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Review Article

TRANSMISSION OF NOVEL HUMAN CORONA VIRUS

ABSTRACT

Background: With emergence of COVID -19 pandemic, the potential of bidirectional transmission of coronavirus has been alarming and of global concern. Various illicit human activities and ecological dynamics are blameable for various spillovers. Community transmission is the major cause of escalation of this disease.

Aim: The article highlights the bats to be epicentre of all the three corona viral outbreaks namely, SARS-CoV, MERS-CoV and COVID-19. It reveals that the coronavirus crossed the species barrier via camels, civet cats and pangolin's considering them as intermediate host. Now this novel coronavirus has become toll for *Homo sapiens* through multiple modes of transmission. The potential and stringency of this contamination is dictated by genetics and immunological status of the human host. In this review, various case studies of human to animal transmission have also come into limelight.

Conclusion: Dissemination of COVID-19 virus in human community through respiratory droplet transmission has been confirmed and documented. The tradition of including wild animals in meals in some of developing countries like China and other intruding activities in the environment should be limited as it is feared of causing zoonosis and anthropozoonosis. The challenge has globally put healthcare workers on war footing in combatting the disease. The disease would continue to pose threat in community and within healthcare setting unless proper administrative, clinical, and physical measures are taken. Various struggling practices and adoptive preventive measures such as lockdown, social distancing and wearing masks or other barriers have flattened the epidemic curve of COVID -19 as reported globally.

Key words: Corona, virus, sars, Spillover, bidirectional transmission, zoonosis, anthropozoonosis

INTRODUCTION

The 21st century has experienced a renascent interest in the variegation of coronavirus in the rouse of pandemic. This spiralling coronavirus scenario has aroused curiosity in zoonotic and anthropozoonotic transmission of this novel virus that has posed a significant threat to vulnerable species on earth as the host range of this coronavirus is considered to be promiscuous [1]. These transmissions are apprehended to be instigated by globalization, the loss of natural habitats and exposure to new hosts. In this review, we explore the host and viral dynamics that shape these CoV populations for viability, proliferation, and persistence in naive hosts. Many domestic and wild animals, including camels, cattle, cats, and bats, may serve as hosts for coronaviruses [2]. Primitively, coronavirus was considered to be non-pathogenic to humans[3]. Coronavirus glared publicity when diseases such as Severe Acute Respiratory Syndrome (SARS), Middle East Respiratory Syndrome (MERS), and 2019-nCoV pneumonia stormed the human species through cross species transmission. Over a few decennary numerous animals have been monitored in the vicinity of which bat species being the oldest mammals are claimed to be indigenous source for novel viral species by Anthony et al. in 2013[4,5]. Inevitably, Luis et al., 2013 hypothesized that the great diversity of bats and their long co-progressive relationships with pathogens provide the opportunity for spillover and maintenance of quasi-species pools of viruses that can infect a range of hosts [6].

The reoccurrence of atypical pneumonia in Wuhan in conjunction to the Huanan seafood wholesale market, suggesting a possible zoonosis . The live animals such as snakes, marmots, birds, frogs, and hedgehogs captured the seafood market. Currently, there is no evidence suggesting a specific wildlife host as a virus reservoir. Studies of relative synonymous codon usage (RSCU) between viruses and their hosts suggested that viruses tends to evolve codon usage bias that is comparable to their hosts[7]. Results from our analysis suggest that 2019-nCoV has most similar genetic information with bat coronavirus and possess same codon usage bias with snake[8]. More interestingly, an origin-unknown homologous recombination may occurred within the spike glycoprotein of the 2019-nCoV[8] which may explain its cross-species transmission.

Even though the bats have given prominence for nurturing coronavirus virome, still minor remodelling is required in the genome of CoVs to seed their emergence in human species. There are some mutated core viral requisite factors to cripple species barriers without

sacrificing the form or function of other important elements. This dichotomy in CoVs is governed by two distinct mechanisms: fidelity and gene acquisition [6]. Despite of being the largest members of the Nidovirales order, they won over this barrier by formation of a complicated replication complex with known RNA synthesis and modification activities that include a proofreading machine, mediated primarily via the 3′–5′ exoribonuclease activity of non-structural protein (nsp)14[9]. By the virtue of this large and complex RNA replication machinery, CoVs achieved ownership of 30 kb in size and even retained functional components required for viability. Peck et al.in 2015[10]presented the blueprint of gene acquisition processes like recombination, horizontal gene transfer, gene duplication, and alternative open reading frames in Corona Virus to expand its host range and cell tropism. Fidelity compounded with gene acquisition have honed and refined CoV proteins, which can be divided into three broad groups based on selective pressure: spike, conserved, and variable protein. Togetherness of these three domains is responsible for novel CoV adversity.

Human coronaviruses (HCoVs) represent a major group of coronaviruses (CoVs) associated with multiple respiratory diseases of varying severity, including common cold, pneumonia and bronchiolitis [11]. Hitherto, six known HCoVs have been identified, namely HCoV-229E, HCoV-NL63, HCoV-OC43, HCoV-HKU1, severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV); of which HCoVs (HCoV-229E, HCoV-NL63, HCoV-OC43 and HCoV-HKU1) are globally circulated. Walsh et al in 2013[12] warned about these four HCoVs can cause life-threatening pneumonia and bronchiolitis in all age groups especially in immunocompromised patients caused by these four HCoVs. Acc to Smuts in 2008, patient also encounters enteric and neurological diseases.

INCIDENCES OF TRANSMISSION OF CORONAVIRUS

The city Guangdong, China observed first incidence of SARS-CoV in 2002–2003 as a typical pneumonia marked by fever, headache and subsequent onset of respiratory symptoms such as cough and pneumonia, which may further develop into life-threatening respiratory failure and acute respiratory distress syndrome[13]. Being communicable among humans, it can quickly cross the boundaries of 29 countries, infecting more than 8000 individuals with a mortality rate of about 10% [14]. Wang et al in 2015[15]pointed palm civets as a culprits and were thought to be the natural reservoir for the virus. However, subsequent phylogenetic studies by Hu et al [16] alarmed about the sequences of SARS-like virus found in bats considering bat to

be the seedbed. In 2012 the MERS-CoV epidemic surfaced in Saudi Arabia with similar clinical symptoms as SARS-CoV but with a much higher fatality rate of about 35% [17]. Graham et al [13] further documented that Unlike SARS-CoV, which exhibits super-spreader events, transmission of MERS-CoV is geographically limited. In fact, reported cases by Oboho et al in 2015[18] of MERS-CoV often stem from outbreaks within the Middle Eastern countries. The strongest and direct evidence of transmissibility of MERS-CoV from dromedary camels to humans is the isolation of near-identical MERS-CoV strains from epidemiologically linked humans and bats. Thus, bats are a putative origin of MERS – CoV.

In 2020, Huang et al [19]talked about a mysterious pneumonia exploded the Huanan Seafood Wholesale Market, in Wuhan, Hubei, China in late December 2019. This disease was manifested by fever, hacking cough, and fatigue. Multiple systems of human body were in the trap of this virus including respiratory (cough, short of breath, sore throat, rhinorrhoea, haemoptysis, and chest pain), gastrointestinal (diarrhoea, nausea, and vomiting), musculoskeletal (muscle ache), and neurologic (headache or confusion) fever, dry cough, and fatigue and occasional gastrointestinal symptoms. The infection is acute without any carrier status. This new coronavirus is phylogentically related to the virus that causes severe acute respiratory syndrome is named as SARS-CoV-2. SARS-CoV-2 causes the illness known as COVID-19. It is dangerous because it can be easily transmitted among human species, whether the person is exhibiting symptoms or not. It shows that the transmission rate of SARS-CoV-2 is higher than SARS-CoV and the reason could be genetic recombination event at S protein in the Receptor Binding Domain region of SARS-CoV-2 may have enhanced its transmission ability. Initially, Lu et al [20] and Chan et al [21]propounded the snakes to be possible host, however the genomic homology assured that not snakes but only bats could be the zoonotic source.

Fundamentally, it was proffered that disease ridden patients of Wuhan in China may have visited the seafood market where live animals were sold or may have used infected animals or birds as a source of food. Nevertheless, the individuals with no record of visiting the seafood market have also contracted this infection. Currently, Phan et al[22] apprehended that there is a pervasiveness of this virus among human population which has been subsequently reported globally. The human to the human spreading of the virus occurs due to close contact with an infected person via respiratory droplets or aerosols.

ANIMAL TO HUMAN TRANSMISSION

Cross-Species Transmission (CST), also called interspecies transmission, host jump, or spillover, is the potential of a foreign virus to invade a new host species and become pervasive among entire species [23]. Parrish et al.[24] postulated that 'Host range is a viral characteristic considering natural hosts to be part and parcel of a principal transmission cycle or "spillover" infections into alternative hosts'. Thus, the accessibility to new host is seldom and transmission is either to increased exposure or mutations which often ends in devastating outbreaks. The cascade of events includes intrusion of virus into host followed by the replication of virus in the body of host resulting in the outburst of viral disease among the populations of the new host. Spillover of the emerging bat viruses requires a series of hierarchical enabling conditions: reservoir hosts must be *present*; reservoir hosts must be *infected*; if transmission is indirect, reservoir hosts must be *shedding* pathogen and virus must *survive outside* of its reservoir host with access to the recipient host; recipient hosts must be *exposed* to the source of the virus in sufficient quantity for an infection to establish; and recipient hosts must be *susceptible* to the virus.

There are three cognitive factors which support this transmission are:

Host attribution to transmission primary host

Bats of order Chiroptera, suborders Megachiroptera and Microchiroptera are considered to be primitive mammalian species harbouring genetically diverse coronavirus species[25]. Being the second largest group of mammalian species, it is definite host for many viruses[26]. Bat virome includes rabies virus and other *Lyssavirus* (Family Rhabdoviridae), *Nipah* and *Hendra* viruses (Family Paramyxoviridae), *Ebola* and *Marburg* viruses (Family Filoviridae), SARS-CoV and MERS-CoV (Family Coronaviridae)[27]. The determinants like evolution and phylogeny of bats, nutrition selection, symbiotic and non-symbiotic nature, population pattern, flying capability, seasonal migration and daily movement patterns, torpor and hibernation, life span, roosting behaviours, ability to echolocate, virus susceptibility enables these flying mammals to become natural reservoir [28]. Thus, these flying foxes are presented as an ideal 'Virus spreader'. The ecological and epidemiological studies hypothesized various factors responsible for spillover from bats to human as bats overmaster the eco diversity because of ubiquitous nature[29]. Firstly, human and bats might have domesticated the same biosphere either through butchering or coal mining and even the habitat loss due to the developmental activities cause migration of bats to inhabit human territory; Secondly, they

may be act as pollinators in the case bananas and mangoes; Thirdly, bats might have become prey of cats, chemical residues, emissions and other effects of urbanisation. Then eating habits may have contributed a lot as some are insectivorous, few are frugivorous and couple of them are hematophagous. Even, their excretions is being used as a fertilizer and for manufacturing soaps, gasohol, and antibiotics.

Secondary host

When a virus frisks the species barrier and spills over into humans, the mystery sometimes deepen over the missing link in coronavirus jump from bats to humans which mayhaps civet cats in case of SARS outbreak, dromedary camels happen to be culprit in MERS[30] and perhaps pangolins transmitted COVID -19 to human species. The systematic comparison and analytical studies on the composition and divergence in the key amino acids of S protein receptor binding domain (RBD) of coronavirus and host receptor indicated potential intermediate hosts. All the epidemics resulting from SARS-CoV and MERS-CoV to SARS-CoV-2, put bats in the cart for being their natural habour with unpredictable and varying intermediate hosts. However, the study of the structural binding mechanism enables us to strengthen the target of intermediate host in the case of SARS in 2002 and MERS in 2012. Earlier, MERS-CoV was suggested to be originated from bats, but later dromedary camels were identified as a reservoir host fuelling spill over to humans is unequivocally dromedary camels[31]. Bats have been considered to be the reservoir host for both closely related species SARS-CoV and SARS-CoV-2[32,33] and palm civets and racoon dogs apprehended to be intermediate hosts for zoonotic transmission of SARS-CoV between bats and humans[34], the intermediate host for SARS-CoV-2 still remains unknown. The recurrent spillovers of coronaviruses in humans along with detection of numerous coronaviruses in bats, including many SARS-related coronaviruses (SARS-CoVs), suggest that future zoonotic transmission events may continue[35].Generally, a natural host does not show severe disease while intermediate host manifest some clinical symptoms as suggested by authors. Previously, based on relative synonymous codon usage bias resembling snake to other animals, the snake was suspicioned to be the wildlife animal reservoir for SARS-CoV-2[8]. But now it has verified that they nevertheless transmitted the coronaviruses to humans, which makes it difficult to target them as intermediate hosts of SARS-CoV-2 in the short term. Considering pangolins to be the most trafficked mammal in the world and the nutrition and ecological niche similarity with bats, flags them to be the intermediate host for COVID-19.

The pangolins are illegaly traded as it is believed that their scales and blood have medicinal properties and their flesh is considered a delicacy in some parts of world. Systematic and long term monitoring of coronaviruses suggest that snakes and pangolins, turtles (*C. picta bellii, C. mydas*, and *P. sinensis*) to be potential intermediate hosts transmitting SARS-CoV-2 to human, although second thought is needed [36].

Virus attribution to transmission

The three viral determinants of host range expansion are[37]): i) the transition within the S1 dominion of spike proteins; Spike glycopeplomers is second enormous proliferated protein in the host cell across the replication phase which has divided into two apportions: S1 and S2. Though both apportions possess good grading of mutation that rounds up the host diversity, considerably S1 domain ignites the process of attachment in virtue of the receptor binding domain (RBD) residing in it and ought to be the determing factor in selection of host[38]. The ORF1 at 3′ end is often the scapegoat for mutations and recombinations owing to the unique reverse genetic system of coronavirus. ii) Spike RBD: a miscellanea of Allelic constraints; Molecular analysis affirm the existence of mutational hotspots within the S1 dominion of spike protein, panacea for species specificity. Hotspots include nsp3, a cleavage product from the ORF1a, S - Protein, ORF3 and ORF8[39], all are lineated in receptor binding domain of S1 subunit. All these moieties are of variable size ranging from 180 -330 amino acids and their loci within the sequence also differ[40]. These independently folded regions are virus distinct and discrete. Babcock et al[41] has unveiled the structure of RBD of SARS-CoV complexed with human ACE2 receptor. Hu et al[42] worked on civets to ponder the sequences of RBD region of spike coronavirus in initial phase of infection as well as in the delayed phase. His studies summarizes that the isolates of initial infectivity stages is on positive selection mode in terms of alleles whereas the later ones switch off to negative selection with decrease in allelic diversity. iii) Molecular Evolution and longevity: the peculiar large RNA genome works as a platform for genetic modification leading to the interspecies co-evolution and proving advantageous for the emergence of novel CoVs under favourable conditions. This large genome is assisted by the open reading frames and protein functions, subjected to mutations very often. Akin to the RNA virus, coronavirus enhance the biosynthesis of new viral RNA via the production of RNA -dependent RNA polymerase complex, facing inaccuracy of about 10^{-3} to 10^{-5} for each nucleotide in every run[43]. Addition and subtraction in any of the RNA modifying enzymes of this complex can reduce the veracity of this

complex , illustrated by the case study in murine hepatitis virus (MHV) by suppressing the activity of nsp14 of ORF1, exonuclease N (ExoN) responsible for RNA proofreading activities can affect the operation 10 times comparable to mutant with the error rate of 3.2×10^{-5} and of wild type with 2.6×10^{-6} [44,45]. The mutations in SARS CoV retrospected the same results. The practicality emphasized that this mechanism have lowered the spread of disease by compromising the change in RNA polymerase complex owing to adaptive capability of coronavirus.

The homologous recombination is another method in evolution of coronavirus and determines host tropism[37]. Each ORF at 5′ end is prone to the recombination mechanism, generally subjected to the array of 5-7 nucleotides constituting transcription regulatory sequence or TRSs that mediates the leader sequence on subgenomic RNAs usually. Experiments in 2003 outbreak signifies that SARS -CoV as a resultant of gene reshuffling, flaunting with miscellaneous parentage:3′ end with avian lineage and 5′end with mammalian origin, except the spike protein possessing the traits of both the lineages showing high resemblance to Feline Infectious Peritonitis Virus (FIPV) with an exception of approx. sequence of 200 nucleotides (ranging from 2472 to 2694) acquired by avian infectious bronchitis virus (IBV).

The homologue scanning and receptor/coreceptor shifting emphasize on longevity of virus in the host cell. As the entry and docking of virus in the host cells is augmented by spike proteins, therefore any alteration in the genetic makeup of spike protein may expand the range of host cells, if switched on to positive selection. The foremost mechanism directs the virus for its diversion to different receptor or crawl for a coreceptor as a portal accomplishing its successful access to host cell.

Virus – host synergy for transmission

The coaction of the receptor binding domain (RBD) of the spike protein and host cell receptor is of utmost importance in surmising the host range of the coronaviruses. Generally, the host immune response the RBD in the S protein of a CoV interacts with the cellular receptor and is intensely selected by the host antibody response. Phylogenetic reconstruction determines the evolutionary relationship and host selection between spike glycoproteins in the human-close beta coronaviruses. The recombination of SARS-CoV is the exemplar of stabilizing selection during this third spillover[46].

Molecular scrutiny of SARS-CoVs in both human and civet has decided that mutations within the RBD region of spike permitting its rigorous domestication in various hosts such as bat, civet, mouse and raccoon dog[46]. The RBD is confined to 318th from 510th amino acids on the S1 domain[37]. It is notified that difference of only 6 amino acid residues were observed out of which 4 are positioned in the receptor-binding region. Two crucial replacements in Civet SARS-CoV i.e. S487T and K479N enhances the bonding of spike protein with human ACE2 receptor thus confirming the accommodation of virus within host [37].

On this third upsurge of coronavirus, research disclose that SARS-CoV-2 is kith and kin of SARS-CoV with 30% of genomic difference in the S1 domain of the spike protein[21] and the same cellular receptor[33]. These modifications increases the chemistry of human ACE2 and SARS-CoV S protein by 10- to 20-fold, fact revealed by a cryo-EM study[47]. Natheless, studies to discover coreceptors enabling SARS-CoV-2 transmission is on the line. Interestingly, ACE2 receptor binds with a different part of Spike protein of HCoV-NL63 [48]. Beside ACE2, receptors such as aminopeptidase N for HCoV-229E, and 9-O-acetylated sialic acid for HCoV-OC43 also persists urging for the successful adaptation in humans after jump over from their animal hosts.

The host reliance and restriction factor also command the successful interspecies transmission the deviation from these two may also hamper this spillover. For intervening the host, the virus has to capsize host restriction factors and seize host reliance. Molecular strategy in this regard is still in the stage of infancy.

HUMAN TO HUMAN TRANSMISSION

Community transmission

Coronavirus is considered to be one of the respiratory pathogens; communicable through respiratory droplets packed with viral agents. The three approaches involved in the transmission of this virus's origin, passage and destiny (either inhalation or deposition) of respiratory droplets. In 2014 Bourouiba et.al [49] defined respiratory droplets as a small aqueous droplet varying in both size and content and are produced within the human respiratory tract by exhalation, consisting of saliva or mucus and saturated with infectious agents present in different respiratory tract surfaces. The term droplet is often considered to be the droplets >5 μm in diameter remain confined to the upper respiratory tract constituting

oropharynx — nose and throat areas that eventually comes into the influence of gravitational force and falls to the ground thus can travel a very short distance(e.g. ≤1 m) , whilst the droplets ≤5 μm are termed as droplet nuclei have the potential to be inhaled into the lower respiratory tract viz the bronchi and alveoli remain suspended in air for significant periods of time, allowing them to be transmitted over distances >1 m[50]. Temporary interruptions of breathing such as coughing or sneezing and other dormant activities such as talking, breathing, or laughing are the portals for the respiratory droplets. In 2008, Weber and Stilianakis[51] described in their literature that the respiratory droplets can transmit the pathogen through three means viz "contact," "droplet," and "airborne". Considering contact transmission, the transmission is through pathogen-laden droplets; movement of viruses from one infected or colonized person to another through physical touch e.g., licking, touching, biting is categorized as direct contact transmission, whereas transfer facilitated by vectors that allow transmission of agent causing disease without any physical contact is termed as indirect contact transmission. Moving to the next mode is the droplet transmission mode in which large droplets are expelled out by violent and non - violent expiratory events that subsequently scattered and positioned themselves upon the surfaces like conjunctiva or mucus membranes of a person. Since large droplets gravitationally settle rather quickly, droplet transmission is considered important at close range: in still air, a 50-micron droplet crosses a vertical 1.5 m distance in 20s [52]. Third mode is aerosol transmission propounded as airborne transmission, includes the dispersion of small respiratory droplets (typically smaller than 10 microns: a 10-micron droplet settles gravitationally in still air within approximately 9 min). By the dint of their small size, these droplets can be traced even in the alveolar region of respiratory tract. These droplets, often referred to by the confusing term "droplet nuclei," are small enough to remain airborne for sufficient time to transmit the pathogen. Hence, physical contact is not a requisite for airborne transmission. As there is futile knowledge about the droplet physical properties or their dynamics, thereof the segregation among these three modes of transmission is still in dilemma. However, the little literature glimpsed that the size of droplets determine the classification of these modes. The scrutiny of fluid respiratory dynamics explains the process of droplet generation and also depicts the properties of expelled droplets like density, size and velocity. Nevertheless, the settling distance, movement of the particles and evaporation time like attributes can also be determined simultaneously. Though this study is also looking for the effect of extrinsic factors like air currents, humidity and temperature .

For example, droplets formed by airways may be transported by a turbulent jet and subsequently inhaled. The modes of transmission has classified on the basis of size of the droplets. The size of the expelled droplets has been a subject of considerable research and controversy (partly attributable to different instrumentation or collection methods). Nevertheless, it is reasonable to consider that diameter of respiratory-droplet vary from 0.5 microns to 1000 microns [53]. Care should be exercised in interpreting droplet sizes. Respiratory droplets are generated in a nearly 100% relative-humidity environment. Upon exhalation into the lower-humidity ambient environment they shrink by evaporation (a fast molecular process, of the order of seconds or less, depending on droplet size, composition, and relative humidity) to reach their equilibrium diameter. Some estimates suggest that droplets may shrink to about half their original size [54].

While social distancing and sanitation are the only two effective measures to restraint the crisis right now, the one major tension that remains at large is the silent transmission. People showing atypical symptoms, or not getting detected in time and spreading the infection is one of the prime reasons community transmission is on the rise and that is what also happened in hotbed districts- including the travelling ships and cruises which had to be quarantined because of the same.

DIRECT TRANSMISSION

Droplet Transmission

Droplet transmission is one of the usual forms to transmit the viruses from one person to person. This transmission is the repercussion of coughing or sneezing, drip or exhalation. Being enlarged and dense, droplets travel only short distances before settling, usually less than 3 feet. These typically 5-10 microns sized droplets are often loaded with infectious particles.

This virus-laden mucus droplet becomes the primary mode of transmission as it can be disseminated sprightly from diseased person to another within the confined zone of approx. 6 feet/1.8metres [55]. In this shortest route spread, the mucosae of mouth and nose or conjunctiva of eyes are more prone to potentially infective respiratory droplets which may increase the fatality.

Vector Transmission

There's one other route that's thought to play a role in the spiralling COVID-19: vector transmission through fomites. The droplet spray in short range transmission has the potential to transmit this virus effectively, If concisely demonstrated, viral particles expelled from the respiratory tract of an infected individual through any means will land on a surface of inanimate objects and remain infectious for hours which may eventually become contagious as hands will come in contact with these surfaces and thus virus will sneak into the body of individual via the mucous membranes and conjunctiva and so on. The frequently contacted objects on which virus may land includes **c**omputer mouse**, t**rash cans**, s**ickbed handrails**,** doorknobs, and other personal items comprising mobiles, pens, reading glasses with endless list. Natheless, the prolong duration of contamination on objects and surfaces is supplementing the effect of this mode of transmission. The recent studies discovered the length of time of viable SARS-CoV-2 on various objects f'rinstance the duration of virus on plastic and stainless steel is up to 2-3 days and wood is for 1 day and on copper and other metals it can survive for 4 hours. Contact transmission has also criticized as vector transmission in the case of Diamond Princess Cruise ship in Italy and other European nations.

Air Borne Transmission

It has been notified from most of the previous studies that airborne transmission is considered to be aerosol transmission as the caravan for airborne respiratory disease transmission is the droplet nuclei, constituting of evaporated remains of droplets mayhap with pathogen [56]. Virus-loaded small (<5 μm) aerosolized droplets is somehow able to remain hanging in air for considerable proportion of time and travel long distances to infect passers-by which is another complicating factor in figuring out this transmission. By the virtue of their light weight, these droplets can be propagated through a large distance more than 3.3 metres. Add on to this, the current study on SARS-CoV-2 circulated in one of journal of the US CDC, *Emerging Infectious Diseases*, on April 10 divulged that the utmost distance travelled by aerosols of SARS-CoV-2 is likely to be 4 m" (13.1 feet) and is extensively available in the air and on object surfaces in both general ward (GW) and the ICU, indicating threat of infection in medically professional personnel's[57]. The sources from The New England Journal of Medicine on March 17 insights that the SARS-CoV-2 can remain viable "in aerosols up to 3 hours" which is experimentally verified by induced aerosol-generating procedure". This states that formerly called HCoV-19 is a culprit of pandemic because of aerosol transmission and surface stability. Beside these, various extrinsic factors such as

moisture content in the air and thermal effect has been observed showing prominent effect on aerosol transmission [58]. They attune the livelihood of viruses by modifying the membrane and spike protein of viruses.

Faecal -Oral Transmission

An additional mode of transmission i.e. faecal–oral transmission of SARS-CoV has been highlighted in numerous studies [59]. Ample evidences favouring the identification and isolation of SARS-CoV-2 in faecal samples of patients have been reported. Abnormal gastrointestinal mechanisms have been observed in COVID -19 suspects signalling the transmission of virus through faecal–oral route, though diarrhoea has seldom reported [60]. The sources like contaminated water and sewage waste, air condition system and fomites for the transmission of this virus cannot be undervalued which is clearly manifested with the 742 confirmed cases out of 3,700 in Diamond Princess Cruise ship. To evaluate the role of faecal–oral transmission in this superspreading event, it is needed to investigate it in depth.

HUMAM TO ANIMAL TRANSMISSION

The literature regarding the first outbreak of coronaviruses demonstrates the SARS inoculation experiments on ferrets and domestic cats. It was found that domestic cats didn't contract any symptoms of SARS but these inoculated cats was able to disseminate the virus following 2 days of inoculation and this process of pharynx shredded virus continued till 10 - 14 days of inoculation. Whilst, after administration of virus into the ferrets, dormancy was observed in three out of six within 4 days, and one among three inactive ferrets died on IV day. On the grounds of this weekly oriented experiment, domestic cats might be considered as reservoir for this SARS-CoV indicating their effective transmission to uninfected accompanying them. Nevertheless, cats cannot be chosen as experimentals. Though SARS like coronavirus can likely to prey on Chinese ferret badgers (*Melogale moschata*), masked palm civets (*Paguma larvata*) and raccoon dogs (*Nyctereutes procyonoides*) as suggested by Serological and virological studies. *in vivo* studies certified the above mentioned experiment Domestic cats living in the Amoy Gardens apartment block in Hong Kong, where more than 100 residents contracted SARS last year, were also found to be infected with SARS-CoV.

Zooanthroponosis has become the major worry in the case of COVID 19. Though rudimentary knowlegde about reverse zoonosis disease transmission is available . Yet there are instances supporting the context. Human to animal transmission has seldom imposed

threat to any species. But this scary disease has crossed this barrier also which can be illustrated by the incidents reported in various part of the world.

The first incidence which shocked the entire world was the death of the pet dog that contracted a "low-level" COVID-19 infection from its owner, according to news reports. The mystery deepens over exact cause of death as the dog was not autopsied. On march 4, 2020,South China Morning Post in sighted the news that the 17-year-old Pomeranian was first tested "weak positive" for the virus on February 28, and experts from the University of Hong Kong, City University and the World Organisation for Animal Health "unanimously agreed" that the test results reflected a plausible case of human-to-animal transmission. Thereafter, the dog was quarantined at a government facility from February 26 to March 14, after it finally tested negative for the virus and was allowed to return home. The dog's owner intimated about its death on March 16 to Hong Kong Agriculture, Fisheries and Conservation Department (AFCD).

On examining specifically the cause of death of the dog, the sequel was initiated by the dog owner, a 60-year-old woman who first tested positive for COVID-19 on Feb. 25 and was hospitalized immediately. After recovery she was back on March 8. The AFCD confirmed that the similarity report between the genetic makeup of the coronavirus and the virus found in the woman's Pomeranian resultant that virus is likely to diemminate from the diseased human to animals.

The COVID- positive minks at two fur farms were found in the Netherlands with some clinical manifestations of respiratory system. The Dutch Ministry of Agriculture comprehended that some staff at both the farms suspicious for combating the disease thereof it signals towards the human-to-animal transmission. Thus, it has been proved that ferrets and minks are susceptible to COVID-19 contamination. However, not only minks and ferrets, even the cats showed the similar symptoms which is evident in the New York assuming that cats might have got infected from people in their households or neighbourhoods. Another incidence added by the Agricultural and Fisheries department of the Hong Kong stated that contamination in the pet cat for the novel coronavirus after its master was confirmed to be COVID positive in the Hong Kong. They mentioned that the cat had not shown any symptoms earlier but the samples were collected from the cat's mouth, nose, and rectum confirmed it positive.

In the growing list of the animals susceptible to Coronavirus, lions and tigers have also attained a special place**.** Nadia, a four-year-old tiger at the Bronx Zoo, New York who has been infected by this virus . Nadia developed a dry cough after coming in contact with an asymptomatic employee and was tested positive for coronavirus with a fast recovery rate.

As the world continues to try and grapple with the COVID-19 outbreak, Japan's national broadcaster NHK has conducted an experiment that successfully demonstrates how SARS-CoV-2 can spread in buffets and gatherings. In the wake of several Japanese cruise ships becoming hotbeds for COVID-19 infection, NHK teamed up with infectious disease experts to map the spread of the virus in crowded eating locations such as buffet line at restaurants or cruise ships. The experimenters chose ten participants who were asked to pick and eat food from a buffet line and contact the surfaces normally, as they would. One of the participants, however, was marked with fluorescent paint (ergo, acting as virus) on his palm which can only be visible in darkness or under blacklights. The person was asked to mingle with the others. By the end of 30 minutes, experiments turned off the light to trace the trajectory of the fluorescent paint during the course of the meal. They found that bits of the paint had found their way on almost all persons present in the room as well on several items on the buffet table implying that the virus, which spreads through respiratory droplets and frequent touching of surfaces, could find a way to infect almost everyone. The experiment is meant to display the rapid and inevitable transmission of coronavirus in crowded locations when an infected person is part of the crowd.

CONCLUSION

Over the past decades, the bat virome has been extensively studied and it is impressed upon that this mammal is deadly sharing its role in the evolution of coronavirus. Abundant availability of bats on the planet make them natural host of these coronavirus and invasion of human activities in their habitat mayhaps resulted in easy spillover but various connecting links regarding zoonotic origin of SARS-CoV-2 are still uncertain. Studies reflecting camels, civet cats and pangolion as the intermediate host coronavirus hinted the primary host and secondary host might have shared the same ecological niche. Studies on the interactions of this secondary host with human are yet to be clarified. Sero prevalence and experimental studies suspects various mammals including domestic ones to be target of SARS-CoV-2

With the albatross of SARS, MERS now COVID-19 has frightened the various animal species on the earth through zoonosis and reverse zoonosis. With so much still unknown about SARS -CoV-2, it is too early to say exactly how it spreads from person to person. Virologists have envisioned that respiratory droplets and aerosols of COVID -positive are inoculum shed of SARS-CoV-2. These are brooded as the airborne transmission of COVID-19. However, the R & D regarding the physics of the virus loaded showers is still in pipeline. However, on the basis of incidences quoted above, the possibility of transmission of SARS-CoV from human to animals especially pets cannot be downplayed. The veterinary medicine group says limited information is available so far in context of risk of pets spreading. However, they mainly stress on human to human transmission in driving the global pandemic

The cases and lab experiments show that there is public health need to recognize and investigate the potential chain for transmission and will elucidate the evolutionary pathway of SARS-CoV-2 in animals, with important implications in the prevention and control of COVID-19. WHO continues to emphasize the utmost importance of frequent hand hygiene, respiratory etiquette and environmental cleaning and disinfection, as well as the importance of maintaining physical distances and avoidance of close, unprotected contact with people with fever or respiratory symptoms.

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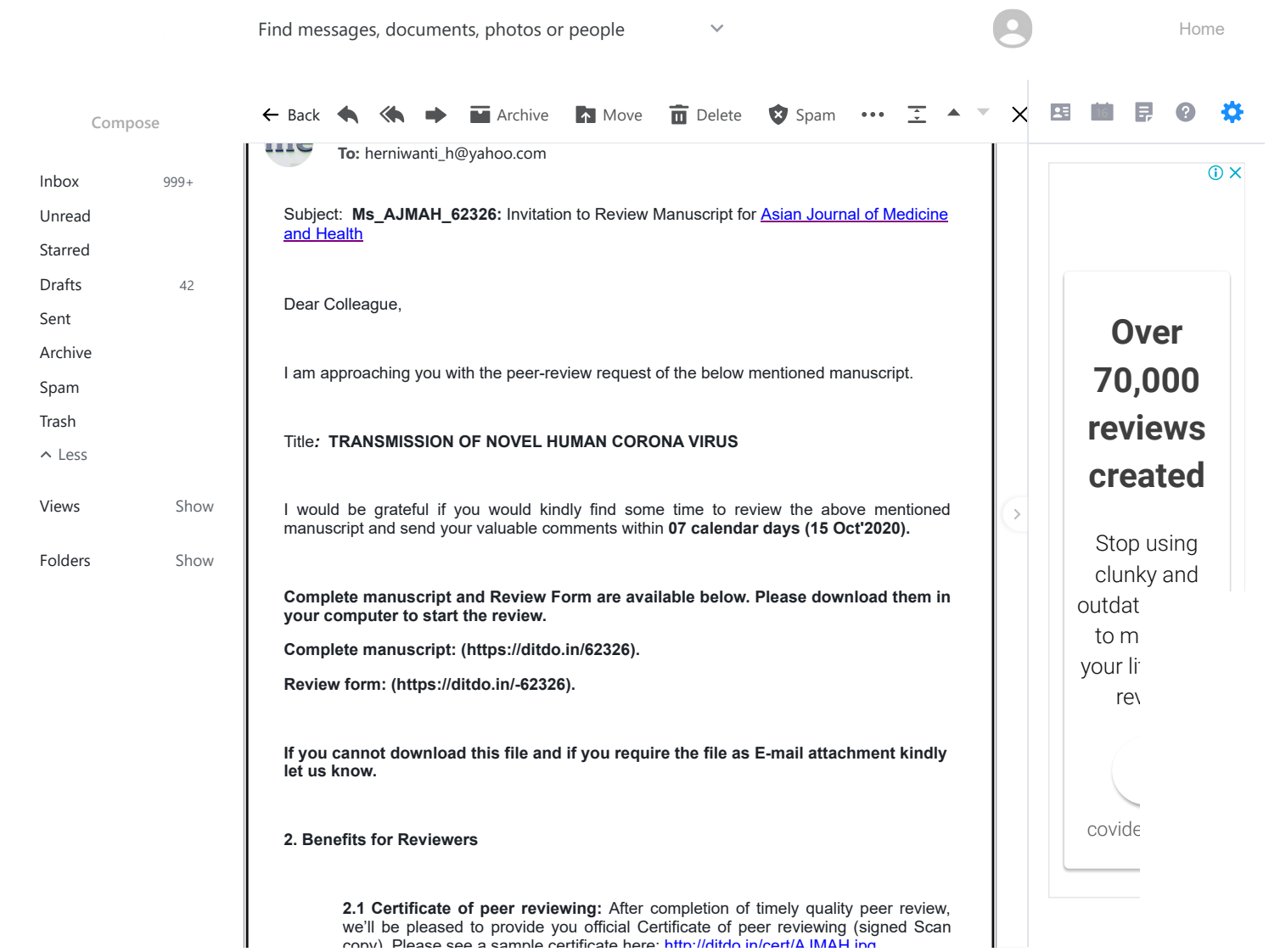
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