RESEARCH ARTICLE

AN AMINO ACID SEQUENCES BASED COMPUTATIONAL ANALYSIS OF ENZYME CYTIDYLATE KINASE

Nitin Kumar Verma[1, 2]*, Balwinder Singh[3], Vibha[4]

[1] Department of Biotechnology and Bioinformatics, Uttaranchal College of Science and Technology, Dehardun, Uttarakhand, INDIA
[2] Faculty of Life Science, Uttarakhand Technical University, Dehradun, Uttarakhand, INDIA
[3] Department of Science, Ek Onkar Scholar Degree College, Shahbjnagar, Shahjahanpur, Uttar Pardesh, INDIA
[4] Genetics and Tree Propagation Division, Forest Research Institute, Dehradun, Uttarkhand, INDIA
Email: nittinkumarverma@gmail.com

Received-01.08.2016, Revised-17.08.2016

Abstract: Computational analysis has been established for hypothetical study of amino acid sequences of the enzyme cytidylate kinase that derived from various programs and databases. Cytidylate kinase enzyme is widely distributed enzyme among bacteria and fungi. In the present study, thirteen full length amino acid sequences cytidylate kinase were retrieved, collected and subject to multiple sequence alignment (MSA), regular expression identification, domain identification, discovering individual amino acid composition, and construction of phylogenetic trees. Multiple sequence alignment revealed that three glycine, one lycine, one arginine and one valine were identically found in all the bacterial and fungal sources of cytidylate kinase. The two major sequence clusters were constructed by phylogenetic analysis. One cluster contains two species of fungi and six species of bacteria, where as other contain five species of only fungi. The amino acid composition results revealed that the average frequency of amino acid leucine is 9.29 % in fungi, where as alanine 13.61 % in bacteria. In addition, six unique motifs were also identified in the group analysis.

Keywords: Motif, Phylogentic analysis, Multiple sequence alignment, Cytidylate Kinase, Domain

REFERENCES

Altschul, S.F., Gish, W., Miller, W., Myers, E.W., Lipman, D.J. (1990). Basic local alignment search tool. J. Mol. Biol. 215, 403–410.

Bailey, T.L., Williams, N., Misleh, C., Li, W.W. (2006). MEME: Discovering and analyzing DNA and protein sequence motifs. Nucleic Acids Res. 34, 369–373.

Bateman, A. (2007). ClustalW and ClustalX version 2.0. Bioinformatics 21, 2947–8.

Blenis, J. (1993). Signal transduction via the MAP kinases: proceed at your own RSK. Proc. Natl. Acad. Sci. U. S. A. 90, 5889–5892.

Briozzo, P., Golinelli-Pimpaneau, B., Gilles, A.-M., Gaucher, J.-F., Burlacu-Miron, S., Sakamoto, H., Janin, J., Bârzu, O. (1998). Structures of Escherichia coli CMP kinase alone and in complex with CDP: a new fold of the nucleoside monophosphate binding domain and insights into cytosine nucleotide specificity. Structure 6, 1517–1527.

Cheek, S., Zhang, H., Grishin, N. V. (2002). Sequence and structure classification of kinases. J. Mol. Biol. 320, 855–881.

Finn, R.D., Mistry, J., Tate, J., Coggill, P., Heger, A., Pollington, J.E., Gavin, O.L., Gunasekaran, P., Ceric, G., Forslund, K., Holm, L., Sonnhammer, E.L.L., Eddy, S.R., Bateman, A. (2010). The Pfam protein families database. Nucleic Acids Res. 38, D211–D222.

Leipe, D.D., Koonin, E. V., Aravind, L. 2003. Evolution and classification of P-loop kinases and related proteins. J. Mol. Biol. 333, 781–815.

Liou, J., Dutschman, G.E., Lam, W., Jiang, Z., Cheng, Y. (2002). Characterization of Human UMP / CMP Kinase and Its Phosphorylation of d- and l-Form Deoxycytidine Analogue Monophosphates Characterization of Human UMP / CMP Kinase and Its Phosphorylation of D - and L -Form Deoxycytidine Analogue Monophosphates. Cancer Res. 62, 1624–1631.

Michalovich, D. (2002). Protein sequence analysis in silico: application of structure-based bioinformatics to genomic initiatives. Curr. Opin. Pharmacol. 2, 574–580.

Pellegrini, M. (2001). Computational methods for protein function analysis. Curr. Opin. Chem. Biol. (5)1,46-50

Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., Kumar, S. (2011). MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol. Biol. Evol. 2731-9

Verma, K. N., Singh, B. (2013). Insight from the structural molecular model of cytidylate kinase from *mycobacterium tuberculosis*. Bioinformation. (9)13, 680-684

*Corresponding Author