ESTABLISHING NOVEL DRUG LEADS OF MONKEYPOX VIRAL RECEPTOR USING HIGH-THROUGHPUT SCREENING FROM MEDICINAL HERBS

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ABSTRACT

Introduction: Monkeypox virus (MPV or MPXV), is a double- stranded DNA virus that is caused by the monkeypox virus, which comes from the family *Poxviridae* and genus *Orthopoxvirus* the name was given after isolating it from monkeys . It is oval like shaped structure with a outer membrane of lipoprotein. Its genome is approximately around 200kb long chain coding for approximately 200 proteins, it is similar to the smallpox virus with milder rash and lower mortality rate. It has two clades which was isolated and observed in Central Africa, where the strains are more virulent than the second clade that is Western Africa. Monkeypox is although a DNA viruses, they avoid the host cell's nucleus completely, conducting all of their genome replication, transcription, translation and new virus assembly in the host cell cytoplasm.

Methodology: The FASTA/ FASTQ sequence of the (gene: BR209) was retrieved from SRA database to galaxy and the sequence quality was checked using FASTQC tool. Further, we modelled the 3D structure of the FASTA protein sequence using modeller. The best model was selected using Ramchandran plot. Phytocompounds from medicinal plants like (*Tinospora cordifolia, Aegle marmelos, Gmelina arborea, Oroxylum indicum, Premna serratifotia, Solanum indicum*) was considered as novel drug leads is retrieved from PUBCHEM databases. The phytocompounds are checked for drug- like properties using molinspiration software. The compounds having so violations were considered for further docking studies.

Results: The phytocompounds having least docking score and most interactions is considered as the drug lead for Monkeypox virus. Further receptor ligand binding assay studies will be done to establish the compound as drug for the above disease.

Keywords:- *Monkeypox, Phytocompounds, Novel drug, Virus, Monkey*

INTRODUCTION

Monkey pox is a rare disease caused by infection with the monkey pox virus. Monkey pox virus falls in the same family of variola virus (Xiang and White, 2022). It is also known as viral zoonosis (a virus transmitted to humans from animals) (Moore et. al., 2022). Monkeypox virus is an enveloped double – stranded DNA virus that belongs to the *Orthopoxvirus* genus of the *Poxviridae* family (Lansiaux et. al., 2022). The first Human monkeypox was identified in 1970 at the Democratic Republic of the Congo in a 9-month-old boy in a region where smallpox had been eliminated in 1968 (Ladnyj et. al., 1972). Monkeypox is a disease which is similar to smallpox and chickenpox but the protein receptor acting on it makes it different, BR-203 and BR-209 are the two receptor which are not in small pox (Weaver and Issacs, 2008). Since then, most cases have been reported from rural, rainforest regions of the Congo Basin, particularly in

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the Democratic Republic of the Congo and human cases have increasingly been reported from across central and West Africa. There are two distinct genetic clades of the monkeypox virus: the central African (Congo Basin) clade and the west African clade (Kindrachuk, *et. al.,* 2012). The congo basin clade has historically caused more severe disease and was thought to be more transmissible (Sunder Sham et al., 2022). The transmission is believed to occur via saliva/respiratory excretions or contact with lesion exudate or crust material (Miaojin Zhu et. al., 2022). As per clinical studies it is seen that monkey pox virus closely resembles the one of smallpox but the major difference seen in monkey pox virus is the lymph node enlargement that occurs early, often at the onset of fever (Sklenovská and Van Ranst, 2018).

The clades of Monkeypox Virus

Experts in pox virology, evolutionary biology and representatives of research institutes from across the globe reviewed the phylogeny and nomenclature of the known and new monkeypox virus variants or clades (WHO, 2022). The discussed the characteristics and evolution of monkeypox virus variants, their apparent phylogenetic and clinical differences, and potential consequences for public health and future virological and evolutionary research (Sklenovská and Van Ranst, 2018).

The researches reached consensus on new nomenclature for the virus clades that is in line with best practices. They agreed on how the virus clades should be recorded and classified on genome sequence repository sites (www.ncbi.nlm.nih.gov).

Consensus was reached to now refer to the former Congo Basin (Central African) clade as Clade one (I) and the former West African clade as Clade two (II). Additionally, it was agreed that the Clade II consists of two subclades (www.ncbi.nlm.nih.gov).

Gene involved

1. **BR-203:** BR-203's encoded protein has a role in avoiding apoptosis of infected lymphocytes (Hendrickson et.al. 2010; Weaver and Isaacs, 2008).
2. **BR-209: BR-209** encodes a 326 aa protein that functions as an interleukin-1β (IL-1β) binding protein that prevents IL-1β from binding to the IL-1 receptor (Jessica R., 2008)

There are 5 stages of monkeypox:

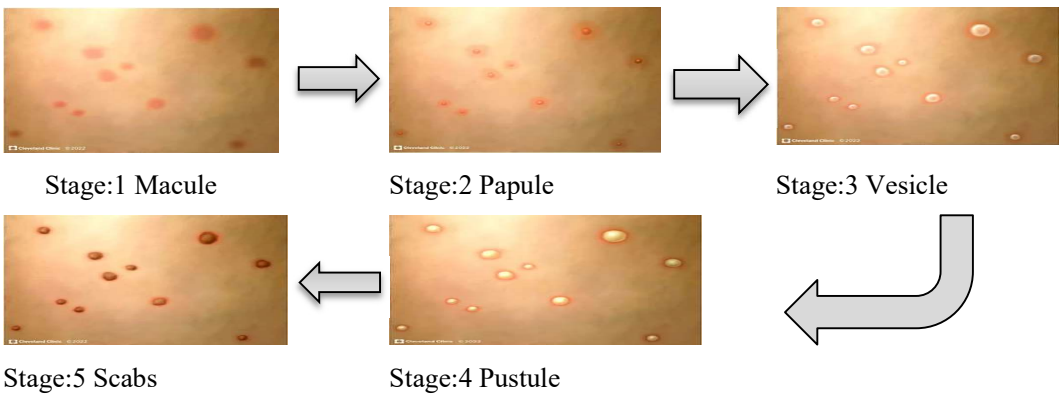


Fig. 1 Stages of monkeypox (clevelandclinic.org; cdc.gov)

Stage 1: Macule - The rash starts as flat, red spots (last for 1-2 days).

Stage 2: Papule – The spots become hard, raised bumps (lasts for 1-2 days)

Stage 3: Vesicle –The bumps get larger. They look like blisters filled with clear fluid (lasts for 1-2 days)

Stage 4: Pustule –The blisters fill with pus (lasts for 5-7 days)

Stage 5: Scabs –The spots crust over and become scabs that eventually fall off (lasts for 7- 14 days)

METHODOGY:

The FASTA sequence of the receptor proteins BR 203 and BR 209 were retrieved. Their 3d structures were modelled using MODELLER (Webb B and Sali, 2016). Their template information was obtained using BLAST and 3d structures were downloaded from RCSB PDB. Modeller generated 5 modes. The generated models were verified using Ramachandran Plot (Willard et. al., 2003). The best model was selected for further docking studies.

The traditional plants were considered as therpeutics for the disease.

Phytocompounds from medicinal plants *Tinospora cordifolia, Aegle marmelos, Gmelina arborea, Oroxylum indicum, Premna serratifotia, Solanum indicum* were selected and their SMILES was retrieved from PUBCHEM database. The phytocompounds were studied and selected using Lipinski's rule of five by using Molinspiration (molinspiration) software. The selected compounds were docked using docking server (Bikadi and Hazai, 2009).

RESULTS

Homology modelling of the receptors were modelled using modeller. The template information was retrieved using BLAST (Table 1).

Gene receptor	Accession id of the receptor	Identified homologous templates using BLAST
BR-203	SRR18666718	1E8SS 1E80E 4UE5E
BR-209	SRR18666719	2FFKA 2GRKA 1CQ3A

The Ramachandran Plot analysis of the modeller generated models is given in Table 2 and Fig. 2.

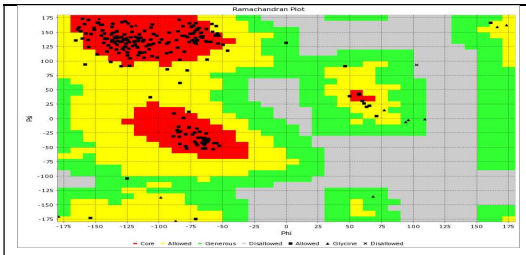
Table 2 (a): Ramachandran Plot analysis of MPXV

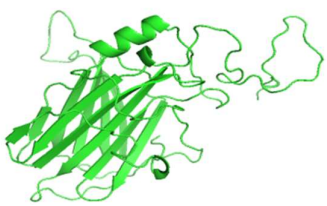
	# res in phipsi core (www.bionmr.ualberta .ca)	# res in phipsi allowed (www.bionmr.ualberta .ca)	# res in phipsi generous (www.bionmr.ualberta .ca)	# res in phipsi outside (www.bionmr.ualberta .ca)	
Model1	215 (87%)	28 (11%)	3 (1%)	0 (0%)	

(MPXV001)					
Model 2 (MPXV002)	220 (89%)	23 (9%)	2 (0%)	1 (0%)	Selected
Model 3 (MPXV003)	217 (88%)	26 (10%)	2 (0%)	1 (0%)	
Model 4 (MPXV004)	214 (86%)	25 (10%)	5 (2%)	2 (0%)	
Model 5 (MPXV005)	211 (85%)	30 (12%)	3 (1%)	2 (0%)	

Table 2 (b): Ramachandran Plot analysis of BR

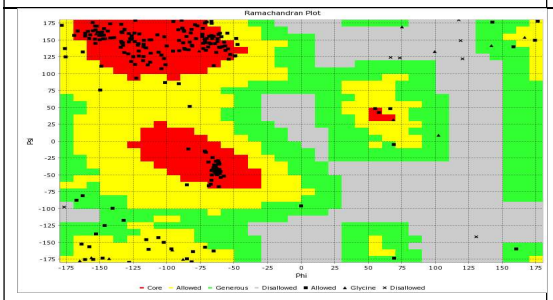
	# res in phipsi core (www.bionmr.ualberta.ca)	# res in phipsi allowed (www.bionmr.ualberta.ca)	# res in phipsi generous (www.bionmr.ualberta.ca)	# res in phipsi outside (www.bionmr.ualberta.ca)	
Model 1 (BR001)	178 (72%)	45 (18%)	12 (4%)	11 (4%)	
Model 2(BR002)	192 (78%)	36 (14%)	11 (4%)	7 (2%)	Selected
Model 3 (BR003)	179 (72%)	46 (18%)	14 (5%)	7 (2%)	
Model 4 (BR004)	189 (76%)	41 (16%)	8 (3%)	8 (3%)	
Model 5 (BR005)	186 (75%)	43 (17%)	10 (4%)	7 (2%)	

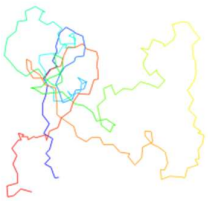




Ramachandran Plot of the selected model (MPXV 02)

3d structure of Model 2 (MPXV 02)





Ramachandran Plot of the selected model (BR 02)

3d structure of Model 2 (BR002)

Fig. 2: Ramachandran Plot and 3d structure of the selected models.

The SMILES of the phytocompounds were retrieved from PubChem (Table 3).

Table 3: Phytocompounds and their SMILES

SCIENTIFIC NAME	**SMILES**
Tinospora cordifolia	
Piperidin	C1CCNCC1
Piperine	C1CCN(CC1)C(=O)/C=C/C=C/C2=CC3=C(C=C2)OCO3 (d3amtssd1tejdt.cloudfront.net)
Tinosporin	CC(C(=O)C1=CC2=C(C=C1)OCO2)C(=O)C3=C(C=C(C=C3)OC)OC (d3amtssd1tejdt.cloudfront.net)
Aegle armelos	
Anhydromarmeline	CC(=CCOC1=CC=C(C=C1)/C=C/NC(=O)/C=C/C2=CC=CC=C2)C
Aegeline	COC1=CC=C(C=C1)C(CNC(=O)/C=C/C2=CC=CC=C2)O
Marmeline	CC(=CCOC1=CC=C(C=C1)C(CNC(=O)/C=C\C2=CC=CC=C2)O)C
Marmesin	CC(C)([C@@H]1CC2=C(O1)C=C3C(=C2)C=CC(=O)O3)O
Lignans	COC1=CC(=CC(=C1OC)OC)[C@H]2[C@H]3C(COC3=O)[C@H](C4=CC5=C(C=C24)OCO5)O
Gmelina arborea	
Isoborneal	C[C@@]12CC[C@@H](C1(C)C)C[C@H]2O
Luteolin	C1=CC(=C(C=C1C2=CC(=O)C3=C(C=C(C=C3O2)O)O)O)O (bioinfo.nrc.ca)
Quercetin	C1=CC(=C(C=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)O)O)O (bioinfo.nrc.ca)
Oroxylum indicum	

Baicalein (www.cheminfo.org)	C1=CC=C(C=C1)C2=CC(=O)C3=C(O2)C=C(C(=C3O)O)O
Chrysin (www.cheminfo.org)	C1=CC=C(C=C1)C2=CC(=O)C3=C(C=C(C=C3O2)O)O
Ellagic acid	C1=C2C3=C(C(=C1O)O)OC(=O)C4=CC(=C(C(=C43)OC2=O)O)O
Aloe-emodine	C1=CC2=C(C(=C1)O)C(=O)C3=C(C2=O)C=C(C=C3O)CO
Apigenin	C1=CC(=CC=C1C2=CC(=O)C3=C(C=C(C=C3O2)O)O)O
Premna serratifolia	
Olivil	COC1=C(C=CC(=C1)C[C@]2(CO[C@@H]([C@H]2CO)C3=CC(=C(C=C3)O)OC)O)O
2- Methyl Aceptophenone	CCC(=O)C1=CC=CC=C1
3- Methoxy-2, 5-Dimethylpyrazine	CC1=CN=C(C(=N1)CC2CC3=C(C=C(C=C3)OC)OC2)C (d3amtssd1tejdt.cloudfront.net)
Premcoryoside	C[C@H]1[C@@H]([C@H]([C@H]([C@@H](O1)O[C@@H]2[C@H]([C@@H](O[C@@H]([C@H]2OC(=O)/C=C/C3=CC(=C(C=C3)O)O)COC(=O)C4=CO[C@H]([C@H]5[C@@H]4CC[C@]5(C)O)O[C@H]6[C@@H]([C@H]([C@@H]([C@H](O6)CO)O)O)O)OCCC7=CC(=C(C=C7)O)O)O)O)O)O (d3amtssd1tejdt.cloudfront.net)
Solanum indicum	
Indioside E (d3amtssd1tejdt.cloudfront.net)	C[C@@H]1CC[C@@]2([C@H]([C@H]3[C@@H](O2)C[C@@H]4[C@@]3(CC[C@H]5[C@H]4CC=C6[C@@]5(CC[C@@H](C6)O[C@H]7[C@@H]([C@H]([C@H]([C@H](O7)CO)O)O[C@H]8[C@@H]([C@H]([C@@H](CO8)O)O)O)O[C@H]9[C@@H]([C@@H]([C@H]([C@@H](O9)C)O)O)O)C)C)C)OC1
Protodioscin (www.cheminfo.org)	C[C@H]1[C@H]2[C@H](C[C@@H]3[C@@]2(CC[C@H]4[C@H]3CC=C5[C@@]4(CC[C@@H](C5)O[C@H]6[C@@H]([C@H]([C@@H]([C@H](O6)CO)O[C@H]7[C@@H]([C@@H]([C@H]([C@@H](O7)C)O)O)O)O)O[C@H]8[C@@H]([C@@H]([C@H]([C@@H](O8)C)O)O)O)C)C)O[C@@]1(CC[C@@H](C)CO[C@H]9[C@@H]([C@H]([C@@H]([C@H](O9)CO)O)O)O)O
Solavetivone (www.cheminfo.org)	C[C@@H]1CC(=O)C=C([C@]12CC[C@H](C2)C(=C)C)C
Scopoletin	COC1=C(C=C2C(=C1)C=CC(=O)O2)O
Isofraxidin (d3amtssd1tejdt.cloudfront.net)	COC1=C(C(=C2C(=C1)C=CC(=O)O2)OC)O
Fraxetin (d3amtssd1tejdt.cloudfront.net)	COC1=C(C(=C2C(=C1)C=CC(=O)O2)O)O

Using Lipinski rule of five the above phytocompounds' drug-likeliness was obtained (Table 4).

Table 4: Drug-like properties of phytocompounds obtained using molinspiration

Phytocompounds	**miLogP**	**TPSA**	**natoms**	**MW**	**nON**	**nOHNH**	**volume**	**nrotb**	**nviolations**
Anhydromarmeline	5.51	38.33	25	333.43	3	1	328.00	7	1

Aegeline	2.64	58.56	22	297.35	4	2	281.45	6	0
Marmeline	4.32	58.56	26	351.45	4	2	342.23	8	0
Marmesin	2.18	59.67	18	246.26	4	1	218.00	1	0
Lignans	1.32	92.70	30	414.41	8	1	354.43	4	0
Isoborneol	2.35	20.23	11	154.25	1	1	165.72	0	0
Luteolin	1.97	111.12	21	286.24	6	4	232.07	1	0
Quercetin	1.68	131.35	22	302.24	7	5	240.08	1	0
Baicalein	2.68	90.89	20	270.24	5	3	224.05	1	0
Chrysin	2.94	70.67	19	254.24	4	2	216.03	1	0
Ellagic acid (D. Benvenuto et al., 2020)	0.94	141.33	22	302.19	8	4	221.78	0	0
Aloe-emodine (D. Benvenuto et al., 2020)	2.42	94.83	20	270.24	5	3	223.43	1	3
Apigenin (D. Benvenuto et al., 2020)	2.46	90.89	20	270.24	5	3	224.05	1	0
Olivil	1.39	130.61	27	376.40	7	4	337.32	6	0
2- Methyl-acetophenone	2.34	17.07	10	134.18	1	0	136.39	2	0
3- Methyl-2, 5-Dimethylpyrazine	3.17	44.25	21	284.36	4	0	271.18	3	0
Premcoryoside	-1.41	380.21	69	982.93	24	13	832.47	17	3
Indioside E	2.03	235.70	60	855.03	16	8	782.64	7	3
Protodioscin	-0.21	346.07	73	1049.21	22	13	949.24	14	3
Solavetivone	3.73	17.07	16	218.34	1	0	232.13	1	0
Scopoletin	1.33	59.67	14	192.17	4	1	162.15	1	0
Isofraxidin	1.54	68.91	16	222.20	5	1	187.70	2	0
Fraxetin	1.27	79.90	15	208.17	5	2	170.17	1	0

Docking was performed using the phytocompounds having nviolations 0 above with the best models selected in Table 2. The docking scores obtained are given in Table 5 and docking results are given in Table 6.

Table 5(a): Docking Result of PROTEIN BR.B99990002

Phyto- compound	**Docking score**	**No. of interactions**	**Docking (yes / no)**
Aegeline	-4.46kcal/mol	08	Yes
Marmeline	-4.16kcal/mol	13	Yes

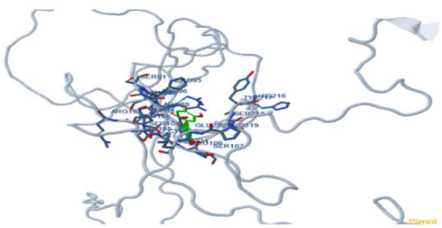
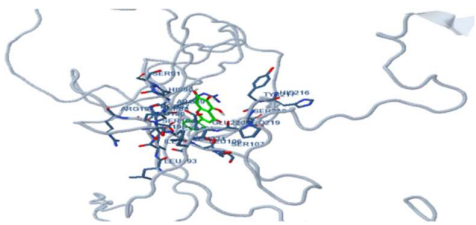
Marmesin	-5.40kcal/mol	13	yes
Lignans	-4.74kcal/mol	09	Yes
Isobornoel	-4.32kcal/mol	09	Yes
Luteolin	-5.77kcal/mol	15	yes
Quercetin	-5.28kcal/mol	18	Yes
Baicalein	-5.37kcal/mol	21	Yes
Chrysin	-5.67kcal/mol	14	Yes
Ellagic acid	-4.02kcal/mol	11	Yes
Apigenin	-5.76kcal/mol	12	yes
Olivil	-5.62kcal/mol	15	Yes
2 methyl acetophenone	-4.82kcal/mol	11	Yes
3 methyl 1-2, 5 dimethyl pyrazine	-5.34kcal/mol	10	Yes
Solavetivone	-5.19kcal/mol	12	Yes
Scopoletin	-4.32kcal/mol	14	Yes
Isofraxidin	-4.94kcal/mol	08	Yes
Fraxetin	-4.02kcal/mol	10	Yes

Table 5(b): Docking Result of PROTEIN MPXV.B99990002

Pyto- compound	**Docking score**	**No. of interactions**	**Docking (yes /no)**
2,methylacetophenone	-4.75kcal/mol	09	Yes
3methyl12,5dimethylpyrazine	-5.63kcal/mol	08	Yes
Aegeline	-5.07kcal/mol	14	Yes
Apigenin	-4.28kcal/mol	08	Yes
Baicalein	-6.04kcal/mol	10	Yes
Chrysin	-6.16kcal/mol	13	Yes

Ellagic acid	-4.25kcal/mol	17	Yes
Fraxetin	-4.26kcal/mol	06	Yes
Isoborneol	-4.49kcal/mol	07	Yes
Marmesin	-4.61kcal/mol	15	Yes
Isofraxidin	-4.45kcal/mol	05	Yes
Lignans	+13.06kcal/mol	29	Yes
Luteolin	-4.00kcal/mol	12	Yes
Marmeline	-2.53kcal/mol	14	Yes
Olivil	-3.80kcal/mol	19	yes
Quercetin		17	Yes
Scopoletin	-4.31kcal/mol	10	Yes
Solavetivone	-5.05kcal/mol	08	Yes

Table 6(a): Receptor-ligand docking results of PROTEIN BR.B99990002.

	
Luteolin docking	Luteolin docking with interacting amino acids
	
Baicalein docking	Baicalein docking with interacting amino acids

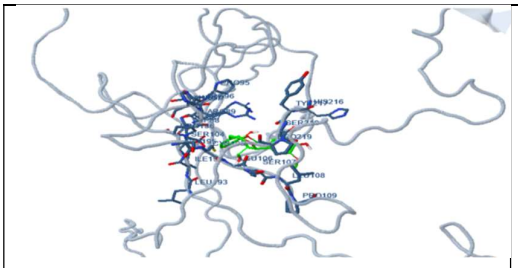
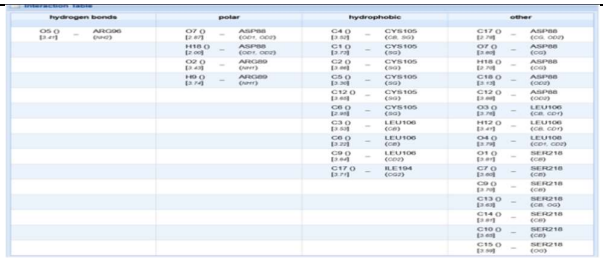
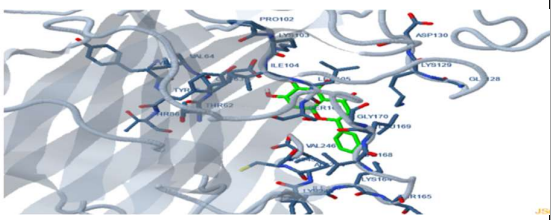
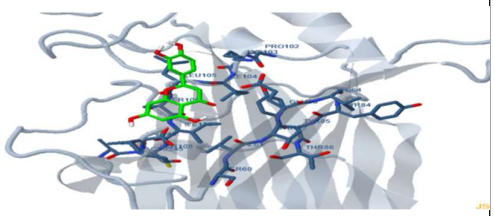
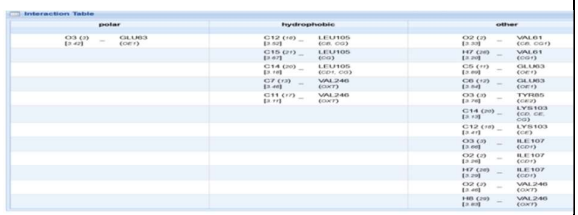
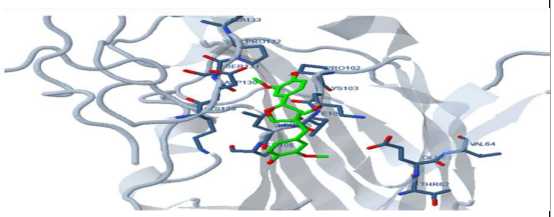
	
Olivil docking	Olivil docking with interacting amino acids

Table 6(b): Receptor-ligand docking results of MPXV.B99990002

	
Baicalein docking	Baicalein docking with interacting amino acids
	
Luteolin docking	**Luteolin** docking with interacting amino acids
	
Olivil docking	**Olivil** docking with interacting amino acids

DISCUSSION

As per the docking result it is seen that compound Baicalein docks with BR.B99990002 with a docking score of -5.37 kcal/mol with 21 interactions and with protein MPXV.B99990002 with a docking score of -6.04kcal/mol and 10 interactions.

Luteolin docks with BR.B99990002 with a docking score of -5.77 kcal/mol with 15 interactions and with protein MPXV.B99990002 with a docking score of -4.00 kcal/mol and 12 interactions.

Olivil docks with BR.B99990002 with a docking score of -5.62 kcal/mol with 15 interactions and with protein MPXV.B99990002 with a docking score of -3.80 kcal/mol and 19 interactions.

CONCLUSION

The phytocompound Baicalein, Luteolin, olivil has the least docking score and high interactions with BR203 and BR209.

These phytocompounds are considered as novel drug leads for Monkeypox virus.

Further receptor ligand binding assay can be done to prove its efficacy as drug for the disease.

REFERENCES

- Adnan N, Haq ZU, Malik A, Mehmood A,Ishaq U, Faraz M, Malik J, Mehmoodi A (2022). Human monkeypox virus: An updated review. Medicine (Baltimore) 101(35). Bikadi, Z., Hazai, E. (2009). Application of the PM6 semi-empirical method to modeling proteins enhances docking accuracy of AutoDock, J. Cheminf. 1, 15 Dinarello CA, Simon A, van der Meer JW. (2012). Treating inflammation by blocking interleukin-1 in a broad spectrum of diseases. Nat Rev Drug Discov. Aug;11(8):633-52

- Domenico Benvenuto, Serena Vita, Stefano Pascarella, Martina Bianchi et al (2022). "The evolution of Monkeypox virus: a genetic and structural analysis reveals mutations in proteins involved in host-pathogen interaction", Cold Spring Harbor Laboratory.
- Hendrickson RC, Wang C, Hatcher EL, Lefkowitz EJ. (2010). Orthopoxvirus genome evolution: the role of gene loss. Viruses.Sep;2(9):1933-1967
- https://my.clevelandclinic.org/health/diseases/22371-monkeypox
- https://www.cdc.gov/poxvirus/monkeypox/clinicians/clinical-recognition.html#:~:text=The%20evolution%20of%20lesions%20progresses,before%20scabbing%20over%20and%20desquamation.
- https://www.molinspiration.com/
- Information Systems Design and Intelligent
- Applications (2015), Springer Nature.
- Jessica R. Weaver. (2008) "Monkeypox virus and insights
- into its immunomodulatory proteins", Immunological
- Reviews, 10.
- Kindrachuk J, Arsenault R, Kusalik A, Kindrachuk KN, Trost B, Napper S, Jahrling PB, Blaney JE. (2012). Systems kinomics demonstrates Congo Basin monkeypox virus infection selectively modulates host cell signaling responses as compared to West African monkeypox virus. Mol Cell Proteomics. Jun;11(6)
- Ladnyj ID, Ziegler P, Kima E. (1972). A human infection caused by monkeypox virus in Basankusu Territory, Democratic Republic of the Congo. Bull World Health Organ;46(5):593-7.
- Lansiaux E, Jain N, Laivacuma S, Reinis A. (2022). The virology of human monkeypox virus (hMPXV): A brief overview. Virus Res. 2022 Dec;322:198932.
- Miaojin Zhu, Jia Ji, Danrong Shi, Xiangyun Lu,
- Baohong Wang, Nanping Wu, Jie Wu, Hangping Yao,
- Lanjuan Li. (2022) "Unusual global outbreak of monkeypox: what should we do?", Frontiers of Medicine.
- Mohammed Baqur S. Al-Shuhaib, Hayder O. Hashim, Jafar M.B. Al-Shuhaib (2021). "Epicatechin is a promising novel inhibitor of SARS-CoV-2 entry by disrupting interactions between angiotensin-converting enzyme type 2 and the viral receptor binding domain: A computational/simulation study", Computers in Biology and Medicine.

- Monjur Ahmed Laskar, Moriom Begam, Manabendra Dutta Choudhury. (2020) "In Silico Screening of SomeAntiviral Phytochemicals as Drug Leads Against Covid-19", American Chemical Society (ACS).
- Monkeypox: Experts Give Virus Variants New Names, WORLD HEALTH ORGANIZATION, 2022.
- Monkeypox: experts give virus variants new names. Neurosciences (Riyadh),(2022) Oct;27(4):284-286.
- Moore MJ, Rathish B, Zahra F. (2022). Mpox (Monkeypox) [Updated 2022 Nov 30]. In: StatPearls [Internet]. Treasure Island (FL)
- Sklenovská N, Van Ranst M. (2018). Emergence of Monkeypox as the Most Important Orthopoxvirus Infection in Humans. Front Public Health. Sep 4;6:241.
- Sunder Sham, FNU Sapna, Vivek Podder, Hansini Laharwani, FNU Anjali, Ahmed Bandari, Hossein Hosseini (2022). "The Changing Global Epidemiology of Re-emerging Human Monkeypox Virus Infection: A Systematic Review", Cold Spring Harbor Laboratory.
- Xiang Y, White A. (2022). Monkeypox virus emerges from the shadow of its more infamous cousin: family biology matters. Emerg Microbes Infect. Dec;11(1):1768-1777.
- Weaver JR, Isaacs SN. (2008). Monkeypox virus and insights into its immunomodulatory proteins. Immunol Rev. Oct;225:96-113.
- Webb B, Sali A. (2016). Comparative Protein Structure Modeling Using Modeller. Current Protocols in Bioinformatics 54, John Wiley & Sons, Inc., 5.6.1-5.6.37.
- Willard L, Ranjan A, Zhang H, Monzavi H, Boyko RF, Sykes BD, and Wishart DS (2003). "VADAR: a web server for quantitative evaluation of protein structure quality" Nucleic Acids Res.July 1; 31 (13): 3316–3319