Research Article

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Transmitting, Mutational and Pandemic Nature of Corona: The Role oF Transposons, IS1::Tn::IS1 and CRISPR- CAS-9.

Nitosh Kumar Brahma[1]*

1Ex Faculty IIT-Kharagpur.721302,IGE (Institute of Genetic Engineering) India.

***Corresponding Author**
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Abstract

Corona/ Covid19/Omicron / SARS/ MARS similar viruses have no individual genetic mechanism to make them encapsulated spore forming microbes similar to bacteria, fungi, algal blooms involved spreading allergy. Transmission in all such cases need fluid dynamics of water and air. This flow does not require any support of matrix, i.e. nano particles of carbon, silicates and dust of animate inanimate molecules. They enter into lung alveoli surface epithelial cell, adhere on the surface of body saliva, originated due to cold and other infections. In support of ACE-I and II (Angiotensin Converting Enzyme I and II) [1]. So, there are two releasing mechanisms are existing in corona infection; one is the release of corona virus from the alveoli cells with matrix binds of one co-morbid patients directly to other healthy recipient at the distance of 6 m in a closed environment by its self-development irritation and allergy, as received by sudden irritating smoke developed from kitchen, pollen, that grows during grass cutting, cleaning and sanitization. Transcription of m-RNA, in a matrix based single corona after entering into lung alveoli starts to transcribe and translate to many molecules of corona viruses, damages alveoli cells of lung, caused due to individual physiological conditions, old (above 70 years) and young (below 40), co-morbid(sick) and healthy people at similar age groups. IS::Tn::IS), Crispr/Cas-9 DNA transposons existing in corona m-RNA starts to act during transcription, and translation.

Keywords: Transposons, Alveoli, Transcription, Translation, Mutation and Infections.

1. Introduction

An AAIR(Antiadherent Immune Response) experimental was initiated in Bulb/C mic against serotype 026: EPEC (Enteropathogenic (invasive) Escherichia coli) a fatal diarrheagenic E.coli , killing mice over night at (8 hours) found unique support of hybrid genetically engineered E.coli, carrying MRHU(+) donor plasmid in support of trascojugated pRT (Plasmid Ronald Taylor) of Yale University , USA, 1980, expressed MRHU(+) plasmid in auxotrophic genetically Engineered (GE) Immune responses, revealed that the mice were resistant against the donors 026:EPEC, even at highest dose of 10^8 cells / 0.2 ml, intraperitoneal inoculum, without pre-inoculated Balb/ C mice were killed at low intra peritoneal dose inoculum of 101 cells / 0.2 ml. The investigation revealed that some IS based transposons support the expression of MRHU (+) hemagglutination in hybrid genes of Escherichia coli. By increasing antibiotic profiles, as occurred due to IS (Insertion Sequence) as represented by IS1, IS2, IS3…IS10 DNA sequences change the flanking nature of transposons (Tn), their expressions in foreign DNA, chromosome and plasmids. The antibiotic resistant profiles initiate the illegitimate recombination nature of microbes, their surface antigenic, fimbriae(pili) profile and adherence, colonization profile. The process was studied carefully in 1980 in the lab of Prof. H. Saedler, Biology-III Genetic Engineering, Dept, ALU, Freiburg, Germany. In case of increasing fatality of corona antibiotic treatments is therefore recommended.

Considering the fatality rate of corona as pandemic globally, the author has attempted to recapitulate the possible application of AAIR by generating hybrid plasmid cloned m-RNA, expressing spike proteins. IS:Tn::IS and Crispr/Cas-9 modified corona viral cells involved in designing vaccine against corona, to prevent corona virus to adhere on trachea and lung cells, to repair and to bring healthy life to mankind. IS::Tn::IS was observed/studied/ discovered in Maize by Barbara Mc Clintock, USA, Peter Starlinger and Heinz Saedler, Germany studied the same in bacteria. Due to spontaneous mutations in corona, it is speculated by the author, that “IS::Tn::IS” DNA sequences might be present in corona, to mutate and to change the adhering, invasive and infective spike protein. The presence of IS-Tn-IS sequence have not been studied in SARS-COV-2, COVID-19, and corona. The sequence length, varied from IS1 (0.8kb) to IS10, (1.2 kb) (kilo base pairs) showed the potentiality spontaneous to do illegitimate recombination. If any

of the sequence IS1, IS2, IS3…IS10 found common among HIV, MERS, SARS, Influenza, and H1N1 viruses, it could be useful to develop AAIR. Both AAIR vaccine concept and recent revolution in DNA editing, Crispr/cas-9(Clustered, Repeat Interspaced Short Palindromic Repeat), / (Crispr-associated protein-9) both could essentially be used, bidirectional in corona vaccine to protect pandemics and their repeats in future.

The IR mechanisms which is proposed is supposed to be controlled by IS: Tn:IS transposons failed to attach the spike proteins. Hybrid DNA as involved in formation of AAIR as monoclonal antibody will block the adherence of corona spikes. Crispr/cas-9 will repair in addition to the transmitting, invasive nature of corona. In the process the programmable DNA of non-pathogenic influenza virus. The author describes few of those possible mechanisms of Crispr transposons involved in changing protein structures of spike protein of corona. Jumping gene, transposons, if programmed non-pathogen m-RNA could be used in the form of vaccine. Bacteriophage Lambda , x similar and other fusion to change the mode of infection to coccucea are the present thought, changing the direction of corona to human trillion microbes involved in Pneumonia

1. Materials and Methods

Different Isolated DNA and RNA of different bacteria and viruses were used. P32 radioisotope dATP, EcoR1, Pst1, HindIII, Bam H1, restriction enzymes were purchased from Boeringer Manheim Germany. Labelling of DNA and RNA were made to find the similarities , the presence and absence of IS1. The study inspired not only to study genetic rearrangements and illegitimate recombination , as occurred when corona infections are moving downwards(i.e. many varieties of antibiotics are applied, various sanitations are used in commonplaces, when for survivals corona stats to mutate and exposed as antibiotic resistant human system surviving with bacterial strains , namely pneumococcal strains significantly participate the micro evolution of living world. Fig. (d), represents the ampicillin resistant Tn. Fig.1 (e), shows the segregating colour changes among maize seeds, as caused by transposons. Fig.1 (f) is reproduced with the legendary personality of Barbara Mc Clintock, who identified colour changes in maize seeds due to presence of spm transposons in maize seeds DNA in 1931, and received Nobel Prize in 1983, [1].

IS based Tn (Transposons) are involved in higher and lower groups of plant and animal kingdom, including the evolution of viruses and bacteria. The camouflaging infective nature of SARS COV-2 corona virus, covid-19 could be associated with Tn, as proposed by the author, [10-14]. Jumping-genes as retro transposons [9] hijacks special cells called nurse cells, produce invasive nature of DNA driving evolution, and causing diseases.

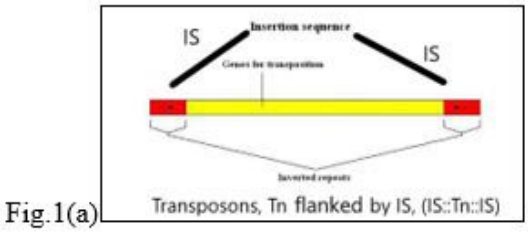

Fig.1(a)

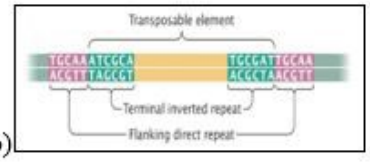

Fig.1(b)

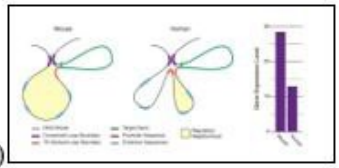
Fig.1(C)


1(d) 1


(e)

Fig.1 (a) shows one transposons, flanked by IS elements (IS::Tn::IS), Fig1(b) shows the repeats and inverted repeats DNA sequences involved of IS elements. Fig.1(C) shows the mechanism of Tn enzymes involved in illegitimate recombination and rearrangements. “Cut and Paste and Copy and Paste “foreign DNA have been identified in such illegitimate recombination where IS elements support to insert foreign DNA into host recipient DNA [1]. In Fig.1 (C).Histogram compares the chromatin folding frequencies among mouse and human. It shows that transposons based chromatin folding in mouse is higher compared to human. IR(Immune Response) in mouse is stable, compared to human. MHC-HLA gene, responsible for IR in human chromosome 17 is susceptible compared to chromosome 6 in mouse [2-9] Chromatin loops are important for gene regulation because they define a gene's regulatory neighbor-hood, which contains the promoter and enhancer sequences responsible for determining its expression level. Remarkably, transposable elements (TEs) are responsible for creating around 1/3 of all loop boundaries in the human and mouse genomes, and contribute up to 75% of loops unique to either species. When a TE creates a human-specific or mouse-specific loop it can change a gene's regulatory neighborhood, leading to altered gene expression. The illustration shows a hypothetical region of the human and mouse genomes in which four enhancer sequences for the same target gene fall within a conserved loop. In this example, a TE-derived loop boundary in the human genome (orange bar) shrinks the regulatory neighborhood, preventing two

of four enhancers from interacting with their target gene's promoter sequence. The net result is reduced gene expression in human relative to mouse. Looping variations such as these appear to be an important underlying cause of differential gene regulation across species and between different human cell types, suggesting that TE activity may play significant roles in evolution and disease. The method was studied by radio isotopic IS DNA labelling and southern hybridization. The method proves also how one IS elements jumps from plasmid to chromosome and back to plasmid. Almost half of our DNA sequences are made up of jumping genes, known as transposons. They jump around the genome in developing sperm and egg cells and are important in cellular evolution [15] and cause new mutations that lead to diseases. Remarkably little is known about when and where these movements started in development of reproductive cells. The key process that ensures their propagation for future generations with possible genetic disorders. Animals have developed a powerful using suppressing activities of jumping gene, non-coding pi RNAs[15-17], that recognize jumping genes and suppress their activity.

Some information has been recorded that virus, Covid-19, originated from Wuhan, China, and was spreaded all over the world, representing no RNA variations. Measurement of antibodies to SARS-CoV-2 will improve disease management, if used correctly. In late 2019, China reported a cluster of atypical pneumonia causative agent, responsible for severe acute

2. Conclusion

Microbes and the climate change are proportionally related oscopic An outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was first reported in Wuhan City, China, in December 2019. Since then, the outbreak has grown into a global pandemic, and neither a vaccine nor a treatment for the disease, termed coronavirus disease 2019 (COVID-19), is currently available. The slow translational progress in the field of research suggests that a large number of studies are urgently required. In this context, this review explores the impact of bacteriophages on SARS-CoV-2, especially concerning phage therapy (PT). Bacteriophages are viruses that infect and kill bacterial cells. Several studies have confirmed that in addition to their antibacterial abilities, bacteriophages also show antiviral and antifungal properties. River Ganges in India, for centuries, has been revered for its “self-cleansing and special healing properties”. More than 450 million people depend on the waters of Ganges for many aspects of their life. In 1896, one of the first published works on Ganges water by Ernst Hankin, a British bacteriologist demonstrated antibacterial property of Ganges water against Vibrio cholera [1]. Further work by French microbiologist D’Herelles in the beginning of the twentieth century established that the antibacterial property of Ganges water to be due to a factor, later named “bacteriophage” [2]Virus Bacteria, (Unorganised without nucleas) Fungi, Mould and Algae (Organize with nucleas) are propagating and changing their non-pathogenic mode to pathogenic mode quickly and slowly based on their pro(unorganised) karyotic and Eu (organised, nuclear material)

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