Evolution of amino acid biosynthesis and enzymes with broad substrate specificity

Hiromi Nishida

Institute of Molecular and Cellular Biosciences, The University of Tokyo, Tokyo 113-0032, Japan

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ABSTRACT

Summary: I selected 82 proteins that were related to amino acid biosynthesis in the genome of Escherichia coli. I then searched the extensive sequence homology for each of the selected proteins from among the proteins of E.coli. The result showed that 30 proteins of the selected proteins had extensive sequence homology within the selected proteins, and 21 proteins had extensive sequence homology to proteins outside the selected proteins. In addition, the enzymes with broad substrate specificity play an important role in the amino acid biosynthesis. I demonstrate here that some substrate-specific enzymes evolved from an ancestor enzyme with broad substrate specificity.

Contact: hnishida@iam.u-tokyo.ac.jp

RESULTS AND DISCUSSION

The 22 proteins of the selected proteins function at more than two steps of the amino acid biosynthetic pathway. Those are ArgD, AspC, HisB, HisD, HisI, IlvB, IlvC, IlvD, IlvE, IlvG, IlvH, IlvI, IlvM, IlvN, LeuC, LeuD, MetL, PheA, ThrA, TrpC, TrpD, and TyrA. Thus, the enzymes with broad substrate specificity play an important role in the amino acid biosynthesis.

The result of the BLAST sequence homology search is available on http://www.iam.u-tokyo.ac.jp/misysyst/Bresult.html. The result showed that 30 proteins of the selected 82 proteins had extensive sequence homology within the selected proteins, and 21 proteins had extensive sequence homology to proteins outside the selected proteins (Table 1). Among the 30 proteins that showed sequence homology within the selected proteins, 16 proteins (ArgF, ArgI, AspC, IlvB, IlvG, IlvH, IlvI, IlvM, LysC, MetL, SdaA, SdaB, ThrA, TyrB, YhaP, and YhaQ) are homologous to the enzymes that recognize the same substrate, and the other 14 proteins (ArgE, ArgH, AspA, CysK, CysM, DapE, HisA, HisC, HisF, IlvA, MetB, MetC, TdcB, and YfdZ) are homologous to the enzymes that recognize the different substrates during amino acid biosynthesis.

I believe the latter 14 proteins had the broad substrate specificity in the past. Those proteins include the following six enzymes whose evolutionary relationships have been reported: phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (HisA), succinyl-diaminopimelate desuccinylase (DapE), and cystathionine γ-synthase (MetB) have similarity and
Table 1. Result of the BLAST search

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<th>Categories</th>
<th>Proteins</th>
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A common evolutionary origin with cyclase (HisF), acetylornithine deacetylase (ArgE), and cystathionine β-lyase (MetC), respectively (Belfaiza et al., 1986; Boyen et al., 1992; Fani et al., 1994). On the other hand, the other eight proteins are newly reported in this paper. I show here that histidinol-phosphate aminotransferase (HistC) and asparate ammonia-lyase (AspA) have extensive sequence homology to N-succinyl-diaminopimelate aminotransferase (YfdZ) and argininosuccinate lyase (ArgH), respectively, and that threonine deaminase (TdcB), threonine deaminase (IlvA), cysteine synthase (CysK), and cysteine synthase (CysM) have homology.

The homologues of the 14 proteins are distributed among prokaryotes. I performed the phylogenetic analysis using MEGA (Kumar et al., 2000). The phylogenetic trees and alignments are available on http://www.iam.u-tokyo.ac.jp/misyst/tree1.pdf and http://www.iam.u-tokyo.ac.jp/misyst/AAlign.html, respectively. This phylogenetic analysis indicates that each of the 14 proteins has a common ancestor with a different functional protein, and that the ancestor probably had broad substrate specificity. The results support the idea that the substrate specificity of enzymes evolves from broad substrate specificity. Primitive organisms probably had more proteins with broad substrate specificity.

REFERENCES