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IN SILICO STUDIES ON DENGUE AND LASSA VIRAL PROTEINS WITH SELECTED AZADIRACHTA INDICA LEAVES CONSTITUENTS

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ABSTRACT

Dengue virus contains seven proteins and Lassa virus contains four proteins, which are considered to be most effective for drug designing. Recent studies have shown that these proteins can effectively inactivate the dengue and lassa diseases in humans. *Azadirachta indica* phytochemicals are found to have anti cancer and anti-bacterial properties. In the particular study, the binding efficiency of five compounds that are present in the *Azadirachta indica* with all the eleven proteins through in silico methods was carried out. By our virtual screening and molecular docking result, we found that the 9,12,15 - Octadecatrienoic acid,(Z,Z,Z) and 8,11,14- Eicosatrienoic acid have highest binding affinities with the proteins and we also predicted the amino acid residues in the binding site and the type of hydrogen bonding.

KEYWORDS: Neem, molecular docking, hydrogen bonding, 9, 12, 15 - Octadecatrienoic acid, 8, 11, 14- Eicosatrienoic acid.

1. INTRODUCTION

Neem tree belongs to the family Meliaceae which is found abundance in tropical and semitropical regions like India, Pakistan, Nepal and Bangladesh. It is a fast-growing tree with

20–23 m tall, straight trunk and has a diameter around 4-5 ft. The Latinized name of the neem is derived from the Parsian,'' *Azadirachta indica*''.[1] Therapeutic properties of neem (*Azadirachta indica*) have been recognized since ancient times and have been extensively used in ayurveda, unani, and homoeopathic medicine.[2] Recent studies have shown that neem possesses anti-inflammatory, antiarthritic, antipyretic, hypoglycemic, antigastric ulcer, antifungal, antibacterial, and antitumor activities.[3-7] Neem-coated urea is being used in India as an alternate to plain urea fertilizer. It decreases the pollution, improves fertilizer's efficacy and soil health.[8,9] More than 140 compounds have been isolated from different parts of *Azadirachta indica*. There leaves, seeds, roots, fruits, flowers and bark have been used traditionally for the treatment of different disease.

GC-MS chromatogram of the methanolic extract of *Azadirachta indica* showed five major peaks indicating the presence of five phytocomponents. From the results, it was observed that presence of 3, 7, 11, 15-tetramethyl-2-hexadecen-1-ol (synonym:Phytol), 9,12,15-Octadecatrienoic acid(synonym: Linolenic acid; α-Linolenic acid), Tridecanoic acid (synonym:Tridecylic acid) 8,11, 14-Eicosatrienoic acid (Synonym: Homo-γ-linolenic acid), and N-Hexadecanoicacid (synonym:Palmitic acid) were the major.[8] Phytol posses anti-diuretic, antioxidant, anticancer property. Linolenic acid shows Antibacterial and Antifungal properties, Palmitic acid Hypercholesterolemic, Pesticide, antialopecic, antiandrogenic Homo-γ-linolenic acid has Anti-inflammatory and Anticoagulant property.[9]

Dengue is a mosquito-borne viral infection it causes a severe flu-like illness and, sometimes it causes a potentially lethal complication called severe dengue. The incidence of dengue has increased 30-fold over the last 50 years. It is a single positive-stranded RNA virus of the family *Flaviviridae*; genus *Flavivirus*. Four serotypes (DENV-1, DENV-2, DENV-3 and DENV-4)[10] of the virus have been found, all of which can cause the full spectrum of disease.[11] Dengue virus infection presents with a diverse clinical picture that ranges from asymptomatic illness to DF to the severe illness of dengue hemorrhagic fever/dengue shock syndrome (DHF/DSS)[12] Dengue virus gains entry into the host organism through the skin as per an infected mosquito bite. Onset of symptoms is characterized by a biphasic, high-grade fever lasting for 3 days to 1 week.[13,14] Dengue is found in tropical and sub-tropical climates worldwide, mostly in urban and semi-urban areas.[15] Dengue virus has 10 protiens,out of which 3 proteins are structural and 7 proteins are non structural.[16]

The structural protein of dengue virus is the Envelope protein which is involved in the viral assembly. The capsid protein used for this study was from dengue virus type 2 (strain Puerto Rico/PR159-S1/ 1969).[17] It is one of the structural proteins, which is involved in the encapsidation of the viral genome. The RNA – dependent – RNA - polymerase (RdRp) domain of the NS5 protein is a main protein which is involved in the viral genome replication. RNA is synthesized via "de novo" by NS5 protein.[18]

The non structural proteins are NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5, expressed in the host cells that are not incorporated in the viral particle. With the help of host proteins, NS proteins mature the polyprotein,reshape the inner organization of the cell, replicate the viral RNA and help the virus evade the immune system. The integral membrane proteins are NS2A, NS2B, NS4A, NS4B which are important for viral replication.NS1 has different oligomerization states dependent on its glycosylation status[19,20,21]

Lassa virus (**LASV**) belongs to the family arenaviridae and genus arena virus that causes Lassa hemorrhagic fever,[22] a type of viral hemorrhagic fever (VHF), in humans and other primates. It is very common \ in West African countries, especially Sierra Leone, the Republic of Guinea, Liberia and Nigeria, where the annual incidence of infection is between 300,000 and 500,000 cases, resulting in 5,000 deaths per year.[23] Lassa virus genome is bisegmented, single-stranded negative-sense RNA. Their genome is contained in two RNA segments that code for two proteins each, so there are total of four viral proteins.[24] The four proteins are nucleoprotein, glycoprotein, zinc-binding protein and RNA polymerase. The small segment encodes the surface glycoprotein precursor (GP) and the nucleoprotein (NP), the glycoprotein precursor is proteolytically cleaved into the envelope glycoproteins GP1 and GP2 that bind to the alpha-dystroglycan receptor and mediate host cell entry.[25] The large segment encodes a small zinc-binding protein (Z) that regulates transcription and replication,[26][27] and the RNA polymerase (L).

Bioinformatics is an interdisciplinary branch of science which consists and uses statistics, computer and mathematics to analyze the biological data [28]. Bioinformatics is now utilized for many research aspects such as evolution. Protein Data Bank (PDB) is a protein storage bioinformatics tool. It contains the structures of large numbers of proteins, ligands and other macromolecules.[29] Docking analysis could be conducted for the protein and the ligand to analyze the fitness and the interaction with each other in the form of binding energy. This interaction could be used as the pharmaceutical approach for drug production.[30] The aim of

our study is to compare the best docking fit for the selected *Azadirachta indica* leaves constituents with the Dengue and Lassa viral proteins.

2. MATERIALS AND METHODOLOGIES

2.1. Preparation of viral proteins

The protein data bank (PDB) that contains large number of proteins which are experimentally determined and stored, was used to obtain the three-dimensional structure of the macromolecule. PDB The structures are downloaded and saved either in mm CIF or PDB format. Proteins of dengue and lassa virus were used for this study. The 3D structure of all the eleven proteins were downloaded from PDB and saved in PDB format. Only those proteins are downloaded and docked which have PDB ID. The downloaded proteins were viewed in Py-Mol viewer.[31]

2.2. Preparation of ligands

Ligands selected were from the previous studies on GCMS analysis on *Azadirachta indica* leaves extract.[32] 5 ligands were used for the study. Ligands were constructed using ChemSketch.[33] The constructed ligands were optimized to add the hydrogen bonds and the obtained structures were saved in mol for docking analysis and named as A, B and C respectively.

2.3. Docking study

Docking studies were conducting using iGEMDOCK software. IGEMDOCK (Generic Evolutionary Method for molecular Docking) is a graphical-automatic drug design system for docking, screening and post-analysis [34]. The proteins and the ligands were loaded and the out path was set. Standard docking parameters like (population size=200, Number of solutions =2 and generations =70) were used for docking. The docking processwas initiated. After the docking process, the best docking pose can be obtained for all the seven individual ligands of dengue viral proteins. The binding affinities of the compounds the binding pose and the total binding energy values that are best were saved in the output folder. The saved files were visualized in Py-Mol viewer.

3. RESULTS

3.1. Total Binding Energy (kcal/mol) profile for Dengue and Lassa viruses proteins with 5 ligands.

Table 1: **The Total Binding Energy (kcal/mol) profile for Dengue and Lassa viruses non structural proteins with 5 ligands.**

Ligand	Compound name	Dengue Virus					Lassa virus	
		NS1 protein	Transmembrane domain of NS2A	NS2 /NS3 protease	NS3 helicase	NS5 protein	Zn-binding protein	RNA polymerase
A	9,12,15-Octadecatrienoic acid,(Z,Z,Z)-	-90.76	-566.06	-85.18	-113.9	-98.33	-96.79	-81.83
B	3,7,11,15- tetramethyl-2-hexadecen-1-ol	-83.79	-568.42	-79.91	-83.61	-91.27	-75.52	-84.26
C	8,11,14- Eicosatrienoic acid	-110.14	-621.4	-90.77	-112.51	-91.1	-75.64	-85.93
D	Tridecanoic acid	-81.17	-591.3	-64.49	-83.72	-80.19	-74.91	-74.43
E	N-Hexadeconoic acid	-93.03	-583.09	-88.36	-78.83	-90.99	-90.79	-90.74

Table – 2: The Total Binding Energy (kcal/mol) profile for Dengue and Lassa viruses structural proteins with 5 ligands.

Ligand	Compound name	Dengue virus		Lassa virus	
		Capsid protein	Envelope protein	Nucleoprotein	Glycoprotin
A	9,12,15-Octadecatrienoic acid,(Z,Z,Z)-	-84.19	-90.22	-95.67	-84.95
B	3,7,11,15- tetramethyl-2-hexadecen-1-ol	-84.23	-88.04	-81.69	-76.22
C	8,11,14- Eicosatrienoic acid	-101.08	-97.79	-89.7	-77.48
D	Tridecanoic acid	-74.89	-75.95	-76.92	-66.29
E	N-Hexadeconoic acid	-81.74	-90.85	-90.53	-72.34

3.2. H – Bond profile for Dengue and Lassa viruses protein with 5 ligands.

Table 3: H – Bond profile for Dengue and Lassa viruses non structural proteins with 5 ligands.

Ligand	Compound name	Dengue virus					Lassa virus	
		NS1 protein	Trans membrane domain of NS2A	NS2B / NS3 protease	NS3 helicase	NS5 protein	Zn-binding protein	RNA polymerase
A	9,12,15-Octadecatrienoic acid,(Z,Z,Z)-	H-S	-	H-S	H-M H-S	H-M H-S	H-M	H-M H-S
B	3,7,11,15- tetramethyl-2-hexadecen-1-ol	H-M H-S	-	H-M H-S	H-S	H-M	H-M	H-M H-S
C	8,11,14- Eicosatrienoic acid	H-M H-S	H-S	H-S	H-S	H-S	-	H-M H-S
D	Tridecanoic acid	H-M H-S	H-S	H-M	H-M H-S	H-S	H-M	H-M H-S
E	N-Hexadeconoic acid	H-M H-S	-	H-M	H-S	H-S	H-M	H-M H-S

Table – 4: H – bond profile for Dengue and Lassa viruses structural proteins with 5 ligands.

Ligand	Compound name	Dengue virus		Lassa virus	
		Capsid protein	Envelope protein	Nucleoprotein	Glycoprotein
A	9,12,15-Octadecatrienoic acid,(Z,Z,Z)-	H-M H-S	H-S	H-S	H-M
B	3,7,11,15- tetramethyl-2-hexadecen-1-ol	H-M H-S	H-M	H-M	H-M
C	8,11,14- Eicosatrienoic acid	H-M H-S	H-M H-S	H-S	H-S
D	Tridecanoic acid	H-M H-S	H-S	H-M H-S	H-M
E	N-Hexadeconoic acid	H-M H-S	H-S	H-M H-S	H-M H-S

3.3. Amino acid position profile for Dengue and Lassa viruses protein with 5 ligands

Table 5: Amino acid position profile for Dengue and Lassa viruses non structural proteins with 5 ligands.

Ligand	Compound name	Dengue Virus					Lassa virus	
		NS1 protein	Transmembrane domain of NS2A	NS2 /NS3 protease	NS3 helicase	NS5 protein	Zn-binding protein	RNA polymerase
A	9,12,15-Octadecatrienoic acid,(Z,Z,Z)-	Lys(206)	-	Thr(118)	Lys(199)	Gly(86)	Gly(27)	Thr(80)
B	3,7,11,15- tetramethyl-2-hexadecen-1-ol	IIe(242) Lys(206)	-	Asn(152)	Arg(458)	Met(342)	Leu(57) Arg(63)	Phe(147) Arg(161)
C	8,11,14- Eicosatrienoic acid	IIe(242) Ser(252)	Thr(7)	Lys(74)	Arg(458)	Lys(355)	-	Arg(106)
D	Tridecanoic acid	Ser(252) Asn(225)	Asp(1)	IIe(30) Leu(31)	Arg(418)	Arg(211)	Gly(27)	Asp(18) Asp(19)
E	N-Hexadeconoic acid	Lys(206) IIe(242)	-	Val(146)	Arg(530)	Lys(253)	Gly(27)	His(76)

Table 6: **Amino acid position profile for Dengue and Lassa viruses structural proteins with 5 ligands.**

Ligand	Compound name	Dengue virus		Lassa virus	
		Capsid protein	Envelope protein	Nucleoprotein	Glycoprotin
A	9,12,15-Octadecatrienoic acid,(Z,Z,Z)-	Lys(76) Arg(55)	Lys(613)	Asp(105)	Lys(88)
B	3,7,11,15- tetramethyl-2-hexadecen-1-ol	Thr(25) Glu(87)	Pro(635)	Phe(176)	Asn(89) Asn(90)
C	8,11,14- Eicosatrienoic acid	Asn(21) Arg(68)	Thr(579) Asn(663)	Arg(492)	Asp(89)
D	Tridecanoic acid	Ala(77) Lys(45)	Arg(619)	Arg(323)	Lys(88)
E	N-Hexadeconoic acid	Arg(22) Arg(68)	Arg(619)	Thr(178)	Gly(198)

4. DISCUSSION

Considering all the tables from Table 1 to Table 6, the 3D structure coordinates of seven non proteins of Dengue and four proteins of Lassa viruses are optimized and 5 compounds from *Azadirachta indica* leaves extract are identified. The total binding energy of the compounds with all the eleven proteins was calculated using iGEMDOCK. Evaluations of binding conformation of these 5 compounds with seven Dengue as well as four Lassa viral proteins are performed using iGEMDOCK. From docking study, we listed binding affinities of 5 compounds based on ligand binding energy (Table- 1 and Table - 2). The binding pose for each ligand molecule into the Dengue and Lassa viral proteins are analyzed and the one having lowest ligand binding energy with these proteins among the different poses are generated. The lower energy scores represent better protein-ligand target binding affinity compared to higher energy score. Considering the structural proteins of Dengue virus, among the 5 analogs, compound "C" is found to have lower ligand binding energy (binding energy value = -97.79 kcal/mol), than other analogs for Envelope protein. Compound "C" has least binding energy score with capsid protein (binding energy value = -101.08 kcal/mol), the structural proteins of Lassa virus had following binding energies, Nucleoprotein ('A' binding energy value = -95.67kcal/mol), Glycoprotein ('A', binding energy value = -84.95kcal/mol). The non structural proteins of Dengue virus had these binding energy values: Trans membrane domain of NS2A ('C', binding energy value= -621.4kcal/mol), NS2B / NS3 protease ('C', binding energy value = -90.77kcal/mol), NS3 helicase ('A', binding energy value = -113.9kcal/mol), NS5 protein ('A', binding energy value= -98.33 kcal/mol) and NS1 protein ('C', binding energy value = -110.4kcal/mol). And the non structural proteins of Lassa viruses have, Zinc binding protein ('A', binding energy value = -96.79kcal/mol) and RNA polymerase ('E', binding energy value = -90.74kcal/mol). We further analyzed the docked pose for finding the binding mode of compound "A" and compound "C" in to seven dengue and four Lassa viral proteins to validate the reasonable binding conformations.

4.1. Non-Structural proteins of Dengue Virus:

4.1.1. The Total Binding Energy for Dengue virus NS1 protein with 5 ligands

From Table – 1, Table – 3 and Table – 5, the docking simulation of 5 ligands were performed for Dengue virus NS1 protein. From the docking study, we observed that compound-C has best binding affinity with the target NS1 protein with the binding energy value of -110.14kcal/mol. Interaction analysis of binding mode of compound –C in dengue virus NS1 protein reveals that it forms two hydrogen bonds with low energy, with Ile(242) and

Ser(252). A close-up view of the Total Binding Energy (kcal/mol) profile for Dengue virus NS1 protein with 5 ligands: is shown in Fig.1.

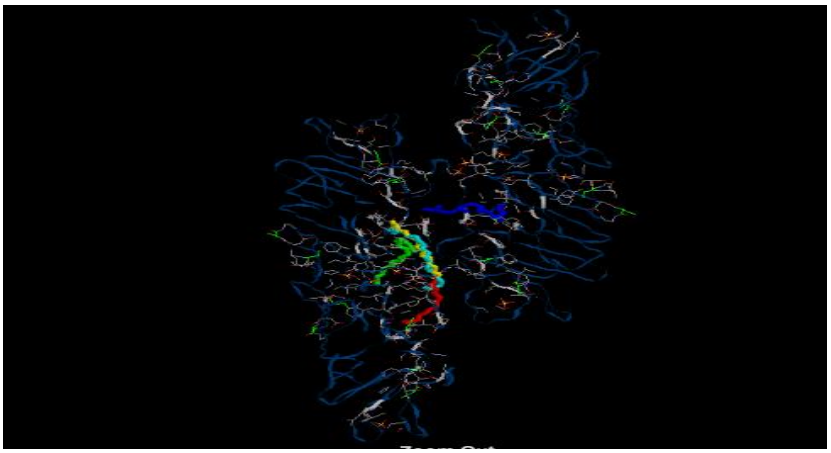

Fig.1: The Total Binding Energy profile for Dengue virus NS1 protein with 5 ligands.

4.1.2. The Total Binding Energy for Dengue virus Trans membrane domain of NS2A with 5 ligands

From Table – 1, Table – 3 and Table – 5, the docking simulation of 3 ligands were performed for Dengue virus Trans membrane domain of NS2A. From the docking study, we observed that compound – C has best binding affinity with the target Trans membrane domain of NS2A with the binding energy value of -621.4 kcal/mol. Interaction analysis of binding mode of compound -C in dengue virus Trans membrane domain of NS2A reveals that it forms one hydrogen bond with low energy, with Thr (7) A close-up view of the Total Binding Energy (kcal/mol) profile for Dengue virus Trans membrane domain of NS2A with 5 ligands: is shown in Fig.2.

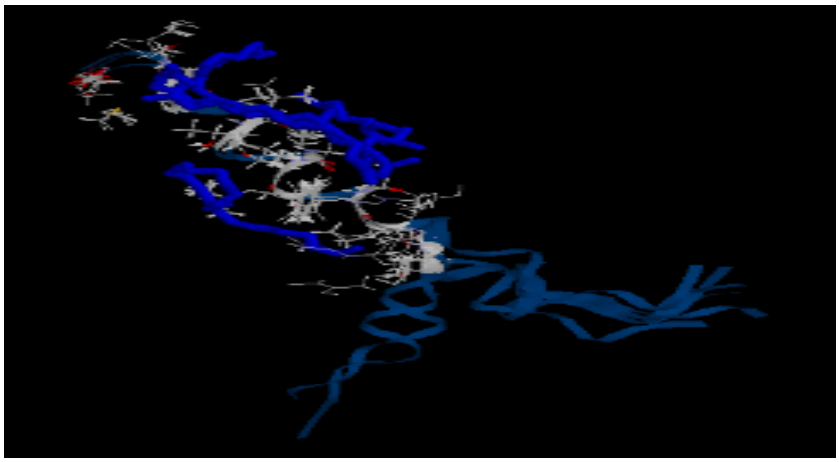

Fig.2: The Total Binding Energy profile for Dengue virus Trans membrane domain of NS2A with 5 ligand.

4.1.3. The Total Binding Energy for Dengue virus NS2B / NS3 protease with 5 ligands

From Table – 1, Table – 3 and Table – 5, the docking simulation of 5 ligands were performed for Dengue virus NS2B / NS3 protease. From the docking study, we observed that compound – C has best binding affinity with the target NS2B / NS3 protease with the binding energy value of -90.77 kcal/mol. Interaction analysis of binding mode of compound –C in dengue virus NS2B / NS3 protease reveals that it forms one hydrogen bond with low energy, with Lys(74). A close-up view of the Total Binding Energy (kcal/mol) profile for Dengue virus NS2B /NS3 protease with 5 ligands: is shown in Fig.3.

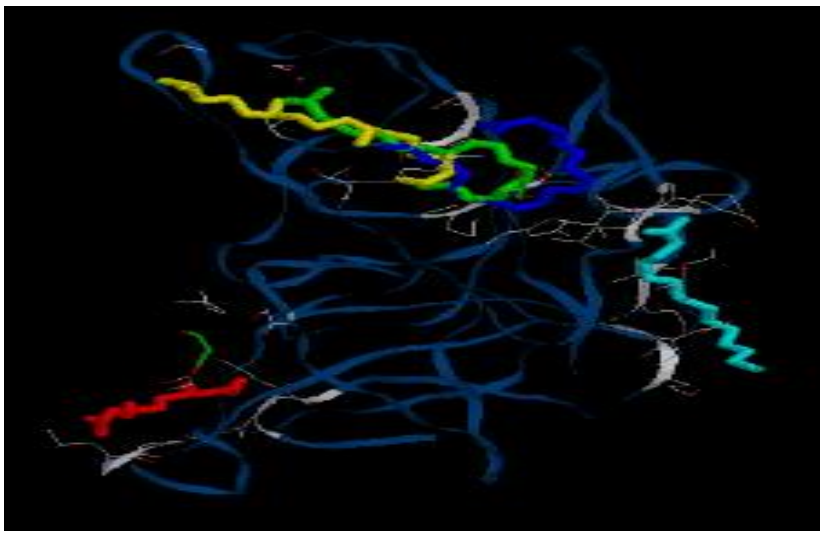

Fig.3: The Total Binding Energy profile for Dengue virus NS2B / NS3 protease with 5 ligands.

4.1.4. The Total Binding Energy for Dengue virus NS3 helicase with 5 ligands

From Table – 1, Table – 3 and Table – 5, the docking simulation of 5 ligands were performed for Dengue virus NS3 helicase. From the docking study, we observed that compound – A has best binding affinity with the target NS3 helicase with the binding energy value of -113.9 kcal/mol. Interaction analysis of binding mode of compound –A in dengue virus NS3 helicase reveals that it forms two hydrogen bonds with low energy, with(Lys199). A close-up view of the Total Binding Energy (kcal/mol) profile for Dengue virus NS3 helicase with 5 ligands: is shown in Fig.4.

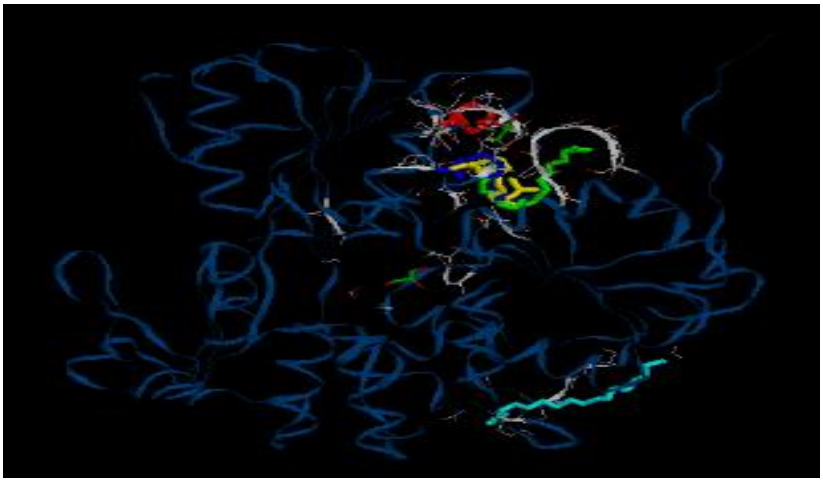

Fig.4: The Total Binding Energy profile for Dengue virus NS3 helicase with 5 ligands.

4.1.5. The Total Binding Energy for Dengue virus NS5 protein with 5 ligands

From Table – 1, Table – 3 and Table – 5, the docking simulation of 5 ligands were performed for Dengue virus NS5 protein. From the docking study, we observed that compound – A has best binding affinity with the target NS5 protein with the binding energy value of -98.33kcal/mol. Interaction analysis of binding mode of compound –A in dengue virus NS5 protein reveals that it forms two hydrogen bonds with low energy, with Gly(86). A close-up view of the Total Binding Energy (kcal/mol) profile for Dengue virus NS5 protein with 5 ligands: is shown in Fig.5

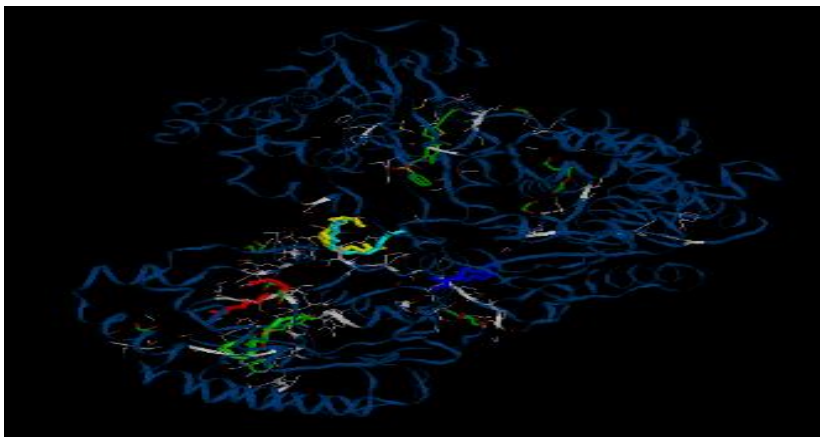

Fig.5: The Total Binding Energy profile for Dengue virus NS5 protein with 5 ligands.

4.2. Non-Structural proteins of Lassa virus

4.2.1.The Total Binding Energy for Lassa virus Zinc binding protein with 5 ligands

From Table – 1, Table – 3 and Table – 5, the docking simulation of 5 ligands were performed for Lassa virus Zinc binding protein. From the docking study, we observed that compounds – A has best binding affinity with the target protein Zinc binding protein with the binding

energy values of -96.79 kcal/mol. Interaction analysis of binding mode of compounds – A in Lassa virus Zinc binding protein reveals that it forms one hydrogen bond with low energy, with Gly(27). A close-up view of the Total Binding Energy (kcal/mol) profile for Lassa virus Zinc binding protein with 5 ligands: is shown in Fig.6.

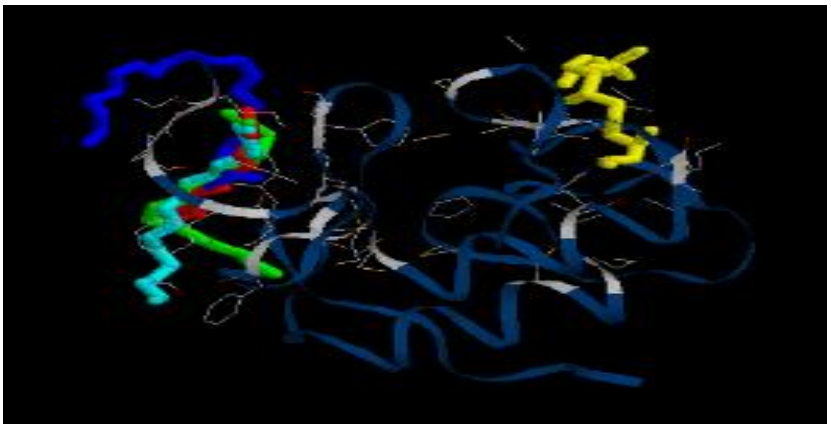

Fig.6: The Total Binding Energy profile for Lassa virus Zinc binding protein with 5 ligands.

4.2.2.Total Binding Energy for Lassa virus RNA polymerase with 5 ligands

From Table – 1, Table – 3 and Table – 5, the docking simulation of 5 ligands were performed for Lassa virus RNA polymerase. From the docking study, we observed that compounds – E has best binding affinity with the target protein RNA polymerase with the binding energy values of -90.74 kcal/mol. Interaction analysis of binding mode of compounds – E in Lassa virus protein RNA polymerase reveals that it forms two hydrogen bond with low energy, with His (76).A close-up view of the Total Binding Energy (kcal/mol) profile for Lassa virus RNA polymerase protein with 5 ligands: is shown in Fig.7.

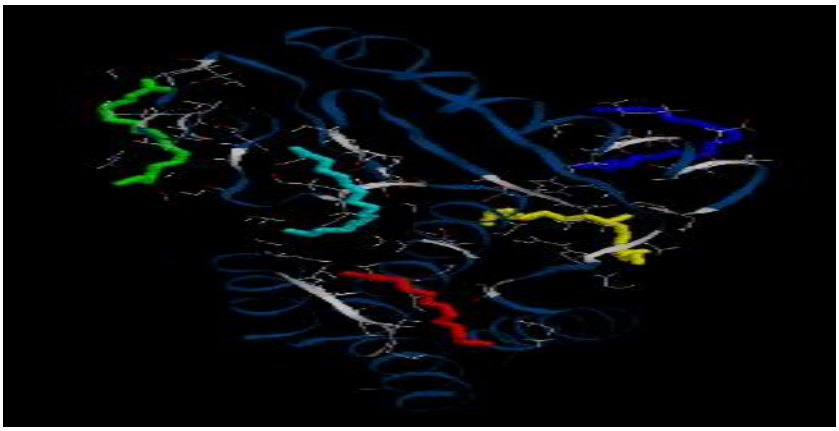

Fig.7: The Total Binding Energy profile for Lassa virus RNA polymerase protein with 5 ligands.

4.3. Structural proteins of Dengue virus

4.3.1. The Total Binding Energy for Dengue virus Capsid protein with 5 ligands

From Table – 2, Table – 4 and Table – 6, the docking simulation of 5 ligands were performed for Dengue virus Capsid protein. From the docking study, we observed that compound – C has best binding affinity with the target Capsid protein with the binding energy value of -101.08 kcal/mol. Interaction analysis of binding mode of compound –C in dengue virus Capsid protein reveals that it forms two hydrogen bonds with low energy, with Asn(21) and Arg(68) residue. A close-up view of the Total Binding Energy (kcal/mol) profile for Dengue virus Capsid protein with 5 ligands: is shown in Fig.8

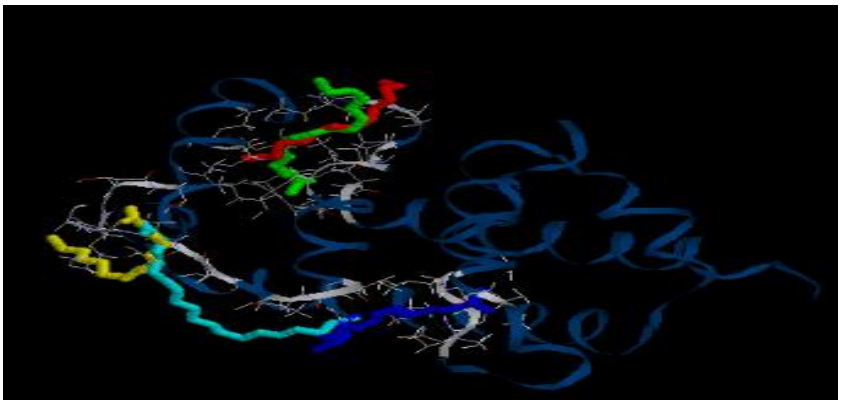

Fig.8: The Total Binding Energy (kcal/mol) profile for Dengue virus Capsid protein with 5 ligands.

4.3.2. The Total Binding Energy for Dengue virus envelope protein with 5 ligands

From Table – 2, Table – 4 and Table – 6, the docking simulation of 5 ligands were performed for Dengue virus envelope protein. From the docking study, we observed that compound – C has best binding affinity with the target envelope protein with the binding energy value of -97.79 kcal/mol. Interaction analysis of binding mode of compound – C in dengue virus envelope protein reveals that it forms two hydrogen bond with low energy, with Thr(579) and Asn(663) residue. A close-up view of the Total Binding Energy (kcal/mol) profile for Dengue virus envelope protein with 5 ligands: is shown in Fig.9.

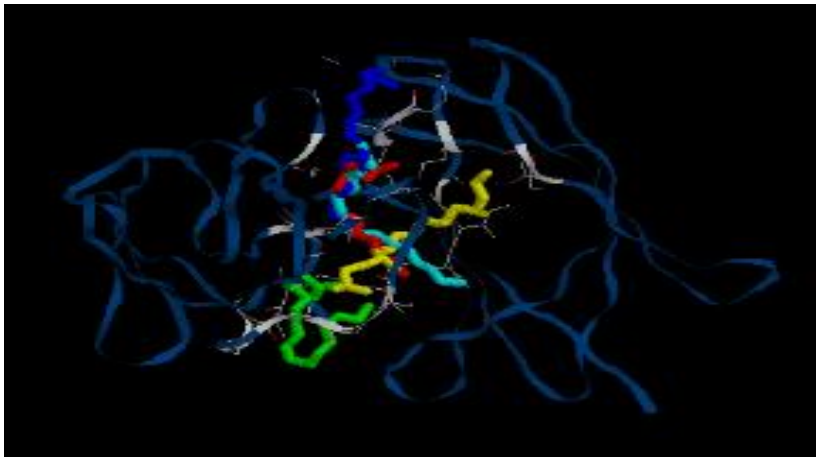

Fig.9: The Total Binding Energy profile for Dengue virus envelope protein with 5 ligands.

4.4. Structural proteins of Lassa virus

4.4.1. The Total Binding Energy for Lassa virus Nucleoprotein with 5 ligands

From Table – 2, Table – 4 and Table – 6, the docking simulation of 5 ligands were performed for Lassa virus Nucleoprotein. From the docking study, we observed that compound – A has best binding affinity with the target Nucleoprotein with the binding energy value of -95.67kcal/mol. Interaction analysis of binding mode of compound –A in Lassa virus Nucleoprotein reveals that it forms one hydrogen bond with low energy, with Asp(105) residue. A close-up view of the Total Binding Energy (kcal/mol) profile for Lassa virus Nucleoprotein with 5 ligands: is shown in Fig.10

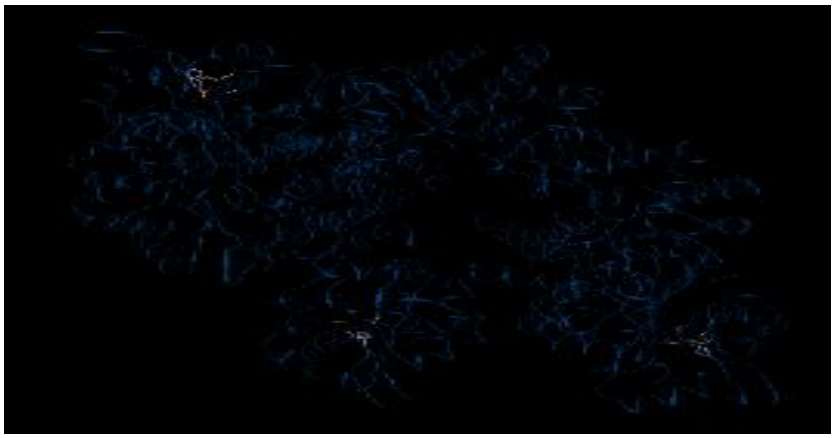

Fig.10: The Total Binding Energy profile for Lassa **virus Nucleoprotein with 5 ligands.**

4.4.2. The Total Binding Energy for Lassa virus Glycoprotein with 5 ligands

From Table – 2, Table – 4 and Table – 6, the docking simulation of 5 ligands were performed for Lassa virus Glycoprotein. From the docking study, we observed that compound – A has

best binding affinity with the target Glycoprotein with the binding energy value of -84.95kcal/mol. Interaction analysis of binding mode of compound –A in Lassa virus Glycoprotein reveals that it forms on hydrogen bonds with low energy, with Lys(88) residue. A close-up view of the Total Binding Energy (kcal/mol) profile for Lassa virus Glycoprotein with 5 ligands: is shown in Fig.11.

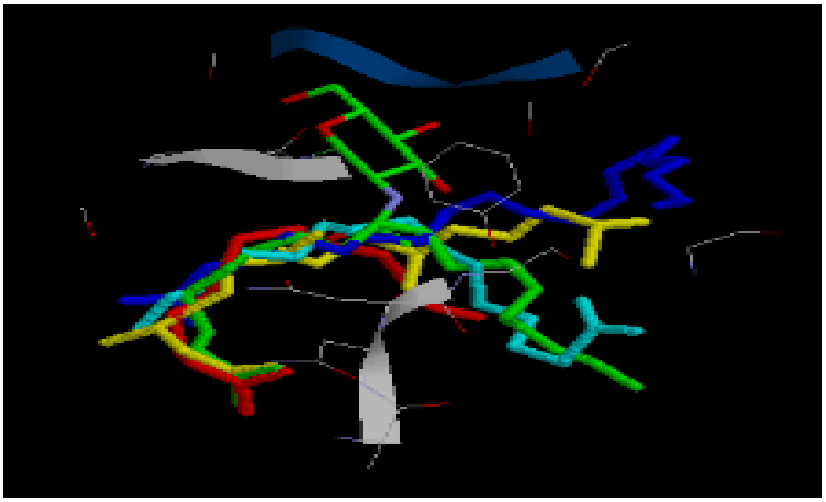

Fig.11: The Total Binding Energy profile for Lassa virus with 5 ligands.

5. CONCLUSION

Our molecular docking studies explored the possible binding modes of 5 compounds that are present in *Azadirachta indica* leaf with seven proteins of Dengue virus and four proteins of Lassa virus. Dengue virus consists of envelope protein, NS1 protein, Transmembrane doamin of NS2A, NS2B/NS3 protease, NS3 helicase, NS5 protein and capsid protein; Lassa virus consists of Glycoprotein, Nucleoprotein, Zinc binding protein,RNA polymerase- 1 protein. It revealed that all the 5 compounds show minimum affinity with all the proteins. The compound 'C' (8, 11, 14- Eicosatrienoic acid) and compound 'A' (9, 12, 15-Octadecatrienoicacid(Z,Z,Z))) shows best results compared to other compounds. On comparing the binding energy and the binding site residues, we found that all the compounds will differ in either of them for hydrogen bond formation. The conclusion which is drawn from our virtual screening and docking result are that the Compound C has highest binding affinity with the structural proteins of Dengue virus and compound A has the highest binding affinity with majority of the structural proteins of Lassa virus. Whereas the compound C is shown to have highest binding affinity with most of the non structural proteins of Dengue virus and the non structural proteins of Lassa virus has highest binding affinities with compound A and therefore it can be used as an effective drug target for Dengue virus as well

as Lassa virus. Hence, the Compound C and A may be considered as the effective drug target for both dengue and Lassa virus because it can effectively bind to most of the proteins of both the viruses. Though, there are many reports on the *in vitro* analysis of these compounds and its medicinal and toxic properties, there are no in silico studies that predict the binding and active regions especially with these proteins. Our study is an attempt to predict the binding site and the binding residues. However, validation of our results through *invivo* and *invitro* experiments and also with animal models will enlighten hope for the future development of more potent drugs for the treating Dengue and Lassa.

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