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In silico structure analysis of potassium channel Bgk toxin and its docking prediction with human voltage gated potassium (Kv) channel

Sriparna Ray[1] and Jayanta Sinha[2]#

[1]*Department of Zoology, B. C. College, Asansol, West Bengal, India*
[2]*Department of Zoology, Vivekananda College, Kolkata, West Bengal, India*

ABSTRACT

Kappa actitoxin Bg1a or Potassium channel Bgk toxin is voltage-gated potassium (Kv) channel blocker toxin extracted from sea anemone Bunodosoma granulifera. The present study represents a detailed in silico analysis of the Bgk toxin. Primary structure and transmembrane helix analysis were done through Pepstat tool and TMHMM server respectively. Secondary structure, signal peptide and cysteine disulfide prediction was made though PsiPred workbench, Signal P server and DiANNA 1.1 web server respectively. Protein disorderliness and immunogenicity prediction were carried on through PrDos and POPI 2.0 server respectively. Docking simulation was performed through the application of ClusPro server. The phylogenetic tree was constructed by COBALT multiple alignment tools and the tree were redrawn through Phifi server. Motif, protein family and hydrophobicity were also predicted through Interproscan, Pfam and Protscale. The paper aimed towards the characterization of kappa Bgk toxin through bioinformatics tools. The input from such bioinformatic analyses will be a novel and important approach for paving a way in searching new products of pharmacological interest and may later be helpful in designing vaccine against this toxin. The primary structure prediction showed that kappa Bgk toxin is a stable and basic protein. The secondary structure prediction revealed that the presence of alpha helices and coils as its secondary structural elements. The hydrophobicity prediction showed that this toxin is of hydrophilic nature. Whereas trans-membrane prediction reflected that this toxin is a soluble protein with no transmembrane domains. Further the toxin has no signal sequence. Three cysteine disulfide bonds were predicted in the toxin. It has only a ShK motif and belongs to Pfam-A family. This toxin showed disorderness and the predicted immunogenecity of CTL response was moderate. The toxin illustrates a distinct phylogenetic relationship with related toxins of other sea anemone species. There are distinct disordered regions on the toxin. Molecular docking of the Bgk toxin with voltage gated potassium channel illustrated a definite binding which may be related to protein disorderness and presence of cysteine disulfide bonds.

Keywords: *in silico* analysis, Kappa actitoxin Bg1a, human voltage gated potassium channel, protein docking.

INTRODUCTION

Sea anemones are a group of aquatic, poisonous predatory animals under phylum Cnidaria; class Anthozoa and subclass Hexacorallia [1]. Most of the sea anemones are sessile polyp and they are attached at the bottom to the surface beneath by an adhesive foot or may be pelagic [2]. Sea anemone produces various types of toxins. Kappa Bgk toxin is derived from sea anemone (*Bunodosoma granulifera*). It affects the voltage gated potassium channel in human being by blocking them [3]. Voltage-gated potassium (Kv) channels are associated with excitability of human cell membrane, as they are responsible for triggering the initiation and mediating propagation of action

potential [4]. During action potential, they play a crucial role in returning the depolarized cell to a resting state [5]. Toxins from *Anemonia sulcata, Bunodasoma granuliferum, Stichodactyla helianthus* also act as blockers of a specific member of the Kv potassium channel family. Kv channels are trans-membrane channels specific for potassium and sensitive to voltage changes in the cell's membrane potentials. These channels are trans-membrane pore forming complexes. There are two subunits-α subunit (actual conductance pore) and β (auxillary proteins). This β-subunit does not conduct current on their own but rather modulate the activity of Kv channels [6, 7]. In this paper, *in silico* study of Kappa actitoxin Bg1a or potassium channel Bgk toxin had been performed. The aim of this work is to predict primary structure, secondary structure, hydrophobicity, motif, cysteine-disulfide bond, transmembrane helix, signal peptide, immunogenicity and phylogenetic tree and also to carry on docking study with a voltage gated potassium channel.

EXPERIMENTAL SECTION

1. Sequence retrieval:
Sequence of potassium channel Bgk toxin was retrieved from uniprot (www.expasy.org/sprot/) (Table 1).

Table 1. Description about potassium channel Bgk toxin.

Toxin name	Sources	PDB ID	PDB code	Uniprot Identifier	Toxin peptide sequence	Sequence length
Kappa actitoxin Bg1a	*Bunodosoma granulifera*	1BGK	P29186	TXT1B_BUNGR	VCRDWFKETACRHAKSLGNCRTSQKYRANCAKTCELC	37 aa

2. Amino acid composition prediction of potassium channel Bgk toxin:
Amino acid composition and other physico-chemical parameters of the potassium channel Bgk toxin was analyzed through Pepstats tool (www.emboss.bioinformatics.nl/cgi bin/emboss/ pepstats). Various physico-chemical parameters analyzed for the given protein sequence include: theoretical pI, amino acid composition, extinction coefficient, estimated half life, instability index, aliphatic index and Grand Average of Hydropathicity (GRAVY).
3. Secondary structure prediction of potassium channel Bgk toxin:
Secondary structure analysis of potassium channel Bgk toxin was carried out using Psipred protein sequence analysis workbench (www.bioinf.cs.ucl.ac.uk/psipred).
4. Hydrophobicity prediction of potassium channel Bgk toxin:
Hydrophobicity prediction was done through Protscale tool (www.expasy.org/protscale).
5. Trans-membrane helices prediction:
Whether the Kv channel Bgk toxin has transmembrane helices or not, were predicted using TMHMM server version_2.0 (www.agro.vbi.vt.edu/cgi-bin/tmhmm).
6. Signal sequences prediction of potassium channel Bgk toxin :
Detection of Signal sequence of potassium channel Bgk toxin protein was carried out using Signal P 4.1 server – CBS (www.cbs.dtu.dk/services/SignalP/).
7. Cysteine-disulfide prediction of potassium channel Bgk toxin:
Positions of the cysteine disulphide bonds were predicted through DiANNA 1.1 web server (www. clarius.bc-edu/ ~cloetelab / DiANNA). This software helps in disulfide connectivity prediction.
8. Motif Prediction of potassium channel Bgk toxin:
Motif prediction were made through the use of Interproscan server (www. ebi.ac.uk/Tools /pfa/ iprscan/).
9. Protein family prediction of potassium channel Bgk toxin:
This was done through Pfam software (pfam.sanger.ac.uk).
10. Phylogenetic tree prediction of potassium channel Bgk toxin:
Phylogenetic tree prediction was done by COBALT multiple alignment tools (www. ncbi.nlm.nih.gov/tools/ cobalt/).This software indicates evolutionary relationship amongst the related sea anemone toxins. The tree is redrawn and refined through Phy.fi online tool (www. cgi-www.cs.au.dk/cgi-chili/phyfi/).
11. **Protein disordered region prediction of potassium channel Bgk toxin**:
Detection of protein disordered region was carried out by PrDos server (www.prdos.hgc.jp).
12. Immunogenecity of MHC Class-1 and Class-2 prediction:
This was carried out through POPI 2.0 server (www.mba.biocuckoo. org).One can compute T-cell immunogenicity through this software.
13. Selection of particular potassium channel (receptor) of Bgk toxin:

A particular voltage gated potassium channel (PDB Id. 3BJ4) was retrieved from protein databank (www. rscb.org/pdb/home/home.do) (Table 2).

Table 2. Description about human voltage gated potassium channel

Toxin name	Source	PDB ID	PDB code	Uniprot Identifier	Sequence length
Potassium channel subunit (Polymer 1; chain A & B)	*Homo sapiens*	3BJ4	P51787	KCNQ1_HUMAN	**676 aa**
Toxin peptide sequence	MAAASSPPRAERKRWGWGRLPGARRGSAGLAKKCPFSLELAEGGPAGGALYAPIAPGAPGPAPPASPAAPAAPPVASDLGPRPPVS LDPRVSIYSTRRPVLARTHVQGRVYNFLERPTGWKCFVYHFAVFLIVLVCLIFSVLSTIEQYAALATGTLFWMEIVLVVFFGTEYVV RLWSAGCRSKYVGLWGRLRFARKPISIIDLIVVVASMVVLCVGSKGQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQ ELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWGVVTVTTIGYGDKVPQTWVGKTIASCFSVFAISFFALPAGILG SGFALKVQQKQRQKHFNRQIPAAASLIQTAWRCYAAENPDSSTWKIYIRKAPRSHTLLSPSPKPKKSVVVKKKKFKLDKDNGVTPG EKMLTVPHITCDPPEERRLDHFSVDGYDSSVRKSPTLLEVSMPHFMRTNSFAEDLDLEGETLLTPITHISQLREHHRATIKVIRRMQY FVAKKKFQQARKPYDVRDVIEQYSQGHLNLMVRIKELQRRLDQSIGKPSLFISVSEKSKDRGSNTIGARLNRVEDKVTQLDQRLALI TDMLHQLLSLHGGSTPGSGGPPREGGAHITQPCGSGGSVDPELFLPSNTLPTYEQLTVPRRGPDEGS				

14. Docking prediction of potassium channel Bgk toxin:

Docking between the Kappa actitoxin Bg1A or potassium channel Bgk toxin and the human voltage gated potassium (Kv) channel protein (receptor) was done by ClusPro 2.0 server (www. cluspro.bu.edu).The docked complex is visualized through JSmol software (www. bioinformatics.org/first glance/fgij/).

RESULTS AND DISCUSSION

In this study, primary structure and physic-chemical properties of potassium channel Bgk toxin was predicted using PEPSTAT tool and the results are shown in Table 3 and Table 4 respectively. The Table 3 shows that cysteines are abundant (16.2%) in this toxin and the least are valine (2.7%), tyrosine (2.7%), tryptophan (2.7%), phenylalanine (2.7%), histine (2.7%), glycine (2.7%) and glutamine (2.7%). Abundant cysteines are frequently involved in disulfide bonds (03 nos. bonds), where pairs of cysteines are oxidized to form a covalent bond. These bonds serve mostly to stabilize the protein structure.

Table 3. Amino acid composition prediction of potassium channel Bgk toxin

Types of amino acid	Amino acid composition (%)	Types of amino acid	Amino acid composition (%)
Ala	10.8	Leu	5.4
Arg	10.8	Lys	10.8
Asn	5.4	Met	0.0
Asp	2.7	Phe	2.7
Cys	16.2	Pro	0.0
Gln	2.7	Ser	5.4
Glu	5.4	Thr	8.1
Gly	2.7	Trp	2.7
His	2.7	Tyr	2.7
Ile	0.0	Val	2.7

Table 4 exhibits the certain physic-chemical properties of the toxin. Calculated isoelectric point (pI) is 8.8823, the protein is basic. The aliphatic index of a protein is defined as the relative volume occupied by aliphatic side chains (alanine, valine, isoleucine, leucine). It may be regarded as a positive factor for the increase of thermostability of globular protein. As the aliphatic amino acid content of this toxin is 8.108 Mol % hence indicates that this protein is not stable for a wide range of temperature. The aromatic amino acid content of this protein (10.811 Mole %) include aromatic ring. Aromatic amino acids strongly promote cross-β amyloid formation; further amyloidogenicity of aromatic residues is due to high hydrophobicity [8, 9]. As this toxin is hydrophilic in nature thus there is no chance of cross-beta amyloid formation. This toxin shows basic properties due to high basic amino acid content i.e. 24.324 Mole % hence it can accept a proton and exists with an overall charge of +1 at physiological pH. Extinction coefficient of this toxin ($6970 M^{-1} cm^{-1}$) indicates how much light, a protein absorbs at a certain wavelength. This toxin absorbs greater amount of light.

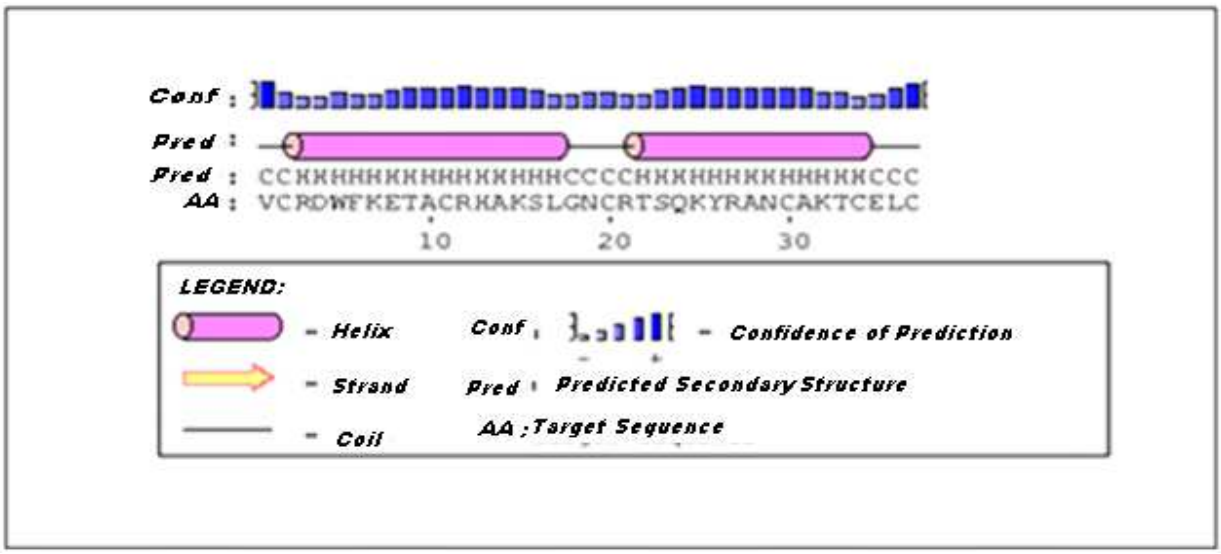
Table 4. Physico-chemical properties of potassium channel Bgk toxin

Toxin name	Mol.wt.	pI	Aliphatic amino acid (Mole %)	Aromatic amino acid (Mole%)	Non polar amino acid (Mole%)	Polar amino acid (Mole %)	Basic amino acid (Mole %)	Acidic amino acid (Mole %)	Extinction co-efficient ($M^{-1}cm^{-1}$)
Kappa actitoxin Bg1a or Potassium channel Bgk toxin	4281.93	8.88	8.108	10.811	45.946	54.054	24.324	8.108	6970

The secondary structure was predicted through PsiPred server. Results showed that the toxin is composed of alpha helix and coils (Table 5).

Table 5. Secondary structure prediction of potassium channel Bgk toxin

Toxin name	Alpha helix (%)	3_{10} Helix (%)	pI helix (%)	Beta Bridge (%)	Extended strand (%)	Beta turn (%)	Bend region (%)	Random coil (%)	Ambiguous state (%)	Other states (%)
Kappa actitoxin Bgk	75.6 (in two areas)	0.00	0.00	0.00	0.00	0.00	0.00	23.07 (in three areas)	0.00	0.00



This toxin is predominant in α-helix and random coil. Presence α-helix in two stretches (75.6 %; 3-17 and 22-34 amino acid positions) points to the fact that it is globular protein. Globular proteins are spherical ("globe-like") proteins that are somewhat water-soluble (they actually form colloids in water), unlike the fibrous or membrane proteins. The molecule's apolar (hydrophobic) amino acids are bounded towards the molecule's interior whereas polar (hydrophilic) amino acids are bound outwards, allowing dipole-dipole interactions with the solvent, which explains the molecule's solubility. The protein partially also exhibits a random coil conformation. The conformational entropy (the energy associated with the physical arrangements of protein chain that assumes a compact and globular state) associated with random coil states appreciably its energetic stabilization and accounts for much of the energy barrier to protein folding. Here, this toxin has 23.07% random coil in three stretches (1-2, 18-21, 35-37 amino acid positions) that represents moderate amount of energetic stabilization.

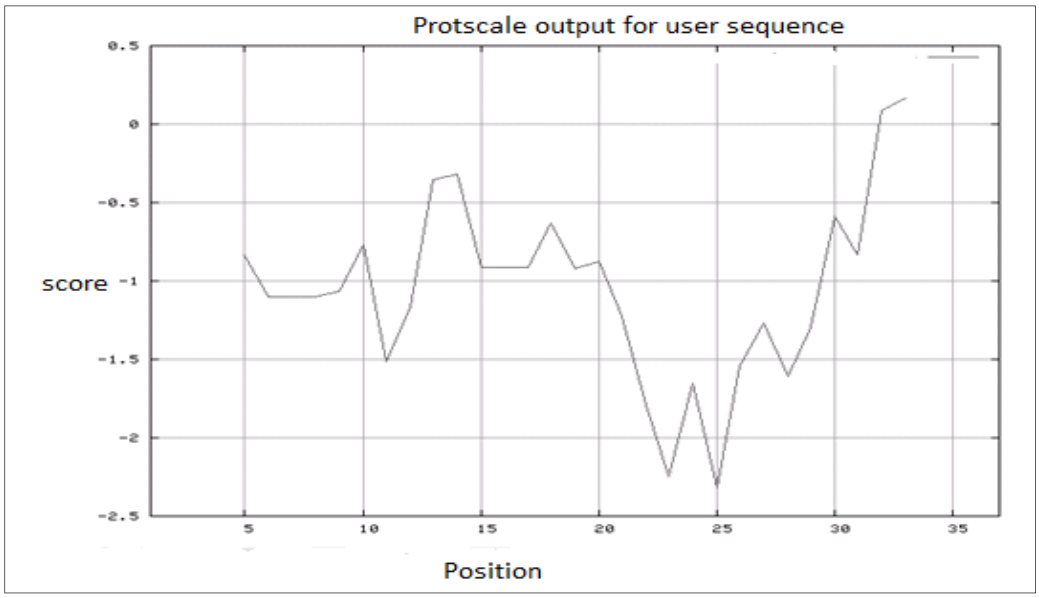
Kyte-Doolite is widely applied scale for determining hydrophobic character of a protein. If the region is greater than zero, then the region is hydrophobic in character [10]. Hydrophobicity of potassium channel Bgk toxin including GRAVY was predicted through Protscale. Table 6, represents the analysis of hydrophobicity of potassium channel Bgk toxin including GRAVY.

Table 6. Hydrophobicity prediction of potassium channel Bgk toxin

Toxin name	Maximum value	Minimum value	GRAVY
Kappa actitoxin Bg1a	0.167	-2.322	-0.738

The GRAVY value for a peptide or protein is calculated as the sum of hydropathy values of all the amino acids, divided by the no. of residues in the sequence. As the GRAVY value is too low (-0.738) it indicates better interaction of the protein with water i.e. hydrophilic in nature. Figure 1, demonstrates the hydropathy plot which corroborates with the GRAVY value.

Figure 1. Hydropathy plot of potassium channel Bgk toxin



The GRAVY value of this toxin initially declined, after that the GRAVY value of this toxin initially declined, thathe GRAVY value increase and made a peak (-0.5) on 12th amino acid position. After making a small peak, the GRAVY value declined again (on 25th amino acid position, GRAVY value was -2.5) and ultimately increased on 33th amino acid position. This time the score was -0.73. This too low score predict that this toxin is hydrophilic.

Table 7, illustrates that potassium channel Bgk toxin has no trans-membrane helix as predicted through TMHMM server.

Table 7. Trans-membrane helices prediction of potassium channel Bgk toxin

Toxin name	Sequence length	No. of Transmembrane helix
Kappa actitoxin Bg1a	37	Not detected

Thus this toxin is predicted to be a soluble protein and globular in nature with huge amount of alpha helix. In a globular protein, the amino acid chain twists and folds in a manner that enhances the protein's solubility in water by placing polar groups of atoms at the protein's surface (where they can contribute in desirable interactions with water molecules. This twisting and folding that ascertain the overall shape of a protein molecule (its tertiary structure) are due mainly to the very complex interplay of intra molecular forces that exists between different groups of atoms within the molecule, and to intermolecular forces working between groups of atoms on the protein and molecules in the protein's immediate surroundings [11].

As revealed from Table 8 which was predicted through Signal P 4.1 server, potassium channel Bgk toxin does not possess any signal peptide in its sequence.

Table 8. Signal peptide prediction of potassium channel Bgk toxin.

Toxin name	Presence of signal peptide sequence	Cleavage site in sequences
Kappa actitoxin Bg1a	Nil	**Nil**

As this Bgk toxin does not possess any signal peptide in its sequence, so it may have been synthesized on free polyribosome [12].

As predicted through DIANNA 1.1 server. Potassium channel Bgk toxin has at least three (03 nos.) disulfide bonds between cysteines in 2 and 11; 20 and 37 & 30 and 34 positions (Table 9).

Table 9 . Cysteine-disulfide bond prediction of potassium channel Bgk toxin.

Toxin name	Sequence length	Cysteine sequence position		Presence of disulfide bond (cysteines in red)
Kappa actitoxin Bg1a	37	1. 2. 3.	2-11 20-37 30-34	VCRDWFKETACRHAKSLGNCRTSQKYRANCAKTCELC
		03 nos. Cysteine disulfide bonds		

Disulfide bonds join the two segments of protein chains, increases the effective local concentration of proteins residues and lowers the effective local concentration of water molecule. As the water molecule strike amide-amide hydrogen bonds and break up secondary structure, so the disulfide bond by excluding the water molecule, stabilize the secondary structure in its vicinity. Disulfide bonds play an important role in the folding and stability of some proteins. To investigate the role of these disulfides in the structure and channel-blocking activity of ShK toxin, Pennington MW et.al, in 1999 synthesized a series of analogues by selective replacement of each pair of half-cystines with two alpha-amino-butyrate (Abu) residues. They did experimentation on ShK toxin. ShK toxin, a potassium channel blocker from the sea anemone *Stichodactyla helianthus*, is a 35 residue polypeptide cross-linked by three disulfide bridges: Cys3-Cys35, Cys12-Cys28, and Cys17-Cys32. They showed that the disulfide bond linking the N- and C-terminal regions is less important for activity than the internal disulfides. NMR analysis of the (Abu12, 28) and (Abu17, 32) analogues indicated that they had little residual structure, in harmony with their significantly reduced activities. By contrast, (Abu3, 35), ShK (12-28, 17-32) had a moderately well-defined solution structure, with a mean pair wise root-mean-square deviation of 1.33 A over the backbone heavy atoms. This structure on the other hand showed significant differences from that of native ShK toxin. The possible interactions of this analogue with the channel and the distinction between native secondary and tertiary structure on one hand and global topology imposed by the disulfide bridges on the other are discussed [13]. As this toxin has a Shk domain (discussed later) there may be a role of disulphide bond in Kv channel blocking.

Table 10, shows that this potassium channel Bgk toxin has one Shk like domain. Shk domain founds in *Stichodactyla helianthus*. This Shk domain is also found in toxin of *Stichodactyla* (sea anemone) that blocks potassium channel [14]. The peptide binds to all four subunits in the Kv tetramer through its interaction with the shallow vestibule at the outer entrance of the ion conduction pathway [15]. Every protein belongs to a specific protein family. Table 10, represents that potassium channel Bgk toxin belongs to pfamA family.

Table 10. Motif and Protein family prediction of Kappa Bbk toxin of potassium channel Bgk toxin

Toxin name	sequence length	Found motif	Protein family
Kappa actitoxin Bg1a	37	ShK domain like	Pfam A

PfamA belongs to sea anemone type 1 potassium channel toxin family and type 1b subfamily [16]. A phylogenetic tree (Figure 2) drawn through COBALT server (and modified in Phy.Fi online tool shows 07(seven) other toxins including query sequence [COHJC3.1 (*Bunodosoma caissarum*), COHJC2.1 (*Bunodosoma caissarum*), P81897.1 (*Actinia equina*), Q9TWG1.1 (*Anemonia sulcata*), P291862 (*Bunodosoma granulifera*, query sequence), QOEAE5.1 (*Anemonia erythraea*) and O168462 (*Heteractis magnifica*)]. The phylogenetic tree shows that COHJC3.1 and COHJC2.1 are sister toxins as are P81897.1 andQ9TWG1.1. These sister toxins are clade to P291862 and P291862 is clad to QOEAE5.1 and O168462. This type of phylogenetic tree was explored in Kv1 potassium channel toxins in sea anemones. In this case, Bgk toxin of *Bunodosoma granulifera* also showed similarities with *Anemonia sulcata*,

Actinia equina and *Anemonia erythraea* [17]. Protein evolution study often involves the comparison of homologs, sequences that have common origins but may or may not have common activity. These homologous sequences are inherited from a common ancestor that possesses similar structure.

Figure 2. Phylogenetic tree prediction of Bgk toxin

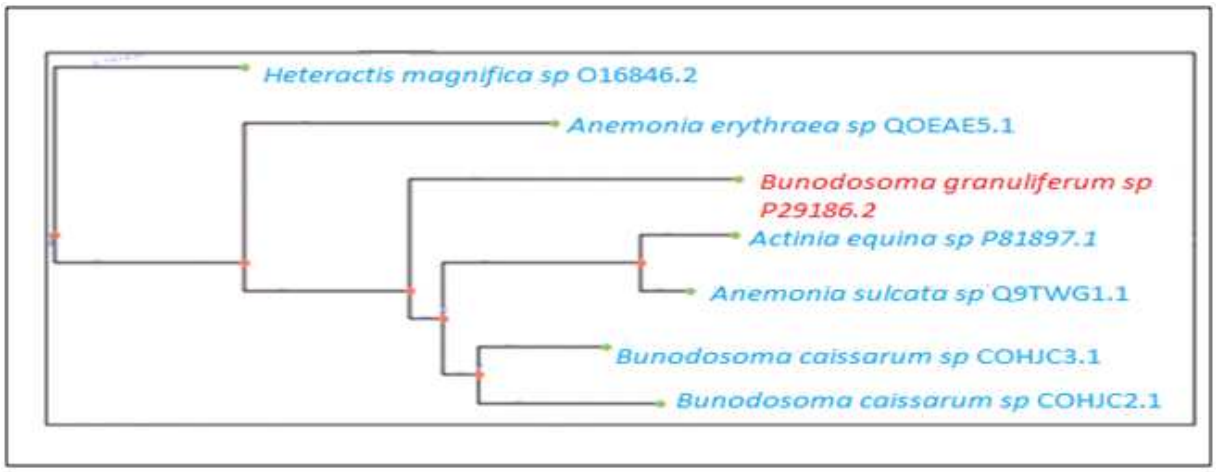


Table 11, shows the protein disordered region of this potassium channel Bgk toxin as predicted PrDos server. The double underlined residues are predicted to be disordered. The predicted disordered regions are useful for annotation of proteins. The disordered regions are supposedly involved in many biological processes, such as cell cycle regulation, cell signaling, cell cycle control, molecular recognition of proteins/DNA/RNA and molecular threading [18,19,20]. Protein disordered percentage is 8.108% that may affect protein protein interaction between the voltage gated potassium receptor and the toxin.

Table 11. Protein disordered region prediction of potassium channel Bgk toxin.

Toxin name	Protein disordered region(double underline portions)
Kappa actitoxin Bg1a	VCRDWFKETA CRHAKSLGNC RTSQKYRANC AKTCELC

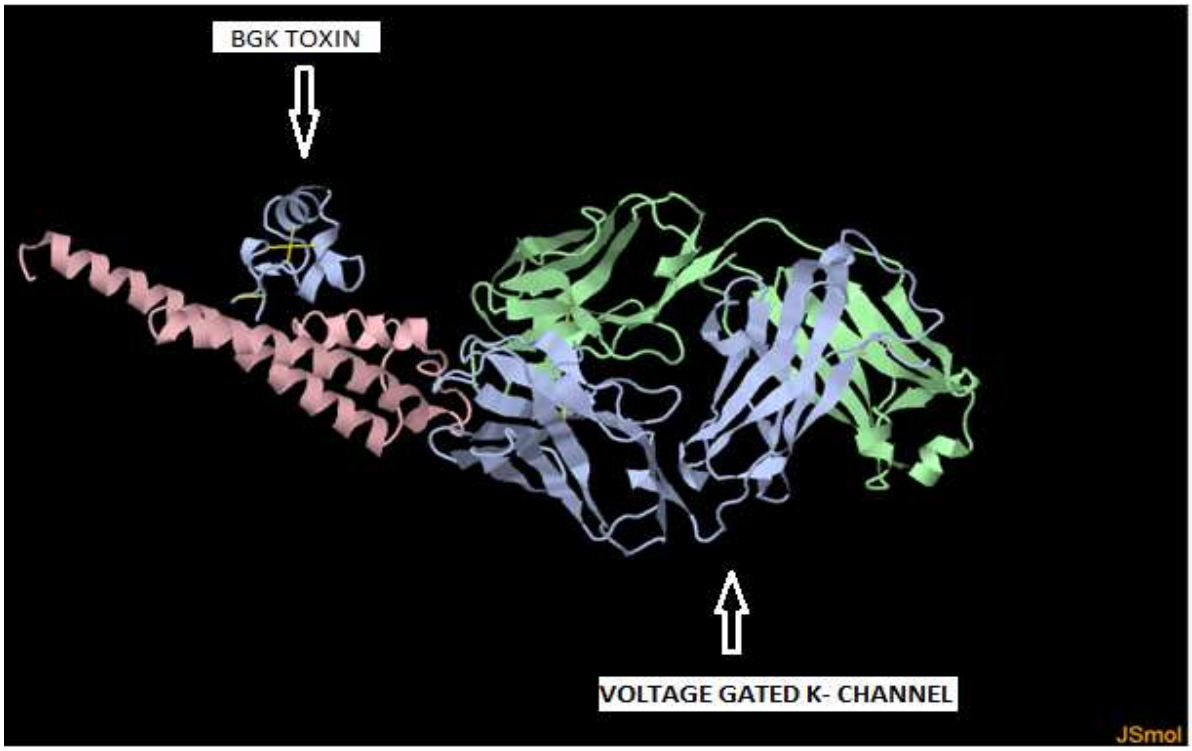
The cytotoxic T cell destroys cancer cell, viruses and bacteria through cytotoxic substances. The helper T cell release lymphokines that increase the response of B cell. Table 12, demonstrates that predicted immunogenicity (prediction made through POPI 2.0 server) of CTL response is moderate and predicted immunogenicity of HTL response is little. This result may be later helpful in designing vaccine against this toxin already studied in Australian box jelly fish [21].

Table 12. Immunogenicity prediction of potassium channel Bgk toxin

Toxin name	Epitope sequences	Predicted immunogenicity CTL response	Predicted immunogenicity HTL response
Kappa actitoxin Bg1a	VCRDWFKETACRHAKSLGNCRTSQKYRANCAKTCELC	Moderate	Little

Figure 3, shows the model of molecular docking between Bgk toxin and voltage gated potassium (Kv) channel created through ClusPro 2.0 server and visualized through JSmol First Glance software (www. bioinformatics.org/first glance/fgij/).

Figure 3. Predicted sea anemone Bgk toxin - voltage gated potassium channel bound complex visualized through JSmol



Docking is a method which predicts the favored orientation of one molecule to a second when bound to each other to form a stable complex [22]. Knowledge of the favored orientation in turn may be applied to predict the strength of association or binding affinity between two molecules using for example scoring function. Most scoring functions are physico-based molecular mechanics force fields that approximate the energy of pose; a low (negative) energy indicates a stable system and thus a likely binding interaction. Figure 3, shows the model of molecular docking between Bgk toxin and voltage gated potassium channel as visualized through JSmol First Glance software [23]. Model with highest negative weighted score was selected amongst list of predicted models that points out towards more efficient docking (Table 13).

Table13. Docking score prediction between Bgk toxin and potassium channel protein

Cluster	Member	Representative	Weighted score
1	84	Center	-766.2
		Lowest energy	-840.7

The weighted score is based upon the following coefficient equation:
$E=0.40Erep+-0.40Eatt+600Eelec+1.00EDARS$ ---------- [24]

Where :
DARS: Decoy as reference state; rep: Lennard- Jones attractive energies; elec: electrostatic; att : Lennard-Jones repulsive energies

M. Dauplais in 1997 found a diad in a K+ channel-blocking toxin (Bgk) from the sea anemone *Bunodosoma granulifera*. The diad is formed between amino acid position of 6, 13, 23, 25, 26 which are similar to the docking position of Bgk and potassium channel receptor. An alanine-scanning-based analysis revealed the functional importance of five residues, which include a critical lysine and an aromatic residue separated by 6.6 +/- 1.0 A. The same diad is found in the three known homologous toxins from sea anemones. More strikingly, a similar functional diad is present in all K+ channel-blocking toxins from scorpions, although these toxins adopt a distinct scaffold. Moreover, the functional diads of potassium channel-blocking toxins from sea anemone and scorpions superimpose

in the three-dimensional structures. Therefore, toxins that have unrelated structures but similar functions possess conserved key functional residues, organized in an identical topology, suggesting a convergent functional evolution for these small proteins [25].

Further, it is clear that for docking involvement of amino acids (i.e. amino acid positions 6, 13, 23, 25 and 26) [25] occurs where disulfide bonds (between amino acid residues 2-11, 20-37, 30-34) are present. This result thus shows the importance of disulfide bonds in protein docking prediction. Further amino acid positions 6, and 26 are aromatic amino acid and positions 10 and 31 and a critical lysine in 25 position that are important for binding. On the other hand disorderness of amino acids (i.e. amino acid positions 1, 35, 36 and 37) in this toxin occurs that too where disulfide bonds are present. Thus disordered region of proteins often bind to structured domains, mediating interactions within and between proteins [26] may be supported by disulphide bonds between cysteines. Thus in the present study the sequence and structure analysis and docking of potassium channel Bgk toxin was done through various bioinformatics tools and software. Based on these findings it can be concluded that further characterization of kappa Bgk toxin may be important for screening new pharmacological molecules and effective toxin's antidote.

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REFERENCES

[1] F Barbara; V Vitor; A Agostinho, *Mar Drugs*., **2012**, 10(8), 1812-1851.
[2] P Castro; ME Huber, Marine Biology, McGraw–Hill, New Delhi, **2010**, p.121.
[3] SM Messerli; RM Greenberg, *Mar. Drugs*., 2**0**06, 4, 70–81.
[4] S Mouhat; N Andreo; B Jouirou; JM Sabatier, *Curr Pharm Des*., **2008**, 14(24), 2503-18.
[5] F Bosman; J Tytgat, *Toxicon.*, **2007**, 49(4), 550-560.
[6] DA Doyale; J Morais; RA Pfuetzner; A Kuo; JM Gulbis; SL Cohen; et al, *Scienc*.,**1998**, **280** (5360), 69–77.
[7] G Feng; P Deak; M Chopra; LM Hall, *Cell*., **1995**, 80,1001-1011.
[8] http://www.biology.arizona.edu/biochemistry/problem_sets/aa/aromatic
[9] Doran, T.M; Kamens, A.J; Byrnes, N.K; Nilsson, B.L. *Proteins*.**2012**; 80(4):1053-65.
[10] Kyte, J; Doolittle, R. *J. Mol. Biol*.**1982**; 157: 105-132.
[11] http:// www.chemistryexplained.com/Ge-Hy/Globular-Protein.
[12] KR Murray; KD Granner; AP Mayes; WR Rodwell, Herper's Biochemistry, 25th edition, Lange Medical Books/Mc Graw Hill, **2000**.
[13] MW Pennington; MD Lanigan; Kalman K; VM Mahnir; H Rauer; CT McVaugh; D Behm; DDonaldson; KG Chandy; WR Kem; RS Norton, *Biochemistry*.,**1999**, 38 (44), 14549–58.
[14] K Kalman; MW Pennignton; MD Larigan; A Nguyen; H Raur; V Mahnir; K Paschetto; WR Kem; S Grissemeo; GA Gutman; EP Christian; MD Cahalan; RS Norton; KG Chandy, *J.Biol.Chem.*,**1998**, 273(49),32699-707.
[15] KG Chandy; H Wulff; C Beeton; M Pennington; GA Gutman; MD Cahalan, *Trends pharmacol.sci*., **2004**, 25(5), 280-9.
[16] http://www.uniprot.org/uniprot/P29186
[17] Y Yamaguchi; Y Hosegawa; T Honma; Y Nagashima; K Shiomi, *Mar Drugs*.,**2010**, 8(12), 2893-2905.
[18] T Ishida; K Kinoshita, *Nucleic Acids Res*., **2007**, **35**.Web server Issue **2007**.
[19] AK Dunker; CJ Brown; JD Lawson; LM Iakoucheva; Z Obradovic, *Biochemistry*., **2002**, 41(21), 6573 - 6582.
[20] LM Iakoucheva; CJ Rown; JD Lawson; Z Obradovic; AK Dunker, I *Journal of Molecular Biology*.,**2002**, 323, 573-584.
[21] J Md Alam; KU Md Ashraf, *Toxicol Int*., **2013**, 20(3), 235-253.
[22] T Lengauer; M Rarey, *Curr. Opin. Struct. Biol*., **1996**, **6**, 402–6.
[23] www.bioinformatics.org/first glance/fgij/
[24] D Kozakov; R Brenke; SR Comeau; S Vajda, *Proteins*., **2006**, 65, 392-406.
[25] M Dauplais; A Lecoq; J Song; J Cotton; N Jamin; B Gilquin; C Roumestand; C Vita; CLC de Medeiros; EG Rowan; AL Harvey; A Menez, *J. Biol. Chem*., **1997**, 272, 4302-4309.
[26] W Khan; F Duffy; G Pollastri; DC Shields; C Mooney, *PLoS ONE*., **2013**, 8(9), e72838.