THE COMPUTER ANALYSIS OF PRIMARY STRUCTURES OF INULINASES FROM VARIOUS PRODUCERS

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Inulinase (EC 3.2.1.7) splits off inulin and others fructose containing polymers, playing the important role in transformation reserve polyfructozydes type inulin or levan in mobile fructose, which is a source of carbon and energy for plants and microorganisms. Biotechnologists began to investigate inulinase because of prospect to use them with the purpose to receipt syrups with the high contents of fructose – perspective substitute of sugar for patients with diabetes, and also for caries and adiposity preventive maintenance.

The purpose of this work was to perform the computer analysis of amino acid sequences of inulinase from various producers, which creates preconditions to drawing up of forecasts concerning molecular features of enzyme, mechanism of catalysis, functional groups of the active center. The detailed analysis of protein macromolecules at all levels of their organization in a combination to classical methods of biochemistry and biophysics allows to define structurally functional properties and molecular mechanisms of inulinase action. For today the opportunity to predict property of protein, proceeding from amino acids sequences, is one of the mainest purposes modern integrative biology.

Data on primary structures of inulinase we received in National Center for Biotechnology Information (http://www.ncbi.nlm.hin.gov/Entrez), alignment of amino acids sequences we spent at use of software package BioEdit.

It is established, that the basic amount of homologous parts is presented by Gln, Asn and Asp residues. These amino acids are possibly responsible for active interaction between protein macromolecule and molecules of water, providing good solubility of enzyme. Carboxyl groups of lateral radicals Asp and Glu, a part active centers of inulinases, can play a role of contact groups for molecules of substrate, and also carry out basic-acids catalysis, influencing on polarity located on the neighborhood with them connections and groups of enzyme-substrate complex or causing displacement of electronic density by formation of hydrogen communications. Comparison of primary structures of inulinases has shown, that frequency of rests replacements during polypeptide chains differs high variability. The phylogenetic tree for inulinases fom various producers is constructed. The high degree of homology is characteristic for enzymes from *Aspergillus awamori*, *A. niger* and *A. ficuum;* it is interesting, that inulinase from *A. fumigatus* stands evolutionally much further from them. Endo- and exo-inulinases possess rather small relationship. The most essential differences are found out between inulinases from *Aspergillus fumigatus* and *Arthrobacter* sp. S37.