Identification Of Functional Subfamilies Of Class I-Type Lysyl tRNA Synthetase Family In Archaeal And Bacterial Members: A Bayesian Evolutionary Tree Estimation (BETE) Approach

D Rao, R Ramanjeneyulu, D Rao, C Kumar

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Abstract

Bayesian Evolutionary Tree Estimation (BETE) identified functional subfamilies of a given protein family multiple sequence alignment of Class I Lysyl t-RNA synthetase family. The importance of BETE is mainly used to identify functional subfamilies and the residues which involved in functional alteration in different subfamilies. Lysyl tRNA synthetases facilitate amino acylation process and play a crucial role in the essential cellular process of translation in all living organisms. Recently, genomic analysis has revealed that the archaeal class I-type tRNA synthetase is detected in Treponema palladium and other spirochetes. The understanding of taxonomical distribution in different organisms provides valuable information about gene transfer in various microbial pathogens.

INTRODUCTION

Lysyl tRNAs are essential for protein biosynthesis by ribosomal mRNA translation in all organisms. They are synthesized by Lysyl tRNA synthetases, a group of enzymes of two unrelated families; Class I tRNA synthetase and Class II tRNA synthetase. In bacteria and eukaryota, all known lysyl t-RNA synthetases are classified as Class II lysyl tRNA synthetases, whereas some archaea have been shown to contain an unrelated Class I-type lysyl tRNA synthetase. Recently, genomic analysis has revealed that the archaeal class I-type tRNA synthetase is detected in Treponema palladium and other spirochetes [Michael Ibba et al., 1997].

The understanding of taxonomical distribution in different organisms provides valuable information about gene transfer in various microbial pathogens. Interestingly, few microbial pathogens such as spirochetes were sequentially close relatives to Archaeal members. This is an evident based on computational analysis of Class I Lysyl t-RNA synthetase revealed that spirochetes may probably evolved from Archaeal kingdom. This computational analysis data would help researchers to understand in identifying common origin genes in different kingdoms and to discover organism specific molecular targets in pathogens which are taxonomical distributed only in bacteria and Archaea.[Terada et al., 2002].

MATERIAL AND METHODS

DETECTION OF SUBFAMILIES

In this experiment, we obtained subfamilies of Class I-type Lysyl tRNA synthetase using Bayesian evolutionary tree estimation(BETE). BETE identifies functional subfamilies of a given protein family multiple sequence alignment. BETE uses dirichlet mixture densities and information theory to construct phylogeny tree and cut the tree in to subtrees to obtain subfamily decomposition. BETE has been demonstrated on set of Lysyl-tRNA synthetases. BETE is mainly used to identify functional subfamilies and the residues which involved in functional alteration in different subfamilies [Sjolander.K. 1998].

SUBFAMILY PROFILE GENERATION AND COMPARISON :

Profile Hidden markov models were constructed to subfamilies of Class I-type Lysyl tRNA synthetases using hmmbuild program in HMMER package [http://genome.wustl.edu/eddy/hmm.html.] that can be used for database searching. Furthermore, we compared Class I-

type Lysyl tRNA synthetase subfamily profiles against Protein data Bank [http://rcsb.org], with the help of hmmsearch program in HMMER package, to find similar structure template to Class I-type Lysyl tRNA synthetase subfamilies.

RESULTS

BETE identified 3 subfamilies: Class I-type Lysyl tRNA synthetase_1, Class I-type Lysyl tRNA synthetase_2 and Class I-type Lysyl tRNA synthetase_3. The list of subfamilies and protein members present in microorganisms are summarized in table 1.

Figure 1

Table 1: The list of subfamilies of Class I-type Lysyl tRNA synthetase and Archaeal and bacterial members sharing different subfamilies.

Subfamily name	Organism name
Class I-type lysyl-tRNA synthetase_1	*Streptomyces coelicolor, Aeropyrum pernix, Methanopyrus kandleri, Halobacterium salinarium, Haloarcula marismortui, Methanobacterium thermoautotrophicum, Methanococcus maripaludis, Methanococcus jannaschii, Picrophilus torridus, Thermoplasma volcanium, Thermoplasma acidophilum, Archaeoglobus fulgidus, Methanosarcina barkeri, Methanosarcina mazei, Methanosarcina acetivorans, Pyrococcus kodakaraensis, Pyrococcus furiosus, Pyrococcus horikoshii, Pyrococcus abyssi, Borrelia garinii, Borrelia burgdorferi, Borrelia afzelii, Treponema pallidum, Treponema denticola.*
Class I-type lysyl-tRNA synthetase_2	*Rickettsia prowazekii, Rickettsia typhi, Rickettsia conorii, Rickettsia felis, Caulobacter crescentus, Rhodopseudomonas palustris, Silicibacter pomeroyi, Rhizobium loti, Brucella melitensis, Brucella suis, Brucella abortus.*
Class I-type lysyl-tRNA synthetase_3	*Cenarchaeum symbiosum*

DISCUSSION

Bayesian Evolutionary Tree estimation (BETE) identified three functional subfamilies of a given Class I-type Lysyl tRNA synthetase multiple sequence alignment. Hidden markov models were useful in construction of subtypes of Class I-type Lysyl tRNA synthetase to search structural template in PDB database. The advantage of subfamily HMMs search against structural database and as well as sequential databases is to select suitable structural template for homology modeling of subfamily members which improves the quality of homology model. Moreover subfamily protein profiles are useful for homology searching and accurate protein family annotation at amino acid residue level which in turn helpful to recognize functionally and structurally important residues in different subfamilies. The family level comparison is not possible to determine exact functional annotation.

The Class I-type Lysyl tRNA synthetase are restricted to Archaeal and bacterial domains but not found in eukaryotes. Recent evidences showed that disease causing microorganisms such as Treponema palladium and Borrelia burgdorferi are orthologues to Archaeal members. The functional orthologous proteins in bacterial species and Archaeal species, not in Eukaryota, are the best drug protein targets.

CORRESPONDING AUTHOR

Dr.Dowlathabad Muralidhara Rao
muralidhararao@yahoo.co.in

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Author Information

D. K. Venkata Rao
Department of microbiology, Sri Krishnadevaraya University

R. Ramanjeneyulu
Department of microbiology, Sri Krishnadevaraya University

DowlathabadMuralidhara Rao
Department of Biotechnology, Sri Krishnadevaraya University

ChittaSuresh Kumar
Department of Biochemistry, Sri Krishnadevaraya University