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GENOMIC STRUCTURAL IDENTIFICATION AND IMMUNOINFORMATICS STUDIES FOR SARS-COV-2

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ABSTRACT: Coronaviruses are a group of viruses that belongs to the Coronaviridae family. These viruses have helical symmetry, enveloped, positive-sense, single-stranded RNA genome with nucleocapsid that causes diseases in birds and mammals. SARS-CoV 2 complete genome has genome size of 29,903 bp, having nine genes identified as Orf1a Polyprotein, Orf1ab Polyprotein, ORF3a Protein, ORF7a Protein, ORF8 Protein, Envelope proteins, Spike Surface glycoprotein, Membrane glycoprotein, and Nucleocapsid Phosphoprotein. Based on the ProtParam result, ORF1a has more molecular weight (489989 daltons), and Envelope protein has a less molecular weight (8365 daltons). The pI is lower in Orf1a polyprotein, Orf1ab Polyprotein, ORF3a Protein, ORF8 Protein, and Spike Surface glycoprotein) and high in ORF7a Protein, Envelope proteins, Membrane glycoprotein, and Nucleocapsid Phosphoprotein. The Orf1a Poly-protein, Orf1ab Polyprotein, ORF3a Protein, Envelope proteins, Spike Surface, and Membrane glycoprotein are stable. The higher aliphatic index and more hydrophobicity of membrane glycoprotein suggest an increase in the thermostability of protein might favor an increase in its solubility. The vaccines like EIAV vaccine gp45, anti-SARS m396 Antibody, EIAV vaccine gp45, and E protein of the Japanese encephalitis live attenuated vaccine virus are less effective than Curcumin for SARS-CoV 2. Hence better vaccines are to be developed for respiratory viruses like SARS-CoV 2 in the future.

INTRODUCTION: Coronavirus disease 2019 (COVID-19) or SARS-CoV 2 (Severe Acute Respiratory Syndrome Related Coronavirus 2) is a new emerged human coronavirus in Wuhan city of China and rapidly spread throughout the world [1, 2, 3]. In December 2019, the authorities of China were declared that the virus is new and emerging that may spread to all over the world. Within short period, the coronavirus was spread to more than 200 countries all around the world.

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On 11-3-2020, WHO (World Health Organization) declared COVID-19 as pandemic disease, an epidemic associated with geographic spread to several countries and cause disease [4]. Scientists and medical researchers have identified several microbial species that cause diseases like Cholera, bubonic plague, smallpox, and influenza that are the most brutal killers in human history [5].

In 1918 influenza virus originated in France, China, and Britain, is a severe pandemic that was occurred in the past, where more than 50 million people had died [6]. In 1956, Asian flu was originated in China and estimated about two million deaths worldwide. In 2002 SARS (Severe acute respiratory syndrome) emerged in China [7], spread to 37 countries, causing global panic with more than 8,000 people infecting and about 750 people have died.

The SARS transmission after 2004 was not reported. In 2009, Swine flu or influenza (H1N1) was first identified in Mexico, with an estimated 151000-575000 people died worldwide. MERS-CoV (Middle East Respiratory Syndrome Coronavirus) first identified in Saudi Arabia spread to 27 countries infected 2400 cases and 912 deaths (4 out of 10 patients died). Like other coronavirus family members, COVID-19 is a novel mutated virus having infected cases of 5, 03, 274 with 22 342 deaths as on 26-3-2020. As on 3-8-2020, the COVID-19 virus having infected cases of 18.305.496 with 694,058 deaths worldwide. The world is commonly called this virus Coronavirus. About 70% of people infected are recovered and developed herd immunity. Hence the emerging viruses originated previously from China, US and Saudi Arabia may be due to eating habits, mobile radiations, advanced microbial researches or climate factors. Coronaviruses (CoVs) cause gastrointestinal and/or respiratory disease/s in humans, cattle, swine, and poultry [8]. The effect of Coronaviruses in chickens and humans are upper respiratory tract infections. In cows and swine, the Coronaviruses cause diarrhea.

The Coronavirus is a viral genetic material with lipoprotein present as a particle outside host machinery [9]. It contains a replicative protein nsp [9] acts as a single-stranded RNA-binding subunit that is distinctive in the world of RNA virus [10]. When the virus enters into living cells, it multiplies fast using host machinery within human cells. The virus reaches into the human system through the nose or mouth or eyes or ears and finally reaches the alimentary canal, blood, liver and lungs. In lungs, the epithelial cells containing ACE2 receptor joins with spike glycoprotein of Coronavirus and kills all epithelial cells in lungs [11, 12]. Within seven to ten days, millions of cells present in human system will be damaged and then coronavirus acts on the Immune system. The genetic material may modify into other forms, infect other parts of the host complex system and may damage complete system.

Humans with a good immune system can be isolated, quarantined/ recovered [13]. The Immune system will protect humans from foreign bodies by passive immunity. If the immune system disturbs, it causes severe effects like dry cough, cold, inflammation, and fever.

Some of the T-cells, with the help of proteins called cytokines, come closer to coronavirus and become non-effective [14]. The resources of host machinery will be used very fast, and coronavirus multiplies rapidly and kills Neutrophils and Killer T-cells. In some cases, the Neutrophils and Killer T cells act as toxic and make other human cells to be self-Killed. If cells in the lungs are killed, it leads to fibrosis and respiratory problems. In some humans with good immune system regains its strength of Neutrophils and Killer T cells and dominates coronavirus, and stop infecting other cells.

In some cases, there will be critical cases that are hidden at present conditions. There may be a flu-like infection that causes pneumonia (due to damage of alveoli), where the patient should be kept in ventilators and should supply oxygen [15]. If the virus spreads to the entire body and controls other bacteria in humans and cells, the patient will die. Quantitative comparisons of quarantine, case identification and isolation, infection control precautions, and immunization interventions are the effectively controlling measures for viral diseases [16].

The slow pandemic viruses like HIV are not that much dangerous as it spreads slowly to the people. The fast Pandemic species like Coronavirus is more dangerous that kills many people and stays for longer periods [17]. The facilities like vaccines, drugs, ventilators, and manpower become less, and many people will have died. To control this situation, the fast-spreading viruses should be converted into slower pandemic species. The infected people should be isolated and treated in the first condition, and other healthy humans should stay away. As there is no proper vaccine in the present condition, human behavior, distance maintenance, and prevention measures can only make fast pandemic coronavirus slow pandemic coronavirus [18]. The hands should be washed with soap (destroy lipid envelop) and sanitizers. The virus may persist on glass, paper, plastic, and wood for 4 days, Aluminum and surgical gloves for 8 days, and steel for 48 days. Like other coronaviruses like SARS, COVID-19 has been predicted to be transferred to humans from animals like Bats [19]. The most common symptoms of COVID-19 are tiredness, fever, and a dry cough, sometimes with a runny nose, sore throat, nasal

congestion and aches and pains or diarrhea. The elderly people having medical problems like diabetes, high blood pressure, heart problems, or chronic respiratory conditions are having greater risk of serious illness and deaths from COVID-19. The virus is stable for several hours to days in aerosols and on surfaces moving smaller distances as particles. The virus can live two to three days on plastic and metals. Immunoinformatics helps in the development and design of novel or enhanced vaccines that target through *in-silico* genome analysis that has great potential to fight against diseases. Several human types of HPV were identified, but vaccines for few types have only developed. The newly emerged virus COVID-19 has several types hence success rate for the development of vaccines may be less.

Antibiotics are of no use, antiviral drugs will not work, and there is currently no vaccine for Coronavirus. Recovery from this disease depends on the strength of the immune system of humans. The present work provides a better understanding of the genome and immune control activity by vaccination using in silico methods.

MATERIALS AND METHODS:

Genome Retrieval: The SARS CoV 2 complete genome sequence is retrieved from the NCBI database with Accession number NC_045512.2 isolate from Wuhan-Hu-1. The genome was analyzed for genomic and immunoinformatics studies for better relevant vaccination.

Gene Prediction: The gene prediction for SARS CoV 2 complete genome was predicted using FGENESV0, a prediction of potential genes in viral genomes server. The server predicts the genes present in the viral genome.

Gene Identification: The gene identification for the protein sequences of SARS CoV 2 was obtained using FGENESV0 is submitted to BLASTp. Based on the predicted alignment scores and the function of proteins can be identified for a better understanding of the character of the virus.

Characterization of Proteins: The proteins present in SARS CoV 2 are characterized using the ProtParam tool present in ExPASy server. The protein characters like Molecular weight, Theoretical pI, estimated half-life, instability index (II), Aliphatic index, and Grand average of hydropathicity (GRAVY) for Coronavirus have been predicted in this method.

Prediction of Antigenic Epitope Regions: Epitope regions in the viral genes have been conducted using the SVMTriP server. The prediction may help the design of vaccine components in recognition of antibodies in cells.

Properties of Computer: The system properties conducted in the present work is as follows:

1. Window Edition: Windows 10 Home
2. Processor: Intel Celeron CPU N3350 of 1.10GHz with RAM of 4GB and x64-based processor

Docking Studies: The modeled structure for Spike glycoprotein of SARS CoV 2 was designed using SWISS-MODEL. The Spike protein (Antigen) was taken as a receptor, and 2O8Y (PDB file) of ACE2 (Antibody) as ligand are selected to check for Antigen-Antibody activity.

The vaccine structures 2g75 (anti-SARS m396 Antibody), 3wmj (EIAV vaccine gp45), 5mv2 (E protein of the Japanese encephalitis live attenuated vaccine virus) were retrieved from Protein DataBank (PDB) and Curcumin E (Designed and optimized by ChemSW software) are used as ligands for Spike glycoprotein. Docking studies are conducted using Hex v8.0.0.

RESULTS:

Genome Retrieval: The SARS CoV 2 genome sequence of NC_045512.2 related to severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome has been retrieved from NCBI. The genome has 29903 bp, ss-RNA with linear structure. As per the genomic data, SARS CoV 2 is a novel emerging coronavirus associated with a severe respiratory disease emerged in Wuhan of Hubei province, China. The virus is formerly called 'Wuhan seafood market pneumonia virus'.

Gene Prediction: The gene prediction for the retrieved SARS CoV 2 genome was predicted using FGENESV0, a Prediction of potential genes in viral genomes server. The number of predicted genes in the 29903bp length genome is nine, and the details are shown in **Table 1**.

TABLE 1: GENE PREDICTION FOR SARS COV 2

Gene number	Strand	Location on genome		Score
		Start	End	
1	+	266	13483	13218
2	+	13768	21555	7788
3	+	21536	25384	3849
4	+	25393	26220	828
5	+	26245	26472	228
6	+	26523	27191	669
7	+	27394	27759	366
8	+	27894	28259	366
9	+	28274	29533	1260

TABLE 2: GENE IDENTIFICATION OF SARS COV 2

Gene number	Identification
1	Orf1a polyprotein SARS 2
2	Orf1ab polyprotein SARS2
3	Surface glycoprotein SARS2
4	ORF3a protein SARS2
5	Envelope protein SARS2
6	Membrane glycoprotein SARS2
7	ORF7a protein SARS2
8	ORF8 protein SARS2
9	Nucleocapsid Phosphoprotein SARS2

Gene Identification: The identification of SARS CoV 2 genes using BLASTp was shown in **Table 2**.

The structure of the identified SARS CoV 2 was shown in **Fig. 1**

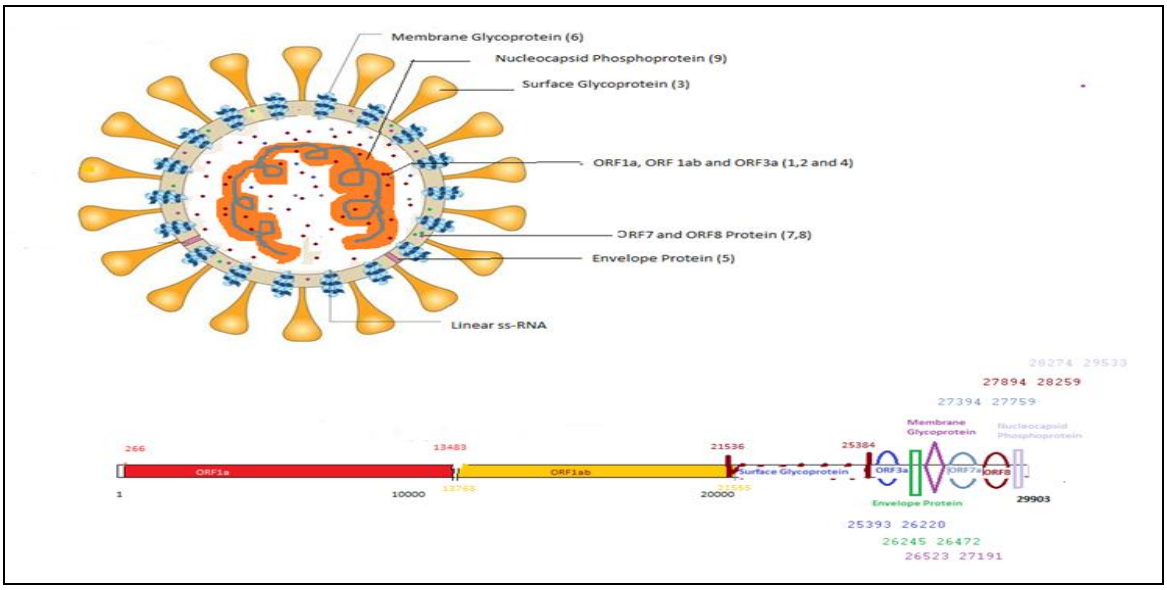


FIG. 1: SARS COV 2 PHENOTYPIC AND GENOMIC STRUCTURE

TABLE 3: PROTEIN CHARACTERIZATION OF SARS COV 2

Protein	Molecular weight	Theoretical pI	Estimated half-life	Instability Index (II)	Aliphatic index	Grand average of hydropathicity (GRAVY)
Orf1a polyprotein SARS 2	489988.91	6.04	30 h (mammalian reticulocytes *in-vitro*)	34.92 stable	88.99	-0.023
Orf1ab polyprotein SARS2	292977.43	6.87		31.14 stable	84.12	-0.132
Spike Surface glycoprotein SARS2	142270.84	6.42	> 20 h (yeast, *in-vivo*)	33.10 stable	84.69	-0.077
ORF3a protein SARS2	31122.94	5.55		32.96 stable	103.42	0.275
Envelope protein SARS2	8365.04	8.57	> 10 h (Escherichia coli, *in-vivo*)	38.68 stable	144.00	1.128
Membrane glycoprotein SARS2	25146.62	9.51		39.14 stable	120.86	0.446
ORF7a protein SARS2	13744.17	8.23		48.66 stable	100.74	0.318
ORF8 protein SARS2	13831.01	5.42		45.79 stable	97.36	0.219
Nucleocapsid Phosphoprotein SARS2	45625.70	10.07		55.09 stable	52.53	-0.971

Characterization of Proteins: The proteins are characterized using the ProtParam tool was shown in **Table 3**. **Table 3** shows that ORF1a has more molecular weight (489988.91), and the Envelope protein has a less molecular weight (8365.04). The pI (Isoelectric point) is the pH at which protein does not migrate in electric field. The antigens with lower pI generally have tissue uptake and a longer half-life. For acidic proteins, the pI will be lower (Orf1a Polyprotein, Orf1ab Polyprotein, ORF3a Protein, ORF8 Protein, and Spike Surface glycol-protein), and for basic proteins, pI will be high (ORF7a Protein, Envelope proteins, Membrane glycoprotein, and Nucleocapsid Phosphoprotein). Orf1a Polyprotein, Orf1ab Polyprotein, ORF3a Protein, Envelope proteins, Spike Surface, and Membrane glycoprotein are stable. The higher aliphatic index (Membrane Glycoprotein) suggests an increase in the thermostability of protein might favor an increase in its solubility. In the GRAVY result, a more positive score present in Membrane Glycoprotein indicates more hydrophobicity.

TABLE 4: ANTIGENIC EPITOPES FOR ORF1A POLYPROTEINS OF SARS COV 2

Rank	Location	Epitope	Score	Recommend*
1	2793 - 2812	VHVMSKHTDFSSEIIGYKAI	1.000	
2	3967 - 3986	AVANGDSEVVLKKLKKSLNV	0.971	
3	571 - 590	DGISQYSLRLIDAMMFTSDL	0.915	
4	288 - 307	VEKKKLDGFMGRIRSVYPVA	0.897	
5	4023 - 4042	AKVTSAMQTMLFTMLRKLDN	0.860	
6	3065 - 3084	MRFRRAFGEYSHVVAFNTLL	0.730	
7	3932 - 3951	EEMLDNRATLQAIASEFSSL	0.721	
8	1450 - 1469	LGYVTHGLNLEEAARYMRSL	0.710	
9	489 - 508	ETVKGLDYKAFKQIVESCGN	0.702	
10	3162 - 3181	KRRVVFNGVSFSTFEEAALC	0.701	

* The epitopes recommended are labeled by the flags

TABLE 5: ANTIGENIC EPITOPES FOR ORF1AB POLYPROTEIN OF SARS COV 2

Rank	Location	Epitope	Score	Recommend*
1	1420 - 1439	VATLQAENVTGLFKDCSKVI	1.000	
2	777 - 796	QYIRKLHDELTGHMLDMYSV	0.618	
3	1202 - 1221	ATNYDLSVVNARLRAKHYVY	0.589	
4	2118 - 2137	LIGEAVKTQFNYYKKVDGVV	0.566	
5	517 - 536	MPNMLRIMASLVLARKHTTC	0.565	
6	249 - 268	DVNLHSSRLSFKELLVYAAD	0.532	
7	2462 - 2481	GSVAIKITEHSWNADLYKLM	0.521	
8	2326 - 2345	NYGDSATLPKGIMMNVAKYT	0.512	
9	1450 - 1469	HLSVDTKFKTEGLCVDIPGI	0.444	
10	1154 - 1173	SRIIPARARVECFDKFKVNS	0.429	

* The epitopes recommended are labeled by the flags

TABLE 6: ANTIGENIC EPITOPES FOR SPIKE SURFACE GLYCOPROTEIN OF SARS COV 2

Rank	Location	Epitope	Score	Recommend*
1	1195 - 1214	LNEVAKNLNESLIDLQELGK	1.000	
2	970 - 989	TLVKQLSSNFGAISSVLNDI	0.987	
3	1019 - 1038	QQLIRAAEIRASANLAATKM	0.963	
4	1158 - 1177	KEELDKYFKNHTSPDVDLGD	0.961	
5	1237 - 1256	VMVTIMLCCMTSCCSCLKGC	0.827	
6	749 - 768	MYICGDSTECSNLLLQYGSF	0.701	
7	891 - 910	ITSGWTFGAGAALQIPFAMQ	0.681	
8	699 - 718	QSIIAYTMSLGAENSVAYSN	0.509	
9	580 - 599	DTTDAVRDPQTLEILDITPC	0.466	
10	604 - 623	VSVITPGTNTSNQVAVLYQD	0.457	

* The epitopes recommended are labeled by the flags

Prediction of protein surface regions that are preferentially recognized by antibodies (antigenic epitopes) can help the design of vaccine components and immunodiagnostic reagents [20].

A method to predict Linear antigenic epitopes is conducted by Support Vector Machine (SVM) has been utilized by combining the Tri-peptide similarity and Propensity scores (SVMTriP).

The antigenic epitopes for Orf1a polyprotein, Orf1ab polyprotein, Surface glycoprotein, ORF3a protein, Membrane glycoprotein, ORF7a protein, ORF8 protein, and Nucleocapsid Phosphoprotein were shown from **Table 4** to **11**. There are no antigenic epitopes found in the Envelope protein of SARS CoV 2.

TABLE 7: ANTIGENIC EPITOPES FOR ORF3A PROTEIN OF SARS COV 2

Rank	Location	Epitope	Score	Recommend*
1	184 - 203	YQIGGYTEKWESGVKDCVVL	1.000	
2	24 - 43	TPSDFVRATATIPIQASLPF	0.563	
3	139 - 158	LLYDANYFLCWHTNCYDYCI	0.510	

* The epitopes recommended are labeled by the flags

TABLE 8: ANTIGENIC EPITOPES FOR MEMBRANE GLYCOPROTEIN OF SARS COV 2

Rank	Location	Epitope	Score	Recommend*
1	96 - 115	FIASFRLFARTRSMWSFNPE	1.000	
2	151 - 170	IAGHHLGRCDIKDLPKEITV	0.255	

* The epitopes recommended are labeled by the flags

TABLE 9: ANTIGENIC EPITOPES FOR ORF7A PROTEIN

Rank	Location	Epitope	Score	Recommend*
1	70 - 89	GVKHVYQLRARSVSPKLFIR	1.000	
2	14 - 33	TCELYHYQECVRGTTVLLKE	0.921	

* The epitopes recommended are labeled by the flags

TABLE 10: ANTIGENIC EPITOPES FOR ORF8 PROTEIN OF SARS COV 2

Rank	Location	Epitope	Score	Recommend*
1	41 - 60	FYSKWYIRVGARKSAPLIEL	1.000	
2	98 - 117	LVVRCSFYEDFLEYHDVRVV	0.700	

* The epitopes recommended are labeled by the flags

TABLE 11: ANTIGENIC EPITOPES FOR NUCLEOCAPSID PHOSPHOPROTEIN OF SARS COV 2

Rank	Location	Epitope	Score	Recommend*
1	239 - 258	QQQQGQTVTKKSAAEASKKP	1.000	
2	276 - 295	RRGPEQTQGNFGDQELIRQG	0.865	
3	217 - 236	AALALLLLDRLNQLESKMSG	0.676	
4	186 - 205	SSSRSRNSSRNSTPGSSRGT	0.663	
5	359 - 378	AYKTFPPTEPKKDKKKKADE	0.638	
6	333 - 352	YTGAIKLDDKDPNFKDQVIL	0.471	
7	74 - 93	INTNSSPDDQIGYYRRATRR	0.317	
8	128 - 147	DGIIWVATEGALNTPKDHIG	0.282	
9	29 - 48	NGERSGARSKQRRPQGLPNN	0.221	
10	303 - 322	QIAQFAPSASAFFGMSRIGM	0.216	

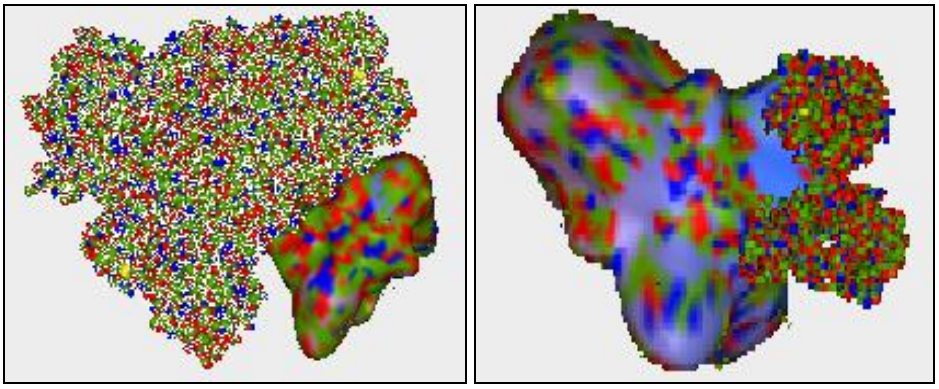
* The epitopes recommended are labeled by the flags

There are more antigenic sites in Orf1a polyprotein, Orf1ab polyprotein, Surface glycoprotein, and Nucleocapsid phosphoprotein of SARS CoV 2. As per the previous studies, it was found that the Coronavirus attaches to a receptor on respiratory cells called ACE2 (angiotensin-converting enzyme 2). The small molecular key present on SARS-CoV-2 that gives an entry of the virus into the host cell is called a spike protein, or Surface Protein, or S-protein.

TABLE 12: DOCKING RESULT OF ACE2 WITH SPIKE PROTEIN OF SARS COV 2

Ligand	Spike protein of SARS CoV 2	
	Total Energy (in KCal/Mol)	Distance (in °A)
ACE2	63	68
anti-SARS m396 Antibody	1105.92	72.8
EIAV vaccine gp45	-99.56	53.6
E protein of the Japanese encephalitis live attenuated vaccine virus	-52.43	63.2
Curcumin E	-195.37	30.4

As per the previous information, lesser the binding energy may be considered as a good inhibitor of Spike Glycoprotein of coronavirus [21, 22]. Hence, the activity of Curcumin E is more on Spike protein of SARS CoV 2. The vaccines like EIAV vaccine gp45, anti-SARS m396 Antibody, EIAV vaccine gp45, and E protein of the Japanese encephalitis live attenuated vaccine virus are less effective than Curcumin for SARS CoV 2 **Table 12** and **Fig. 2**. Hence, better vaccines are to be developed for SARS CoV 2.



ACE2 WITH S-PROTEIN ANTI-SARS ANTI-BODY WITH S-PROTEIN

EIAV GP45 WITH S-PROTEIN E-PROTEIN WITH S-PROTEIN CURCUMIN E WITH S-PROTEIN

FIG. 2: DOCKING RESULT OF SPIKE GLYCOPROTEIN OF CORONAVIRUS WITH SELECTED MOLECULES

DISCUSSION: As on 23-3-2020, there are 358803 Coronavirus Cases, 15,433 Deaths, 100,645 Recovered and 242,725 active cases. The linear graph of the growth has been shown in **Fig. 3**.

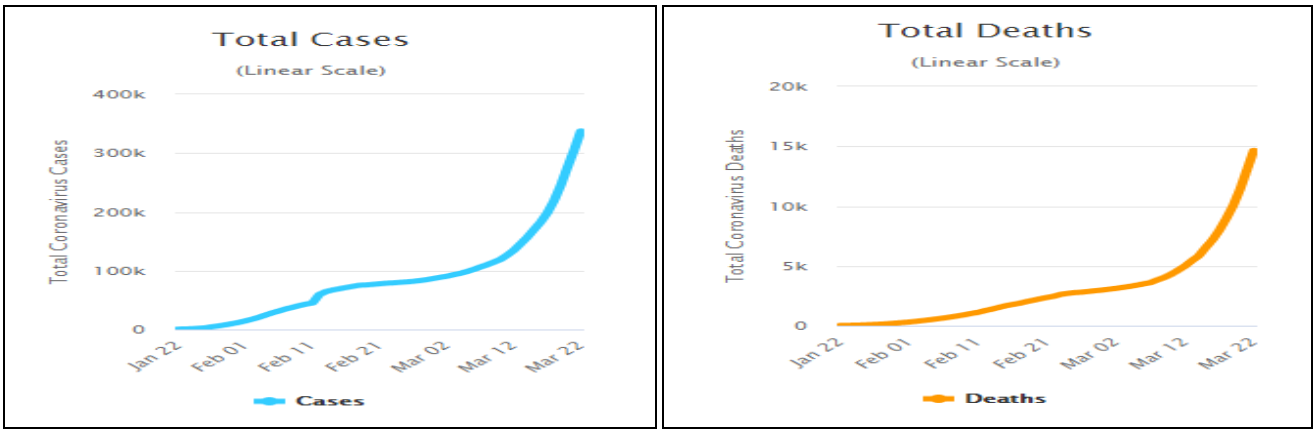


FIG. 3: TOTAL CASES AND DEATHS OF SARS-COV-2 TIMELINE AS ON 23-3-2020

As of 25-3-2020, there are 434654 coronavirus cases, 19604 deaths, 111854 recovered, and 303196 active cases. As on 12-10-2020, there are 37,754,464 Coronavirus Cases, 1,081,500 Deaths, 28,361,239 Recovered and 8,311,725 active cases. The linear graph of the growth has been shown in **Fig. 4**.

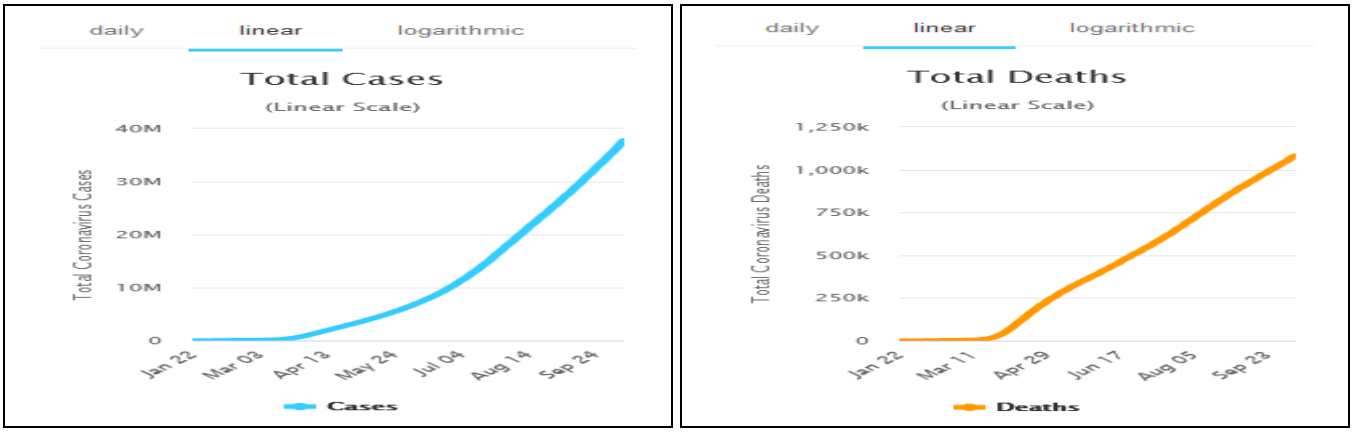


FIG. 4: TOTAL CASES AND DEATHS OF SARS-COV-2 TIMELINE AS ON 12-10-2020

The temperatures on 25-3-2020 in some infected places are shown in **Table 12**. There may be no effect of viral survival and activities based on temperatures but may be active in rainy and winter seasons **Table 13**. The data showed that the origin country of SARS-CoV-2, China, has controlled infections and deaths, and the methodology of control may not be followed by other countries. There may be few more microbial origins in the future that may damage economic and government strategies, which may be dangerous for the human community.

TABLE 13: INFECTIONS, DEATHS AND TEMPERATURES IN SOME COUNTRIES BY SARS-COV-2

Country	25-3-2020				3-8-2020				12-10-2020			
	People		Temperature (in °C)		People		Temperature (in °C)		People		Temperature (in °C)	
	Infected	Deaths	Low	High	Infected	Deaths	Low	High	Infected	Deaths	Low	High
China	81218	3281	7 °C	22 °C	84428	4634	26	38	85578	4634	6	19
Italy	69176	6820	7 °C	13 °C	248229	35166	20	28	354950	36166	8	18
USA	54963	784	3 °C	9 °C	4824715	158484	24	31	7991998	219695	16	19
Spain	47610	3434	1 °C	17 °C	335602	28445	12	29	890367	32929	8	20
Iran	27017	2077	9 °C	15 °C	312035	17405	24	35	500075	28544	11	21
Australia	2423	9	17 °C	23 °C	18318	221	1	11	27285	898	14	23
Japan	1193	43	3 °C	16 °C	36689	1011	25	33	88912	1627	19	25
South Africa	709	0	16 °C	28 °C	511485	8366	7	23	692471	17780	10	16
India	562	10	27 °C	32 °C	1830949	38485	29	36	7120538	109184	27	32
Singapore	558	2	27 °C	29 °C	53051	27	27	31	57876	27	27	31
New Zealand	205	0	13 °C	19 °C	1567	22	11	14	1871	25	12	16
Sri Lanka	102	0	26 °C	32 °C	2824	11	27	30	4752	13	26	29
Bangladesh	39	5	22 °C	33 °C	242102	3184	27	35	378266	5524	27	34

Most humans follow ancient and modern methods of health care products and medicines to keep the health fit with strong immunity [23, 24, 25]. Most of the techniques followed by humans in the past will make a better health habit for future generations. The activity of Curcumin E is more on Spike protein of SARS-CoV-2 compared to selected vaccines. The vaccines like EIAV vaccine gp45, anti-SARS m396 Antibody, EIAV vaccine gp45, and E protein of the Japanese encephalitis live attenuated vaccine virus are less effective than Curcumin for SARS-CoV-2. Currently, there is no effective drug treatment or vaccine exists for the treatment of SARS-CoV-2. Aging diseases like diabetes, cardiovascular disease, hypertension, chronic respiratory disease, and cancer are showing a high risk of death due to SARS-CoV-2 [26].

Remdesivir that is developed for the treatment of viruses like the Ebola virus and Marburg virus is effective against SARS-CoV-2. Hence, better vaccines are to be developed in the future.

CONCLUSION: The viruses that emerge from time to time can spread to several countries and can make pandemics.

Hence the immunity has to be developed, and vaccine development procedures have to be established for the control of novel viruses.

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