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Bioinformatics Characterization Cysteine Protease as Anti-Co Agulant Extracted From Haemonchus Spp

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ABSTRACT

The current study were showed through the period from June 2022 to October 2022, the total of examined samples 20 samples taken from slaughtered camels (DNA sampels after prepration) in Al Najaf province used to identify the score of similarity, the results of in silico of cysteine show the Docking score : -274.20 compare with standred -246.52 was performed test protein interaction between humen fibrin alpha chain (3GHG) with tested protein(modeled) compared with humen CYSTEINE PROTEASE (1CJL).. Gene extraction was done from samples ribosomal DNA was used as a gene marker for rapid PCR for DNA amplification, 20 sample otherwise this prevalence confirmed the resuts with gen bank similarity NCBI bioinformatics.

INTRODUCTION

Bioinformatics in its broadest sense involves the application of computer processes to solve biological problems. A wide range of computational tools are needed to effectively and efficiently process the large amounts of data generated by the latest technological innovations in biology and medicine. Many computational tools have been developed or adapted to handle the experimental richness of complex and multivariate data and the transformation from data collection to information or knowledge. These include various clustering and classification algorithms, including Self-Organizing Map (SOM) artificial neural networks (ANN), support vector machines (SVM), fuzzy logic, and even hyphenated technologies such as neurofuzzy networks. These bioinformatics tools are being evaluated and used in various fields of medicine, including early detection, risk assessment, classification, and prognosis of cancer. The goal of these efforts is to develop and identify bioinformatics methods with optimal sensitivity, specificity, and predictive power.

MATERIALS AND METHODS

The sequences of the nucleotide, were gained to analysed and compared against the sequences database by using BLAST, obtained by the NCBI (http://www.ncbi.nlm.nih.gov), and were aligned and clustered using ClustalW, Jalview, BioEdit and DNAStar programs.

The sequence of P. saltans L. cysteine proteinase amino acid, was obtained by translating the nucleotide sequence using the translation tool at the ExPASy server (http://web.expasy.org/translate/). therefore, by using the Phylogeny. fr Software

(http://www.Phylogeny.fr), and according to (Liolios et al., 2011),the tree of the Phylogenetic of P. saltans L. cysteine proteinase gene was created.

The prediction of Secondary structure was performed according to the SAS online program (sequence annotated by structure) (https://www.ebi.ac.uk/thornton-srv/databases/sas/). Then, the dimensional structure expectation was done by submitting the sequence of the protein to the Swiss model server to obtain the data and the 3D structural prediction, were analysed by using the PDB viewer program.

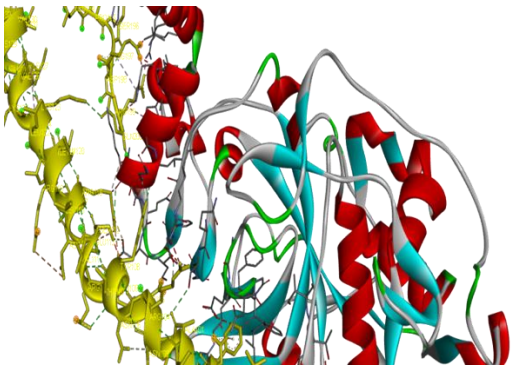
finally, modelling the protein 3D structure were design according to the multiple-threading alignments by using TASSER and LOMET iterative assembly simulation, and The molecular mass and theoretical (pI) values, of the *P.saltans* L. cysteine proteinase were expected by using ProtParam tool, (http://www.expasy.org/tools/protparam.html),(Saeed et al., 2018).

Results

In silico study for cysteine proteinase from Haemonchus spp as Anti-Co agulant

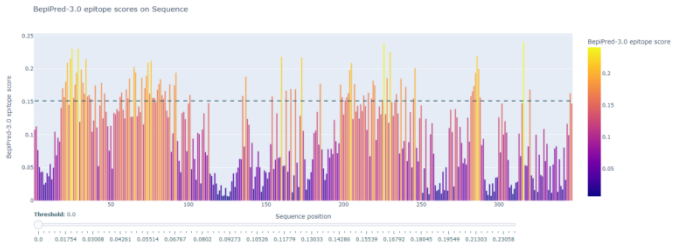
Protein sequence was retrieved from NCBI with accession number AAA29176.1

Secondary structure prediction, The tested sequence was predicted as 2nd structure to obtain the main properties as physiochemical and motif structure by direct uploading the sequence into http://bioinf.cs.ucl.ac.uk/psipred/



This figure show the tested protein structure .This results of in silico of cysteine show the Docking score: -274.20 compare with standred -246.52 Docking

was performed test protein interaction between humen fibrin alpha chain (***3GHG***) **with tested protein(modeled) compared with** humen CYSTEINE PROTEASE (1CJL)



Discussion

The current study determines the prevalence of CYSTEINE PROTEASE enzyme. among abomasum haemonchus samples collected from camels was showed by technique fr Software (http://www.Phylogeny.fr), and according to SAS online program (sequence annotated by structure) (Kozakov.D et al 2017). (https://www.ebi.ac.uk/thornton-srv/databases/sas/ . Although prediction of Secondary structure was performed to perform and only method to determinedgenrally Then, the dimensional structure expectation was done by submitting the sequence of the protein to the Swiss model server to obtain the data and the 3D structural

prediction, were analysed by using the PDB viewer program*3GHG*) with tested protein(modeled, is an application that provides a user friendly interface allowing to analyze several proteins at the same time- (Jordan F et al 2022) , we confrirm Using these two programs significantly reduces model generation effort because the protein primary sequence can be threaded into a 3D template and receive immediate feedback on how well the reference structure accepts the threaded protein before submitting a request to create missing loops, and Improve side chain packaging (James W et al 2020).

REFERENCES

1. Harris TK, Turner GJ. Structural basis of perturbed pKa values of catalytic groups in enzyme active sites. *IUBMB Life.* 2002; 53(2): 85–98.
2. Nabavi R, Eslami A, ShoKrani HR, Bokaie S, Shayan P, Saadati D (2011) Study on the prevalence, intensity, seasonal dynamic of abomasal hel-minths in sheep from different climatic zones of Iran. World Appl Sci ,.12(4): 441-445.
3. Behnam M., Fatemeh J.and Zahra M.(2015) Phylogenetic Study of Haemonchus Species from Iran Based On Morpho-Molecular Characterization . Iran J Parasitol: Vol. 10,. pp.189-196.
4. Alessandro F. T.do A. (2011) Why is it important to correctly identify Haemonchus species?. Rev. Bras. Parasitol. Vet., Jaboticabal, v. 20, n. 4, p. 263-268.
5. Heise M, Epe C, Schnider T.(1999) Differences in the second internal transcribed spacer (ITS-2) of eight species of gastrointerstinal nematodes of ruminants. J Parasitol.; 85 (3):431–435.
6. Michelle C.S.; Mônica R. V.; Maria R. L. and Alessandro F. T. do A.(2014) Differentiation of Haemonchus placei from Haemonchus contortus by PCR and by morphometrics of adult parasites and third stage larvae . Braz. J. Vet. Parasitol., Jaboticabal, v. 23, n. 4, p. 495-500.
7. Bhatnagar A, Apostol M, Bandyopadhyay ID. Amino acid function relates to its embedded protein microenvironment: a study on disulfide-bridged cystine. *Proteins.* 2016;84(11):1576–1589.
8. Jordan Fauser, Nicholas Leschinsky, Barbara N. Szynal, Andrei V. Karginov. Engineered Allosteric Regulation of Protein Function. *Journal of Molecular Biology* 2022, *434* (17) , 167620.
9. Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. 2013. MEGA6: molecular evolutionary genetics analysis version 6.0. Mol Biol Evol. 30:2725–2729.
10. Samson-Himmelstjerna G, Harder A, Schnieder T. (2001) Quantitive analysis of ITS2 sequences in trichostringyle parasites. Int J Parasitol.; 32: 1529– 1535.
11. James W. McCormick, David Pincus, Orna Resnekov, Kimberly A. Reynolds. Strategies for Engineering and Rewiring Kinase Regulation. *Trends in Biochemical Sciences* 2020, *45* (3) , 259-271.
12. Hastie, T., R. Tibshirani, M.B. Eisen *et al.* 2000. "Gene shaving" as a method for identifying distinct sets of genes with similar expression patterns. Genome Biol. 1(2): 0003.1-0003.21 (http://genomebiology.com/2000/1/2/research/0003/).
13. NCBI website