

BIOINFORMATICS STUDY OF PHY GENE ENCODING PHYTASE FROM VARIOUS OF MICROORGANISMS

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Abstract

*Phytase is an important enzyme for livestock especially for monogastric because this enzyme is able to hydrolyze phytic acid. The addition of phytase in ration has been known increased digestibility of phosphate, reduced soil pollution, and increased feed digestibility. In Indonesia, the availability of phytase is limited. The sources and technology to produce phytases is needed. Thus, various studies including bioinformatic study is important to fulfill the requirement of phytase in Indonesia. This study aimed to study phy gene encoding phytase from different microorganismes.. Data regarding a phy gene sequences encoding phytase from different microorganisms, amino acid sequences of phytase, 3D structure with active site and binding site of phytase, the phylogenetic tree of phy gene and phytase were evaluated. The results showed that coding sequence (CDS) size of the phy gene varies from 1104 to 1959 base pairs with the amino acid sequence size from 368 to 652 AA. The active site of phytase from *Aspergillus niger* are the amino acid Histidine (His59) and Aspartic acid (Asp339) where this phytase is dominated by the alpha helix structure. While, phytase from *Bacillus amyloliquefaciens* has 6 calcium binding sites, namely GLU15, PRO29, VAL73, ASP280, ILE 312, dan ASP313, where beta sheet and loop are very dominant in compiling this enzyme. Further study on bioinformatics, gene expressuon, enzyme activities and biological evaluation is needed to support the development of phytase production.*

Key words: bacteria, bioinformatic, feed additive, fungi and gene phy