

Bioinformtic analysis of microbial phytase

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Abstract: A large protion of the phosphorus in food is linked to an acid that called phytic acid[1]that causes lack of minerals in humans and impaired food intake.Phytase attaches to the acid and releases nutrients.other importance include: the production of peroxidase, Supplementation in fish food ,pulp and paper industry,the bakery industry, the isolation of plant proteins[2] , the digestibility of niterogen and amine acid in poultry nutrition.Phytase extraction ways are: the gastrointestinal tract itself , feed in the ration of birds, phytase with the origin of germs found inside the digestive tract By foreign microorganisms[3].

The best and most cost –effective way is by microorganisms,wich is the isolation of viruses and bacteria. Bacteria also show higher levels of phytase activity compared to viruses.

In this study in order to find more stable and resistant phytase to heat 11 microbial phytase were analyzed and the Protparam server was used and the second and third structure of the proteins was drafted by the Psipred and Swiss model server to study the evelutionaly relationships of this phylogeny tree enzyme was construct by the Mega7 server.Among the enzymes examined,4 enzymes in addition to stability also had higher aliphatic than other enzymes:

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| 1)phytase Pseudomonas sp.10_3_11 | aliphatic index:89.95 |
| 2)phytase Pseudomonas geniculate | aliphatic index: 80.84 |
| 3)phytase Aspergillus fumigatus[4] | aliphatic index: 74.75 |
| 4)phytase Pneicillium olsunii | aliphatic index:75.11 |

Keywords: Protparam;Secondary structure prediction; PsIpred; Swiss-model; Phytase extraction; Aliphatic index

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