

KARBOKSYHYDROLAZY *TRICHODERMA REESEI*: BUDOWA, MECHANIZM DZIAŁANIA, REGULACJA I ZASTOSOWANIE

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Carboxyhydrolases of *Trichoderma reesei*: structure, mode of action, regulation and application

Abstract: Cellulose is the most abundant source of carbon in the world. This plant polysaccharide is decomposed by several microorganisms. One of the best producers of cellulases which has found industrial applications are fungi from the type *Trichoderma*. Apart from cellulases, other enzymes which occur in the culture filtrates (i.e. xylanases, proteases, chitinases, and fl-1 „3-glucanases) are also involved in the hydrolysis of plants biomass and play other significant roles. Three different types of enzymes of *T. reesei* are involved in the degradation of cellulose. At least two cellobiohydrolases (CBH), several endo-1,4-glucanases (EG) and β -glucosidases have been identified and characterized. CBHI is the dominant enzyme of cellulolytic complex forming up to 60% of the secreted protein by *T. reesei*. The proportion of CBHII amounts to around 20% and endoglucanase, most of which endoglucanase I (EGI) comprise 10%. β -glucosidases account for only 1% of the total secreted proteins. Molecule of CBHI (which is 18 nm long) consist of three domains: cellulose binding domain, hinge domain and catalytic core domain. Genetic improvements of *T. reesei* QM6a and its derivatives for cellulase production has been investigated in several laboratories and hyperproductive mutants were obtained by treatment with UV light, gamma irradiation or diethyl sulphate. The application of genetic engineering to *Trichoderma* has made it possible to modulate cellulase production in such away that new *T. reesei* strains producing novel cellulase profiles are now available. Irrespective of genetic engineering advancement, it seems that the knowledge of regulatory mechanism of cellulases is required for increased production of these enzymes. β -1,4-xylan, next to cellulose is the most abundant hemicellulose fraction. Due to structural

heterogeneity, xylan degrading enzyme system includes several hydrolytic enzymes. One of the best known of these enzymes are endo- β -1,4-xylanases which attack the main chain of xylan and β -xylosidase which hydrolyses xylooligosaccharides to D-xylose. Recently, trend of research seems to develop towards production cellulase-free β -1,4-xylanases. Such preparations are used in kraft pulp for bleaching processes as an alternative to chlorine-based methods.

1. Introduction. 2. Characteristic of cellulolytic enzymes complex of *Trichoderma reesei*. 2.1. Cellobiohydrolases. 2.2. Endoglucanases. 2.3. β -glucosidases. 3. Molecular structure of cellulases. 4. Cellulases genes from *T. reesei*. 5. Genetical modification of *T. reesei*. 5.1. Mutagenisation. 5.2. Genetic engineering. 6. Regulation of production and secretion of cellulases. 6.1. Regulation of cellulases formation on molecular level. 6.2. Induction and inducers of production of cellulases. 6.3. Carbon catabolite repression of biosynthesis of cellulases. 6.4. Secretory pathways of cellulases of *T. reesei*. 7. Application of cellulases of *T. reesei*. 8. Additional enzymes of culture filtrates of *T. reesei*. 8.1. Xylanases. 8.2. Application of xylanolytic enzymes of *T. reesei*. 8.3. Proteases. 8.4. β -glucanases. 8.5. Chitinases. 8.6. Application of lytic enzymes of *T. reesei*. 9. Final remarks

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