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Molecular Modeling and *Insilico* Analysis of Tumor Necrosis Factor Receptor Superfamily Member 1A involved in Mumps Disease

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ABSTRACT

The mumps virus is a negative-strand RNA virus in the family Paramyxoviridae. Mumps infection results in an acute illness with symptoms including fever, headache, and myalgia, followed by swelling of the salivary glands. Complications of mumps can include meningitis, deafness, pancreatitis, orchitis, and first-trimester abortion. Symptoms of mumps usually appear within two weeks of exposure to the virus. Mumps virus doesn't respond to antibiotics or other medications. Vaccination is the only way to prevent mumps. Therefore, every newborn infants and children receive the vaccine against measles, mumps, and rubella (MMR) at the same time. The MMR vaccine is currently given on a two-dose. One dose of mumps containing vaccine has an efficacy of 88%, with efficacy increasing to approximately 95% with two doses. In silico tools and techniques which are include retrieval of Tumor necrosis factor receptor superfamily member 1A protein sequence from the UniProt KB database and physicochemical parameter analyzed by using Protoparam tool. In that Leucine had a maximum amino acid composition. The structure of a protein has a very important role in its function. The secondary structure was predicted by using SOPMA tool which indicated that the percentage of Random coils was higher than the percentage of alpha helix and extended strand. Then the 3D structure of Tumor necrosis factor receptor superfamily member 1A was predicted by using SWISS MODEL server and the model was validated by using PROCHECK analysis after validation of the model, the validation score was 94.7%.

Keywords : Mumps, *Insilico*, Random Coil, secondary structure, Protparam, Tumor necrosis factor receptor superfamily member 1A

I. INTRODUCTION

Mumps is an acute respiratory infectious disease caused by the mumps virus(MuV), is transmitted to a person primarily through contact, and droplets. The main clinical manifestation of mumps is unilateral or bilateral parotid gland swelling, accompanied by pain and fever [1,2]. Although its common symptoms seem mild, mumps can cause serious complications such as permanent deafness, encephalitis, pancreatitis, oophoritis, and orchitis, which may result in disability or death and bring a heavy economic burden to families and societies [3,4]. This disease is highly contagious and often occurs in childhood [5]. Mumps can be prevented by administration of live attenuated vaccine which is usually delivered as a component of measles/mumps/rubella vaccine (MMR)2. With the use of mumps vaccine, mumps incidence had a significant drop in countries with high vaccine coverage rates. However, some countries such as the United States are experiencing some large mumps outbreaks occurring in highly vaccinated populations [6,7]. The septic effect of vaccination is related to factors such as age, coverage, and inoculation times. However, the recovery and outbreaks of mumps have not stopped, even in some

developed countries with higher immunization rates, such as the United States, France, Britain, and Australia, which has once again aroused concern and attention [8].

Mumps virus (MuV) is a member of the family Paramyxoviridae in the genus Rubulavirus. It has a negative-sense, nonseg-mented RNA genome of 15,384 nucleotides. According to the WHO, the MuVs strains are classified into 12 genotypes, designated as A to N, based on nucleotide sequence analysis and containing genes encoding for nucleocapsid (N), phospho (P), matrix (M), fusion (F), small hydrophobic (SH), hemagglutinin-neuraminidase (HN) and large (L) proteins. Each of these proteins plays a crucial role for virus entry, replication, assembly and budding. Briefly, the N, P and L proteins are located inside MuV virion and account for genome transcription and replication [9]. In the present study, we used different In-Silico tools and techniques for characterization, homology modeling of Tumor necrosis factor receptor superfamily member 1A protein. The first step includes retrieval of Tumor necrosis factor receptor superfamily member 1A sequence from UniProt KB database. The physiochemical properties were analyzed by using ProtParam tool and the secondary structure was predicted by using SOPMA secondary structure prediction tool. Later the 3D structure was predicted by using SWISS-MODEL server and the model was validated by using PROCHECK method.

II. MATERIAL AND METHODS

1. Retrieval of Sequence

The protein sequence of Tumor necrosis factor receptor superfamily member 1A proteins was retrieved from UniProtKB protein database and saved in FASTA file format. UniProtKB is a protein sequence database which is freely accessible to the public and it contains the amino acid sequences of proteins [10].

2. Physicochemical Analysis

The physicochemical properties of Tumor necrosis factor receptor superfamily member 1A proteins were analyzed by ProtParam analysis tool. The ProtParam tool calculates parameters such as amino acid composition, molecular weight theoretical pI, instability index, aliphatic index and grand average of hydropathicity (GRAVY) [11].

3. Secondary Structure Prediction

The secondary structure was predicted by SOPMA (Self- Optimized Prediction Method with Alignment) method. It was employed for calculating the secondary structural of Tumor necrosis factor receptor superfamily member 1A proteins. The SOPMA method correctly predicts the secondary structure α-helix, β-sheet and coil [12].

4. Homology Modeling and Model Validation

The of Tumor necrosis factor receptor superfamily member 1A sequence was used for comparative homology modeling using SWISS MODEL server. SWISS-MODEL is a fully automated protein structure homology modeling server to make the protein models accessible to all biotechnologist [10]. After modeling, to check the quality and validation of the model was carried out by PROCHECK Ramchandran plot method using PDBsum server [13].

5. Identification of Domain function and analysis

Identification of domain and its biological function of Tumor necrosis factor receptor superfamily member 1A proteins were determined from Pfam domain identification database. The Pfam database is a large collection of protein families, each represented by

multiple sequence alignments and hidden Markov models (HMMs) [14].

III. RESULTS AND DISCUSSION

Retrieval of protein Sequence

The protein sequence of Tumor necrosis factor receptor superfamily member 1A proteins was retrieved from UniProt KB database and the sequence was saved in FASTA file format in notepad. The protein name, organism name, UniProt KB ID and sequence length were shown in table 1.

Protein Name	Organism Name	UniprotKB ID	Sequence Length
Tumor necrosis factor receptor superfamily member 1A	Homo sapiens	P19438	455

Table 1. Retrieval of sequence

Physicochemical analysis of Protein

The physicochemical properties were analyzed by using ProtParam tool and the results were enlisted in table 2. As per the table, the Tumor necrosis factor receptor superfamily member 1A is unstable and basic in nature. The total number of positively charged residues (Arg+Lys) and negatively charged residues (Arg+Glu) are same in number as shown in Table 2.

Parameters	Values
Total no. of Amino acids	455
Molecular weight	5049.87
Theoretical pI	6.23
UniprotKB ID	P19438
The no. of positive amino acid (Arg+Lys)	47
The no. of negative amino acid(Arg+Glu)	51
Extinction coefficient	0.965
Aliphatic index	79.91
GRAVY	-0.285

Table 2. Physicochemical parameters of Protein.

Secondary Structure Prediction

The secondary structure was predicted by using SOPMA method. The secondary structure elements like alpha helix, beta sheets, extended strand and random coils were enlisted in Table 3. From the table, the percentage of coils in Tumor necrosis factor receptor superfamily member 1A proteins was higher than the percentage of alpha helix and extended strand as shown in Table 3.

Secondary Structure elements	Number of residues	Percentage
Alpha helix	122	26.81%
Extended stand	54	11.87%
Beta turn	19	4.81%
Random coil	260	57.14%

Table. 3 Secondary Structure Prediction

Homology Modeling and Model Validation

The 3D structure of Tumor necrosis factor receptor superfamily member 1A proteins was predicted by the SWISS Model server. The sequence template Tumor necrosis factor receptor superfamily member 1A was selected as template for prediction of homology modelling. The quality and validation of the model was carried out by Ramchandran plot analysis using PDBsum server. Ramchandran plot analysis showed that the percentage of favored region

is 94.7% which was higher than the percentage of additional allowed region it's conclude that the predicted model was reliable and good quality shown in Fig.1. Further model was visualized in RasMol visualization software package as shown in figure2.

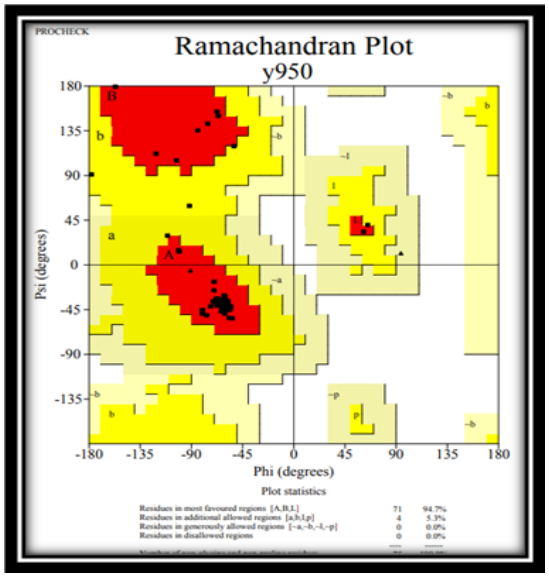


Fig.1 Protein model validation by PROCHECK

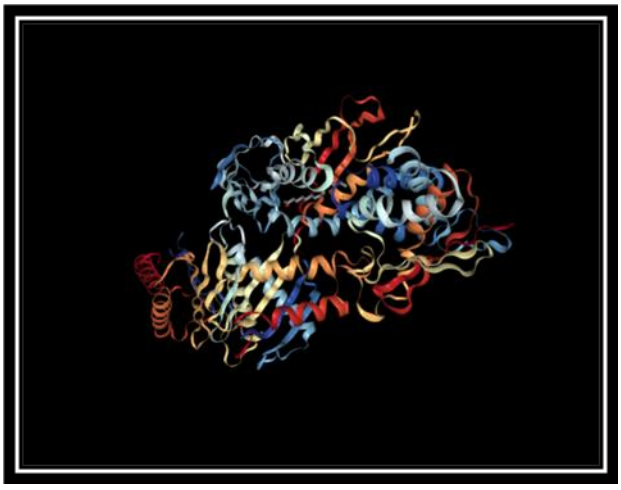
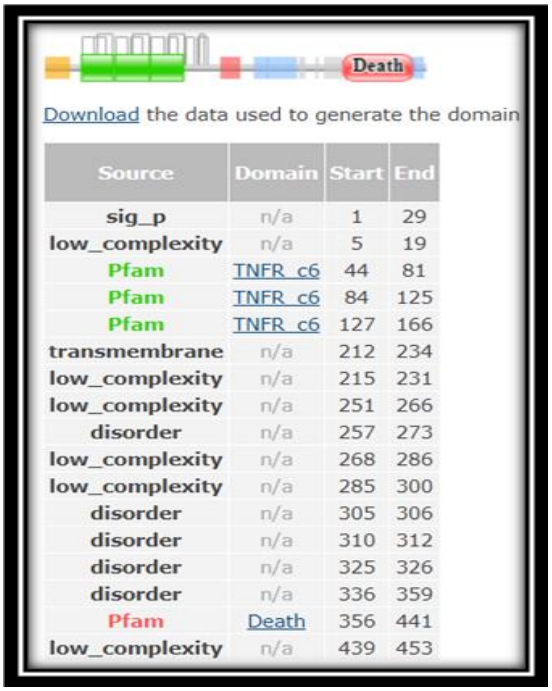


Fig.2. Visulatization of Predicted 3D structure by RasMol

Identification of Domain function and analysis

The Protein domain and protein family analysis of Tumor necrosis factor receptor superfamily member 1A by Pfam database. The domain of Tumor necrosis factor receptor superfamily member 1A proteins and its sequence length was shown in Fig. 3.



Source	Domain	Start	End
sig_p	n/a	1	29
low_complexity	n/a	5	19
Pfam	TNFR_c6	44	81
Pfam	TNFR_c6	84	125
Pfam	TNFR_c6	127	166
transmembrane	n/a	212	234
low_complexity	n/a	215	231
low_complexity	n/a	251	266
disorder	n/a	257	273
low_complexity	n/a	268	286
low_complexity	n/a	285	300
disorder	n/a	305	306
disorder	n/a	310	312
disorder	n/a	325	326
disorder	n/a	336	359
Pfam	Death	356	441
low_complexity	n/a	439	453

Fig. 3. Domain identification with its sequence length

IV. CONCLUSION

The present preliminary investigation mainly leads to understand the basic primary, secondary structure and tertiary structure of Tumor necrosis factor receptor superfamily member 1A proteins. In-silico tools and techniques. The Tumor necrosis factor receptor superfamily member 1A proteins were retrieved from UniprotKB database and it is having length of 455. The primary protein sequence analysis carried out using protparam tool and it retrieval that having a Molecular weight - 5049.87 Da, Theoretical pI -6.23, The number of positive amino acids (Arg + Lys): 47, The number of negative amino acids (Arg + Glu): 51 respectively. Aliphatic index: 79.91, GRAVY: -0.285. Secondary structure of the Tumor necrosis factor receptor superfamily member 1A proteins was predicted by SOMPA having alpha helix-73, beta turns 21, extended strands 42; random coils 87 so protein was highly stable. The Modelling of 3D structure of Tumor necrosis factor receptor superfamily member 1A proteins was build by Swiss model 2xfc. Structure was validated using

PROCHECK having model quality was 94.7%. This present study put molecular insight into the further studies to find the structural and functional properties of these Tumor necrosis factor receptor superfamily member 1A proteins to find or design the novel antiviral drugs.

V. REFERENCES

[1]. Foy, H.; Cooney, M.; Hall, C.; Bor, E.; Maletzky, A. Isolation of mumps virus from children with acute lower respiratory tract disease. Am. J. Epidemiol. 1971, 94, 467–472.

[2]. Philip, R.; Reinhard, K.; Lackman, D. Observations on a mumps epidemic in a virgin population. Am. J.Hyg. 1959, 69, 91–111.

[3]. Hviid, A.; Rubin, S.; Mühlemann, K. Mumps. Lancet 2008, 371, 932–944.

[4]. Galazka, A.M.; Robertson, S.E.; Kraigher, A. Mumps and mumps vaccine: A global review. Bull. World Health Organ. 1999, 77, 3–14.

[5]. Marshall, H.S.; Plotkin, S. The changing epidemiology of mumps in a high vaccination era.LancetInfect. Dis. 2019, 19, 118–119.

[6]. Barskey, A. E. et al. Mumps outbreak in Orthodox Jewish communities in the United States. N Engl J Med 367, 1704–1713, 10.1056/NEJMoa1202865 (2012).

[7]. Jin, L. et al. Genomic diversity of mumps virus and global distribution of the 12 genotypes. Rev Med Virol 25, 85–101, https://doi.org/10.1002/rmv.1819, Epub2014 Nov 1026 (2015).

[8]. Vygen, S.; Fischer, A.; Meurice, L.; Mounchetrou Njoya, I.; Gregoris, M.; Ndiaye, B.; Ghenassia, A.; Poujol, I.; Stahl, J.P.; Antona, D.; et al. Waning immunity against mumps in vaccinated young adults, France 2013. Eurosurveillance 2016, 21, 30156.

[9]. Paterson, R. G. & Lamb, R. A. RNA editing by G-nucleotide insertion in mumps virus P-gene mRNA transcripts. J. Virol.64, 4137–4145.

[10]. O'Donovan, C.; Martin, M. J.; Gattiker, A.; Gasteiger, E.; Bairoch, A.; Apweiler, R. (2002). "High-quality protein knowledge resource: SWISS-PROT and TrEMBL". Briefings in Bioinformatics. 3 (3): 275–284.

[11]. Gill, S. C, von Hippel, P. H. (1989) Calculation of protein extinction coefficients from amino acid sequence data. Anal. Biochem. 182, 319–326.

[12]. Wang T., He G.Z., Yang G.Y., Fei Y.X., Zhang Z.H., Wang C.D., Yang Z., Lan J.C., Luo L., Liu L. Cloning, expression and evaluation of the efficacy of a recombinant Baylisascaris schroederi Bs-Ag3 antigen in mice. Vaccine. 2008;26:6919–6924.

[13]. Westbrook J., Feng,Z., Chen,L., Yang,H. and Berman,H.M. (2003) The Protein Data Bank and structural genomics. Nucleic Acids Res., 31, 489–491.

[14]. Finn RD, Tate J, Mistry J, Coggill PC, Sammut SJ, Hotz HR, Ceric G, Forslund K, Eddy SR, Sonnhammer EL, Bateman A (2008). "The Pfam protein families database". Nucleic Acids Res. 36 (Database issue): D281–8.

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