Viva Origino 33 (2005) 41－172

S1-1

Characteristics of Enzymes Participating in D-Amino Acids Metabolism

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Various D-amino acids occur widely, and are metabolized by several enzymes such as amino acid racemases. These are unique in catalysis: they catalyze the removal of α-proton from either enantiomer of amino acid, and subsequent non-stereospecific reprotonation. Most require pyridoxal phosphate, but glutamate racemase and aspartate racemase depend on no coenzymes and metals. Their substrate specificities are very high except arginine racemase and amino acid racemase with low substrate specificity, which were demonstrated by us. The primary structure of glutamate racemase of *Pediococcus pentosaceus* is similar to none of other enzymes, but that of active center resembles those of hemin binding sites of myoglobin and hemoglobin. The enzyme is inhibited by hemin, which stoichiometrically binds with the active center, whose structure is quite similar to that of the hemin binding pocket of myoglobin. D-Amino acid aminotransferase(D-AAT) acts on D-amino acids exclusively, and shows the analogous primary structure to only branched-chain L-amino acid aminotransferase, Only both enzymes catalyze the *pro*-R hydrogen transfer between the α-C of substrate and the C-4' of coenzyme. The catalytically important amino acid residues including Lys145 of D-AAT are located on the *re*-face in contrast to those of Asp-AT.