International Conference on Recent Research Development in Environment, Social Sciences and Humanities
University of Delhi (DU), Conference Centre, New Delhi (India) (ICRRDESH-15)
27 September 2015, www.conferenceworld.in ISBN: 978-81-931039-8-2

PREDICTION OF ANTIGENIC EPITOPE FROM D. MEDINENSIS: NEW PARADIGM OF SYNTHETIC VACCINE DEVELOPMENT

Sonu Mishra[1], Virendra S. Gomase[2]

[1,2]*Department of Biotechnology, Mewar University ,Chittorgarh, (India)*

ABSTRACT

Dracunculus medinensis is popularly known as Guinea worm disease, the only species which infects human. The dracunculus parasite larvae are ingested by Cyclops (the small water fleas which is the intermediate source. When people consume the stagnant contaminated unfiltered water from the source this after reaching to the stomach it digested by digestive juices and causes release of the larvae.This larvae travels and penetrate the digestive wall into the body cavity and get entry in abdominal cavity and retroperitoneal space. These larvae develop and mature into adults. After the copulation the ovoviviparous female mature and grows in size whereas the male dies. The utrophin protein of 88 amino acid residue is used for the identification of the antigenicity through B- cell epitopes prediction methods .The result obtained shows that the region of maximal hydrophilicity is likely to be antigenic site having the hydrophobic characteristics and contain the segments of low complexity and high-predicted flexibility. This predicted antigenic protein from D. medinensis could be the new paradigm of synthetic vaccine development and target validation.

Keywords*: *Antigen, Dracunculus medinensis, Epitope, Protein, Utrophin, Vaccine

I. INTRODUCTION

*Dracunculus medinensis*is the largest of the tissue nematode parasite affecting humans, have an unusual life cycle with incubation period of the approximately 1 year and six developmental stages and clinically important parasite needs to be eradicated after small pox [1]. By the time produced millions of eggs in its uterus, and is predominantly localized in the lower extremities(80-90%).After an incubation period the female worm release which induces a painful blister (1 to 6cm diameter) on the skin of lower limbs; the person develop a slight fever , local skin redness , swelling and severe pruritus around the blister . The presence of other symptoms like diarrhea, nausea, vomiting and dizziness has been seen. The blister burst within 1 to 3 days and female worms one or more slowly comes out from the wounds which causes an excoriating burning sensation and pain[2].Immersing or pouring water over the blister provide pain reliever. But this the moment that adult female is exposed to the external environment [3]. During emergence of the limbs in open water sources it recognizes the temperature difference and releases the milky white liquid in the water which contains millions of immature larvae, when larvae released in water are ingested by copepods where they mount twice and become infective larvae within two weeks [4]. The *D.medinensis* antigen peptides are most suitable for the subunit vaccine development because with the single epitope, the immune response can be generated in large population. This approach is based on the phenomenon of cross-protection, whereby infected with the mild strain and is protected

against a more severe strain of the same. The phenotype of the resistant transgenic hosts includes fewer centers of initial infection, a delay in symptom development and low accumulation. In this study utrophin protein has been used to investigate its role in antigenicity. Utrophin protein encoded gene belongs to cytoskeleton components. Utrophin has got homology with dystrophin, it was found during investigation of Duchenne's muscular dystrophy. Duchenne's muscular dystrophy (and female carriers) the utrophin level is comparatively seen higher), both in those muscle fibers lacking dystrophin and in rare, revertant fibers that express dystrophin. Utrophin found to be located at the neuromuscular synapse and myotendinous junctions in normal muscle cells. This protein is essential for normal membrane maintenance and also helps in the acetylcholine receptor clustering. The abundance of this protein has been demonstrated mostly in the brain, kidney, liver, lung, muscle, spleen and stomach. At the stage of muscle differentiation in the human fetus utrophin is found at the sarcolemma but at later on stages when the fetus begins to express dystrophin it disappears [5]. Antigen protein prediction from *D. medinensis* is necessary for few paradigms of synthetic vaccine development and target validation [6-7].

II. METHODOLOGY

B-cell epitopes are the sites of molecules that are recognized by antibodies of the immune system. Knowledge of B-cell epitopes may be used in the design of vaccines and diagnostics tests. It is therefore of interest to develop improved methods for predicting B-cell epitopes [8]. In this research work antigenic epitopes of antigen protein utrophin from *D.medinensis* is determined using the Gomase in 2007, Bepipred Linear Epitope Prediction, Emini Surface Accessibility Prediction, Karplus& Schulz Flexibility Prediction, Kolaskar & Tongaonkar Antigenicity, Parker Hydrophilicity Prediction[9-13].

III. RESULT AND INTERPRETATIONS

The utrophin protein sequence (88 amino acid) is analyzed through different types B- cell epitope prediction methods. Through Bepipred linear epitope method and Karplus and schulz flexibility prediction method we found the higher peak of the peptide sequence of 6 residue (TESQDS) with start and end position between 20-25.The highest score for the residue indicates the probability to be a part of the epitope (Residue colored in yellow) [Figs.1 & 2]. Similarly, the other methods is used and analyzed the utrophin protein by Emini surface accessibility prediction and Parker hydrophilicity prediction and the larger score were obtained with start and end position between 40-45 with 6 residue (LDDEQN)[Figs. 3& 4]. Whereas, the peak of higher score is obtained through Kolaskar and Tongaonkar Antigenicity with start and end point between 47-57 with 11 residues (SLLQZKLVNA) [Fig. 5]. Considering all the output of the result we can predict that the residue's highest peak with higher score is between the positions 40-57. This in turns indicates that there might be probability of residue to be a part of the epitope. We found that the region of maximal Hydrophilicity is likely to be an antigenic site, having hydrophobic characteristics, because the terminal regions of antigen protein is solvent accessible and unstructured, antibodies against those regions are also likely to recognize the native protein. It was seen that an antigen protein is hydrophobic in nature and contains segments of low complexity and high-predicted flexibility (Figs. 1-5). The predicted antigenic protein segments of utrophin can take active

part in the host immune reactions. In future study the predicted antigenic protein utrophin fragments can be used in the investigation of MHC molecules binding and it can be the first bottlenecks in vaccine design.

IV. FIGURES AND TABLES

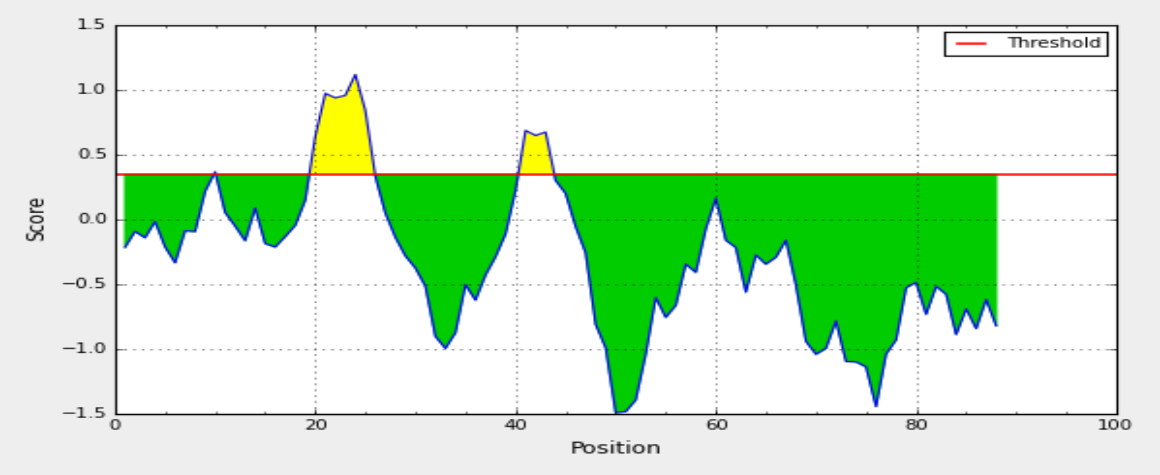

Fig. 1. Bepipred Linear Epitope Prediction graph

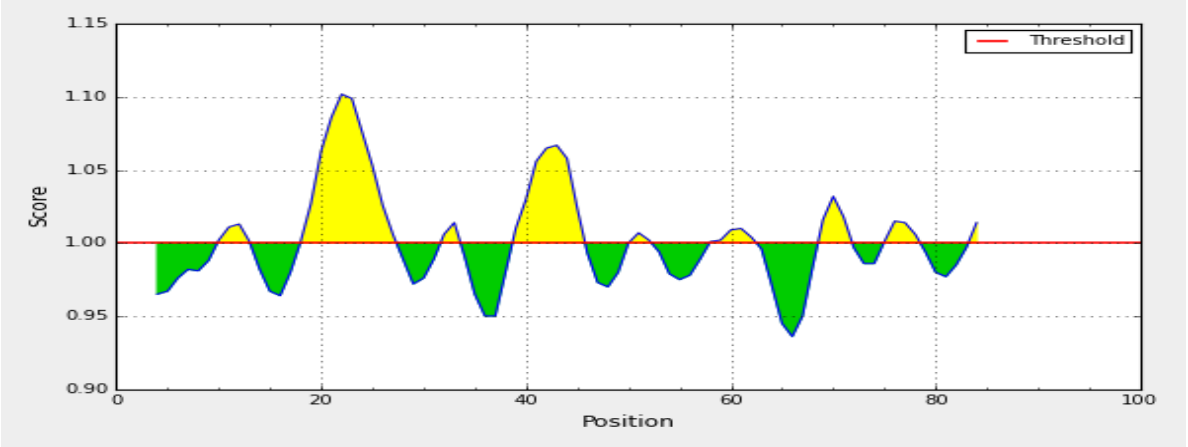

Fig. 2-Karplus& Schulz Flexibility Prediction graph

Fig. 3-Emini Surface Accessibility Prediction

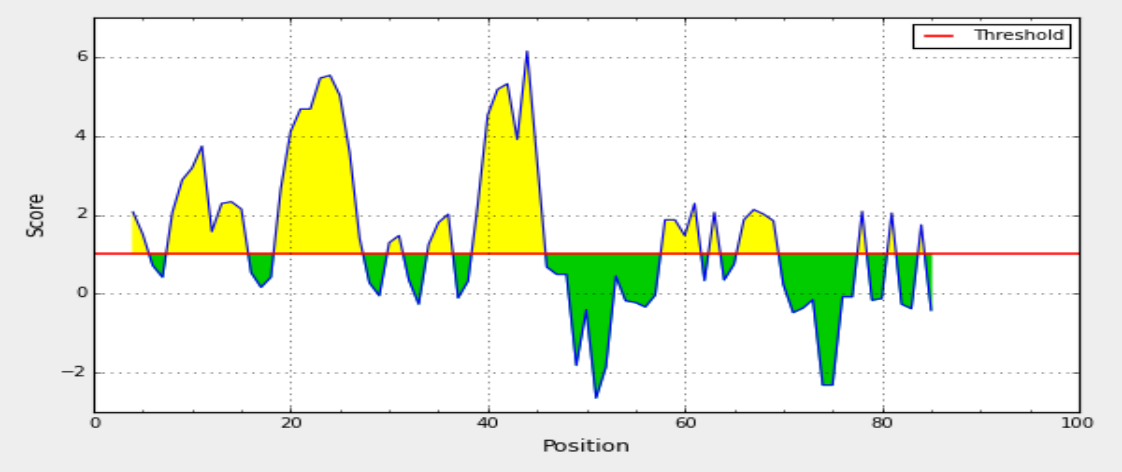

Fig.4-Parker Hydrophilicity Prediction graph

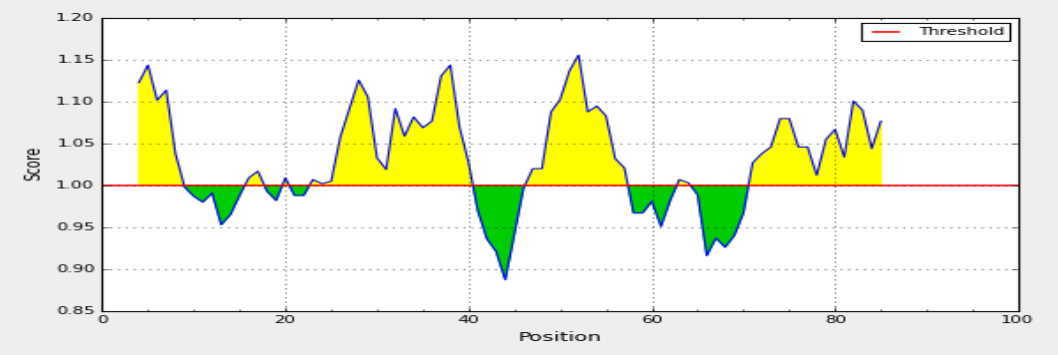

Fig.5- Kolaskar&Tongaonkar Antigenicity Prediction graph

Table: Kolaskar &Tongaonkar Antigenicity Prediction Table

	Predicted residue scores						Predicted peptides				
	Position	Residue	Start	End	Peptide	Score	No.	Start	End	Peptide	Length
	47	S	44	50	QNMSLLS	1.02					
	48	L	45	51	NMSLLSQ	1.02	1	23	40	QDSVGRVLHRGNVICQKL	18
	49	L	46	52	MSLLSQL	1.088	2	47	57	SLLSQLKLVNA	11
Kolaskar & Tongaonkar Antigenicity Prediction	50	S	47	53	SLLSQLK	1.103					
	51	Q	48	54	LLSQLKL	1.137					
	52	L	49	55	LSQLKLV	1.156					
	53	K	50	56	SQLKLVN	1.088					
	54	L	51	57	QLKLVNA	1.095					
	55	V	52	58	LKLVNAK	1.083					
	56	N	53	59	KLVNAKW	1.032					
	57	A	54	60	LVNAKWE	1.021					

V. CONCLUSION

An antigenic protein utrophin from *D. medinensis*can play an important role in vaccine development. The peptide fragments of antigen protein can be used to select nonamer for use in rational vaccine design and can develop the understanding of roles in the immune system in infectious disease.

VI. ACKNOWLEDGEMENTS

We gratefully acknowledge the support and many helpful discussion of Dr. Gomase.

Conflicts of Interest

The authors declare no conflict of interest.

REFERENCES

[1] Greenaway C.Dracunculiasis (Guinea worm disease). CMAJ 170(9): (2004); 495-500.

[2] Miillner A, Helfer A ,KotlyarD.Oswald J, EfferthT.Chemistry and pharmacology of neglected helminthic disease.Curr Med Chem;18(5): (2011) 767-789.

[3] Ruiz-Tiben E, Hopkins DR.Dracunculiasis (Guinea worm disease) eradication .AdvParasitol; 61(2006),275-309.

[4] IriemenamNC,Oyibo WA, Fagbenro-Beyioku AF.Dracunculiasis – The saddle is virtually ended. Parasitol Res 102(3): (2008);343-347.

[5] Bakiri, A. H., & Mingomataj, E. C.. Parasites Induced Skin Allergy: A Strategic Manipulation of the Host Immunity. Journal of Clinical Medicine Research, 2(6), (2010)247–255

[6] Nwoke, B. E.. Behavioral aspects and their possible uses in the control of dracunliasis (guinea-worm) in Igwun river basin area of Imo State, Nigeria. Angew. Parasitol. 33: (1992);205–210.

[7] Muller R..Life cycle of DracunculusMedinesis .In workshop on opportunities for control of dracunculiasis : contaminated papers, washinton,DC:National Academy Press(1985)]

[8] Larsen JE, Lund O, Nielsen M. Improved method for predicting linear B-cell epitopes. Immunome Res. 2006; 2:2.

[9] V.S.Gomase, K.V. Kale, N.J.Chikhale, S.S. Changbhale,."Prediction of MHC Binding Peptides and Epitopes from Alfalfa mosaic virus". Curr. Drug Discov. Technol., 4(2), (2007),117-1215.

[10] V.S.Gomase and K.V.Kale."In silico prediction of epitopes: a new approach for fragment based viral peptide vaccines". Int. J. of Applied Computing, 1(1), (2008); 39-46.

[11] V.S.Gomase and K.V.Kale, "Approach of proteomics system architecture in plant virus's database". Int. J. of Applied Computing, 1(1), (2008); 33-38.

[12] Gomase VS, Chitlange NR. Sensitive Quantitative Predictions of MHC Binding Peptides and Fragment Based Peptide Vaccines from Taeniacrassiceps. J Vaccines Vaccin (2012); 3:131.

[13] Gomase VS, Chitlange NR (2012). Microbial Proteomics Approach for Sensitive Quantitative Predictions of MHC Binding Peptide from Taeniaovis. J Data Mining Genomics Proteomics(2012); 3:121.