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An Anthropological review on COVID-19 and its Reflection in Indian Demography

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Abstract: COVID-19 pandemic is a global issue and the morbidity is increasing day by day. Social Distancing is one of the imperative tools to resist this deadly virus accepted by majority of the country, but this can't be a permanent solution. Whole India lockdown and a universal guideline can't help India for long run. Every State and zone has their own cultural identity. The aim of this paper is to understand the structural aspect of the viruses, its genetic orientation as well as its effect on the demographic shift faced by India. A comprehensive literature string search was performed by using 'Google Scholar', 'PubMed', 'PMC' and 'Academia' to search for citation published till 6th June, 2020 using the key terms Coronaviruses, taxonomy, genetics, India. 88 papers were fulfilled the eligible criteria. The findings indicated that the structure and genetic organization and taxonomy of coronaviruses were not new for academic field. The study of coronaviruses started from late 60s. A specific species of it was widespread from China (SARS-CoV-2) on the late December 2019 and nowadays different countries were in its trap. Researchers of different nations were focusing their research on trial of various drugs and till the discovery, social distancing was the ultimate weapon. In case of secular country like India, every state has its own growth level of affecting cases and morbidities. Different kind of strategies to different states and trial of diverse drugs and antiviral treatment are needed. An Anthropological view is to find out the solution with the help of local remedies and processes.

Keywords: COVID-19 pandemic, Coronaviruses, Anthropological genetics, Demography, Epidemiology, India.

I. INTRODUCTION

The aftermath of COVID-19, represents a picture of World population, where India is now in a transitional phase viz. economically, demographically and health wise [12]. According to World Health Organization's latest update, already 465,740 deaths were registered because of COVID-19 [132]. Ample number of original studies and review articles was already published on this pandemic disease, where a demographic transition was observed along with its determinants. Various comprehensive studies had been done by using Auto Regressive Integrated Moving Average (ARIMA) model, Exponential Smoothing methods, and SEIR (Susceptible - Exposed - Infectious - Recovered - Susceptible model, Network Modeling, Pattern Mining Model and Regression Model to understand the trends of this disease in a particular geographical region [48]. Apart from that, there are very few studies are till now published based on the anthropological genetic of COVID-19.

Anthropological genetics is solely diverse from human genetics because of theoretical orientation, methodical approach and procedure of application. Unique socio-demographic structures of population, temporal and comparative dimensions were the essential tool and methodology of anthropological genetics [18]. The question of anthropological genetics is about population variation which is totally dependent on population sizes and fluctuations, mating pattern, structural aspects of migration and many other things provided by anthropological demography [85].

Coronaviruses, the cause behind this pandemic can be a key tool to study the anthropological genetics and demography to understand the future shift regarding socio-cultural, economic-political, and psycho-biological health aspects of Indian population and helps in further implementations in policy strategies.

After gaining humongous knowledge about its function and historical dreadful effect on human population, it is very important to understand the structure and molecular genetics of largest single strand RNA virus [2]. In India, the transmission of infection doesn't follow any mathematical model proposed earlier by several scholars. Everyday its increasing in an exponential manner, and nowadays the number of getting infected are more than five thousands per day in India [3]. The varied degree of lethality of this virus and human to human transmission may create bio-terrorism all over the world [7]. The approach of resisting this heinous situation, Government of India is increasing the period of lock down, but without having a proper knowledge about this virus and how human population are getting affected; it would be really difficult to plan a model by governments and planners for making strategies to resist it [20]. Thus the aim of this review paper is to understand the genetics and the epidemiology of COVID-19 and the demographical shift as an effect of COVID-19 in India.

II. SEARCH PROCEDURE

A detailed, comprehensive string search was conducted in Google Scholar, PMC and PubMed and Academia databases. Special focus were given to the websites of World Health Organization (WHO), World Trade Organization (WTO), National Institute of Health(NIH) and Centre for Disease Control and Prevention(CDC) to collect the updated information regarding Coronavirus. Relevant search terms are 'COVID-19', OR 'Coronavirus' AND 'Taxonomy of Coronavirus', AND 'Epidemiology' AND 'Genetics', OR 'Genetic Organization of Coronavirus', AND 'Macro and Micro-evolution of Coronavirus' OR 'Origin and Evolution of Coronavirus' OR 'Epidemiology' AND 'India'.

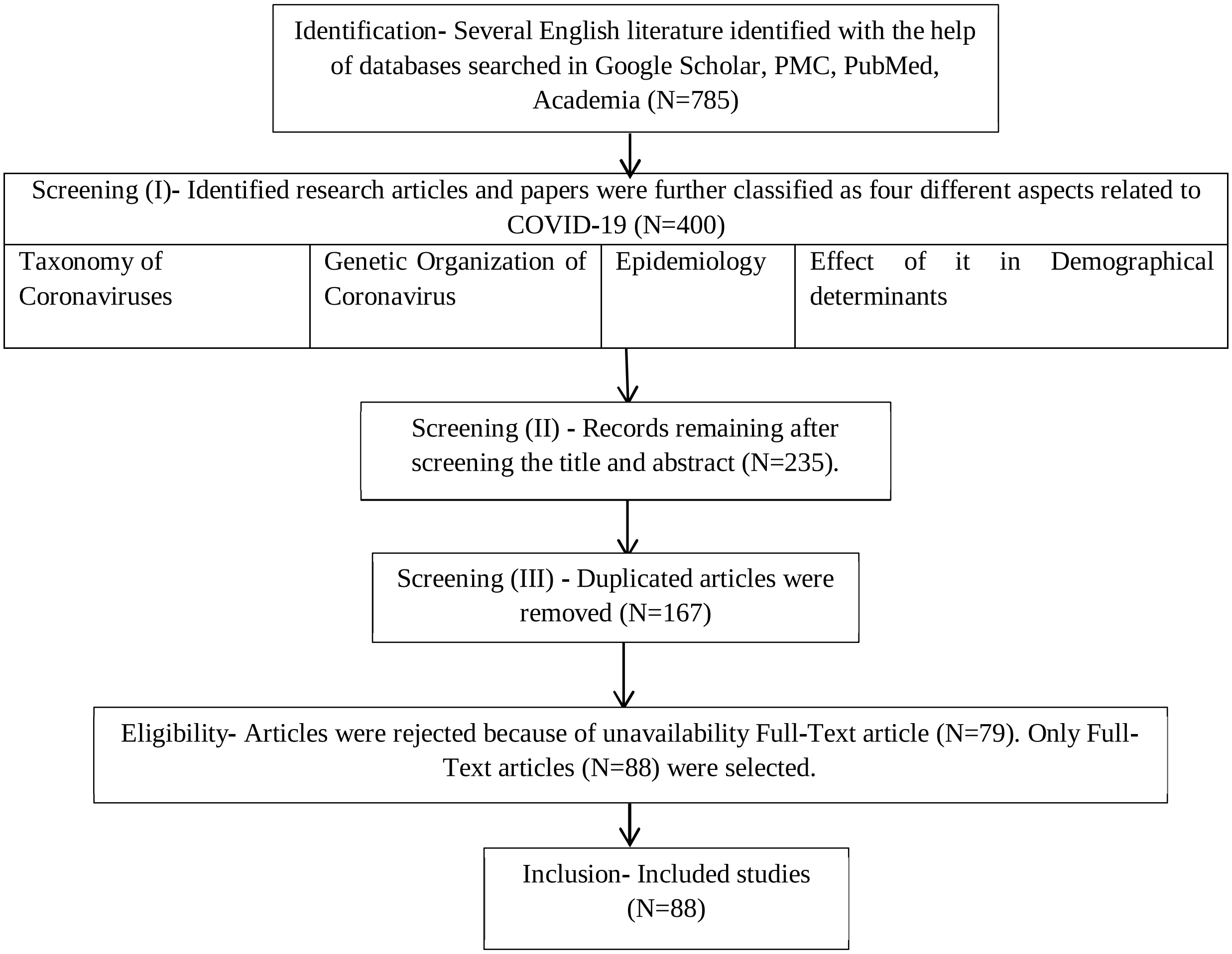
III. SELECTION PROCEDURE

The inclusion criteria are followed: (i) All study is based on human, (ii) All the study is based on review as well as original article. (iii) Article based on Indian context was preferred purposefully.

IV. RESULT

In the initial search 785 research papers/articles were selected based on selection strategy. The potential articles were further categorized four parameters i.e. Taxonomic Classifications, genetic Organizations, Epidemiology and Effects of pandemic in Demographical determinants special references to Indian context. After that 400 articles/research papers were selected as a potential paper for inclusions. Based on objectives, searching terms and titles the further selection procedure was filtered and 235 were selected. Among these, 68 research articles/papers were duplicate and left with 167 articles. After screening, 79 articles were eliminated due to unavailability of full text articles. Thus 88 research paper/articles were considered to be highly potential research articles for this review article.

V. DIAGRAM OF REVIEW PROCESS



Identification- Several English literature identified with the help of databases searched in Google Scholar, PMC, PubMed, Academia (N=785)

Screening (I)- Identified research articles and papers were further classified as four different aspects related to COVID-19 (N=400)

Taxonomy of Coronaviruses	Genetic Organization of Coronavirus	Epidemiology	Effect of it in Demographical determinants

Screening (II) - Records remaining after screening the title and abstract (N=235).

Screening (III) - Duplicated articles were removed (N=167)

Eligibility- Articles were rejected because of unavailability Full-Text article (N=79). Only Full-Text articles (N=88) were selected.

Inclusion- Included studies (N=88)

VI. BRIEF UNDERSTANDING ABOUT CORONAVIRUSES

Taxonomy, genetic organization and the virion are the core concept to understand the orientation of any virus which contains diverse family and Coronavirus is one of them [42]. It infects many species includes mammals and birds ranging from in cows, pigs and chickens to potentially lethal human respiratory infection ([42], [121]).

VII. TAXONOMY

Coronaviruses are enveloped, linear, unimolecular, infectious, single stranded, positive sensed, largest RNA genome with a length of 26-32bp ([17], [69], [112], [122], [127]). These groups of viruses belong to the order Nidovirales, family Coronaviridae, which are classified in two subfamilies viz. Coronavirinae and Torovirinae, further classified on the basis of phylogenetic relationship into four different genera i.e. Alpha, Beta, Gamma, and Delta, further segregated in twenty-seven sub-genus and ample numbers of species. Among them seven species are Human coronaviruses specified in tables ([58], [130]).

Table I: Taxonomic classification of Human Coronaviruses

Taxonomic Unit	Classification of Coronavirus													
Order	*Nidovirales*													
Family	Arteriviridae	Roniviridae	Mesoniviridae	*Coronaviridae*										
Subfamily				*Torovirinae*		*Cornavirinae*								
Genus	Arterivirus	Okarivirus	α-Mesonivirus	Bafinivirus	Torovirus	*Alpha*		*Beta*					*Gamma*	*Delta*
Species						*229E*	*NL63*	*HKU1*	*C43*	*SARS*	*MERS*	*SARS2*		

(Source: [58], [101])

VIII. THE VIRION

Virion should be an imperative aspect to understand the characteristics of a particular virus as it provide proper size and shape. It consists of an entire particle of virus along with its outer protein shell and the inner core [94]. The virion of coronavirus was spherical with the radius of 62.5nm ([8], [91]). The spherical outer layer consists of ample number of spikes (20nm long) or peplomer [84], thus it looks like a crown and thus the virus named as Corona [34]. Despite of that, five encoding structural protein consisting genome are the fundamental units of coronavirus viz. Spike Glycoprotein(S), Membrane Glycoprotein(M), Envelope Glycoprotein(E), Hemagglutinin Esterase (HE) and Nucleocapsid (N) protein which primarily encoded in the 3′end. ([30], [34], [118]).

S-Protein: The most prominent, large, multifunctional and N-exo/C-endo trans-membrane protein that accumulates into trimmers ([31], [82], [84]). The C and N- terminal has specific functional orientation. On one hand C-terminal interacts with M protein and N –terminal reacts with the membrane of host cells. Synthesized as a heavily glycosylated polypeptide is a promising character of S protein [30], thus the masses of full length monomers of glycosylated S protein falls under 150-200kDa, otherwise it seems to have 128-160KDa monomeric masses [84].

M-Protein: This is the most copious ([84], [116], [117]) structural protein [36] and fundamental building block of coronavirion [30]. M-polypeptide has 221-262 amino acids and its sizes ranges from 25-30 kDa, which represent its smallness as a protein during pre-glycosylated phase ([35], [83]). On the other side, during SDS-PAGE electrophoresis, M-protein showed a multiple times higher molecular masses during glycosylated form ([68], [84]). It is consist of small N-terminal which is glycosylated ecto-domain and comparatively larger C-terminal and i.e. endodomain that encompasses 6–8 nm into the viral particle [35]. After N-terminal there were three trans-membrane segments and then a large carboxy terminus comprising the major part of the molecule. This latter domain is situated in the interior part of the virion or on the face of cytoplasm of intracellular membranes, thus it can communicate with different organelles [107]. M-Protein is hydrophobic but not more than E-Protein. The function of M protein is to triggers the formation of interacting virions in this endoplasmic reticulum-Golgi apparatus intermediate compartment (ERGIC) with this complex ([29], [34], [43]).

E-Protein: Most divergent, small polypeptide protein ranges from 8.4-12kDa, having 76-109 amino acids, represent as a minor constituent of this virion [84].E-Protein individually or along with M-Protein virus like particles are formed. The appearance of this protein creates an interaction between host and virus and inducting apoptosis [129].

N-Protein: This protein constitutes three domain regions, among them Domain1 and 2 are highly variable. The molecular mass of this protein ranges from 43-50kDa, which is the fundamental components of nucleoplasmid and where RNA resides in beads on a string fashion ([74], [84]). It not only plays an important role in virion structure but also in replication and transcription of coronaviruses ([34], [93], [102], [122]).

HE-Protein: Hemagglutinin Esterase (HE) present only in β-coronavirus and also have a spike structure varied from 5-7 nm. When HE synthesized individually, it contains 42kDa apoprotein, but when it is synthesized, the glycosylated mass increased to 65kDa [129].

IX. GENETIC ORGANIZATION

A non-segmented, positive-sense, 27-31kb in size [30], largest RNA genome contained numerous amount of Open Reading Frames (ORFs) [84] along with 5′ cap structure and 3′ poly (A) tail, which played an important role as an mRNA for translation of the replicase polyproteins ([30],[72], [78], [85], [89], [113]). This both termini encompassed un-translated regions (UTRs) [97] and this genome had fixed order of occurrence of distinctive genes i.e., 5`S-E-M-N `3 and among this region, 5′ UTR nucleotides were varied in 210-530 range and the on the other side 3′ UTR, nucleotides were varied in 270 to 500 range ([30], [84], [97]). At the end of the leader sequence present at 3′, there is Transcription Regulatory Sequence (TSR) which has a specific function. The replicase gene encodes two part, one is the nonstructural proteins (nsps, 20kb) occupies two-thirds of the genome, and structural accessory proteins (10kb), which is one-third of genome [35]. The G+C content of this virus varied from 32%-43% from species to species [97]. Open Reading Frame doesn't have any stop codons and through the process of translation it may produce different kinds of proteins [43], and in case of coronaviruses ORF1ab subjugates more than 50% of the whole genome. Another most ingesting slippery sequence (UUUAAAC) is predominantly present in all coronaviruses which form a pseudo knot structure in the junction of ORF1a and ORF1b. Despite of that there are small ORFs present between several condensed genes, and there functions are still unknown [97].

X. EPIDEMIOLOGY

Epidemiology of Coronaviruses is one of the vivacious factors as it is not all about this present pandemic, the outbreak of this virus was faced by human population in the past through the passage of time. In 1960s, the first outbreak of coronavirus had been taken into consideration ([52, [62]). There were 7 species of coronavirus, which affects human and among them MERS-CoV and SARS-CoV outbreak were came into a frame in 2002 and 2012 [60]. According to World Health Organization the first outburst of SARS-CoV began in China. After that, 8,437 SARS cases, 7452 recovered and 813 deaths were reported from November 2002 to July 2003 from different geographical locations. MERS-CoV was first acknowledged in 2012 in Saudi Arabia and 2400 cases were confirmed. SARS-CoV-2 was first observed on 12th December, 2019 in Wuhan, China in a seafood market ([11], [47], [96]). A study by Zhou et al, (2020) assessed that Bat CoV RaTG13 shown 96.2% similarities with SARS-CoV-2 in genome sequence. This study can conclude that Bat CoV RaTG13 and SARS-CoV-2 shares a common ancestor [141]. A study by Kumar et al, (2020) addressed the spreading history of COVID-19/2019-nCoV. He further illustrated that Thailand was the first country, which experience the trauma of this virus on 13th January, 2020, after that gradually different Asian countries like UAE (29/1/2020), Korea (20/1/2020), Japan (15/1/2020), Malaysia (26/1/2020), Sri Lanka (28/1//2020), Cambodia (28/1/2020), Vietnam (24/1/2020), Nepal (25/1/2020), India (30/1/2020) and Japan (06/2/2020) were experiencing the same situation. Afterwards it spreads into different developed country like USA (23/1/2020), Germany (28/1/2020), Australia (25/1/2020), France (25/1/2020), Italy (31/1/2020) and many others [69].

The effect of COVID-19 pandemic creates a horrendous effect not only on economy, demography and health system but also various socio-cultural dimension of human population will be changed. A review study by Bandyopadhyay et al, (2020) focused on genetic heterogeneity of ACE2 (Angiotensin Converting Enzyme 2), as it SARS-CoV-2 bind to their target cells through it. A study by China CDC Weekly found out that 17% were having a huge history of critical morbidities among the patient of COVID-19 [7]. Another study by Wu et al, (2020) stated about the three factors regarding the development of any epidemic, i.e. Source, Susceptible individual having proper characteristics for virus to cross the threshold in his/her body and Transmission path/ mechanisms. The paper further described the exponential outbreak of SARS-CoV-2 in China and globally after few months [133].

WHO declared about COVID-19 in 11th March 2020, as a global pandemic, but the first case in India was detected in Kerala, on 30th January,2020 from a student who returned from Wuhan, China([13], [41], [56]). The first death was reported in 12th March, 2020 [63]. According to Government of India latest update on 23rd June, 2020, the total deaths were registered 13699, total active cases

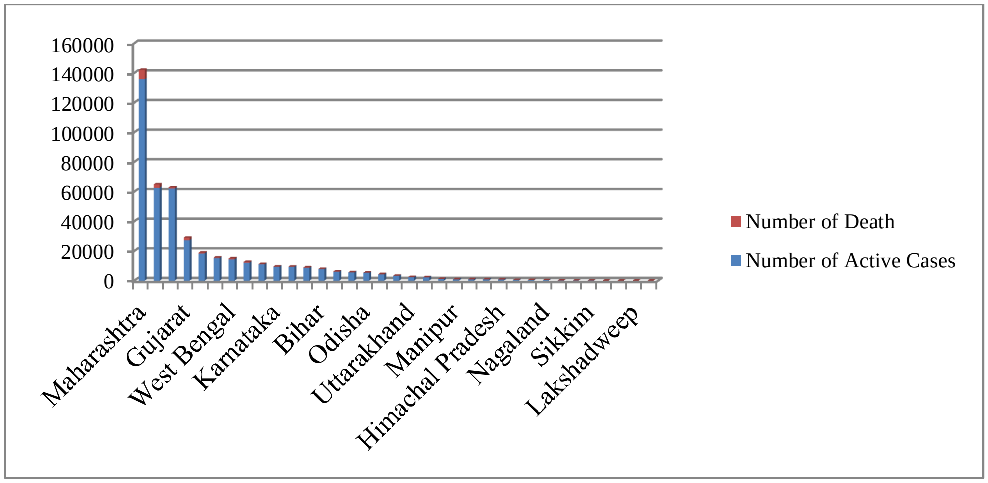
178014 [91]. But the state wise cases were showing different pictures in the table 2. An extensive growth study based on COVID-19 categorized the growth level of COVID-19 into four stages specially focusing on Indian scenario. The Stage1 different states/countries are experienced a case that have a travel history from virus prone zone. Next in Stage 2 those region and countries were experiencing new cases that had no history of any travel. On Stage 3 the transmission phase were observed, in which new cases had been coming up, that doesn't had any previous contact with individuals who had travel history. The final one is Stage 4, where the situation is uncontrollable and countries have ample number of case histories. This study also concluded that state wise strategies should be considered as India is the most diverse country so the approach should be different for each state and not be a homogeneous strategy for a whole country [41].

Table II: Distribution of death and active cases of COVID-19 state wise in India

Sl. No	Name of State	Number of Active Cases	Number of Death
1.	Maharashtra	135796	6283
2.	Delhi	62655	2233
3.	Tamil Nadu	62087	794
4.	Gujarat	27285	1684
5.	Uttar Pradesh	18322	569
6.	Rajasthan	15232	356
7.	West Bengal	14358	569
8.	Madhya Pradesh	12078	521
9.	Haryana	11025	169
10.	Karnataka	9399	142
11.	Andhra Pradesh	9372	111
12.	Telengana	8674	217
13.	Bihar	7825	55
14.	Jammu and Kasjmir	6088	85
15	Assam	5586	9
16.	Odisha	5303	15
17.	Punjab	4235	101
18.	Kerala	3310	21
19.	Uttarakhand	2402	28
20.	Chhattisgarh	2303	12
21.	Tripura	1237	1
22.	Manipur	898	0
23.	Goa	864	1
24.	Ladakh	847	1
25.	Himachal Pradesh	727	8
26.	Chandigarh	411	6
27.	Pondicherry	383	8
28.	Nagaland	280	0
29.	Arunachal Pradesh	139	0
30.	Dadra Nagar Haveli	91	0
31.	Sikkim	78	0
32.	Andaman and Nicobar	48	0
33.	Meghalaya	44	1
34.	Lakshadweep	0	0
35.	Daman and Diu	0	0

(Source- http s://www.mygov.in/corona-data/covid19-statewise-status/ accessed on 23rd June, 2020; 03:43PM)

Graphical Representation of Table I



XI. PRESENT SOCIO-DEMOGRAPHICAL CHANGE

There are bounteous amount of variables which affect the demographic determinants like economy, health, migration, global as well as local environment and other socio-cultural aspect. The effect of COVID-19 is not an exception [22]. Demographic analysis is dependent on a gigantic figures which represents the population [21]. A study conducted in Miami, Florida, discussed the vast impact of COVID pandemic in HIV positive patients [5]. Another interesting rapid online survey was conducted in USA among Men who have sex with men (MSM) (N=1051) and its impact on their sexual health. This survey reveals that there was not only a general impact on wellbeing, social interactions, money, food, use of drugs and alcohol consumption but also interruption in HIV related services [112]. Another online survey in Tunisia (N=284) showed that 89% were aware about food wastage, 93% of respondents were had a huge impact because of the COVID-19 pandemic. Attitude towards food wastage were highly modified during the period of lockdown [61]. A cross sectional KAP (Knowledge, Attitude and Practice) survey was conducted in USA (N=630) found out that despite of having a very critical condition individuals are not changing their daily life plans and greater public health efforts were needed to create more awareness [130]. Health Care workers (HCW), doctors are forefront soldiers of this battle between human population and COVID-19 pandemic. A living rapid review was conducted on the basis of electronic databases, shown that they experienced significant burdens because of this pandemic [26]. Another significant study on HCW showed the post-traumatic stress after COVID-19, will create an interruption in their psychological wellbeing [4]. Fertility is important demographic determinants and also a health indicator of a population. Several studies had shown the effect of COVID-19, on fertility treatment clinics and hospitals. Those studies tried to create awareness about pregnant women so that they were not having a chance of severe infections [106]. A study focused on the importance of Indian Medicine and plant medicine to find out the drug/ anti-virus of COVID-19 [124].

The anthropological essence is to understand the large population as well as the several strata of a population which don’t fit into the broader scale. Anthropology doesn’t always promote village studies or rural research orientations. The crux of the subject also lies in the domain of human genetics, public health, urban disparities [115], space orientations [115] and many bridges of bio-cultural domain. This present socio-demographic changes are the idle place for anthropological discussion and getting probable solutions in community level as well as globally. Every ethnic population or specific communities were facing some change in the course of pandemic. Their socio-cultural and biological life-style may have changed the shape due to it. Diverse myriad of anthropological research can capture those changes in human population.

XII. GLIMPSE OF ANTHROPOLOGICAL GENETICS

Anthropology, always tried to investigate the cultural and biological variation and evolution of a particular species, known as Homo sapiens [103]. This effect of COVID-19 crafts a huge demographical change in present situation and may create a genetic as well as proteomic changes in human genome. Thus the genetic configuration of this Coronaviridae family is very important to focus on. As anthropology covers a huge arena, where human as well as non-human primate’s falls in, it is very imperative to highlight a non-human primate strategic model to resist this and also understand the pathogenesis. Ample numbers of studies have conducted on nonhuman primates especially on SARS-CoV and MERS-CoV.

A study conducted among macaques and provided a new model to test preventive and therapeutic strategies [107]. But the study was conducted among cynomolgus macaque (*Macaca fascicularis*) was the first animal subjected to experimental infection with SARS-CoV ([37], [68], [129]). Not only the clinical symptoms but also it was very important to understand the behavioral changes of those affected primates. This kind of anthropological research enormously helps to recognize the probable future health and behavioral issues of human population.

XIII. DISCUSSION

At the end of December 2019, a viral pneumonia was identified because of unknown viral microbial agent and after couples of weeks its spread all over the world ([79], [140]). Different varieties of pipeline drugs, clinically used drug were on trials and according to World Health Organization Chloroquine and hydroxychloroquine have been found to be effective against COVID-19 in laboratory studies and in-vivo studies [124]. Till now social distancing is the primary strategies followed by government. But the fallacy of this strategy embedded in its own loop holes. It was very difficult for any social animal especially human being to resist them for a longer period of time. So for better understanding this problem, we need to dig out from the root. The structure of Coronavirus should be understood by lot of scholar from the beginning of 1960s [129]. Not only that the characteristics RNA, the structure of proteins were very important. Apart from the structure the function of coronavirus along with its impact on human being on the domain of public health, genetics, socio-cultural and politico-economy is the major concern of anthropological research. There are few studies were conducted on the anthropological context. An ethnographic study conducted in the sub-urban part of West Bengal found out the issues of social distancing, the strategies of black marketing, and many things [88]. Another important article tried to give idea about the importance of Medical Anthropology during the time period of economic, social and political fallout [83]. Another extensive study conducted in USA about pregnancy and birth and how the strategies changes during the period of social distancing, how people were comfortable in midwifery concept and avoid hospitals was the main concern of that study [28].

XIV. CONCLUSION AND LIMITATION OF THE STUDY

Year 2020, started with huge obstacles and every individual was facing minor to major problems because of this unknown viral microbial agents. This is a high time for anthropological research should contribute in a holistic approach in the field of socio-cultural as well as biological aspects. In India there are few papers was published regarding the Indian scenario of COVID-19, through the lens of anthropology. India is a diverse country; every state has its own hues of cultural essence, socio-political identity, biological and linguistic diversity. From this point of view every state need a special, individualistic, diversified approach which should be different from another. Thus the strategy should be viewed through the anthropological lens for better understanding and full-proved results. Unfortunately there is very slight effect of the anthropological approach to fight with COVID-19 in Indian context. Anthropology can understand the macro as well as the micro-population and their layers. So author emphasized more anthropological work related to the phase of COVID-19 in the Indian subcontinent.

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