Phylogenetic Characterization of Ureases

Andreis, F.C.; Ligabue-Braun, R.; Carlini, C.R.; Verli, H.

Centro de Biotecnologia, UFRGS, Rio Grande do Sul, Brazil

Ureases (EC 3.5.1.5) are nickel-dependent enzymes which catalyze urea hydrolysis into ammonia and carbon dioxide. They are widely distributed in plants, fungi and bacteria. In plants and fungi, ureases exist as hexamers or trimers. In bacteria, they possess two or three smaller subunits, approximately 55% identical to the single-chained plant enzymes. In this context, the current work intends to obtain a phylogenetic characterization of evolutionary relations among ureases of different organisms, contributing to the understanding of the alterations of polypeptide chain numbers of these enzymes among different taxa. Accordingly, urease protein sequences, obtained from the NCBI database, were submitted to initial filtering, eliminating incomplete and incorrectly labeled sequences. The remaining dataset was submitted to sequential multiple alignments (ClustalW algorithm) aiming to reduce the redundancy of information, resulting in 126 representative sequences. For better understanding, phylogenetic trees using Maximum-Likelihood (MEGA 5 software) and Bayesian (MrBayes software) algorithms were constructed with different sets of sequences (complete, conserved and hypervariable regions, detected with SimPlot software). So far, phylogenies of conserved regions using both methods converged, suggesting that single-chained ureases of plants and fungi originated from those of bacteria (triple-chained). In addition, as expected, Archeal ureases appear as the most primitive. Two-chained enzymes, present in Helicobacteraceae and presumed intermediates between single- and triple-chained ureases, branched as special cases among triple-chained ureases, opposing the previous hypothesis. Based on the data, we suggest a horizontal gene transfer among taxa.

Keywords: enzyme, phylogeny, urease

Supported by: FAPERGS, CNPq and CAPES