MOLECULE PHYLOGENETIC ANALYSIS OF GENE ENCODING ASPARTATE AMINOTRANSFERASE

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Abstract: Aspartate aminotransferases is an effective catalyst in the amino-transformation rection, and plays an important role in the metabolism of carbon and nitrogen in cells. In this study, the conserved genes encoding Aspartate aminotransferase in different species were analyzed by bioinformatics, and found gene (AAF19543) from *Arabidopsis thaliana* shows obvious comparability with those from some species in Dicotyledon and Monocotyledon. Furthermore, The phylogenetic tree showed that these species analyzed were divided into two branch, one branch was composed of Protist, Eukaryotes, the other consist of *Pan troglodytes* and *Tribolium castaneum*, and the Eukaryotes was further divided into two branch, which is mostly consistent with biology system.

INTRODUCTION

Aminotransferases was firstly found in 1930, could transfer the amido from α-amino acid to α-keto acid, and then catalyze the synthesis and hydrolysis (Francisco et al., 1991; Puppo et al., 1992; Mavrides and Orr 1975; Gall et al., 1983). Aspartate aminotransferases belongs to Aminotransferases A, currently is found in animal, plant and microbe, and exhibits significant catalysis in the metabolizing process of nitrogen and carbon. When pyridoxal phosphate is its coenzyme, Aspartate aminotransferases catalyzes the reverse reaction between do-carboxyl amino acid and α-keto acid (Christen and Metzler 1985), therefore the functions of Aspartate aminotransferases are very abroad, mostly participates in convergency, transfer and stockpile of nitrogen, and the synthesis and hydrolysis of amino acid.

At present, the theory research of Aspartate aminotransferases is performed in the molecular level (Jager and Pauptit 1994). Along with development of biology technology, the catalyse mechanism Aspartate aminotransferases is studied by molecule simulation, and then instruct its reconstruction and reasonable design. In this article, the gene encoding Aspartate aminotransferases in various species was analyzed by bioinformatics in order to provide reference for further theory and application studies of Aspartate aminotransferases.

MATERIALS AND METHODS

Materials

The gene encoding Aspartate aminotransferases was screened in http://www.ncbi.nlm.nih.gov/blast/Blast.cgi, its GenBank accession number and source from different sources were shown in Table 1. In this article, the amino acid sequences of Aspartate aminotransferases were used to analyze the evolution relationship.

Methods

The amino acid sequence of every gene encoding Aspartate aminotransferases in Table 1 was analyzed by

DNAMAN software, and the gene tree was constructed to study the evolution relationship among gene encoding Aspartate aminotransferases in different species.

Table 1 The source and GenBank accession number of gene encoding Aspartate aminotransferases

	Source	GenBank accession number
1	*Arabidopsis thaliana*	AAF19543
2	*Populus trichocarpa*	ABK95824
3	*Vitis vinifera*	CAO65506
4	*Daucus carota*	P28734
5	*Lupinus angustifolius*	AAA50160
6	*Oryza sativa Japonica Group*	NP_001044317
7	*Glycine max*	AAC50015
8	*Panicum miliaceum*	CAA45023
9	*Medicago sativa*	CAA43779
10	*Lotus japonicus*	CAA63894
11	*Triticum aestivum*	ABY58643
12	*Apis mellifera*	XP_396131
13	*Securigera parviflora*	AAL09704.
14	*Chlamydomonas reinhardtii*	XP_001695040
15	*Dictyostelium discoideum*	XP_646849
16	*Solanum tuberosum*	ABB55364
17	*Xenopus laevis*	NP_001080255
18	*Phaseolus vulgaris*	AAN76499
19	*Xenopus tropicalis*	NP_001016933.
20	*Ornithorhynchus anatinus*	NP_001016933.
21	*Lotus corniculatus*	AAC12674.
22	*Ustilago maydis 521*	XP_756742
23	*Oryza sativa*	AAO23563
24	*Macaca fascicularis*	Q4R559
25	*Tribolium castaneum*	XP_969549
26	*Drosophila pseudoobscura*	XP_001356945
27	*Mus musculus*	AAB91426
28	*Monodelphis domestica*	XP_001376001

	Source	GenBank accession number
29	*Yarrowia lipolytica CLIB122*	XP_500415
30	*Rattus norvegicus*	NP_037309
31	*Bos taurus*	NP_777231
32	*Macaca mulatta*	XP_001103601
33	*Cryptococcus neoformans var. neoformans JEC21*	XP_568414.
34	*Pan troglodytes*	XP_523381
35	*Gallus gallus*	7AAT_A
36	*Pongo pygmaeus*	Q5REB0
37	*Sus scrofa*	NP_999093
38	*Danio rerio*	NP_998544
40	*Canis lupus familiaris*	XP_535278
41	*Homo sapiens*	AAH00525
42	*Laccaria bicolor S238N-H82*	XP_001873821
43	*Sus scrofa domestica*	0308236A
44	*Malassezia globosa CBS 7966*	XP_001731601
45	*Tetrahymena thermophila SB210*	XP_001017054
46	*Pan troglodytes*	NP_001092011

RESULTS AND DISCUSSIONS

The amino acid sequence of Aspartate aminotransferases (AAF19543) from *Arabidopsis thaliana* was used to search databank by BLAST, and obtain conserved gene encoding Aspartate aminotransferases from various species. These amino acid sequences of Aspartate aminotransferases from different species were compared by DNAMAN, and discovered that Aspartate aminotransferases (AAF19543) from *Arabidopsis thaliana* shows obvious comparability with some species belonging to Dicotyledon and Monocotyledon, 71%~75% or so. In order to further analyze the evolution relationship among these genes, the phylogenetic tree was constructed with amino acid sequences of Aspartate aminotransferases by DNAMAN. As shown in Fig. 1, the phylogenetic tree was divided into two branch, one branch was composed of Protist, Eukaryotes such as plant, animal and fungal, and the other consist of *Pan troglodytes* and *Tribolium castaneum*. Moreover, the Eukaryotes was further divided into two branch, one was made of green alga, Dicotyledon and Monocotyledon belonging to Angiosperm, and according to the evolution relationship, the other branch consist of in turn some species belonging to Protozoa

such as *Dictyostelium discoideum AX4*, *Yarrowia lipolytica CLIB1229*, *Ustilago maydis 521*, *Malassezia globosa CBS 7966*, *Cryptococcus neoformans var. neoformans JEC21* and *Laccaria bicolor S238N-H82*, *Drosophila pseudoobscura* and *Apis mellifera* in Phylum Arthropods, and animals in Craniota.

Furthermore, it was found in the phylogenetic tree that the relationship between *Pan troglodytes* (NP_001092011) and *Hono sapiens* is far, and the comparability is 48.9%, but Pan troglodytes (XP_523381) exhibit higher similarity with *Hono sapiens*, 99.5%. The amino acid sequence of NP_001092011 and XP_523381 was further compared, their similarity is merely 48.6%, which probably shows that *Pan troglodytes* NP_001092011 andXP_523381 are paralog. Wherease, *Pan troglodytes* (NP_001092011) and *Tribolium castaneum* (XP_969549) were clustered together, and exhibit parallel relationship with other species. Therefore, it is presumed that gene (NP_001092011) in *Pan troglodytes* might be evolved from gene (XP_523381). In addition, based on the phylogenetic tree, we also found *Tetrahymena thermophila SB210* belong to Protozoa which is the furthest primal phylum in animal kingdom, *Dictyostelium discoideum AX4* which is one kind of amoebae locates in the bottom of Matazoa, and fungi has closer relationship with animal than plant.
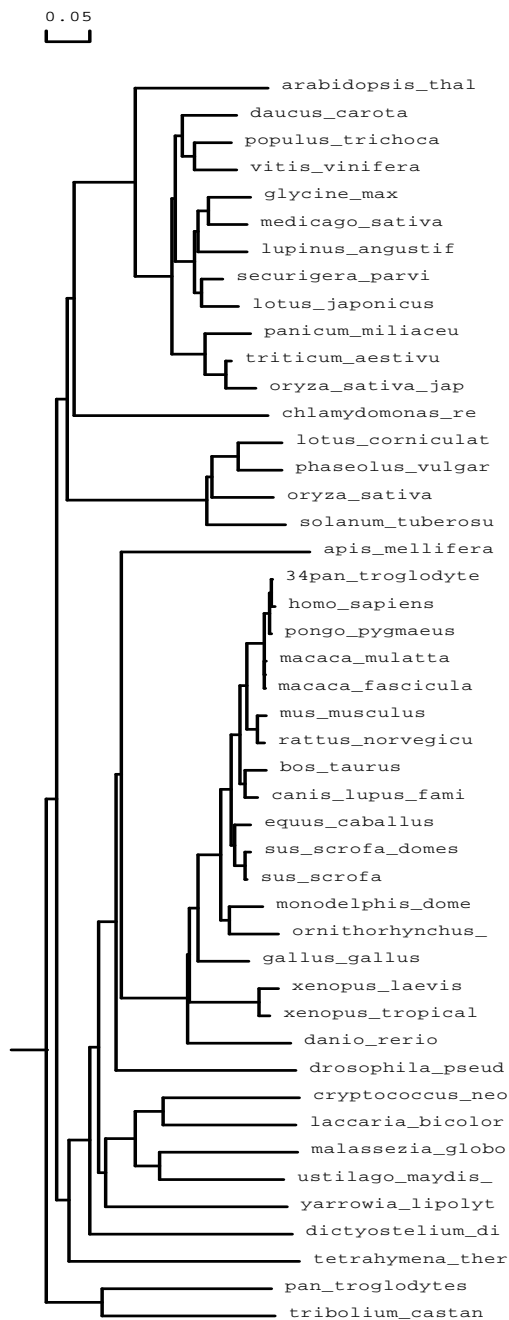
Fig. 1 The phylogenetic tree was constructed based on amino acid sequences of Aspartate aminotransferases from various species, the scale bar represents the branch length.

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