ISSN 1996-3351

# Asian Journal of Biological Sciences

http://knowledgiascientific.com

Knowledgia SCIENTIFIC
A Place to Publish Outstanding Research

Asian Journal of Biological Sciences 4 (4): 352-361, 2011
ISSN 1996-3351 / DOI: 10.3923/ajbs.2011.352.361


# Homology Modeling and Docking Studies Between AC1 Rep Protein of *Begomovirus* and Whey α-lactalbumin

R. Prajapat, R.K. Gaur and A. Marwal
Department of Science, Faculty of Arts, Science and Commerce, Mody Institute of Technology and Science, Lakshmangarh, Sikar-332311, Rajasthan, India

*Corresponding Author: R.K. Gaur, Department of Science, Faculty of Arts, Science and Commerce, Mody Institute of Technology and Science, Lakshmangarh, Sikar-332311, Rajasthan, India Tel: 9352911723*

## ABSTRACT

Structural bioinformatics is concerned with computational approaches to predict and analyze the spatial structure of proteins and nucleic acids by using different tools and techniques. The aim of present study was to carry out the homology modeling study of AC1 Rep protein and docking between α-lactalbumin and Rep protein of *Begomovirus* by using modeling and docking (Hex 6.3) softwares. This model show that 35% identity is enough for receptor based antiviral agent designing. The closest homologue of Rep protein was 1L2M|A, with the highest sequence identity of 81% that was selected as representative model using homology modeling softwares. The model was validated by using protein structure checking tools such as RAMPAGE server and Prochek for reliability. On the basis of RMS and energy values, the best docking orientation -1.00 was selected. This study will be used for the screening of inhibitors against Begomoviral proteins and can be further applied in future antiviral agent designing.

**Key words:** *Begomovirus*, RAMPAGE, Hex 6.3, 1L2M|A, prochek

## INTRODUCTION

X-ray protein crystal structures and NMR classified protein families based on a limited set of folding patterns. Homology modeling is a helpful tool for the production of 3D structure of protein by using *in-silico* methods and this approach can overcome the limitations of X-Ray crystallography and NMR (Mount, 2004). Structure of unknown proteins can be identified on the basis of amino acid sequence pattern by matching of both known and unknown proteins. By selecting best homologous proteins which showing maximum sequence similarity with the unknown protein for homology search, predict that their structure could be similar (Prajapat *et al*., 2010). Homology modeling is a multi step processes that can be summarize in four steps, includes selection of template, target template alignment, construction of model, analysis and assessment of model (Marti-Renom *et al*., 2000).

In the field of Molecular modeling, docking (Kartasasmita *et al*., 2010) is used to predict the binding orientation of small molecule drugor antiviral agents to their protein targets also for protein-protein docking in order to predict the affinity and activity of the small molecule (Kitchen *et al*., 2004).

Geminiviruses were recognized by the International Committee on the Taxonomy of Viruses (ICTV) on the basis of their unique virion morphology and possession of ssDNA as their genomic material (Briddon *et al*., 2002). Geminiviruses serve as a major plant pathogens in tropical and

subtropical countries (Moffat, 1999; Boulton, 2003; Mansoor *et al*., 2003), affecting higher range of crops, weed and other plants that cause disastrous impact on productivity. The family *Geminiviridae* members have a circular, single-stranded DNA (ssDNA) genome, approximately 2.7-5.2 kb. Based on their genome arrangement and biological properties, geminiviruses are classified into four genera: *Mastrevirus, Curtovirus, Topocuvirus* and *Begomovirus* (Stanley *et al*., 2005). Genera *Begomovirus* contains almost 200 species (Fauquet *et al*., 2008) that are transmitted by dicotyledonous infecting whitefly (Bemisia tabac), having either bipartite genomes (DNA-A and DNA-B) or monopartite genomes resembling DNA-A.

DNA-A component of *Begomovirus* encode various proteins and one of them is AC1/Rep (Replication initiation proteins). Rep is a multifunctional, oligomeric protein that initiates replication at plus strand and plays important role in conferring origin of replication (Chatterji *et al*., 2001). Rep found in the nuclei of infected plant cell (Nagar *et al*., 1995) and involves in viral DNA replication and transcription (Laufs *et al*., 1995). This protein possesses site specific DNA binding, ligation and nicking and site specific topoisomerase activity, ATPase and helicase activities (Pant *et al*., 2001; Choudhury *et al*., 2006). On the basis of available literature the whey proteins fractions (α-lactalbumin, β-lactoglobulin and lactoferrin) can be used as an inhibitor of Tomato Yellow Leaf Curl Virus (TYLCV) which infects tomato plants (Abdelbacki *et al*., 2010).

*In silico* approach for Replication Initiation Protein (Rep) as possible receptor for α-lactalbumin was applied on the basis of modeling and docking (protein-protein docking) study. Viruses strain responsible for the disease in *Begomovirus* infected plant species are identified by using gene specific primers in Polymerase Chain Reaction (PCR) (Adjata *et al*., 2008) therefore these *in silico* approaches of present study not only support antiviral agent designing, primer designing for PCR based study but also helpful in developing viral resistant through gene silencing (Dhakar *et al*., 2010).

## MATERIALS AND METHODS

In present study we used different bioinformatics tools and biological databases for Rep protein and α-lactalbumin fraction to confirming the epidemic of *Begomovirus*, like GenBank-NCBI, PDB (Protein Data Bank), UCLA-DOE and softwares like Hex, UCSF Chimera etc. The homology modeling procedure can be divided into four sequential steps: template selection, target template alignment, model construction and model assessment (Marti-Renom *et al*., 2000). This work was carried out as a part of Ph.D research project at the Department of Science (Mody Institute of Technology and Science, Lakshmangarh, India) from 2009 to 2010. Rep sequence of Sweet potato leaf curl Lanzarote virus, in FASTA format was mined from GenBank-NCBI database (>gi|262530246|ref|YP_003288785.1| Rep [Sweet potato leaf curl Lanzarote virus]) for homology modeling and docking study.

**Template selection and sequence alignment:** BLAST (Basic Local Alignment Search Tool) (BLASTP 2.2.24+) was used (Altschul *et al*., 1997; Altschul *et al*., 2005) to search against the PDB (Protein Databank) to find out the related homologues of the query/template (Rep, YP_003288785) sequence (http://blast.ncbi.nlm.nih.gov/Blast.cgi). The homology modeling requires a query sequence with unknown 3D structure and target sequence that have known 3D structure with at least 35% similarity. By the BLAST search, we selected the closest homologue of Rep, it was 1L2M|A (Replication initiation protein of Tomato yellow leaf curl virus-Sardinia) with the highest sequence identity of 81%, Positives 91% and gaps are 0%.

**Target sequence:** The PDB file of the target sequence of Rep protein was downloaded from PDB (http://www.rcsb.org/pdb) and the FASTA format of target sequence was mined from GenBank-NCBI as follows:

PDB: 1L2M_A
>gi|253722967|pdb|1L2M|A Chain A, Minimized Average Structure Of The N-Terminal, DNA-Binding Domain Of The Replication Initiation Protein From A Geminivirus (Tomato Yellow Leaf Curl Virus-Sardinia)
SGRFSIKAKNYFLTYPKCDLTKENALSQITNLQTPTNKLFIKICRELHENGEPHLHILIQFEGK
YNCTNQRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDVLEWGTFQIDGR

**Template sequence:** The template sequence for the query (accession no. YP_003288785) was searched from NCBI and mined in the FASTA format as follows:

>gi|262530246|ref|YP_003288785.1| Rep [Sweet potato leaf curl Lanzarote virus]
MPRAGRFNIKAKNYFLTYPQCSLTKEEALDQLLHLNTPTNKKFIKICRELHENGEPHLHVLL
QFEGNYQCTNQRFFDLVSPSRSSHFHPNIQRAKSSSDVKSYVDKDGDTIEWGEFQVDGRSAR
GGQQTANDAAAEALNSGSKEAALQIIREKLPEKFIFQYHNLCGNLDRIFSPPPSVYSSPFSSSS
FNAVPDIISDWAAENVMDSAARPDRPISIVIEGPSRIGKTVWARSLGPHNYLCGHLDLSPKVY
SNSAWYNVIDDVNPQYLKHFKEFMGAQKDWQSNCKYGKPVQIKGGIPTIFLCNPGEGSSFK
LWLDKPEQGALKNWATANAIFCDVQSPFWVQEEVSHSGATAHRGEEGQEESS

The FASTA sequences of query (accession no. YP_003288785.1) were uploaded on the 3D-Jigsawn (Protein Comparative Modeling Server) for the construction of its PDB files. 3D-Jigsawn (bmm.cancerresearchchuk.org/~3djigsaw) sends the PDB files on the e-mail address that was assigned to the modeling server. The PDB file of query and homologous target sequence were further utilized for 3D model energy validation and docking studies (Heinrichs, 2008).

**Model building**

**Evaluation and validation:** UCLA-DOE server http://nihserver.mbi.ucla.edu) provides various softwares for the study of different aspects of browsed PDB files e.g., Verify3D, Procheck etc. The Verify 3D and Procheck (Laskowski *et al*., 1993) outcomes displayed in the form of profile search and Ramachandran plots (Prajapat *et al*., 2010, 2011). In order to study the energy validation of query and homologous target proteins, we uploaded PDB files of both proteins on structure analysis and validation server (SAVA, http://nihserver.mbi.ucla.edu/sava/). SAVA programs should require some time interval for the processing and display various results, this service provided by NIH-MBI laboratory for structural genomics and proteomics (Bowie *et al*., 1991; Luthy *et al*., 1992). In this study the model was checked with Verified-3D (Goh *et al*., 2008) server (Fig. 2) and Ramachandran plot at RAMPAGE (Lovell *et al*., 2003) server (Fig. 3).

PDB file of both query and homologous target proteins were utilized for the structural model construction using offline bioinformatics softwares e.g., UCSF Chimera (Fig. 1). By using Chimera we can study the position of different amino acids present in the active site of proteins and find out the position of conserved regions and mutational sites.

**Docking of α-lactalbumin and Rep protein:** The aim of protein docking is to predict how proteins interact with each other and automated comparative docking was done in between α-lactalbumin and Rep protein by the program Hex 6.3 (Ritchie *et al*., 2008). Hex is a primarily docking program; it demonstrates the potential for performing fast 3D superpositions using the SPF correlation approach. Hex reads protein and DNA molecular structures in PDB files format. The proteomics research develops this approach as a separate program for high throughput ligand screening (Balakrishnan *et al*., 2010).

The FASTA sequence of α-lactalbumin (accession No. ACI62509, Source: Bos Taurus) was mined from GenBank-NCBI and by the help of 3D-Jigsawn server its PDB file was designed. The PDB files of Rep protein and α-lactalbumin were uploaded as inputs into Hex for protein-protein docking. These are treated as a receptor and a ligand respectively. All the input files and the constructed model were analyzed using the protein docking and spherical harmonic surfaces of the Hex. Structure refinement and energy minimization was performed with Hex itself, Hex sorts the generated orientations by docking energy and prints a summary of the 10,000 highest scoring (lowest energy) orientations. Regularization is a procedure for fitting a protein model with the ideal covalent geometry of residues to the atomic positions of the target PDB structure (Ritchie *et al*., 2008). Based on the energy minimization the best pose of the docked complex was selected.

## RESULTS AND DISCUSSION

In this study the 3D structure of Rep protein of Sweet potato leaf curl Lanzarote virus was built by homology modeling based on the PDB file obtained from 3D JIGSAW by using UCSF Chimera software. The secondary structure of Rep protein has 5 α helix and 5 β sheets (Fig. 1).

Profile score above zero in the Verify 3D graph (Bowie *et al*., 1991; Luthy *et al*., 1992) corresponds to acceptable environment of the model. The high score of 0.63 indicates that environment profile of the model is good (Fig. 2).

The Ramachandran plot contributes to the final values of Rep protein e.g., 87.3% of residues comes in the most favoured regions, 11.4% residues in allowed region and 1.3% residues in outlier regions (Table 1, Fig. 3a). Non-proline residues, non-glycine residue regions were 98.7% and most disallowed regions were 1.3% in the plot (Fig. 3b).

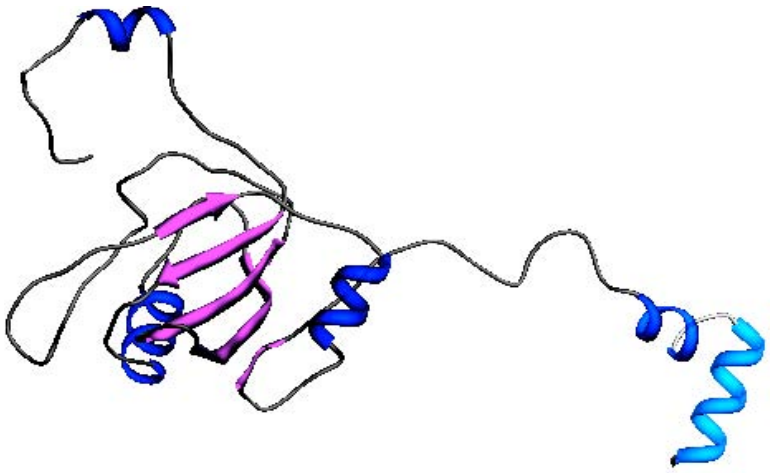

Fig. 1: Ribbon diagram of Rep protein, designed by using UCSF Chimera

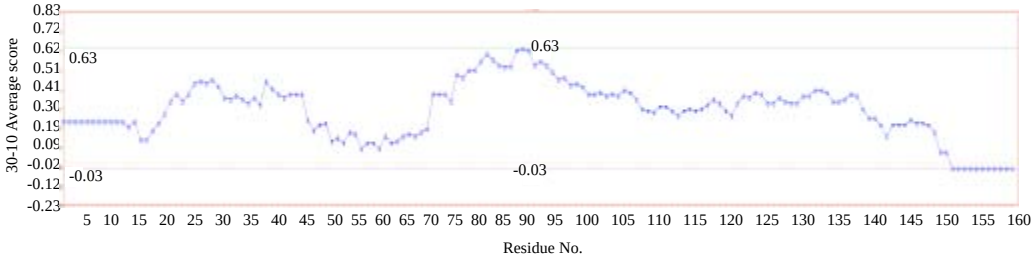


Fig. 2: Verified 3D graph of Rep protein of Sweet potato leaf curl Lanzarote virus

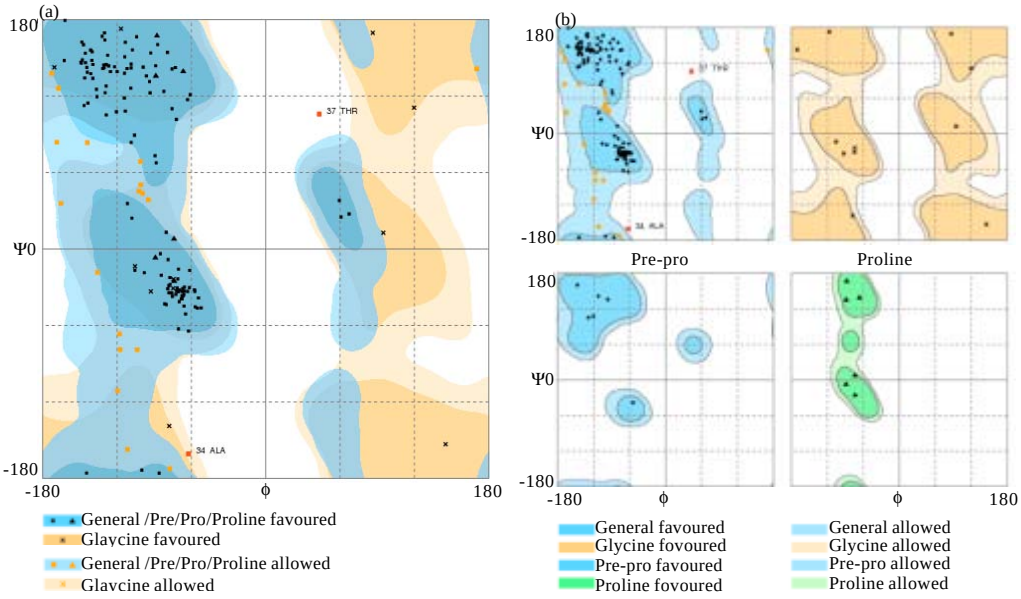


Fig. 3: (a) Ramachandran plot of 3D model of Rep protein of Sweet potato leaf curl Lanzarote virus, (b) Non-proline residues and non-glycine residue regions

Table 1: Results summary of the Ramachandran plot

| S.No | Accession no. | Protein | Virus strain | Residues in favoured region (%) | Residues in allowed region (%) | Residues in outlierregion(%) |
|---|---|---|---|---|---|---|
| 1 | YP_003288785.1 | Rep | Sweet potato leaf curl Lanzarote virus | 87.3 | 11.4 | 1.3 |

A good quality Ramachandran plot has over 90% in the most favoured regions (Xiao *et al*., 2004; Balakrishnan *et al*., 2010) but the Ramachandran plot of Rep protein has only 87.3% of residues in the most favoured regions therefore it is near to good quality model (Table 1).

Hex assigns multiple local coordinate systems to the larger molecule (receptor) and docks the ligand around each local coordinate frame on the receptor. Rep protein has 161 residues atoms of the residues.

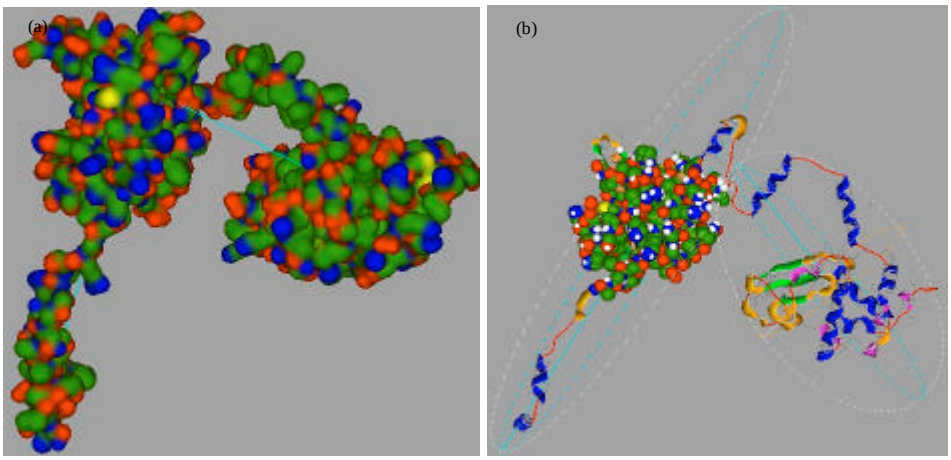


Fig. 4: A Hex scene showing the Rep protein (left) domain and α-lactalbumin (right) in Van der Waals mode and with the intermolecular axis drawn in blue (a) and solid surfaces (b)

Table 2: Cluster found (Found 1687 clusters from 2000 docking solutions).

| Clst | Soln | Models | Etotal | Eshape | Eforce | Eair | Vshape | Vclash | Bmp | RMS |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 1 | 000:000 | -657.0 | -657.0 | 0.0 | 0.0 | 0.0 | 0.0 | -1 | -1.00 |
| 1 | 2 | 000:000 | -641.4 | -641.4 | 0.0 | 0.0 | 0.0 | 0.0 | -1 | -1.00 |
| 1 | 5 | 000:000 | -581.7 | -581.7 | 0.0 | 0.0 | 0.0 | 0.0 | -1 | -1.00 |
| 1 | 7 | 000:000 | -569.0 | -569.0 | 0.0 | 0.0 | 0.0 | 0.0 | -1 | -1.00 |
| 1 | 90 | 000:000 | -448.5 | -448.5 | 0.0 | 0.0 | 0.0 | 0.0 | -1 | -1.00 |
| 1 | 199 | 000:000 | -426.0 | -426.0 | 0.0 | 0.0 | 0.0 | 0.0 | -1 | -1.00 |
| 1 | 1 | 000:000 | -657.0 | - 657.0 | 0.0 | 0.0 | 0.0 | 0.0 | -1 | -1.00 |

The binding sites exhibit chemical specificity, a measure of the types of ligand that bond and the affinity that measure strength of the chemical bond (Balakrishnan *et al*., 2010). The binding site for Rep protein model was predicted using Hex 6.3. The Etotal, Eshape and Eforce values for the model were -657.0, -657.0 and 0.0 (Table 2). Best start orientation is alpha 26 (E = -837.44) was at 42477/128790 (Emin is -912.92, Emax is -794.03). On the basis of the RMS and energy values the best docking orientation was selected. The better RMS value of docking was -1.00 (Fig. 5, 6).

Figure 4 represents Hex scene of Rep protein domain and α-lactalbumin in van der waals mode, with the intermolecular axis (4a) and solid surfaces form (4b). Figure 5 illustrate spherical harmonic surfaces to order L = 12 for the Rep protein domain (left) and α-lactalbumin (right) (Fig. 5a). Illustration of the Rep protein/α-lactalbumin complex shown as contoured Gaussian density surfaces and background modes (Fig. 5b). Figure 6 illustrate docking control results in the form of side chains (6a), solid models (6b) and solid surface (6c) model view of Rep protein (Receptor: 262530246/YP_003288785.1) and whey α-lactalbumin (Ligand: 209570117/ACI62509) complex. These docking results suggest that the whey α-lactalbumin interact with the Rep protein of Begomovirus and block the replication initiation. The binding pocket values for Rep protein model were predicted by using Hex 6.3. The predicted two pockets by the software with different primary surface area and volume shown in Table 3.

Computational Biology and bioinformatics not only speeding up the antiviral agent discovery process but also reducing the costs and provide a new dimension to structural proteomics. How two protein molecules fit together in 3D space can be studied by docking process. The protein-protein

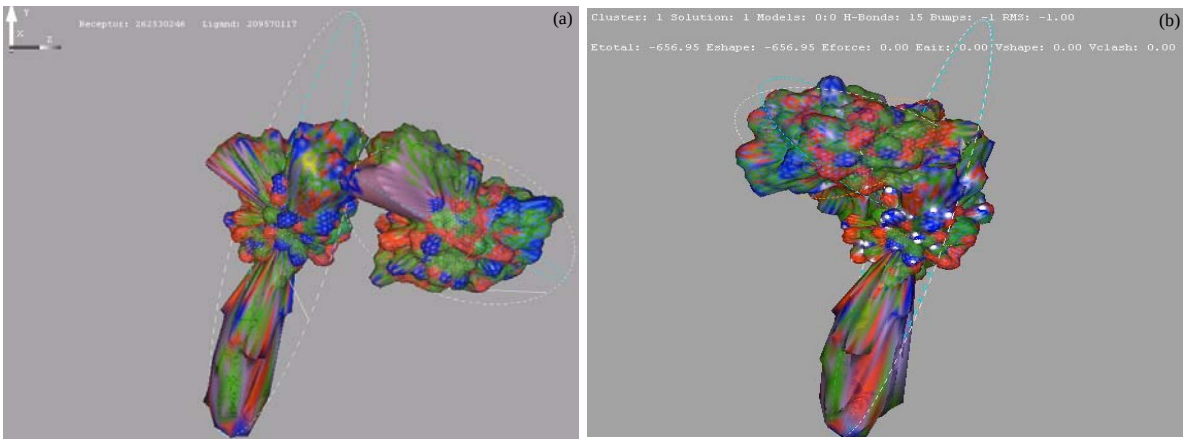


Fig. 5: Illustration of spherical harmonic surfaces to order L = 12 for the Rep protein domain (left) and α-lactalbumin (right) (a). Illustration of the Rep protein (Receptor: 262530246) and α-lactalbumin (Ligand: 209570117) complex shown as contoured Gaussian density surfaces and coloured by chain colour, drawn using perspective (keyboard P) and background (keyboard B) modes (b)

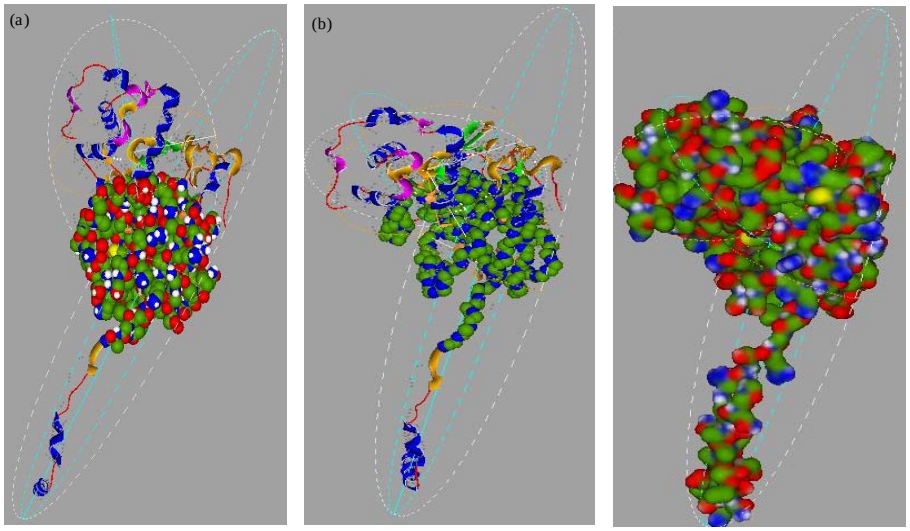


Fig. 6: Docking results illustrate side chains (a), solid models (b) and solid surface (c) view forms of Rep protein/α-lactalbumin complex

Table 3: Binding site model Rep protein

| Pocket | Polar probe | Apolar probe | Primary surface: area | Primary surface: volume | Typical edge arc | Typical edge length (Å) | Average radius (Å) | Surface area (Å) | Triangles | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | Min. | Max. | Avg. |
| 1 | 0.00A | 0.00A | 13012.13 | 16440.48 | 4.62° | 1.28 | 15.83 | 10864.54 | 0.07 | 108.16 | 2.41 |
| 2 | 0.00A | 0.00A | 12088.25 | 15794.49 | 4.62° | 1.45 | 17.97 | 7737.93 | 0.40 | 16.54 | 1.72 |

interaction plays a significant role in structural based antiviral agent designing. In the present work we have selected receptor Replication Initiation Protein (Rep) and identified the antiviral agent against it that could inhibit Begomovirus infection at molecular level.

Docking can be used in several ways like to study the mechanism of an enzymatic reaction, to identify possible binding modes for a ligand and to screen a database (Morris *et al*., 2008). Hex is user friendly docking software that calculates protein ligand docking with assuming the rigidity of ligand and it can superpose pairs of molecules using only knowledge of their 3D shapes. Hex also calculating, displaying feasible docking modes of pairs of protein (protein-protein docking) and DNA molecules. A few amino acids were found to be conserved in Rep, that forming the binding cavity for the whey α-lactalbumin. Interaction of whey α-lactalbumin with Rep, stop different function that carryout by this protein in infected host cell and this leads to inhibit Begomovirus infection.

Homology modeling and protein-protein docking allows expanding the number of other viral protein sequences and also used to support anti-viral agent design research. Information obtain by this study will be used in screening of other inhibitors of the begomoviral protein and can be further applied in future antiviral agent design.

## CONCLUSION

The present data demonstrate that homology modeling and docking plays an important role in various structural proteomics and *in silico* antiviral agent designing. This result may raise the attention to interaction of whey α-lactalbumin with Rep of Begomovirus, may stop molecular changes at cellular level carryout by this protein in infected host and this leads to inhibit Begomovirus infection because its infection causes an estimated yield loss up to 80-100% in various part of world.

## ACKNOWLEDGMENT

The authors are thankful to Prof. Shakti Baijal, Dean, FASC, MITS, Rajasthan. The authors are also thankful to Department of Biotechnology (DBT), India and Department of Science and Technology, India for financial support for the present studies.

## REFERENCES

Abdelbacki, A.M., S.H. Taha, M.Z. Sitohy, A.I.A. Dawood, M.M.A.E. Hamid and A.A. Rezk, 2010. Inhibition of tomato yellow leaf curl virus TYLCV using whey proteins. Virol. J., 7: 26-26.

Adjata, K.D., E. Muller, M. Aziadekey, Y.M.D. Gumedzoe and M. Peterschmitt, 2008. Incidence of cassava viral diseases and first identification of *East African cassava mosaic virus* and *Indian cassava mosaic virus* by PCR in Cassava (*Manihot esculenta* Crantz) fields in Togo. Am. J. Plant Physiol., 3: 73-80.

Altschul, S.F., T.L. Madden, A.A. Schaffer, J. Zhang, Z. Zhang, W. Miller and D.J. Lipman, 1997. Gapped BLAST and PSI-BLAST: A new generation of protein database search programs. Nucl. Acids Res., 25: 3389-3402.

Altschul, S.F., J.C. Wootton, E.M. Gertz, R. Agarwala, A. Morgulis, A.A. Schaffer and Y.K. Yu, 2005. Protein database searches using compositionally adjusted substitution matrices. FEBS J., 272: 5101-5109.

Balakrishnan, M., R.C. Srivastava and M. Pokhriyal, 2010. Homology modeling and docking studies between HIV-1 protease and carbamic acid. IJBT, 9: 96-100.

Boulton, M.I., 2003. Geminiviruses: Major threats to world agriculture. Ann. Applied Biol., 142: 143-143.

Bowie, J.U., R. Luthy and D. Eisenberg, 1991. A method to identify protein sequences that fold into a known three-dimensional structure. Science, 253: 164-170.

Briddon, R.W., S.E. Bull, S. Mansoor, I. Amin and P.G. Markham, 2002. Universal primers for the PCR-mediated amplification of DNA β: A molecule associated with some monopartite begomoviruses. Mol. Biotechnol., 20: 315-318.

Chatterji, A., R.N. Beachy and C.M. Fauquet, 2001. Expression of the oligomerization domain of the replication-associated protein (Rep) of tomato leaf curl New Delhi virus interferes with DNA accumulation of heterologous geminiviruses. J. Biol. Chem., 276: 25631-25638.

Choudhury, N.R., P.S. Malik, D.K. Singh, M.N. Islam, K. Kaliappan and S.K. Mukherjee, 2006. The oligomeric Rep protein of mungbean yellow mosaic India virus MYMIV is a likely replicative helicase. Nucleic Acids Res., 34: 6362-6377.

Dhakar, K., V.K. Gupta, M.S. Rathore and R.K. Gaur, 2010. Virus resistance and gene silencing in plants infected with begomovirus. J. Applied Sci., 10: 1787-1791.

Fauquet, C.M., R.W. Briddon, J.K. Brown, E. Moriones, J. Stanley, M. Zerbini and X. Zhou, 2008. Geminivirus strain demarcation and nomenclature. Arch. Virol., 153: 783-821.

Goh, K.M., N.M. Mahadi, O. Hassan, R.N. Zaliha R.A. Rahman and R.M. Illias, 2008. Molecular modeling of a predominant β-CGTase G1 and analysis of ionic interaction in CGTase. Biotechnology, 7: 418-429.

Heinrichs, A., 2008. Proteomics: Solving a 3D jigsaw puzzle. Nat. Rev. Mol. Cell Biol., 9: 3-3.

Kartasasmita, R.E., R. Herowati and T. Gusdinar, 2010. Docking study of quercetin derivatives on inducible nitric oxide synthase and prediction of their absorption and distribution properties. J. Applied Sci., 10: 3098-3104.

Kitchen, D.B., H. Decornez, J.R. Furr and J. Bajorath, 2004. Docking and scoring in virtual screening for drug discovery: Methods and applications. Nat. Rev. Drug Discovery, 3: 935-949.

Laskoswki, R.A., M.W. MacArthur, D.S. Moss and J.M. Thornton, 1993. PROCHECK: A program to check the stereochemical quality of protein structures. J. Applied Cryst., 26: 283-291.

Laufs, J., W. Traut, F. Heyraud, V. Matzeit, S.G. Rogers, J. Schell and B. Gronenborn, 1995. *In vitro* cleavage and joining at the viral origin of replication by the replication initiator protein of tomato yellow leaf curl virus. Proc. Natl. Acad. Sci., 92: 3879-3883.

Lovell, S.C., I.W. Davis, W.B. Arendall 3rd, P.I. de Bakker and J.M. Word *et al.*, 2003. Structure validation by Calpha geometry: Phi, psi and Cbeta deviation. Proteins, 50: 437-450.

Luthy, R., J.U. Bowie and D. Eisenberg, 1992. Assessment of protein models with three-dimensional profiles. Nature, 356: 83-85.

Mansoor, S., R.W. Briddon, Y. Zafar and J. Stanley, 2003. Geminivirus disease complexes: An emerging threat. Trends Plant Sci., 8: 128-134.

Marti-Renom, M.A., A.C. Stuart, A. Fiser, R. Sanchez, F. Melo and A. Sali, 2000. Comparative protein structure modeling of genes and genomes. Ann. Rev. Biophys. Biomol. Struct., 29: 291-325.

Moffat, A.S., 1999. Plant pathology: Geminiviruses emerge as serious crop threat. Science, 286: 1835-1835.

Morris, G.M. and M. Lim-Wilby, 2008. Molecular Docking, Methods in Molecular Biology. In: Molecular Modeling of Proteins, Kukol, A. (Ed.). Humana Press, Totowa, New Jersey, pp: 365-382.

Mount, D.M., 2004. Bioinformatics: Sequence and Genome Analysis. 2nd Edn., Cold Spring Harbor Laboratory Press, New York.

Nagar, S., T.J. Pedersen, K.M. Carrick, L. Hanley-Bowdoin and D. Robertson, 1995. A geminivirus induces expression of a host DNA synthesis protein in terminally differentiated plant cells. Plant Cell, 7: 705-719.

Pant, V., D. Gupta, N.R. Choudhury, V.G. Malathi, A. Varma and S. Mukherjee, 2001. Molecular characterization of the Rep protein of the blackgram isolate of Indian mungbean yellow mosaic virus. J. Gen. Virol., 82: 2559-2567.

Prajapat, R., R.K. Gaur, R. Raizada and V.K. Gupta, 2010. *In silico* analysis of genetic diversity of begomovirus using homology modelling. J. Biol. Sci., 10: 217-223.

Prajapat, R., V. Bajpai and R.K. Gaur, 2011. Structural modeling and validation of rep protein of begomovirus strains (TLCBV and TYLCTHV). Nature Publishing Group. http://precedings.nature.com/documents/5617/version/1.

Ritchie, D.W., D. Kozakov and S. Vajda, 2008. Accelerating protein-protein docking correlations using a six-dimensional analytic FFT generating function. Bioinformatics, 24: 1865-1873.

Stanley, J., D.M. Bisaro, R.W. Briddon, J.K. Brown and C.M. Fauquet *et al.*, 2005. Family geminiviridae. In Virus Taxonomy: Eighth Report of the International Committee on Taxonomy of Viruses.

Xiao, J.F., Z.S. Li, M. Sun, Y. Zhang and C.C. Sun, 2004. Homology modeling and molecular dynamics study of GSK3/SHAGGY-like kinase. Comput. Biol. Chem., 28: 179-188.