and the limit of irreversible inhibition. *Nat Chem Biol*. 2020;16:686–694. doi: 10.1038/s41589-020-0498-9.
5. Dindo M., Grottelli S. et al. Cycloserine enantiomers are reversible inhibitors of human alanine:glyoxylate aminotransferase: implications for Primary Hyperoxaluria type 1. *Biochem J*. 2019;476:3751–3768. doi: 10.1042/BCJ20190507.