Computational Approach to Explore *Taenia solium* paramyosin Structure

Pranati swain

Orissa university of agriculture and technology, Bhubaneswar, Odisha

dedicated to my beloved parents & sister Mrs. Pritilata nayak & Mr. purnananda swain, miss prativa swain

Abstract- **Cysticercosis disease generally found in developing countries which also lead to death of the patients at times. Due to lack of awareness people feed on the pork meat and pig is the intermediate host of T.solium worm. The paramyosin protein which is produced by the worm inactivates the host(human) immune system causing infections. So the main objective of the work is to understand the structure, property and function of the protein. The analysis, functional charaterisation, sterio-chemical activity, physico-chemical activity, evaluation of the models were studied by using different bioinformatics tools. From the observation it was easy to get brief idea about the paramyosin protein of *Taenia solium.***

***Indext Terms- T.solium*, paramyosin, cysticercosis, 3D structure modelling**

I. INTRODUCTION

Cysticercosis is specially found in those people who feed on pork meat. The disease is generally caused by a tapeworm known as *Taenia solium*(pork tapeworm). It generally infects the tissues affecting skin, muscles and also the CNS mainly brain. The disease is spread by eating vegetable, meat and by drinking the water which contains porkworm's egg. When the worm affects the intestine of human then the disease is known as taeniasis. This worm use human as the main host and pig as an intermediate host. The main source of infection to human is undercooked pork which contains viable cysticerci. After entering it moves towards intestine and get attatched to the small intestine with the help of it's scolex. Then the proglottid chains grow. Ova released by mature worms are digested in the stomach with the help of digestive enzymes and release oncospheres which penetrate the intestinal wall and reach the bloodstream. These oncospheres develope into cysticerci mainly in brain, subcutaneous tissue and eyes. The symptoms of this disease generally involve myositis, with fever, eosinophilia, and muscular pseudohypertrophy leading to muscle swelling and later progress to atrophy and fibrosis. Neurocysticercosis is the state of disease when the worm exists in parenchyma of the brain. If the cyst is present in ventricles then it stops the outflow of cerebrospinal fluid which increases intracranial pressure. When the cyst is present in subarachnoid space then it causes racemose neurocysticercosis . The worm also damage the eye causing retinal edema, hemorrhage, loss in vision. In eyes the cysticerci may be found in the globe, extraocular muscles, and subconjunctiva. Diagnosis of disease involve various techniques i.e, Ophthalmic cysticercosis can be diagnosed by fundoscopy. Diagnosis of stool sample is also a traditional method to find the presence of *Taenia.* EITB (Enzyme Linked Immunotransfer Blot) assay and in CSF by ELISA methods are alos used for diagnosis by using lentil-lectin (agglutinin from Lens culinaris) antibodies to the cysticerci is demonstrated in serum. CT scan and MRI scan also gives successful diagnosis result. CT scan shows both calcified and uncalcified cysts whereas MRI scan helps in detection of intraventricular cysts. S3PVAC vaccine is mainly used for treatment. The vaccine generally contains 3 protective peptides: KETc12, KETc1 and GK1 having similarity with the sequence of antigens that are present in the different developmental stages of *T. solium* and other cestode parasites. Non-infected pigs are vaccinated with S3Pvac . The S3Pvac vaccine is owned by the National Autonomous University of Mexico. The Neurocysticercosis is treated with niclosamide, Antiparasitic treatment should be given in combination with corticosteroids and anticonvulsants. Infections in eyes are treated with surgery, praziquantel and albendazole. The best way for prevention is to avoid the uncooked meat, to keep the surrounding neat and clean, avoid using of contaminous vegetables and water.

The *Taenia solium* contains a protein known as paramyosin which was identified in PMY gene. Paramyosin is a major structural component of many thick filaments isolated from invertebrate muscles. It acts as an antigen in human cysticercosis that acts as a modulator of the host immune response. It helps in binding of collagen and has complement inhibitor activity. The protein shows identity to taenia saginata, echinococcus granulosus, echinococcus multilocularis. The paramyosin protein helps in catalysis of movement along a polymeric molecule such as a microfilament or microtubule, coupled to the hydrolysis of a nucleoside triphosphate.

II. MATERIALS AND METHODS

Selection of Cysticercosis Parasite:

The *Taenia solium* is selected as a candidate organism because it cuases cysticercosis in human beings and also cause taeniasis. This disease is mainly found in developing countries. Though many awareness informations are available, but lots of people are getting affected by the disease in their day to day life. Here the main objective is to explain how the paramyosin protein works and how it interacts with the human body. When the worm attacks the brain it may lead to death. Complete genome sequence of *T. solium* is available. Taenia solium shows high frequency of resistance to available drugs in the market. Resistance towards the presently available drugs was due to improper identification of *T.solium* and abnormal drug dosage without specificity to the *T.solium* and finally parasite becomes resistant to the available drugs very rapidly. So new drugs should be introduced. This is the main motive of my present study to choose *T.solium* as a target species.

Sequence analysis of paramyosin of *Taenia solium:*

The uniprot ID of the protein is P35418.
The aminoc acid sequence was downloaded in FASTA format from NCBI(http://www.ncbi.nlm.nih.gov/)/Uniprotdatabase(http://www.rcsb.org/pdb/home/home.do).

The retrived amino acid sequence was submitted to PBLAST (http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome) to obtain similar structural protein against the PDB-RCSB database(http://www.rcsb.org/pdb/home/home.do) keeping default parameters like E-value threshold 10, word size 3 and Blosum 62 Matrix.

The PBLAST algorithm helps to obtain global alignments, regions of similarity embedded in the respective protein. The result page of BLAST template sequences which were structurally homolog to the query sequence. The paramyosin protein of *Taenia solium* showed homology to smooth muscle myosin heavy chain of Gallus gallus with the PDB ID OF 1I84_S. The template protein sequence was derived from uniprotKB for further analysis. Multiple sequence alignment of both target and template was performed using CLUSTAL_W2(http://www.ebi.ac.uk/Tools/msa/clustalw2/). Regions of conservation and variation were detected from CLUSTAL_W2 result.

Functional Characterization of paramyosin of *Taenia solium*:

Functional characterization of paramyosin protein sequence was done by detecting the Motifs and domains. Motif scan tool (http://myhits.isb-sib.ch/cgi-bin/motif_scan) was used to find the motifs.
The domains were obtained by using Prodom database(http://prodom.prabi.fr/prodom/current/html/form.php).

Physico-Chemical Characterization of paramyosin of *Taenia solium*:

The basic physicochemical properties of the paramyosin protein sequence were calculated using the ProtParam tool(http://web.expasy.org/protparam/). Molecular weight, theoretical pI, amino acid composition, atomic composition, extinction coefficient, estimated half-life, instability index, aliphatic index and grand average of hydropathicity19 (GRAVY) was computed by ProtParam.

Secondary Structure prediction of *paramyosin* using CFFSP server:

CFFSP (chou & fasman secondary structure prediction) server (http://www.biogem.org/tool/chou-fasman/) was used to obtain the secondary structure of paramyosin protein. Secondary structure prediction is the definition of each residue into either alpha helix, beta sheet or random coil secondary structures.

SWISS model:

This is a protein homology modeling tool (http://swissmodel.expasy.org/interactive). This modeling server is accessible via the expasy web server. It gives the clear tertiary structure of a protein model showing the regions of alpha helix, beta sheets, beta turns, coils, helix etc.

CPH Model:

This is a protein homology modeling tool(http://www.cbs.dtu.dk/services/CPHmodels/). It is a web-server predicting protein 3D-structure which uses single template homology modeling is a group of high performing 3D-prediction tools. It is quite fast than in comparision to other protein modeling tools.

Phyre2:

This is also a homology modeling tool for proteins (http://www.sbg.bio.ic.ac.uk/phyre2/html/page.cgi?id=index). It also generates 3D model of a protein.

Evaluation of the obtained models of paramyosin protein:

The models which were obtained by SWISS-MODEL,PHYRE2 and CPHmodels-3.0 were further evaluated by using following servers.

PROCHECK saves server:

This server is generally used to find the region of allowed and disallowed regions of a protein. It also shows the phi-psi angles. It gives the sterio-chemical evaluation. The model file is generally uploaded in the server which analyses the backbone confirmation of a protein.
(http://services.mbi.ucla.edu/SAVES/Ramachandran/)

ProSA:

This server generally helps in the structural validation of a protein (https://prosa.services.came.sbg.ac.at/prosa.php)**.** PDB file of the model is given as an input. It can also be applied to low resolution structures and approximate models obtained early in the structure determination process

III. Results And Discussion

Selection of Target Protein and Retrieval:

paramyosin protein of *T.solium* generally induces the cysticercosis in human beings. It acts as an antigen to human body by affecting the immune system. It prevents the binding of collagen. The main objective is drug target to design lead molecules for the inhibition of growth. The target protein sequence was retieved from UNIPROT.

Sequence analysis of paramyosin of *Taenia solium*

Blast Results:

The pBLAST was performed to find the hits against the source sequence. The first hit with the PDB ID of 1I84_S was considered for further analysis. The best match to the target protein was smooth muscle myosin(contractile protein) heavy chain of gallus gallus.

Clustal W2 Results:

From the pBLAST result, 1I84_S was considered as a template for target protein to find the homologous structure. The 1I84_S was retrieved and subjected for multiple sequence analysis. The result shows the similarity and dissimilarity among the proteins.

```
1I84_U|PDBID|CHAIN|SEQUENCE      RRAAEGSSNVFSMFDETEIEDFKEAFTVIDQNA----------------- 38
1I84_Z|PDBID|CHAIN|SEQUENCE      RRAAEGSSNVFSMFDETEIEDFKEAFTVIDQNA----------------- 38
1I84_T|PDBID|CHAIN|SEQUENCE      -----------CDFSEEQTAEFKEAFQLFDRTG----------------- 22
1I84_W|PDBID|CHAIN|SEQUENCE      -----------CDFSEEQTAEFKEAFQLFDRTG----------------- 22
1I84_S|PDBID|CHAIN|SEQUENCE      KKMQQQMLDLEEQLEEEEAARQKLQLEKVTADGKIKKMEDDILIMEDQNN 1000
1I84_V|PDBID|CHAIN|SEQUENCE      KKMQQQMLDLEEQLEEEEAARQKLQLEKVTADGKIKKMEDDILIMEDQNN 1000
sp|P35418|MYSP_TAESO             KQLEIEIREITVKLEEAEAFATREGRRMVQKLQN---------------- 730
                                              :.* :    :     .

1I84_U|PDBID|CHAIN|SEQUENCE      ----DGIIDKDDLRETFAAMGRLNVKNEELDAMIKEASG-----PINFTV 79
1I84_Z|PDBID|CHAIN|SEQUENCE      ----DGIIDKDDLRETFAAMGRLNVKNEELDAMIKEASG-----PINFTV 79
1I84_T|PDBID|CHAIN|SEQUENCE      ----DGKILYSQCGDVMRALGQNPTNAEVMKVLGNPKSDEMNLKTLKFEQ 68
1I84_W|PDBID|CHAIN|SEQUENCE      ----DGKILYSQCGDVMRALGQNPTNAEVMKVLGNPKSDEMNLKTLKFEQ 68
1I84_S|PDBID|CHAIN|SEQUENCE      KLTKERKLLEERVSDLTTNLAEEEEKAKNLTKLKNKHESMISELEVRLKK 1050
1I84_V|PDBID|CHAIN|SEQUENCE      KLTKERKLLEERVSDLTTNLAEEEEKAKNLTKLKNKHESMISELEVRLKK 1050
sp|P35418|MYSP_TAESO             -----------RVRELEAELDGEIRRAKEAFANARKYERQFKELQTQSED 769
                                               :    :     . :      .  .        .

1I84_U|PDBID|CHAIN|SEQUENCE      ------FLTMFGEKLKGADP---EDVIMGAFKVLDPDGKGSIKKSFLEEL 120
1I84_Z|PDBID|CHAIN|SEQUENCE      ------FLTMFGEKLKGADP---EDVIMGAFKVLDPDGKGSIKKSFLEEL 120
1I84_T|PDBID|CHAIN|SEQUENCE      ------FLPMMQTIAKNKDQGCFEDYVEG-LRVFDKEGNGTVMGAEIRHV 111
1I84_W|PDBID|CHAIN|SEQUENCE      ------FLPMMQTIAKNKDQGCFEDYVEG-LRVFDKEGNGTVMGAEIRHV 111
1I84_S|PDBID|CHAIN|SEQUENCE      EEKSRQELEKIKRKLEGESSDLHEQIAELQAQIAELKAQLAKKEEELQAA 1100
1I84_V|PDBID|CHAIN|SEQUENCE      EEKSRQELEKIKRKLEGESSDLHEQIAELQAQIAELKAQLAKKEEELQAA 1100
sp|P35418|MYSP_TAESO             DKRMILELQDLLDKTQIKMKAYKRQLEEQEEVSQLTMSKYRKAQQQIEEA 819
                                        *  :   :      .:            .:      :.

1I84_U|PDBID|CHAIN|SEQUENCE      LTTGGGRFT------------PEEIKNMWAAFPPDVAGNVDYKNICYVIT 158
1I84_Z|PDBID|CHAIN|SEQUENCE      LTTGGGRFT------------PEEIKNMWAAFPPDVAGNVDYKNICYVIT 158
1I84_T|PDBID|CHAIN|SEQUENCE      LVTLGEKMT------------EEEVEQLVAGHE-DSNGCINYEELVRMVL 148
1I84_W|PDBID|CHAIN|SEQUENCE      LVTLGEKMT------------EEEVEQLVAGHE-DSNGCINYEELVRMVL 148
1I84_S|PDBID|CHAIN|SEQUENCE      LARLEDETSQKNNALKKIRELESHISDLQEDLESEKAARNKAEKQKRDLS 1150
1I84_V|PDBID|CHAIN|SEQUENCE      LARLEDETSQKNNALKKIRELESHISDLQEDLESEKAARNKAEKQKRDLS 1150
sp|P35418|MYSP_TAESO             EHRADMAER---------------TITIKRTIGGPGSRAVSVVREINSVS 854
                                                         :            .  .    :

1I84_U|PDBID|CHAIN|SEQUENCE      HGEDAEGE-------------------------- 166
1I84_Z|PDBID|CHAIN|SEQUENCE      HGEDAEGE-------------------------- 166
1I84_T|PDBID|CHAIN|SEQUENCE      SG-------------------------------- 150
1I84_W|PDBID|CHAIN|SEQUENCE      SG-------------------------------- 150
1I84_S|PDBID|CHAIN|SEQUENCE      EELEALKTELEDTLDTTATQQELRGSDYKDDDDK 1184
1I84_V|PDBID|CHAIN|SEQUENCE      EELEALKTELEDTLDTTATQQELRGSDYKDDDDK 1184
sp|P35418|MYSP_TAESO             RGNRATSIM------------------------- 863
```

fig.1 clustal w2 showing the result of similarity between two proteins

Functional Characterization of paramyosin protein of *Taenia solium*:

The functional characterization of the protein was studied by submitting the amino acid sequences to the PRODOM tool which helped to obtain the domains and the motifs were obtained by using the MOTIF SCAN tool

Table-1 Domains obtained in *paramyosin* Protein of T.solium using PRODOM

Domain ID	Begin	End	Length	Identity	Score	E-value	Positives	No. of domain in family
PD789382	412	500	96	100%	433	2e-41	100%	243
PD480776	699	772	74	100%	366	9e-34	100%	354
PD001052	777	834	58	100%	289	7e-25	100%	303
PDA1G0Z0	650	698	49	100%	239	100%	5e-19	205
PD625694	602	647	46	100%	225	100%	2e-17	228
PDA20526	157	202	46	100%	192	100%	2e-13	15
PD190210	295	391	97	86%	399	1e-37	86	3006
PD488869	61	156	96	85%	372	2e-34	85%	288

PDB0B378	204	259	56	80%	224	80	3e-17	14
PD345047	526	601	76	77%	264	6e-22	77%	347
PDB0B0I9	2	60	59	61%	156	11%	2e-09	15
PD000023	1725	1904	180	44%	345	3e-31	68%	9431
PDB1J295	273	416	144	44%	258	3e-21	63%	4
PDB3U373	526	601	76	41%	103	67%	0.003	2
PDA8R9B9	87	322	236	34%	282	5e-24	59%	5
PD190210	1260	1372	113	34%	136	11%	5e-07	3006

Table-2 Motifs obtained in *paramyosin* Protein of T.solium using MOTIF SCAN

Motif name	**Position**	**Raw score**	**E-value**
Myosin_tail_1 *Myosin tail*	1-842	1449.2	0
Myosin_tail_1 *Myosin tail*	1-842	1451.1	0
Taxilin *Myosin-like coiled-coil protein*	77-344	-158.5	0.0035
Tropomyosin *Tropomyosin*	547-756	-117.0	0.0016
Filament *Intermediate filament protein*	190-451	-136.2	3.9e-06
DUF2130 *Uncharacterized protein conserved in bacteria*	344-573	-89.0	0.0014
Cenp-F_leu_zip *Leucine-rich repeats of kinetochore protein Cenp-F/LEK1*	572-705	-16.3	0.0036
Rho_Binding *Rho Binding*	403-446	10.2	0.0009
Shugoshin_N *N-terminal coiled-coil region of kinetochore-attachment protein*	316-360		0.0026
BAR domain profile	283-551	396	0.0059

Physico chemical characterization of target protein:

The physico-chemical properties of a protein generally involves it's weight, theoretical pI, amino acid composition, atomic composition, extinction coefficient, estimated half-life, instability index, aliphatic index and grand average of hydropathicity (GRAVY) . The Physico chemical characters of paramyosin protein was analysed by using Protparam tool.

Table-3 Amino acid composition of paramyosin of *T.solium*

Amino acid	**Number**	**Percentage**
Ala (A)	96	11.1%
Arg (R)	89	10.3%
Asn (N)	50	5.8%
Asp (D)	53	6.1%
Cys (C)	0	0.0%
Gln (Q)	49	5.7%
Glu (E)	120	13.9%
Gly (G)	21	2.4%
His (H)	8	0.9%
Ile (I)	33	3.8%
Leu (L)	103	11.9%
Lys (K)	60	7.0%
Met (M)	25	2.9%

Phe (F)	9	1.0%
Pro (P)	2	0.2%
Ser (S)	53	6.1%
Thr (T)	48	5.6%
Trp (W)	0	0.0%
Tyr (Y)	9	1.0%
Val (V)	35	4.1%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%

Table-4 Atomic composition of *T.solium* paramyosin

Element	**Symbol**	**No.of atoms**
Carbon	C	4168
Hydrogen	H	6999
Nitrogen	N	1305
Oxygen	O	1419
Sulfur	S	25

Table-5 Physico-chemical properties of paramyosin of *T.solium*

Property	**Value**
Number of amino acids	*863*
Molecular weight	*98899.8*
Theoretical pI	*5.31*
Total number of negatively charged residues (Asp + Glu)	*173*
Total number of positively charged residues (Arg + Lys)	*149*
Total number of atoms	*13916*
Aliphatic index	*84.35*
Grand average of hydropathicity (GRAVY)	*-0.903*
Ext. coefficient	*13410*
Estimated half-life	30 hours
Instability index (II)	*46.91*
Formula	$C_{4168}H_{6999}N_{1305}O_{1419}S_{25}$

Secondary structure prediction of target protein:

CFFSP (chou & fasman secondary structure prediction) server was used to predict the secondary structure of paramyosin protein. The secondary structure showed that it has total 863 number of amino acids, 780 number of total residues. The diagram shows the regions of helix, sheet, turn, coils. The secondary structure of protein is showed in fig.2.

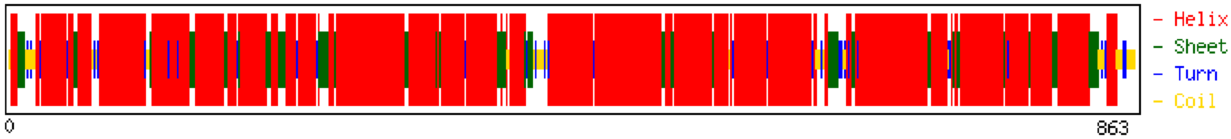

fig.2 secondary structure predicted by CFFSP (chou & fasman secondary structure prediction server)

Table-6 Different servers used to generate best model of the target protein

Server	Template
SWISS-MODEL	2tma.1.B
PHYRE2	C1c1gA
CPH-Models-3.0	1I84_S

The 3D structures of protein which were obtained by using Swiss-model, CPHmodels-3.0, Phyre2 server are given in fig.3, fig.4, fig.5 . The resulted models were visualized by using pymol visualization tool. The models are presented in the form of spherical structure. This 3D models show the alpha helix, beeta sheets and turns also.

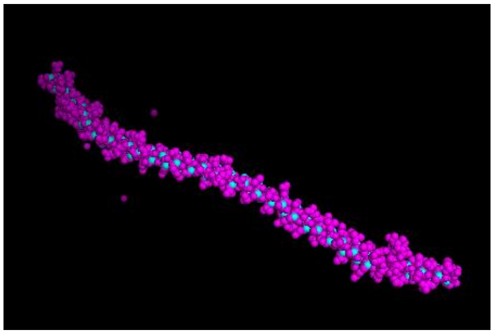

fig.3 3D structure of paramyosin protein obtained by Swiss-model

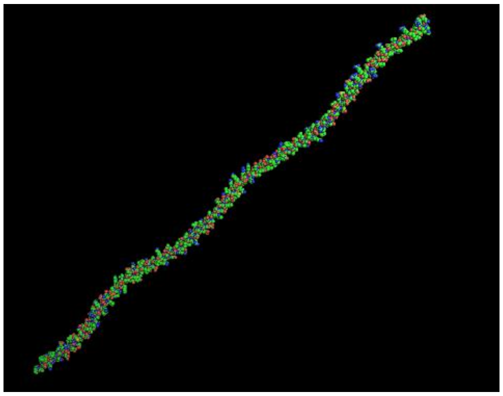

fig.4 3D structure of paramyosin protein obtained by Phyre2

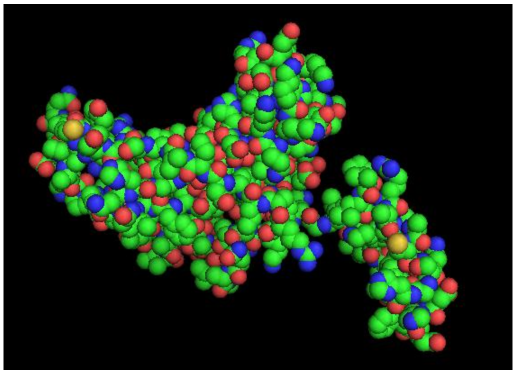

fig.5 3D structure of paramyosin protein obtained by CPHModel-3.0

The models which were obtained were further analysed by using PROCHECK saves server. It shows the allowed and disallowed regions along with the back bone confirmation of proteins. The model which built by using CPHModel-3.0 lies in 83.1% of the favoured regions, the model which built by using Phyre2 server lies in 88.9% of the favoured regions, the model which built by using swiss-model lies in 93.0% of the favoured regions. The details of the back bone confirmations of protein is given in fig.6, fig.7, fig.8.

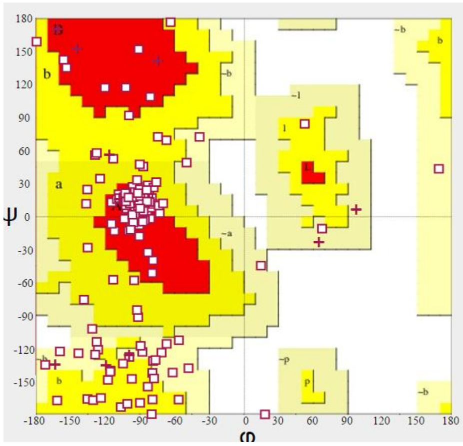

fig.6 Ramachandran plot of the paramyosin protein (Cph model)

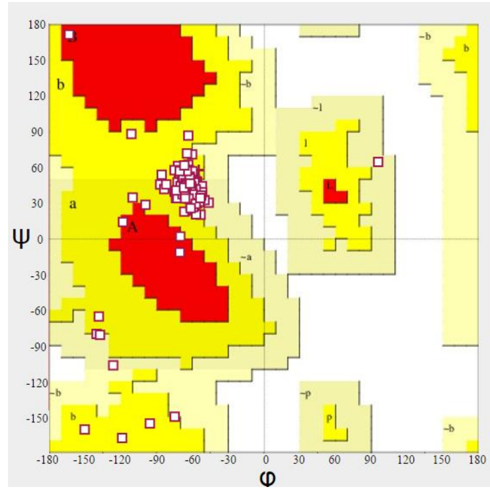

fig.8 Ramachandran plot of the paramyosin protein (swiss-model)

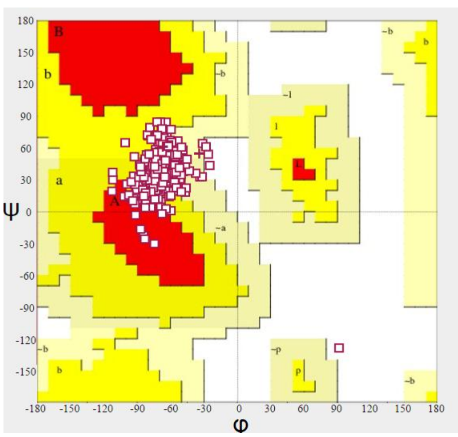

fig.7 Ramachandran plot of the paramyosin protein (Phyre2)

Table-7 Model quality of Target protein obtained from different servers based on Ramachandran Plot using PROCHECK saves server, Z- Score using ProSA

Server	**ProSA**		**PROCHECK**	
	Z- Score	***Amino acids***	***Residues in outlier region(%)***	***Residues in favoured regions (%)***
CPHModel-3.0	-0.6	174	3.5%	83.1%
Phyre2	-1.44	281	1.8%	88.9%
swiss-model	-1.74	302	0.8%	93.0%

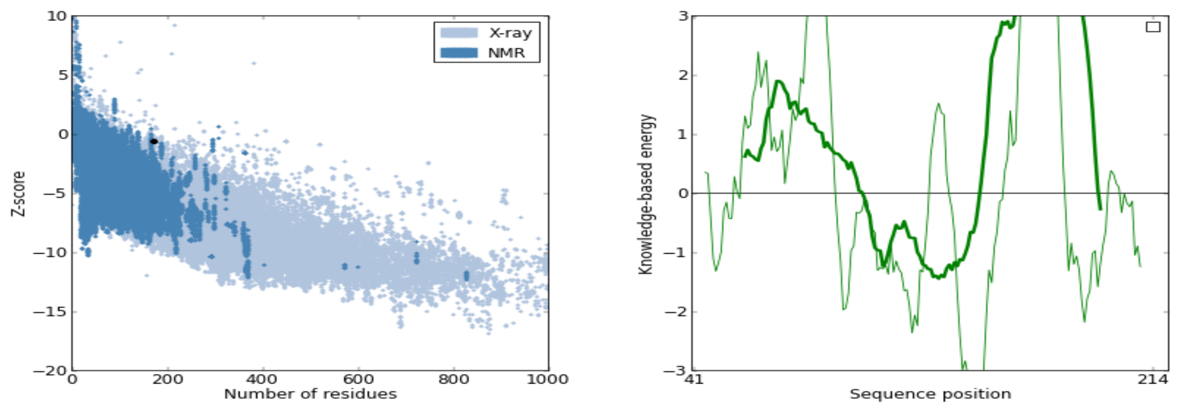

fig.9 Model quality of paramyosin protein obtained by ProSA (CPHModel-3.0 server model)

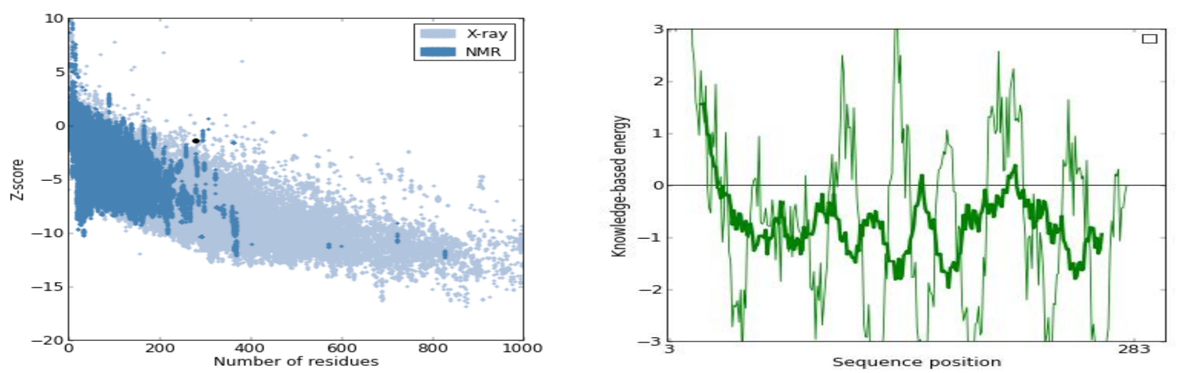

fig.10 Model quality of paramyosin protein obtained by ProSA (phyre2 server model)

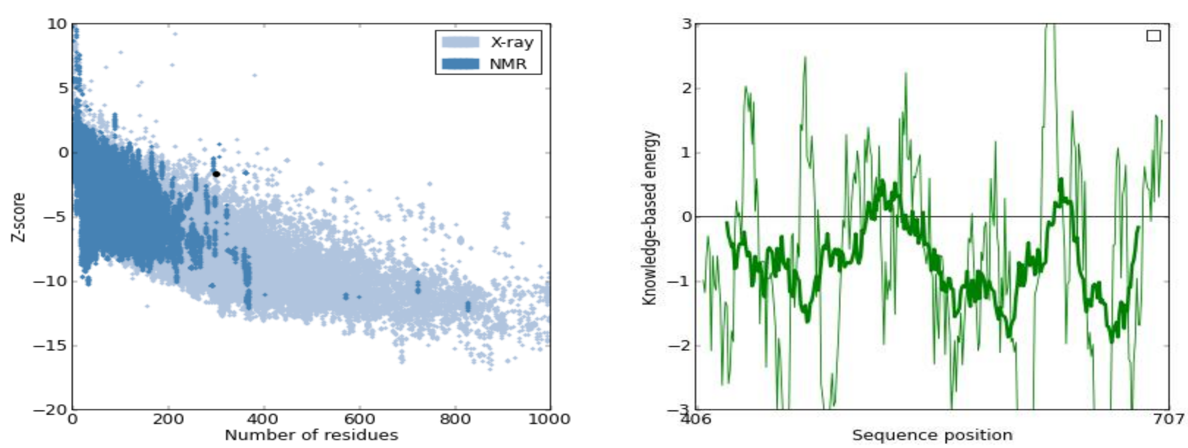

fig.11 Model quality of paramyosin protein obtained by ProSA (swiss model server model)

IV. CONCLUSION

The drugs which are available in market are not sufficient to fight against cystecercosis. The situation continues to be more frightening, with the geographical spread of resistance widening to previously unaffected areas and a ruthless augmentation both in the incidence and degree of drug resistance. So its really important to develop some new drugs which can fight successfully against the infection. Awareness about the disease and the functional characters of protein helps to find out new drugs which can fight successfully against the disease. This hypothesis describes the modeling and validation of *paramyosin* of *T.solium*, which will provide insight into its structure and aid in drug designing.

REFERENCES

[1] Arnold, K., Bordoli, L., Kopp, J. and Schwede, T by The SWISS-MODEL Workspace: A web-based environment for protein structure homology modelling, *Bioinformatics*, (22),195-201(2006).

[2] Schwede, T., Kopp, J., Guex, N. and Peitsch, MC., by an automated protein Homology modeling server', *Nucleic Acids Research*., (31),3381-3385(2003).

[3] Puntervoll P., Linding R., Gemünd C., Chabanis-DavidsonS., Mattingsdal M., Cameron S., Martin D. M. A., Rahman S.A. and Schomburg D by Observing local and global properties of metabolic pathway - load points and choke points in the metabolic networks, *Bioinformatics,* 10(22), 1767–1774.(2006).

[4] Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W. and Lipman D.J., by Gapped BLAST and PSIBLAST a new generation of protein database search programs, *Nucleic Acids Res.*, (25), 3389-3402(1997).

[5] 5-Gasteiger E., Hoogland, C., Gattiker, A., Duvaud, S., Wilkins, M.R., Appel, R.D.and Bairoch, A., by Protein Identification and Analysis Tools on the ExPASy Server' *The Proteomics Protocols Handbook,* 18,571-607.,(2005).

[6] 6-Guex, N. and Peitsch, M. C., by SWISS-MODEL and the Swiss-PdbViewer: An environment for comparative protein modeling'., *Electrophoresis.*, (18),2714-2723.,(1997).

[7] 7-Laskowski, R A., MacArthur, M W., Moss, D S. and Thornton, J M. by PROCHECK - a program to check the stereochemical quality of protein structures'., *J. App. Cryst*., (26),283-291(1993),.

[8] 8-Kumar S*, Nath O, Govil S, Pathak A. N by Computational 3D Structure Prediction, Evaluation and Analysis of Pyruvate Dehydrogenase an Effective Target for Filarial Infection by *Brugia pahangi* Using Homology Modeling Approach. International Journal of Pharmaceutical Sciences and Drug Research 2014; 6(2): 120-123.(2014).

[9] 9-Jr m a r, santos j m s d, gomes e c d s, rocha m a, rocha c f, carvalho g t c d, costa b s by 114 Treatment of cerebral cysticercosiswith albendazole in elevated dosages. arq neuropsiquiatr 2008;66(1):114-116(2008)

.

[10] 10-K sivakumar, * s balaji, gangaradhakrishnan(2007) *in silico* characterization of antifreeze proteins using computational Tools and servers *j. Chem. Sci.*, vol. 119, no. 5, september 2007, pp. 571–579.

[11] 11-Prasad k n*, prasad a, verma a, singh a k by human cysticercosis and indian scenario: a review. *J. Biosci.* 33 571–582(2008).

[12] 12- Via A, Tramontano Aby Protein Structural Motifs: Identification, Annotation and Use in Function Prediction(2010) .

[13] 13-Roy S*, Maheshwari N, Chauhan R, Sen N K, Sharma A by Structure prediction and functional characterization of secondary metabolite proteins of *Ocimum.* Bioinformation 6(8): 315-319(2011).

[14] 14- Antón F S by immunoreactive proteins in *taenia solium.* Isbn 978-91-7457-655-9(2012).

[15] 15-Julie D.Thompson, Desmond G.Higgins+ and Toby J.Gibson* by CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research, 1994, Vol. 22, No. 22 4673-4680(1994).

[16] *16-García H H, Gonzalez A E, Evans C A W, Gilman R H, by Taenia solium* cysticercosis. *Lancet* 2003; 362: 547–56*(2003)*.

[17] 17-Dorny P, Flisser A, Geerts S, Kyvsgaard N C, McManus D, Nash T, Pawlowski Z by WHO/FAO/OIE Guidelines for the surveillance, prevention and control of taeniosis/cysticercosis. ISBN: 92-9044-656-0(2005).

[18] 18-Gasteiger E, Hoogland C, Gattiker A, Duvaud S, Wilkins M R, Appel R D, Bairoch A. Protein Identification and Analysis Tools on the ExPASy Server. The Proteomics Protocols Handbook.

[19] 19-Khor B Y, Tye G J, Lim T S, Noordin R, Choong Y S*(2014) The Structure and Dynamics of *bm*r1 Protein from *Brugia malayi*: *In Silico* Approaches. *Int. J. Mol. Sci.* 2014, *15*, 11082-11099; doi:10.3390/ijms150611082.

[20] 20-Sinha S *, Sharma B S by Neurocysticercosis: A review of current status and management. Journal of Clinical Neuroscience 16 867–876(2009).

[21] 21-Sippl, M.J.,by Recognition of Errors in Three-Dimensional Structures of Proteins, *Proteins*, **(17)**,355-362(1993).

[22] 22- Nielsen, M., Lundegaard, C., Lund, O. and Petersen, TN., by Remote homology modeling using structure guided sequence profiles', *Nucleic Acids Research*.,**33(38)**,576-81.,(2010).

[23] 23- Contreras-Moreira, B., Bates, P.A., by Domain Fishing: a first step in protein comparative modelling', *Bioinformatics*, **(18)**,1141-1142.,(2002).

[24] 24- Maithri S.K., Ramesh K.V., Dieudonné Mutangana and Deshmukh Sudha., by Molecular Modeling and Docking Studies of PirB Fusion Protein from Photorhabdus Luminescens, *ISCA J. Biological Sci*, **(1**), 7-18.,(2012).