

A New-fangled Corona virus coupled with Human Respiratory and AI in COVID-19 Discovery

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Article History: Received: 10 November 2020; Revised: 12 January 2021; Accepted: 27 January 2021; Published online: 05 April 2021

Abstract: Recently a very strange time to fight with invisible enemy. The Corona virus ailment 2019 also known as COVID-19 outbreak, which emerged from Wuhan, the Hubei Province, China, had broaden to all the regions of China and 28 additional countries. Corona viruses are a group of viruses with non segmented, single stranded and positive-sense RNA genomes. Corona viruses is also popular to contaminate human hosts and effect respiratory disease like brutal SARS-CoV (Acute Respiratory Syndrome Corona virus) and MERS-CoV (Middle East Respiratory Syndrome Corona virus). In this paper we discussed on detail analysis of COVID-19 disease.

Keywords: Corona virus, COVID-19, Pandemic.

1. Introduction

The name Corona virus is derived from the Latin word corona, meaning “crown” or “halo” because the virus has “crown-like spikes on their surface”. Corona viruses are a ancestors of viruses which start from the widespread cold to MERS corona virus, that is available in MERS (Middle East Respiratory Syndrome) corona virus and SARS (Severe Acute Respiratory Syndrome) corona virus. Corona viruses are mostly found to be circulated in animals but few of these corona viruses have the potential of transit from animals and humans and vice-versa. Corona viruses were primarily discovered among chicks in year 1930 when an finely tuned respiratory contamination of domestic chickens was exposed to be caused by Infectious Bronchitis Virus (IBV). Human corona viruses were discovered in the 1960s.

In today's era due to the emerging infectious disease there is a huge threat in public about these diseases, like SARS (Severe Acute Respiratory Syndrome) and Zika virus disease. In December 2019, SARS-CoV (Severe Acute Respiratory Syndrome β -Corona virus) was detected in Wuhan, China. It was initially named as 2019-nCoV (2019-Novel Corona virus) on 12th January 2020 by World Health Organization (WHO) and later WHO officially named the disease as COVID-19(Corona virus Disease 2019). On 11th February 2020, according to the survey it has also been found that there is a close genetic relationship between SARS-CoV and SARS-CoV-2.

There are many species of virus found in Bats, which are also known as natural resource of viruses such as Nipah, Ebola, Rabies, Hendra and Marburg. α -CoV(Alpha-CoV) and β -CoV(beta-CoV) are also been detected in bats in Asian and African countries and some parts of America. CoV's are single-stranded, optimistic sagacity RNA viruses with a comparatively large genome size 26 to 32 kb. They are classified into four generations namely α - β - γ - δ -CoV. From this α - and β -CoV are highly capable of infecting mammals, while γ - and δ -CoV primarily have a propensity to contaminate birds. The transmission of SARS-CoV-2 mainly takes place from one human being to another i.e. among family unit, relations and acquaintances that came into contact with patients.

How Corona virus can be spread?

There are three major symptoms how a Corona virus is spread:

1. The first major transmission of Corona virus is when a person is coughing and sneezing without covering his/her mouth/nose and spread the droplets in the air.
2. The second reason is when Handshaking or touching an infected person.
3. The third reason is when a person touches a plane or an entity which consist of droplets of disease and after the person touches his/her eyes, nose or mouth.

National Institutes of Health (NIH) provides the different teams of public those who are at high risk due to COVID-19. In this people from age group of 60 and above, children's of age group 0-10 and pregnant ladies are there; also people who are underlying any medical conditions are also prone to such viruses.

Is there a cure for corona virus?

There is no specific treatment available till date, but doctors are using the existing drugs for viruses such as Ebola, malaria and HIV. Development of a vaccine is in progress many scientists are working on it, but it is

unlikely to be available in next year.

Phenotype and Genotype of Covid-19

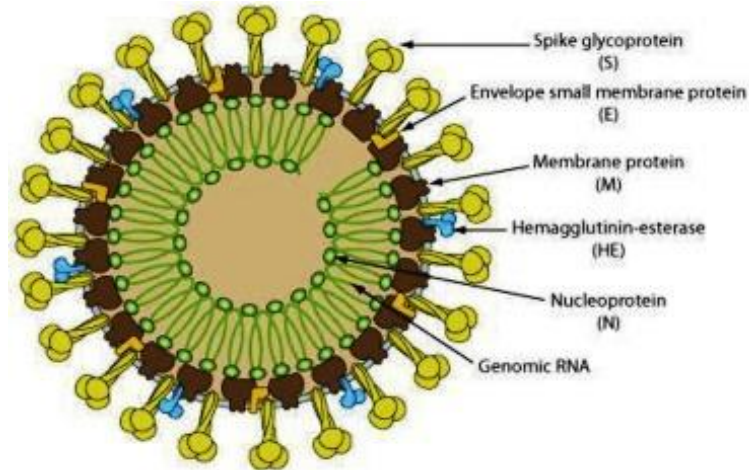


Figure 1. Schematic of a corona virus. (<http://ruleofsix.fieldofscience.com/2012/09/a-new-coronavirus-should-youcare.html>)

Corona virus i.e. COVID19 is a sphere-shaped or pleo-morphic collected particles which consist of single-stranded (positive-sense) RNA linked by means of nucleoprotein inside capsid consisting of surrounding substance protein. The shape of the wrapper is club-shaped glycoprotein projections. Some of the corona viruses also contains a hem agglutinin-esterase protein (HE)[6] (Fig. 1).

Corona viruses owns the major genomes (26.4e31.7 kb) out of all available RNA virus, with G p C stuffing changeable from 32% to 43%. changeable figures of tiny ORFs are there stuck between the variety of sealed genes (envelope, membrane, ORF1a/b, spike, and nucleo capsid). The viral genome also has some typical features, counting a sole N-terminal portion inside the spear protein. Genes for the most important structural proteins in each corona virus take place in the 50e30 classify as S, E, M, and N[7] (Fig. 2).

A distinctive CoV includes a smallest count of six ORFs in its genome. Apart from Gamma corona virus with the aim of lakes nsp1, the primary ORFs (ORF1a/b), with reference to two-thirds from the entire genome measurement lengthwise, encode 16 nsps (nsp1-16). ORF1a and ORF1b hold a frame shift amongst that produce two polypeptides: pp1a and pp1ab.

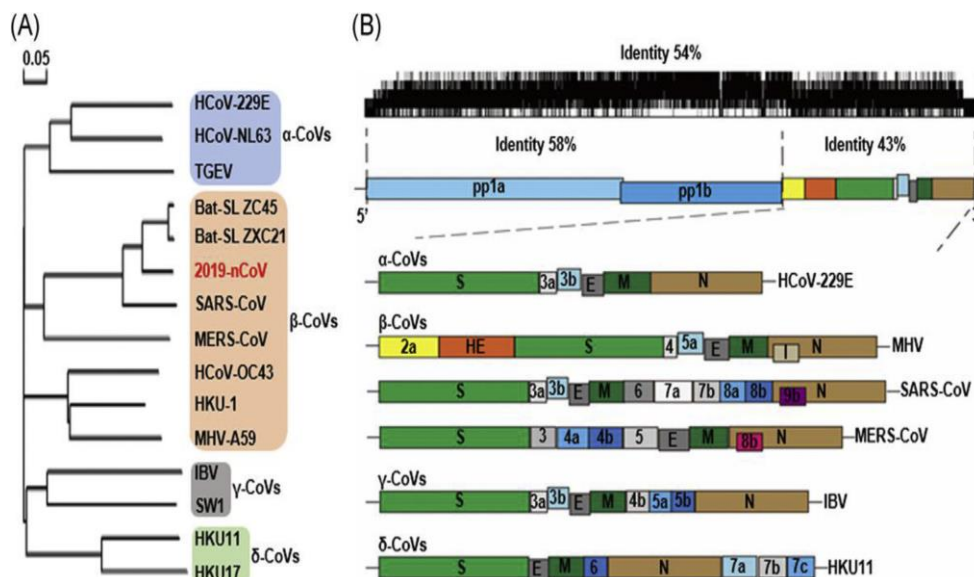


Figure 2. The genomic structure and phylo-genetic tree of corona-viruses. [1]

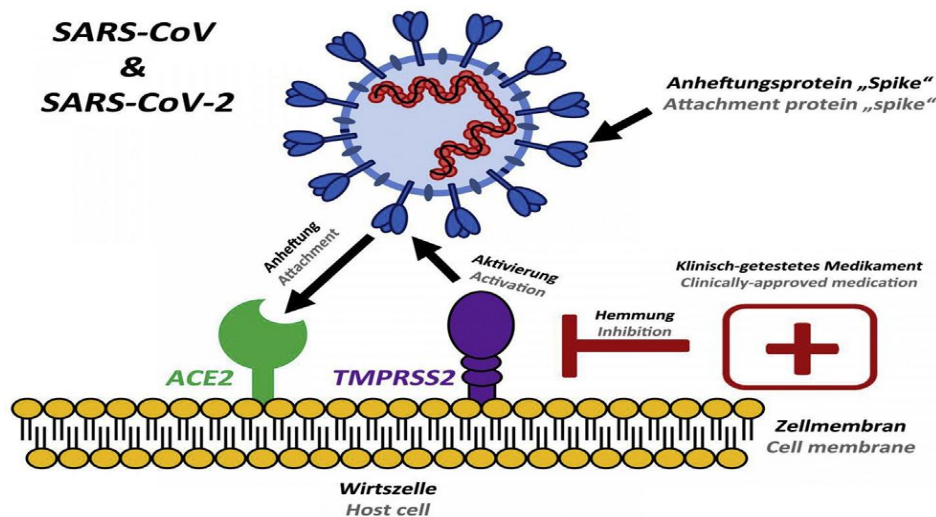


Figure 3. Protein “spike” of the novel corona-virus COVID19 and SARS-CoV make use of identical cellular connection aspect (ACE2) and cellular protease TMPRSS2 to activate themselves. [3]

Difference between SARS-COVID19, SARS-CoV, and MERS-CoV, these 50UTR, 30UTR are mixed up in inter and intra-molecular exchanges which are very significant from the functionally perspective for RNAeRNA exchanges and for fastening of viral and cellular proteins. [4] P1ab is the foremost ORF of the entire genome measurement lengthwise programming non-structural proteins by means of size of 29844bp (7096aa) for COVID-19, 29751bp (7073aa) in SARS-CoV and 30119bp (7078) MERS-CoV, correspondingly. Also when we are comparing the spike protein of all the corona viruses particularly for COVID-19 it is 1273aa, SARS-CoV it is 21493aa, and 1270aa for MERS-CoV. Hereditarily, COVID-19 was found not as much of same as of SARS-CoV (around 79%) and MERS-CoV (around 50%). The understanding of envelope protein(E), nucleocapsid protein (N), and membrane protein (M) among these three corona viruses is different as shown in Fig. 3.[5]

2. Literature Survey

Fan Wu et. al. the study has been carried out on a model of bronchoalveolar lavage fluid out of the 41year old patient recognized novel RNA virus strain commencing the relations Coronaviridae, that is elected here ‘WH-Human1’ coronavirus. Phylogenetic examination of the whole viral genome (29,903 nucleotides) discovered that the virus was mainly strongly associated (89.1% nucleotide similarity) to a cluster of SARS-like corona viruses. This disease damage was nominated as WH-Human 1 coronavirus (WHCV). To conclude the evolutionary associations sandwiched between WHCV and beforehand recognized corona viruses, phylogenetic trees was predictable on the foundation of the nucleotide sequence of the whole-genome sequences, the non-structural protein genes ORF1a and ORF1b, and the chief structural proteins programmed by the S, E, M and N genes. For enhanced accepting the latent of WHCV to contaminate humans, the receptor-binding domain (RBD) of its spike protein was differentiated with others like SARS-CoVs and bat SARS-like CoVs. The RBD sequence of WHCV were further strongly correlated to that of SARS-CoVs.

Shrikrushna Subhash Unhale et. al. as we include witness the coming out of two zoonotic, exceedingly pathogenic HCoV: severe acute respiratory set of symptoms corona virus (SARS-CoV) and Middle East respiratory set of symptoms corona virus (MERS-CoV). Reproduction of HCoV is synchronized by a variety of host factor and induces severe alteration in cellular organization and functioning. In this paper authors has reviewed all the information available related to corona virus including types, life cycle of virus, transmission, symptoms that can be observed, how it can be Diagnosed, available Treatment, and Prevention methods. Statistics on region wise count of cases and death count across all over the world and Indian region wise statistics is also present.

Yan-Rong Guo et. al. with the most recent investigation development of the epidemiology, pathogenesis, and medical distinctiveness of COVID19, and with the existing knowledge of SARS-CoV-2 the authors summarized the information as above: Initially, the rising pneumonia, COVID19, caused by SARS-CoV-2, exhibit muscular contamination but a smaller amount virulence, compared to SARS and MERS, in requisites of morbidity and mortality. Initiating from pool of bats and unidentified transitional hosts, SARS-CoV-2 binds to ACE2 with towering resemblance as a virus receptor to contaminate humans. Secondly, the vulnerable inhabitants involves the old and citizens with convinced original medicinal circumstances, which require added concentration and

care. Thirdly, the underneath treatment, collectively with strong antiviral drugs, such as remdesivir, chloroquine, or lopinavir/ritonavir, were performed with explicit results on treating COVID19 patients.

Lifang Li et. al. [10] during this pandemic situation public use societal medium to get hold of and switch over different types of information at a notable and exceptional level. As the on-spot data is important for the civic and establishment to answer to the outbreak, it became extremely vital to recognize such situational data and to comprehend how it is life form propagated on societal medium. This paper tries to plug this opening by harnessing Weibo data tool and NLP techniques and distinguished the COVID-19-related data in seven different types of situational data like, concern and recommendation, fatalities and harm contributions of money, commodities, or services, people absent, found, or seen.

Wen-Hua Kong et. al. job has been carried out to re-analyse 640 throat swabs composed from patients in Wuhan with influenza-like-illness from 6 October 2019 to 21 January 2020 and bring into being that 9 of the 640 throat swabs were positive for SARS-CoV-2 RNA by quantitative PCR, signifying the public show of SARS-CoV2 in Wuhan in the beginning January 2020. The discovery of SARS CoV- 2 cases amongst confined patients with ILI suggests that the public spread was recognized in Wuhan in the early hours in January. Relating to the current outbreaks episode on the Diamond Princess Cruise ship and Daequ, South Korea, the author suggested the intensification the pathogen observation of ILI cases in all cities facing the hazard of SARS-CoV-2 the public spread.

Michael Dub'e et. al. the Graph Evolution Tool (GET) was build to produce individual get in touch with network on behalf of who can contaminate whom surrounded by a community. GET is prolonged upon to reproduce communities which comprise 512 individuals in up to eight districts, Originally infecting one person in one region and dispersion all the way through a society.

Said Nadeem as this deadly disease is incredibly new and incredibly less methodical matter is obtainable on the subject, a variety of paid journals and companies are contributing by giving free resources in print about the Coronavirus. In this paper, all the articles about Coronavirus that are unreservedly provided by a range of journals and companies in the region of the planet are discussed. This examination is also unbolt to update so if any free starting place can be further added or modernized at this point.

3. Analysis of Corona Virus Diseases

Below Table 1. shows that analysis of coronavirus diseases.

Table 1. Analysis of Coronavirus Diseases

Sr. No.	Year	Disease Name	Details	Symptoms	No. of affected People	No. of people death	Transmission
1	1965	HCoV-OC43-beta coronavirus	Human coronavirus OC43 is a part of the type Betacoronavirus 1 which infects humans and farm animals.	common cold	Millions every year	-	lock contact through contaminated humans or touching a plane that carry the virus.
2	1966	HCoV-229E-alpha coronavirus	Human coronavirus 229E is a type of coronavirus which infects humans and bats.	Starting from the common cold to high-morbidity outcomes such as pneumonia and bronchiolitis .	Millions every year	-	lock contact through contaminated humans or touching a plane that carry the virus.
3	2002	SARS-CoV	SARS-CoV (Severe Acute Respiratory Syndrome), established to transmit amongst civet cats to	Fever, headache and muscle pain , followed in	8,098	774	Supposed to have spread from bats, which contaminated

			humans.	2–14 days by the onset of respiratory symptoms mostly cough, <u>dyspnea</u> , and <u>pneumonia</u> .			civets. Transmitted mostly among humans through close contact.
4	2004	HCoV-NL63 - alpha coronavirus	Human corona-virus NL63 is a species of corona-virus which was recognized in late 2004 in a seven-month-old child with bronchiolitis in the Netherlands.	hoarseness, <u>bronchitis</u> , fever, cough, <u>rhinitis</u> , sore throat, <u>bronchiolitis</u> , <u>pneumonia</u> , and <u>croup</u>	Millions each year.	-	Close contact with contaminated humans or touching a plane that carry the virus.
5	2005	HCoV-HKU1- beta coronavirus	Human coronavirus HKU1 is a species of coronavirus which originated from contaminated mice.		Millions every year.	-	Close contact with contaminated humans or touching a plane that carry the virus.
6	2012	MERS-CoV	Middle East Respiratory Syndrome (MERS- CoV) of 2012 was begin to broadcast from dromedary camels to humans.	fever, cough and tininess of breath. Some also had diarrhea and nausea.	2,521	866	Often from touching contaminated camels or overriding their milk or meat. partial spread between humans throughout close contact.
7	2019	SARS-CoV-2	Initially, scientists thinking the virus may have urbanized in bats, and afterwards pangolins. However, genomic comparisons propose that the SARS-Cov-2 virus is the effect of a recombination among two unlike viruses, meaning the accurate origin of the virus is still unclear.	cough, fever, difficulty breathing, pneumonia in both lungs	more than 1,290,000 till April 7, 2020	76,000 Till April 7, 2020	Likely from touching or eating an infected, as yet unknown animal. Human-to-human transmission occurs through close contact.

4. AI in covid-19 detection

As the COVID-19 epidemic carry on to boost transversely the sphere, Industries and researchers are finding many ways to utilize AI as a technique of solving the challenge of the virus. At this point presently a quantity of the projects by means of AI to that deal with the corona-virus epidemic.

AI system were considered to be amongst the initial to notice so as to the corona-virus outburst, reverse while it was immobile imperfect to a small area of the Chinese city of Wuhan, possibly will turn out to be a full-

on international epidemic. It's consideration that AI-driven Health-Map, which is associated with the Boston Children's Hospital, Collected the improving cluster of mysterious pneumonia belongings soon previous to human being researchers, even though it only rank the outbreak's importance as medium.

An Assistant professor from the department of psychology, Stanford University named Johannes Eichstaedt, had been investigating Twitter posts to guess how COVID-19, and updates are brought to the way how we live our lives, is upsetting our psychological fitness. By means of AI-driven text examination, Eichstaedt queried over two million tweets hash tagged with COVID-related stipulations for the period of February and March, and pooled it with further datasets on applicable factors counting the no. of cases, deaths, demographics and other, to light the virus effects on mental healthiness.

Canadian startup Darwin AI has urbanized a neural network which could monitor X-rays for signs of COVID-19 contagion. When using swabs of patients is default for testing for coronavirus, analyzing chest X-rays might tender a choice to hospitals that does not have an adequate amount of workforce or testing kits to course all of the patients rapidly.

A machine-learning community owned by Google named Kaggle is scenery to no. of COVID19 associated challenge to the members of family, together with fore-casting the no. of cases and fatalities by city as a means of guessing accurately why a variety of spaces are beat inferior than others. Deep Mind, the AI appendage of Google's parent corporation Alphabet, is accessing data on genomes to forecast organisms protein organization, potentially flaking glow on which drugs could work adjacent to COVID19.

No. of research projects are making use of AI to be familiar with drugs which were urbanized so as to struggle further disease although which could now be re-purposed to acquire on corona-virus. By understanding the molecular set of connections of lively drugs with AI, companies want to recognize which ones may disturb the pattern in COVID19 works.

5. Experimental Results

We have analyzed Covid19 dataset of India which is available on Kaggle. The dataset which is used here is collected over period of 30 January 2020 to 16 may 2020.

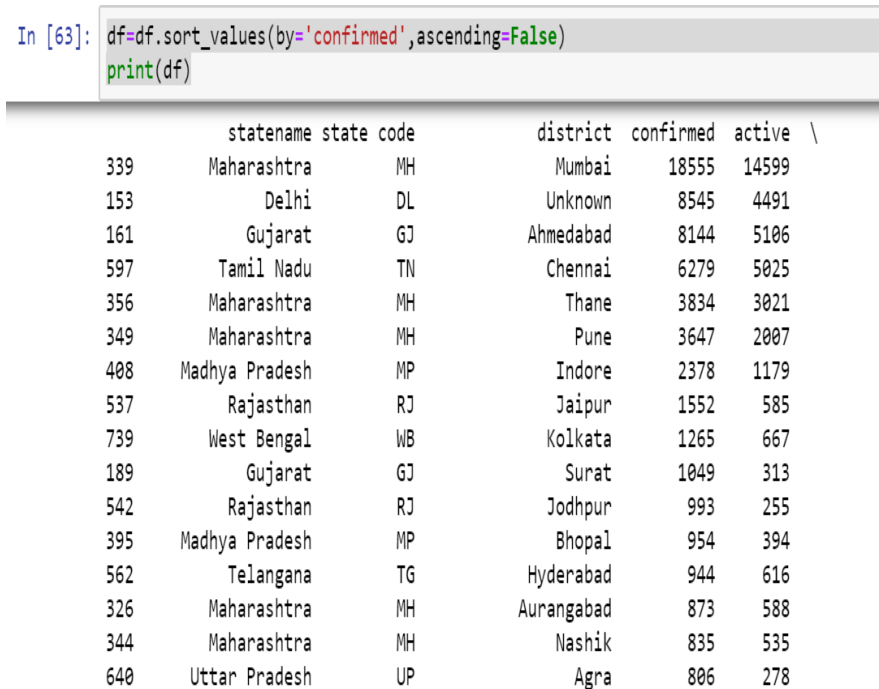


Figure 4. It shows the district wise confirm cases in India in descending order. Where we can see that, Mumbai, capital of Maharashtra is having highest number of covid cases


```
In [62]: df.head()
```

Out[62]:

	statename	state code	district	confirmed	active	deceased	recovered
153	Delhi	DL	Unknown	8545	4491	128	3926
339	Maharashtra	MH	Mumbai	18555	14599	696	3260
161	Gujarat	GJ	Ahmedabad	8144	5106	493	2545
349	Maharashtra	MH	Pune	3647	2007	188	1452
597	Tamil Nadu	TN	Chennai	6279	5025	52	1202

Figure 5. It shows the count of recovered cases of COVID 19 is highest in Delhi

```
In [102]: df.sort_values(by='DeathRate',ascending=False)
```

Out[102]:

	statename	state code	district	confirmed	active	deceased	recovered	DeathRate
573	Telangana	TG	Mancherial	1	0	1	0	100.000000
687	Uttar Pradesh	UP	Lalitpur	1	0	1	0	100.000000
579	Telangana	TG	Narayanpet	1	0	1	0	100.000000
56	Assam	AS	Hailakandi	1	0	1	0	100.000000
546	Rajasthan	RJ	Other State	7	3	4	0	57.142857
201	Himachal Pradesh	HP	Mandi	2	0	1	1	50.000000
390	Madhya Pradesh	MP	Ashoknagar	2	1	1	0	50.000000
357	Maharashtra	MH	Wardha	2	1	1	0	50.000000
690	Uttar Pradesh	UP	Mahoba	3	0	1	2	33.333333
346	Maharashtra	MH	Other State	41	31	10	0	24.390244
548	Rajasthan	RJ	Pratapgarh	5	1	1	3	20.000000
398	Madhya Pradesh	MP	Chhindwara	5	1	1	3	20.000000
543	Rajasthan	RJ	Karauli	10	5	2	3	20.000000
741	West Bengal	WB	Murshidabad	5	4	1	0	20.000000

Figure 6. State wise Death Rate in India: Here states like Telangana, Uttar Pradesh and others are having highest death rate, as the number of confirmed cases are only one.

```
> View(nation_level_daily)
> sum(nation_level_daily$totaldeceased) / sum(nation_level_daily$totalconfirmed)
[1] 0.03261956
```

Figure 7. Death rate in India :3.2.

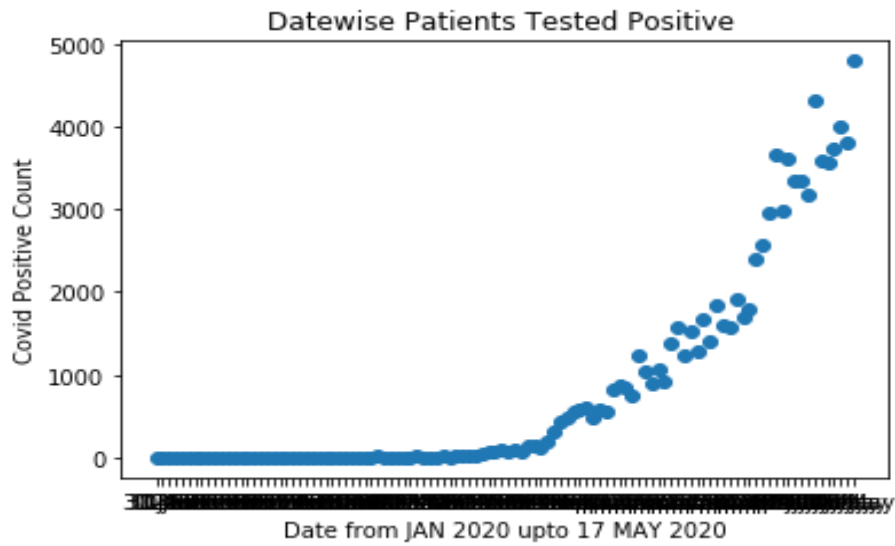


Figure 8. Date wise Tested Positive cases of COVID 19 in India

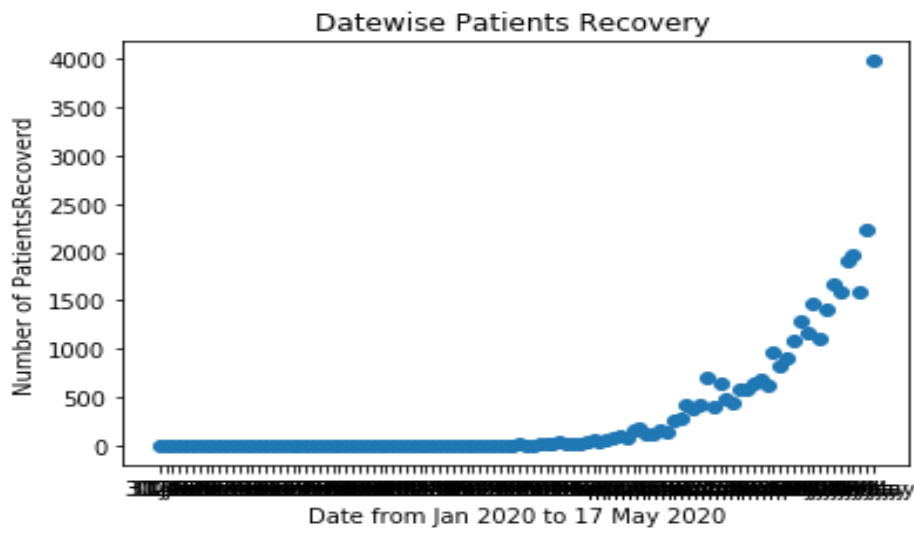


Figure 9. Day wise patients recovery in India

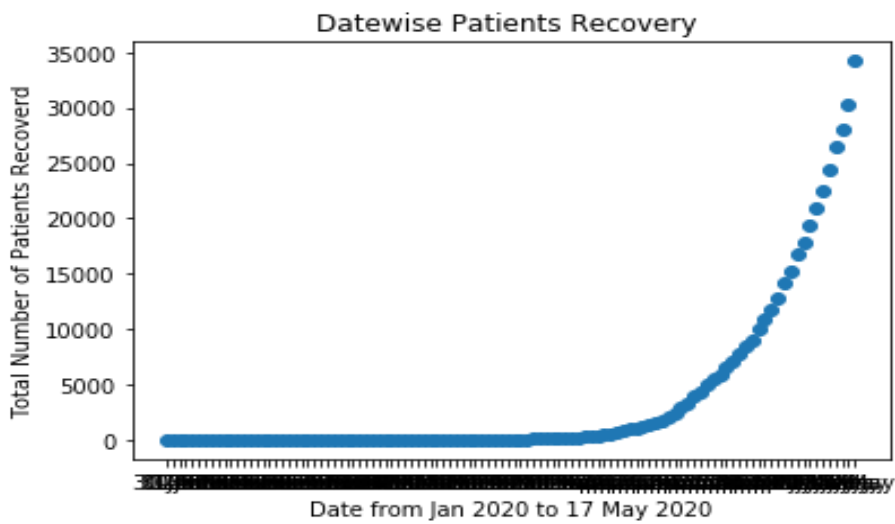


Figure 10. Day wise total number of patients recovered in India.

Here it shows that the lockdown declared in the country worked well to control the spread of Covid-19 and the result also shows that the recovery of patient in India is also good.

6. Conclusion

In this paper we did the detailed analysis of corona virus i.e. COVID-19 with their symptoms and how to take cure. Addressing the different challenges of the viruses by using Artificial Intelligence as a method. AI system were found to be amongst the initial to notice with the aim of corona virus outburst. In this paper we analyzed COVID-19 dataset of India which is available on Kaggle. In India lockdown has been declared to control the spread of COVID-19 and the outcome of this shows that the recovery rate of patients is good.

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