Determination of Symptom Association with COVID-19

By

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Declaration

It is at this moment declared that

1. The thesis submitted is my original work while completing my degree at Brac University.
2. The thesis does not contain material previously published or written by a third party, except where this is appropriately cited through complete and accurate referencing.
3. The thesis does not contain material accepted or submitted for any other degree or diploma at a university or other institution.
4. I/We have acknowledged all primary sources of help.

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Approval

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1) This material is the authors' original work, which has not been previously published elsewhere.

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Abstract/ Executive Summary

SARS-CoV-2 is the ninth known coronavirus that infects people and the seventh discovered in the previous 20 years. Coronaviruses have long been suspected of posing a significant pandemic danger. COVID-19 reveals a wide range of clinical manifestations, severity levels, and mortality rates. Although the deadly impacts of the COVID-19 pandemic can be seen in people of all ages, the most severe health implications and deaths from COVID-19 are connected with older adults, particularly older males. We aim to find the correlation between different demographics such as gender, age, area, symptoms, and comorbidities. We have tested and analyzed over eight months of 2309 covid suspected patients, and among them, 24.0% were positive, and the majority of these positive patients were male. We have also found that people over 70 years are prone to be more affected. These positive patients have a fever, body aches, headache, loss of taste and smell, etc. Our results support the current findings on Covid-19 and show some areas for future research.

Keywords: SARS-CoV-2; COVID-19; Demographics; Age, Gender; Symptoms; Comorbidities

Dedication

Dedicated to my Parents.

Acknowledgment

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List of Acronyms

SARS-CoV-2: Severe Acute Respiratory Syndrome Coronavirus 2

IgG: Immunoglobulin G

HCoV: Human Coronavirus

PCR: Polymerase Chain Reaction

CDCC: Center for Disease Control in China

WHO: World Health Organization

RNA: Ribonucleic Acid

ORF: Open Reading Frames

ADRP: Adipose Differentiation Related Protein

NSP: Nonstructural Protein

Bat-SL-CoV: *Bat* SARS-like Coronavirus

MERS-CoV: Middle East Respiratory Syndrome Coronavirus

RT-PCR: Reverse Transcriptase Polymerase Chain Reaction

ACE2: Angiotensin-Converting Enzyme 2

CFR: Case Fatality Rate

RBD: Receptor Binding Domain

CDC: Center for Disease Control

VTM: Viral Transport Medium

BSC-2: Biosafety Cabinet class 2

P-Value: Probability Value

CI: Confidence Interval

OR: Odds Ratio

H/O: History of

Chapter 1

Introduction

1.1 Background

There is a lack of information on the natural history of a severe respiratory distress syndrome asymptomatic infection, SARS-CoV-2 [1, 2]. Coronaviruses have long been suspected of posing a significant pandemic danger. SARS-CoV-2 is the ninth known coronavirus that infects people and the seventh discovered in the previous 20 years [3, 4]. Like most human viruses, all prior human coronaviruses had zoonotic origins. The establishment of SARS-CoV-2 has some hallmarks of previous zoonotic outbreaks. It is very similar to the SARS-CoV strain that infected people in Foshan, Guangdong province, China, in November 2002, and again in Guangzhou, Guangdong province, in 2003 [5]. Both SARS-CoV emergence events were linked to markets selling live animals and involved species, specifically civets and raccoon dogs[6], which were also sold live in Wuhan markets in 2019 [7]and are susceptible to SARS-CoV-2 infection [8]. Animal merchants working without a SARS diagnosis in 2003 were found to have elevated levels of immunoglobulin G (IgG) of SARS-CoV (13 percent overall and >50 percent for civet traffickers)[9]. Subsequent serological investigations revealed a 3% positive rate of SARS-related coronaviruses (SARS-CoV) in Yunnan province inhabitants living near bat caves [10], showing regular exposure in rural areas. Although animals from this province have been preferentially sampled, the closest known relatives of SARS-CoV and SARS-CoV-2 are viruses from bats in Yunnan. There is a significant geographic gap between Yunnan and the first human cases for SARS-CoV and SARS-CoV-2, underscoring the difficulties in determining the exact pathway of viral development and the need for sampling outside Yunnan. Human coronavirus-OC43 (HCoV-OC43), human coronavirus-HKU1 (HCoV-HKU1), human coronavirus-229E (HCoV-229E), and human coronavirus NL63 (HCoV-NL63) are all endemic human coronaviruses (HCoV-NL63). These viruses are zoonotic, and the circumstances surrounding their emergence are unknown. HCV-HKU1, initially characterized in a big Chinese metropolis (Shenzhen, Guangdong) in the winter of 2004, has an unknown animal origin, a furin cleavage site in its spike protein, and was initially found in a case of human pneumonia [11]. The Covid-19 outbreak on the cruise ship Diamond Princess resulted in 712 people from 3711 passengers and crew, of whom 410 were asymptomatic when the testing occurred, and 410 were

asymptomatic [12]. From Diamond Princess, 96 persons infected with SARS-CoV-2 asymptomatic at the time of the testing were taken to a hospital in central Japan between 19 February and 26 February, together with their 32 cabin mates who tested negative on the ship [13, 14]. The median of four days following the first PCR-test, which meant presymptomatic rather than asymptomatic, was subsequently developed in 11 of these 96 persons with clinical signs and symptoms of covid-19 [12, 15]. With increasing age, the risk of being presymptomatic increases. In the 72 hours following their arrival at the hospital, eight of 32 Cabin mates with a negative PCR test had a positive PCR test but were asymptomatic. In all, 90 individuals with SARS-CoV-2 asymptomatic infection were asymptomatic during and remained asylum-based until the condition was resolved [16]. Fifty-eight passengers and 32 crew members, medium age 59.5 years, have been in the group of persons with asymptomatic SARS-CoV-2 infection [13]. 24 people with hypertension and diabetes had coexisting medical conditions. Six days after the initial positive PCR test on the ship, the first PCR in a hospital was performed [14]. Between the first positive PCR test and the first of the two serial negative PCR tests, the mean number of days was nine days, and the cumulative percentage of those with infection resolution 8 and 15 days later was 48% and 90%—the risk of delayed infection resolution [17].

Fig 1: Wuhan - the city of 11 million where COVID-19 first emerged [18]

1.2 Chronology of the pandemic

The Center for Disease Control in China (CDCC) announced that the first instances of atypical pneumonia were found in Wuhan, the capital of Central China's Hubei province, during the last week of December 2019. After the first cases were identified, Chinese health officials closed Huanan's "wet market" after some investigation revealed that this location was the likely initial site of the virus [19].

During the first week of January, Chinese officials revealed that the new atypical pneumonia was not caused by the SARS or MERS Coronaviruses but by a novel strain of the Coronaviridae family, a virus named SARS-CoV-2 [19].

The first SARS-CoV-2-related fatality was announced on 11 January, and a day later, a group of Chinese researchers disclosed the genome of the virus implicated in the COVID-19 outbreak. The SARS-CoV-2 virus spread worldwide after the first case was discovered in China. The attack originated in Asia, but the first probable cases were identified in Europe and North America only days later. The World Health Organization (WHO) labeled this illness a global pandemic on 11 March. They were using the most recent data from 14 April 2020. Two million people have been infected with the virus, resulting in over 120,000 deaths in over 210 countries worldwide [20].

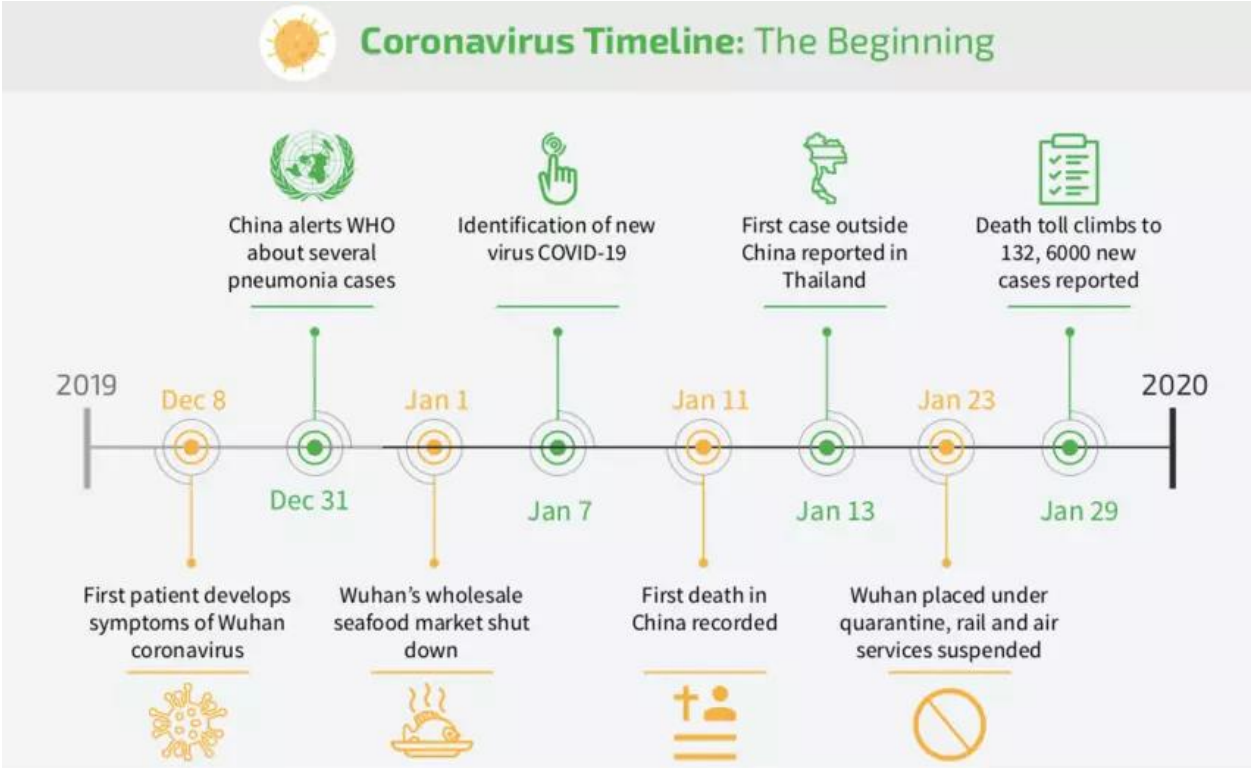

Fig 2: Chronology of the pandemic [21].

1.3 Classification

In the Coronaviridae family of the order Nidovirales, coronaviruses belong to the Coronaviridae sub-family. They can lead to diseases in humans and many other animals in the respiratory, digestive, or nervous systems [22]. The spherical particles of the coronavirus are about 80 to 160 mm in diameter. The spike (S) protein covers the surface of the envelope, and S proteins include the membrane (M) proteins and envelope (E). A helical nucleocapsid located inside the shell is the genomic RNA and the phosphorylated nucleocapsid (N) protein [23]. A single-stranded RNA, positive-stranded genome with a length of 26 to 32 kb is included in the coronavirus genome, the longest known genome of RNA viruses [24].

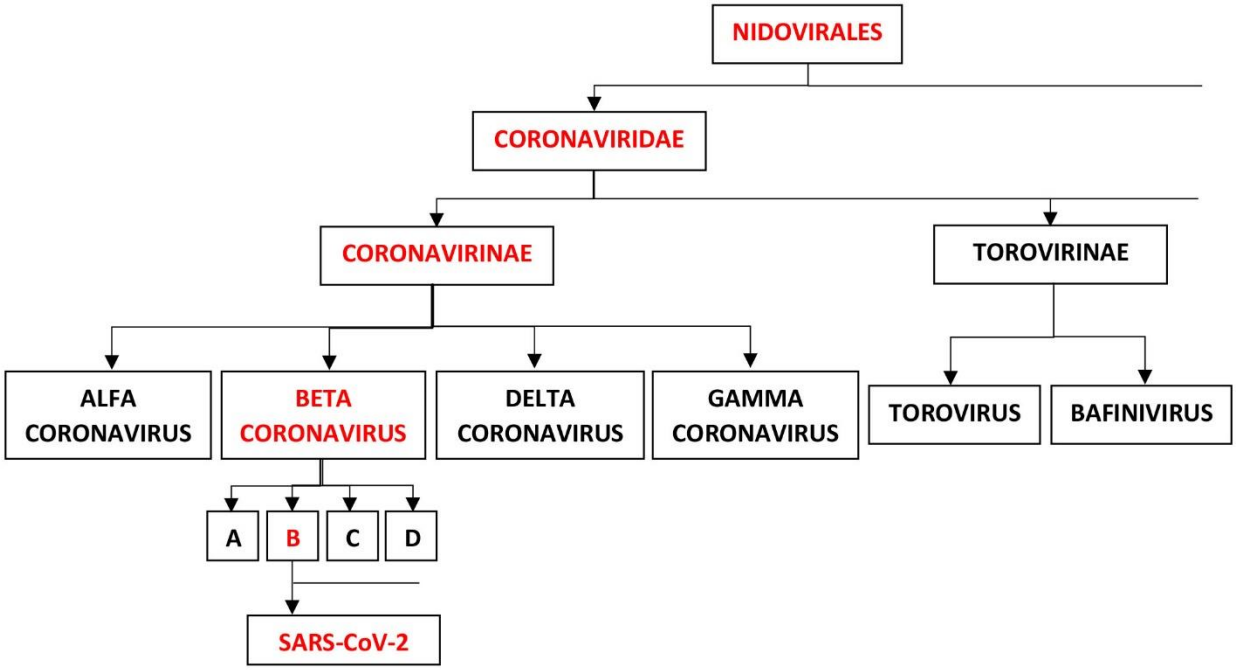

Fig 3: Classification of SARS-CoV-2 [25].

1.4 Differences between SARS-CoV-2 and SARS-CoV

The identification of coronaviruses depends primarily on the resemblance of the amino acid sequences of the seven fields encoded by ORF1ab, including ADRP, nsp5, and nsp12–16, according to the principle of the international commission on virus classification [23]. The amino acid sequences of the seven dominations are very similar (more than 90%), so SARS-CoV-2 and SARS-CoV are both of the Coronaviridae subfamilies of the Nidovirales family and are SARS-like species even if they are classified into different clusters. They belong to

the Coronaviridae group [22]. The first is in the Bat-like Cluster, and the second is in the SARS Cluster, indicating a significant genetic distance. Phylogenetic analysis has shown that SARS-CoV-2 has a longer branch length than its nearest family members, including Bat-SL-CoVZC45 and Bat-SL-CoVZXC21. SARS-CoV-2 has a high genetic space of only 79, 5 and 40 percent SARS-CoV and MERS-CoV homologies. S-protein homology is also relatively low between SARS-CoV and SARS-CoV-2, at 76.5 percent [24, 26].

1.5 Variants of SARS-CoV-2

1.5.1. Alpha (B.1.1.7)

Alpha (B.1.1.7) was the first significant variation of concern to be found. It was discovered in the fall of 2020 in the United Kingdom and spread around 50% faster than the original SARS-CoV-2. There is some sign that the Alpha variation may cause more severe sickness, even though it was formerly known as the Kent variant before the World Health Organization renamed it the alpha variant in May 2021 [27].

Davies et al. discovered that they detected more significant amounts of viral RNA in nasopharyngeal swabs from B.1.1.7 infected patients, as determined by Ct values from qRT-PCR testing2, in specimens collected in the UK in early 2021. However, no experimental data explains why the Alpha variation spreads faster than previous variants [28].

Compared to the reference genome, the Alpha variant of SARS-CoV-2 has 21 nonsynonymous point mutations and three deletions (accession number: NC 0.45512.2) [29]. The spike protein binds with the host cell receptor, angiotensin-converting enzyme 2 (ACE2), and enables viral entrance into host cells[30], with eight mutations and two deletions. These spike mutations include the deletion H69/V70, which has been found in many separate lineages and linked to enhanced infectivity and immune evasion [31].

Older age is a crucial risk factor for death in the Alpha variation, and being they associated over 60 years old with a much higher CFR [32].

The alpha version was prevalent, and a wide variety of additional symptoms associated with Covid was revealed. Chills, lack of appetite, headache, and muscular pains were the most pervasive symptoms among infected patients, along with other characteristic signs. B.1.1.7 an increased risk of hospitalization, as well as a probable increase in severity and mortality [33].

Someone initially detected the Alpha variety in Bangladesh on January 6, 20218, [34]. Its positive rate rapidly rose over time, reaching a peak of 53% in the second week of March 2021 by displacing Wuhan-like and other pre-existing variants.

1.5.2. Gamma (P.1)

In November 2020, SARS-CoV-2 infection resurfaced in Manaus, Brazil, where it had previously shown significant seroprevalence, and the newly emerging virus was identified as P.1 or Gamma [35]. The spike protein of SARS-CoV-2 has 12 mutations in the Gamma version. Three RBD (Receptor Binding Domain) mutations (K417T, E484K, and N501Y) in particular are prevalent in Alpha (N501Y) and Beta (K417 N, E484K, and N501Y) and are related to enhanced transmissibility, immune evasion, and pathogenicity [29].

The Gamma variant has a more significant infection rate and mutation rate than the Beta variant. Gamma variations are more prevalent in those aged 20 to 39. It primarily affects the younger generation, and the symptoms are nearly identical to those of other varieties. However, it is less dangerous than the Alpha version of SARS-CoV-2 [36].

1.5.3. Delta (B.1.617)

Because of its capacity to infiltrate the host's immune system more effectively than the original strain, the delta variation has spread rapidly over 60 nations [37]: In almost three months, the delta variant infected over 26% of the Indian population. The rapid transmission rate is most likely attributable to the delta strain's immunological evasion ability. Furthermore, the delta variation resulted in a loss of population immunity during the second pandemic wave [38]. Despite vaccine efforts and pandemic limitations, infection rates in the United States continue to rise [39].

Compared to the first detected COVID-19 strain (alpha strain), the delta variation of SARS-CoV-2, B.1.617.2, exhibits 23 mutations [40]. The spike protein contains twelve of these mutations. The spike protein enables host cell adhesion, allowing entrance into the cells. The spike protein is also the immune system’s target for viral elimination. Once the immune system recognizes the spike protein as foreign, B cells make antibodies to bind to it to eradicate it. The spike protein comprises two subunits known as S1 and S2. S1 interacts with the ACE2 receptor, and S2 facilitates viral fusion and integration into the host cell [41]. The more the spike proteins change, the more difficult it is for the immune system to recognize

them and for antibodies to bind for later viral elimination. The novel spike protein that evades the immune system allows for better adhesion to human cells, allowing for a more successful infection.

The mutations identified in the spike proteins are the most prominent gene alterations that allow the delta variation to be the most transmissible version. T19R, L452R, T478K, D614G, P681R, and d960N are the spike gene mutations in this B.1.617.2 variation, with deletions at locations 157 158 [42].

Chapter 2

Methodology

2.1. Population: The sample was collected from people of different ages, gender, area, and socioeconomic background who are suspected of covid-19.

2.2. Questionnaire: These patients were provided with a questionnaire to determine their symptoms, chronic diseases, the previous record of being affected, or contact with other covid-19 affected patients.

2.3. Sample Collection and Storage: The sample was collected in a safe environment/sample collection booth wearing PPE, facemask, gloves, and face shield. According to the regulation provided by CDC, both oropharyngeal and nasopharyngeal sample was collected using a swab stick and collected in Viral Transport Medium (VTM). These VTMs produced by Sansure Biotech contain 1ml of sample Storage Reagent. After that, the samples were kept at 0°C – 4°C.

2.4. RT-PCR:

The VTM (Viral Transfer Medium) is then delivered to the laboratory. In the laboratory, two methods are applied before the RT-PCR run. In the Master Mix room, prepare the master mix by mixing the PCR mix and Enzyme mix, and then place them into the PCR tube. Then transfer the PCR tube to the Sample Processing room. In Sample Processing Room, the sample VTM must be put in the BSC-2. Then extract the viral sample from VTM to Eppendorf using sample release reagent and wait 10 minutes for incubation; after incubation, take the PCR tubes that carry the master mix and take the viral sample from Eppendorf to

PCR tubes. Then the tubes are transferred to the PCR room and placed the PCR tubes in the RT-PCR machine. Before putting tubes in the RT-PCR, set up the plate setup protocol. After placing tubes, the RT-PCR machine needs to be started. It takes 1 hour and 40 minutes to complete the RT-PCR run; after completing the run, analyses the reports whether the sample is **Positive** or **Negative**. Then make the reports and give them to the patients.

Fig 4: The Laboratory. (a) Sample Processing Room (b) Master Mix Room

Chapter 3

Data Analysis

IBM SPSS Statistics 25.0 was used to examine the data. In SPSS, all data were coded, and any erroneous data was eliminated. For information, we use descriptive statistics, means, and frequency distribution. First, Pearson's chi-square test established the relationship between independent and dependent variables. Furthermore, we conducted a supplementary bivariate logistic regression analysis to assess the relationship between socio-demographics and depression, anxiety, and stress. The p-value<.05 and confidence interval (CI) of 95% were used to calculate the significance threshold.

Chapter 4

Result

4.1. Demographic characteristics

During eight consecutive months (September 2020- April 2021), we found 2309 COVID-19 suspected participants who willingly consented to participate in the study. The suspects were

of different ages, sex, and region of Bangladesh with one or a few comorbidities (*i.e.,* heart, lung, liver, kidney disease, and diabetes) or with no other comorbidities. The asymptomatic and symptomatic patients were included in this study, where lack of smell, taste, and fever was recognized as common symptoms.

4.2. Gender:

Among these 2309 suspected patients, 1271(55.04%) were male, and 1038(44.96%) were female (Table: 1). none were identified as transgender in this study. In September 2020 the prevalence rate for male was 22.0% (95%CI: 15.4-30.4) and female was 23.5% (95%CI: 14.9-35.1) with an overall prevalence of 22.6% (95%CI: 17.1-29.2). The next three months had a similar prevalence rate noted. October 2020 had overall prevalence of 22.3% (95%CI: 16.9-28.9) male prevalence rate 25.6% (95%CI: 18.5-34.4) female prevalence rate 16.9% (95%CI: 10.0-27.6), November 2020 had the highest prevalence rate in 2020 with an overall prevalence rate of 30.1% (95%CI: 24.6-36.3) male prevalence rate is 35.9% (95%CI: 28.1-44.6) female prevalence rate is (95%CI: 16.4-32.2). December 2020 had the lowest prevalence rate in year 2020 with an overall prevalence rate of 21.0% (95%CI: 16.3-26.5) male prevalence rate 24.3% (95%CI: 18.1-31.9) female prevalence rate 16.0% (95%CI: 10.0-24.6). From January 2021, the prevalence rate started to decrease a bit. In January 2021, it was around 11.1% (95%CI: 8.6-15.8). It decreased more in February which was around 5.8% (95%CI: 3.0-11.7) male prevalence is 6.0% (95%CI: 2.0-17.2) female prevalence rate is 5.6% (95%CI: 2.10-14.2) but it increased threefold in March 2021 and reached to 16.9% (95%CI: 13.7-20.8) male prevalence rate is 17.2% (95%CI: 12.9-22.6) female prevalence rate is 16.6% (95%CI: 12.0-22.4). In April 2021 it increased further, the prevalence rate was 36.4% (95%CI: 32.8-40.2) male rate is 39.9% (95%CI: 34.9-45.1) female rate is 32.3% (95%CI: 27.3-37.9).

Table: one - Prevalence of SARS-CoV-2 during the study period among stratified month

	Overall (n=2309)	Male (n=1271)	Female (n=1038)
Overall prevalence	24.0(22.3, 25.8)	26.5(24.2, 29.0)	20.9(18.5, 23.5)
2020-September	22.6(17.1, 29.2)	22.0(15.4, 30.4)	23.5(14.9, 35.1)
2020-October	22.3(16.9, 28.9)	25.6(18.5, 34.4)	16.9(10.0, 27.6)
2020-November	30.1(24.6, 36.3)	35.9(28.1, 44.6)	23.4(16.4, 32.2)
2020-December	21.0(16.3, 26.5)	24.3(18.1, 31.9)	16.0(10.0, 24.6)

2021-January	11.1(8.6, 15.8)	11.2(6.60, 18.4)	11.1(6.5, 18.1)
2021-February	5.80(3.0, 11.7)	6.0(2.0, 17.2)	5.60(2.10, 14.2)
2021-March	16.9(13.7, 20.8)	17.2(12.9, 22.6)	16.6(12.0, 22.4)
2021-April	36.4(32.8, 40.2)	39.9(34.9, 45.1)	32.3(27.3, 37.9)

4.3. Age:

The population of 2309 was separated into seven different age groups. Using these seven groups, two additional analysis was done. First was the prevalence of both males and females (Table: 2); another was the risk of SARS-CoV-2 among the sex and in the different age groups (Table: 3).

Below the age of 18 the prevalence rate for SARS-CoV-2 is 23.8% (95%CI: 16.6-32.9) and among them the rate for Male patient is 23.6% (95%CI: 14.2-36.7) and for Female it is 24% (95%CI: 14.1-37.8). Their risk of SARS-CoV-2 is 1.38% (95%CI: 1.13-1.67) and have a p-value of 0.002. For the age range of 19-30 years the overall prevalence rate is 13.2% (95%CI: 11.1-15.7), male prevalence rate noted 16.3% (95%CI: 13.0-20.3), female prevalence rate was 10.3% (95%CI: 7.7-13.6). Their odds of SARS-CoV-2 in 19-30 years was [OR=0.53% (95%CI: 0.33-0.86); p=0.010] compared to 18 years. In the middle range which is 31-40 years prevalence is insignificant and the value is around 28.7% [OR=0.53, (95%CI: 24.3-33.5); p-value=0.304]. Their risk of SARS-CoV-2 was higher in 31-40 years compared to 18 years [OR=1.30; 95%CI: 0.79-2.14; p=0.304). For the people in 41-50 years range the prevalence rate for male is 30% (95%CI: 23.9-36.6) and female is 28.5% (95%CI: 22.2-35.7). Overall prevalence rate is 29.2% (95%CI: 24.8-34.1). Patients aged 51-60 years had an insignificant prevalence rate of 27.5% [OR=1.20, (95 % CI: 22.9-32.7); p-value=0] .488]. 61-70 years people range has the overall prevalence rate of 30% (95%CI: 24.1-36.6), where male prevalence is 35% (95%CI: 27.0-44.0) and female prevalence is 23% (95% CI: 15.3-49.4). People above 70 years have the prevalence rate of 31.1% (95%CI: 22.4-41.4), male prevalence rate is 31.7% (95%CI: 21.4-44.3), female prevalence rate is 29.6% (95%CI: 15.3-49.4). Their risk of SARS-CoV-2 found higher in the 70 years old participants [OR=1.58; (95%CI: 1.01-2.26); p=0.049] compared to 18 years old.

Table: 2 - Prevalence of SARS-CoV-2 during the study period among the stratified age group

	Overall (n=2309)	Male (n=1271)	Female (n=1038)

<18 years	23.8(16.6, 32.9)	23.6(14.2, 36.7)	24.0(14.1, 37.8)
19-30 years	13.2(11.1, 15.7)	16.3(13.0, 20.3)	10.3(7.7, 13.6)
31-40 years	28.7(24.3, 33.5)	30.8(25.2, 37.2)	25.2(18.6, 33.1)
41-50 years	29.2(24.8, 34.1)	30.0(23.9, 36.6)	28.5(22.2, 35.7)
51-60 years	27.5(22.9, 32.7)	27.6(21.6, 34.5)	27.5(20.5, 35.8)
61-70 years	30.0(24.1, 36.6)	35.0(27.0, 44.0)	23.0(15.3, 33.0)
>70 years	31.1(22.4, 41.4)	31.7(21.4, 44.3)	29.6(15.3, 49.4)

Table: 3 - Risk of SARS-CoV-2 among the sex and in the different age groups

	OR (95% CI)	p-value
Sex		
Female	Ref.	
Male	1.38(1.13, 1.67)	0.002
<18 years	Ref.	
19-30 years	0.53(0.33, 0.86)	0.010
31-40 years	1.30(0.79, 2.14)	0.304
41-50 years	1.34(0.82, 2.20)	0.245
51-60 years	1.20(0.72, 1.97)	0.488
61-70 years	1.31(0.77, 2.25)	0.313
>70 years	1.58(1.01, 2.26)	0.049

Logistic regression was used to estimate the p-value, and the regression model was adjusted by age and sex.

4.4. Geography:

A higher seroprevalence was noted in Dhaka and then Narayanganj 29.3% (95% CI; 27.1%-31.7%) and 26.0% (95% CI; 18.3%-35.5%) respectively. Whereas a low seroprevalence was observed in Savar and others cities in Bangladesh, which was 15.4% (95% CI; 11.1%-20.9%) and 11.1% (95% CI; 8.70%-14.3%) respectively (Table 4). While a statistical model was fitted to estimate the risk among cities, both the Savar (OR=0.44; 95% CI 0.30-0.64; p<0.001) and other areas (OR=0.30; 95% CI 0.23-0.41; p<0.001) showed lower risk compared to Dhaka city (Table 4)

Table: 4 - Prevalence of SARS-CoV-2 and the risk in the locality among study participants

	Overall (n=2309)	OR (95% CI)	p-value
Dhaka	29.3(27.1, 31.7)	Ref.	
Narayanganj	26.0(18.3, 35.5)	0.85(0.53, 1.34)	0.476
Savar	15.4(11.1, 20.9)	0.44(0.30, 0.64)	<0.001
Outside Dhaka	11.2(8.70, 14.3)	0.30(0.23, 0.41)	<0.001

Logistic regression was used to estimate the p-value, and the regression model was adjusted by sex and locality.

4.5. Symptoms:

Various studies found that among all the symptoms of Sarc-Cov-2, fever, headache, loss of taste, loss of small, weakness, body ache, dry cough, diarrhea, etc., stands out the most [43]. The study gathered data related to these symptoms for the 2309 suspected patients (Table: 5). From these data, it can be found that among these suspected patients, 35.8% [OR=2.10, (95%CI: 30.3-41.9); p-value is less than 0.001] have a fever, which is a significant value... headache is present for 37.2% [OR=2.12%, (95%CI: 29.7-45.4)] with a significant p-value which is less than 0.001. Though 21.8% (95%CI: 20.1-23.7), patients did not face any headaches. Among the patients, 32.6% (95%CI: 26.7-39.1) patients suffer from loss of taste, and 22.0% (95%CI: 20.3-23.8) are unaffected. They have an OR of 1.72% (95%CI: 1.27-2.32) with a significant p-value less than 0.001. 33.5% (95%CI: 27.4-40.1) of the patients are suffering from loss of smell with an OR of 1.79% (95%CI: 1.32-2.43) with a p-value, less than 0.001but 22.0% (95%CI: 20.2-23.8) of them are unaffected. Around 29.0% [OR= 1.43%, (95%CI: 24.2-34.3)] patients feel weakness in their bodies, but the value is insignificant. Of the suspected patients, 39.0% [OR= 2.32%, (95%CI: 32.1-46.2)] have faced body ache. They have a significant p-value, which is less than 0.001. Among the suspected 45.7% [OR=1.63% (95%CI: 36.4-55.3); p-value<0.001] patients had dry cough and have a significant value. However, 21.6% (95%CI: 19.8-23.4) are unaffected Insignificant number 45.7% [OR=0.78% (95%CI: 36.4-55.3); p-value=0.440] of patients are suffering from diarrhea.

Table: 5- Symptom wise seroprevalence among the study participants

Symptoms	Prevalence (95% CI)	OR (95% CI)	p-value
Fever			
Yes	35.8(30.3, 41.9)	2.10(1.58, 2.75)	<0.001

No	21.1(19.3, 23.0)		
Headache			
Yes	37.2(29.7, 45.4)	2.12(.49, 3.03)	<0.001
No	21.8(20.1, 23.7)		
Loss of taste			
Yes	32.6(26.7, 39.1)	1.72(1.27, 2.32)	<0.001
No	22.0(20.3, 23.8)		
Loss of smell			
Yes	33.5(27.4, 40.1)	1.79(1.32, 2.43)	<0.001
No	22.0(20.2, 23.8)		
Weakness			
Yes	29.0(24.2, 34.3)	1.43(1.11, 1.88)	0.007
No	22.1(20.3, 24.0)		
Body ache			
Yes	39.0(32.1, 46.2)	2.32(1.68, 3.16)	<0.001
No	21.6(20.0, 23.4)		
Dry cough			
Yes	45.7(36.4, 55.3)	1.63(1.21, 2.18)	<0.001
No	21.6(19.8, 23.4)		
Diarrhea			
Yes	45.7(36.4, 55.3)	0.78(0.41, 1.48)	0.440
No	21.6(20.0, 23.4)		

4.6. Comorbidities:

For this study, we have collected data for some comorbidities such as Heart disease, Diabetes, Lung disease, Liver disease, kidney disease etc. Among the participants of the study 21.2% [OR= 0.85%, (95%CI: 14.2-30.4); p=0.532] patients have some sort of heart disease and 24.0% (95%CI: 22.2-25.8) have no heart disease. Which is not significant. Among the patients 20.5% [OR=0.81%, (95%CI: 15.1-27.2); p-value=0.294] patients have diabetes16.7% [OR=0.64%, (95%CI: 8.50-30.1); p-value=0.246] patients have some sort of lung disease, 20.5% [OR=0.77%, (95%CI: 10.5-36.2); p-value=0.519] patients have some

sort of liver disease which are not significant either. Only 15.4% [OR=0.53%, (95%CI: 10.6-21.9) of the patients have some sort of kidney disease with a significant p-value of 0.004.

Table: 6- Prevalence of SARS-CoV-2 among the participants with comorbidities

Symptoms	Prevalence (95% CI)	OR (95% CI)	p-value
H/O Heart diseases			
Yes	21.2(14.2, 30.4)	0.85(0.52, 1.40)	0.532
No	24.0(22.2, 25.8)	Ref.	
H/O Diabetes			
Yes	20.5(15.1, 27.2)	0.81(0.55, 1.20)	0.294
No	24.0(22.2, 25.9)	Ref.	
H/O Lung diseases			
Yes	16.7(8.50, 30.1)	0.64(0.30, 1.36)	0.246
No	23.9(22.2, 25.8)	Ref.	
H/O Liver diseases			
Yes	20.5(10.5, 36.2)	0.77(0.35, 1.70)	0.519
No	25.0(23.2, 27.0)	Ref.	
H/O Kidney diseases			
Yes	15.4(10.6, 21.9)	0.53(0.34, 0.82)	0.004
No	25.7(23.8, 27.7)	Ref.	

Chapter 5

Discussion

To the best of our knowledge, this single study attempted to determine the demographics of COVID-19 patients and suspects in Bangladesh with various factors (i.e., age, sex, location, symptoms, and comorbidities) and investigated the statistical correlations between the elements.

Different studies show fundamental variations in men and women's immune systems that may affect our capacity to combat infections, such as SARS-2-CoV-2. Females are often more resistant to diseases than men. [44]. From our study, we can also see that men are more

vulnerable as a result shows that among the taking part suspected Covid-19 patients, 1271 (55.04%) were male and 1038 (44.96%) were female. As these data are from a single institute, there is a lack of data from outside Dhaka so the result might vary. However, this data is closely similar to the datasheet of the Bangladesh Government.

Table:7 - Prevalence of SARS-CoV-2 during the study period among stratified months for the whole of Bangladesh [45].

Date	Total Tested	Total Positive	Prevalence
2020-Sep	345868	44530	12.9
2020-Oct	344001	38568	11.2
2020-Nov	390679	51292	13.1
2020-Dec	393834	41264	10.5
2021-Jan	379717	18275	4.8
2021-Feb	293493	10085	3.4
2021-Mar	563966	62669	11.1
2021-Apr	704431	133789	19

Suppose we compare our study data (Table: 1) and govt. Database data (Table: 7) shows that our population was not sufficient compared to the total affected people of Bangla. Still, there is a striking similarity regarding the increase and decrease of prevalence during these eight months.

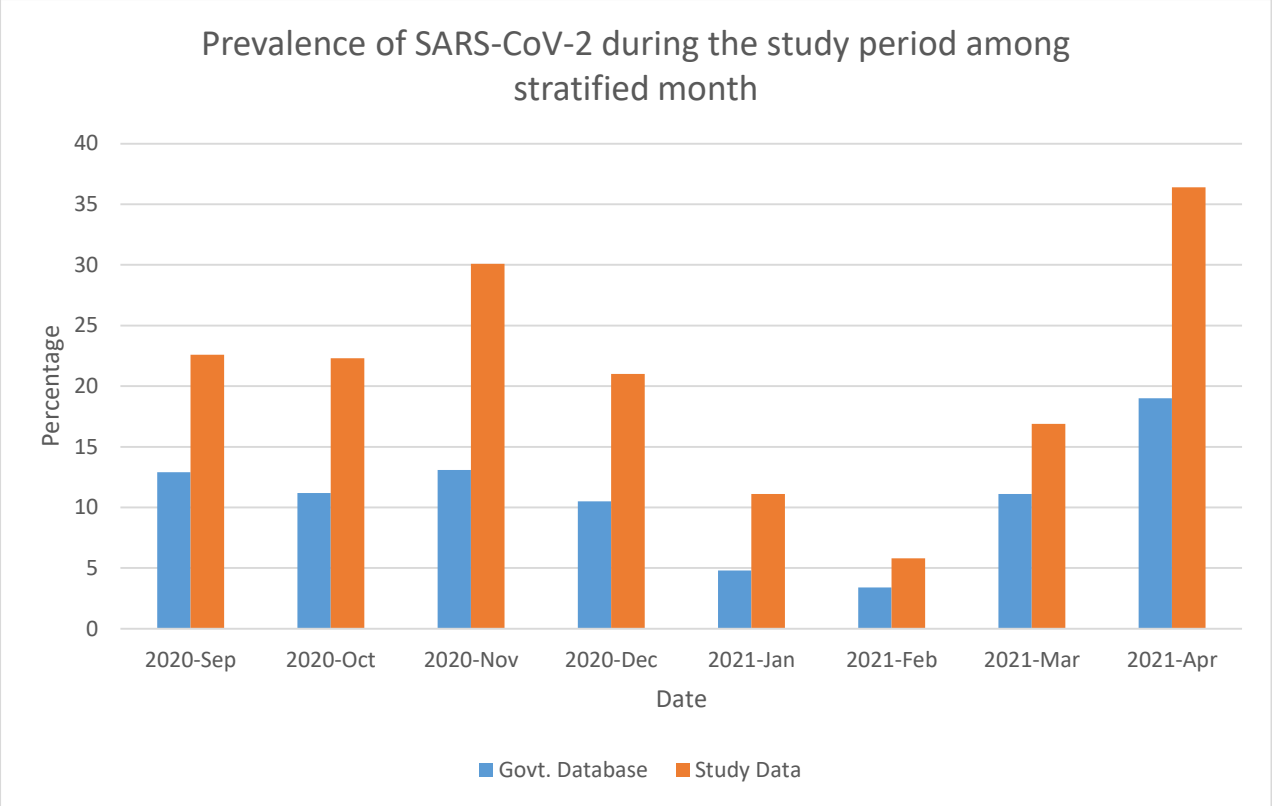

Fig 5: Statistical comparison between data obtained from this study and data obtained from Govt. Database. The data was obtained from September 2020 to April 2021.

From the Fig, we can easily see the changes in the prevalence rate of SARS-CoV-2 patients from both the Govt. database and our studies if we think of September 2020 as the starting point for comparing the rate decreases slightly in October but rises again in November. Then, for the next three months, it decreases continuously. However, it rose again in March 2021, and it grew more in April 201. Now, if we analyze this data with worldwide information, we can see that it correlates with the outbreak of some variants. After comparing it with the WHO database, we see that September 2020 was the 'Alpha' variant period. It decreases slightly in October 2020 but rises again in November 2020, the 'Gamma' Variant period. It fell continuously until March 2021, when the 'Delta' variant was dominant and entered Bangladesh.

Several demographic studies have been done using stratified age groups. Depending on the author, it is verified widely. Still, there are some common grounds between them. They are mainly categorized into three groups – adolescent, young and old. However, for more accessible research, they might have been divided into smaller groups. At Safdarjung Hospital, there is a study where the patients were divided between 0-20 years (4.8%), 21-40

years (47.6%), 41-60 years (38.1%), and greater than 60 years (9.5%) [46]. Another study was performed on the Indian people where the population was stratified into 18-25 years (54.2%), 26-30 years (34.2%), 31-40 years (9.3%), and above 40 years (2.3%) [47]. An analysis done by Zhang[48] shows that 0-14 years have a prevalence of 1.55%, 15-64 years have 76.93%, and above 65 years have a 21.53% of prevalence rate [49].In our studies, it is seen that people whose range is >70 have the most positive prevalence, 31.1% (95%CI: 22.4-41.4), whereas the people around 19-30 have the minor, 13.2% (95%CI: 11.1-15.7). Comparing our data with various other studies, it can be seen that our data varies widely as their studies show that the adolescent group has the least prevalence. In our case, the young group has the lowest. Finally, our study shows the highest prevalence in older adults, similar to a few studies.

Our geographical study shows that urban areas have a higher prevalence than rural areas. Urban areas like Dhaka 29.3% (95% CI; 27.1%-31.7%), Narayanganj 26.0% (95% CI; 18.3%-35.5%) has a higher value, whereas quite suburbs like Savar have 15.4% (95% CI; 11.1%-20.9%) lesser value than the urban area. Rural areas outside Dhaka have the least value, 11.1% (95% CI; 8.70%-14.3%).

Guan et al. released a report on 1099 patients with laboratory-confirmed Covid-19 from 552 hospitals across 30 provinces, autonomous areas, and municipalities in mainland China from January 29, 2020, to January 29, 2021. Fever (43.8% on admission and 88.7% throughout hospitalization) and cough (67.8%) were the most often reported symptoms, whereas diarrhea (3.8%) was infrequent [26]. From our studies, we can also observe that these symptoms are frequent for the patients as it is shown in table-5 that fever 35.8% [OR=2.10, (95%CI: 30.3-41.9); p-value <0.001], cough 45.7% [OR=1.63% (95%CI: 36.4-55.3); p-value <0.001] whereas diarrhea 45.7% [OR=0.78% (95%CI: 36.4-55.3); p-value=0.440] was infrequent. But our studies showed some promising data about other symptoms such as headache 37.2% [OR=2.12%, (95%CI: 29.7-45.4)], body ache 39.0% [OR= 2.32%, (95%CI: 32.1-46.2)], loss of taste 32.6% [OR=1.72% (95%CI: 26.7-39.1)], loss of smell 33.5% [OR=1.79% (95%CI: 27.4-40.1)] which have a significant p-value less than 0.001.

Because COVID-19 has a less severe clinical picture than MERS and SARS, it can spread more freely in the population [50]. Although most individuals have a moderate case of the condition, certain patients, particularly those with other underlying disorders, may experience respiratory failure, arrhythmias, shock, kidney failure, cardiovascular damage, or liver failure

[51, 52]. In another study of 21 patients, Comorbidities were seen in six individuals (28.6 percent). The most typical Comorbidities included hypertension (5 individuals) and diabetes (3 patients). Drugs are used to keep patients under control. One (4.8%) patient diagnosed with anxiety was also seen in patients with hypertension and diabetes mellitus, and hypothyroidism [46]. Our findings from the studies also support these data as there is no significant prevalence regarding the history of comorbidities other than kidney disease 15.4% [OR=0.53%, (95%CI: 10.6-21.9); p-value=0.004] with sars-CoV-2 suspected patients.

Chapter 6

Conclusion

In conclusion, our studies show that the aged male patients living in rural areas are more affected than their counterparts are. As we investigated, the affected patients are shown symptoms such as fever, body ache, headache, loss of taste and smell, etc. These cases, predominantly asymptomatic patient data, need to be further investigated and researched to get further data for the future development of a cure.

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