



# Phylogenetic Tree Construction of Butyrylcholinesterase Sequences in Life Forms

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## Abstract

Butyrylcholinesterase is an enzyme with few known physiological functions. It is related to acetylcholine that was shown to be expressed in a variety of life forms. We performed a search using the human butyrylcholinesterase gene (HGNC:983;MIM:177400), and found the sequence in a broad spectrum including plants, bacteria and animals. Therefore butyrylcholinesterase appears to have evolved early in evolution, and to have been conserved. ©

## INTRODUCTION

Butyrylcholinesterase (BChE; EC 3.1.1.1.8) is an enzyme with few known physiological functions. The ratio of BChE to HDL cholesterol was suggested to be a marker of cardiovascular risk in the metabolic syndrome.<sup>1</sup> However recent studies have suggested that BChE may be only a secondary marker for the metabolic syndrome in obese individuals with the CHE2 C5-phenotype.<sup>2-4</sup>

Acetylcholinesterase (EC 3.1.1.1.7) is a related enzyme with known physiological roles. It occurs in diverse life forms including bacteria, algae, protozoa and primitive plants, suggesting it appeared extremely early in the evolutionary process.<sup>5</sup>

Such analysis is possible following the availability of completely sequenced genomes, which allows comparative genomic analysis. Insights can be obtained into the organization and evolution of biological systems.

Therefore, considering the close structural and functional relationship between butyrylcholinesterase and acetylcholinesterase, and lack of information in terms of phylogenetic aspects, the aim of our study was to construct the phylogenetic tree of butyrylcholinesterase sequence in publicly available genome sequences of a variety of life forms including plants, bacteria and mammals.

## MATERIAL AND METHODS

Sequences were retrieved from National Centre for

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Biotechnology Information (NCBI) and Swiss-Prot datasets.

To collect full length sequence of BChE genes in eukaryotes and prokaryotes we conducted BLASTP searches against the DAD database (all amino acid sequences) on DNA Databank of Japan (DDBJ) Web site ([WWW.ddbj.nig.ac.jp](http://WWW.ddbj.nig.ac.jp)) and chose sequences with E value below 10. A human BChE gene (HGNC:983;MIM:177400) was used as query. Here the nomenclature adopted by HUGO gene nomenclature Committee ([WWW.gene.ucl.ac.uk/nomenclature](http://WWW.gene.ucl.ac.uk/nomenclature)). From the hits obtained by homology search, we took only sequences that contained Butyrylcholinesterase. These sequences were used for further analysis and a Neighbor-joining (NJ) phylogenetic tree was constructed. We searched for BChE genes in three comprehensive datasets, Genbank, dbEST and dbGSS of all species.

Sequence analysis was done using multiple alignments using Clustal X. Score matrices were calculated using BLOSUM 62. This score was given as an input to neighbor-joining algorithm for reconstruction of phylogenetic tree.

We conducted BLASTN searches against plant species database on TIGR gene indices. (<http://www.tigr.org/tdb/tgi/> using gi\_4557350\_ref\_NM\_000055 as query.

## RESULTS

In the plants, when we took an identity of 65% or more as significant, we found it in wheat TC272584, poplar CK104837, Pepper CO911974, Benthamina TC8685, Lotus Japonicus AV778739 and Arabidopsis thaliana BP643359 (Fig. 1). Lesser identity (53-64%) sequences were identified in Rice, Soybean, Potato, Maize, Arabidopsis, Sunflower, Ice plants, Lotus japonicus, Lettuce, Medicago thuruncatula, Spruce,

