

**Special Article**

## **Genomic Implications of Covid-19 Differentials: Analytical Review**

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### **Abstract**

The variability of the novel coronavirus disease causation, spread and treatment modality across culture, colour and geographical location has not been properly studied. This bring to the fore the advocacy on genomic implications of the effect of Covid-19 across the globe. The study evaluate the variability among individuals, ethnicity, race, colour and geographical location as regards Covid-19 disease causation, spread, virulence of the organism, host response and clinical manifestations. The letter- seal- envelope model was conceptualized to underscore the impact of genetic core- host defensive ability- environment to disease causation and prevention. Geographical location and climatic condition have not been scientifically proven to modulate Covid -19 transmission while individual genetic core was considered a factor influencing host responses to disease and treatment modality. Cutting edge genomic medicine is advocated to understand the coronavirus epidemiology, variants, pattern of spread and treatment regimen

**Key Word:** Genomic implications, Covid-19, genetic core, Africa, Model

## **Introduction**

The science of human Genetics and Genomics is critical in precision medicine to further understand the factors responsible for individual, family, racial idiosyncrasies in certain disease conditions (Murray, Kenny, Ritchie, Rader, Bale, Giovanni et al. 2020). Before the close of the last century, genomic implications of development of disease conditions such as hypertension, diabetes, breast cancer, haemophilia, sickle cell disease, polycystic kidney disease, peptic ulcers and cystic fibrosis are well established. Genomic medicine help to explore the specific medical history, genetic makeup, specific diagnosis and personalized treatment of the clinical condition.

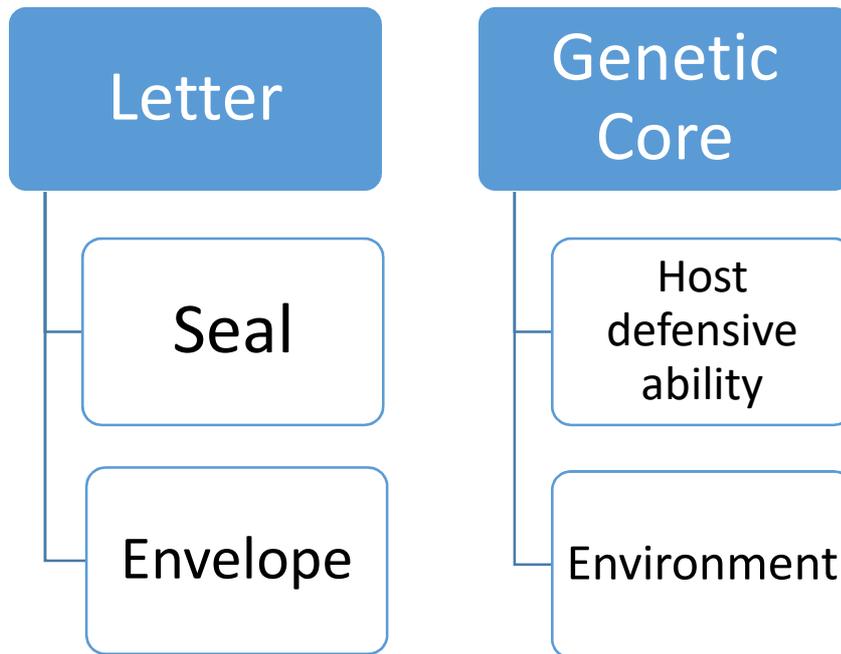
The variation in Covid-19 presenting signs and symptoms, virulence of the organism on the host, incubation period and host responses to the disease condition, death rate, recovery rate as well as the variants of Covid-19 across culture, ethnicity, race and geographical boundaries are all indicative of possible genomic implications (Murray et al. 2020; Khan, Khan, Baig, Ahmad, Farouk, Song, 2020). It is reported that the wave and virulence of the coronavirus was typical in America, Europe and Asia (Badu, Thorn, Goonoo, Dukhi, Fagbamigbe, Kulohoma, 2020; Abdullahi, Emeribe, Ajayi, Oderinde, Amadu, Osuji, 2020; Omotosho, 2020). This inferences gave an idea that geographical location and climatic condition may modulate the spread and the severity of the coronavirus disease (Badu et al. 2020; Gaye, Khoury, Cene, Kingue, N'Guetta, Lassale, 2020; Diop, Ngom, Pougue Biyong, 2020; Bukhari, Massaro, D'Agostino, Khan, 2020; Kotrotsiou et al., 2021). Respiratory diseases such as Influenza is known to increase in cold weather however, there is little scientific evidence to suggest that temperature changes and atmospheric humidity affect the transmission and virulence of the novel coronavirus. A Nigeria study by Ogaugwu, Mogaji, Ogaugwu, Nebo, Okoh, Agbo et al. (2020) revealed that temperature has a significant weak negative correlation with Covid-19 transmission and no significant correlation between atmospheric humidity and mortality from Covid-19. This finding is consistent with the result of some similar studies in China, and also inconsistent with some other studies in the same location. Bukhari et al. (2020)

also observed the conflicting results about the influence of weather on the novel coronavirus in China. Similarly, Gupta, Banerjee, Das (2020) study on the effect of meteorological factors on the transmission of coronavirus in India was also inconclusive. Therefore, more studies is needed to validate the correlation of climatic conditions with the transmission of Covid-19

Furthermore, there was a cynical impression that at the molecular level, Covid-19 has a totally different strain and RNA lipid envelop for the black race. This was widely circulated in Europe and America. It was the first time when scientists could think of genomic undertone of Covid-19 pandemic. However, there was continued variability among people of the same African descents. A cross sectional study in the United States earlier indicated that more of the Black Americans were reportedly dying from Covid-19. This result however was inconsistent with findings and observation elsewhere. In the large African settings especially in the East and West Africa which are far from the Mediterranean Sea, there appeared to be a reduction in the Covid-19 virulence as compared to black Americans and African descents living in part of Europe. Although, it can be argued that much of Polymerase Chain Reaction (PCR) test was carried out in Europe and America than was done on the African continent (Abdullahi et al, 2020; Omotosho, 2020; Bukhari et al. (2020); Seidu, Hagan, Ameyaw, Ahinkorah, Schack, 2020). A perspective is also in the area of incubation period and level of asymptomatic. Epidemiological assessment and mapping show that in Africa a number of infected individual especially among the younger population are asymptomatic as compared to Europe and Asia (Diop et al, 2020). A traditional African mythology is that black descents are known to be resilient and possess innate ability and genetic corrigence which enable them to suppress diseases. It is thought that African food preference and preparation, supplement and choice of plant root, bark, leaf and other indigenous preparations have role to play in the ability of the Africans to prevent diseases. This African psalm of disease control and prevention is not without certain conundrums given that African has been bedeviled with attendant communicable diseases for several years which still require solution (Gaye et al. 2020). Nonetheless, in African setting, it requires a further epidemiological study to

assess and describe how African in particular cope with epidemic and pandemic. Furthermore, due to poor environmental hygiene, inadequate water supply, poor health system as well as illiteracy and poverty in many part of Africa, the coronavirus burden, pattern of spread and virulence was still minimal as compared to most industrialized countries with standard healthcare facilities (Omotosho et al, 2020; Gaye et al. 2020). The predictors of coronavirus disease transmission, clinical manifestations, virulence and susceptible host response variations between Africa and other continents has not been properly studied. Gaye et al further opined that expertise gained from previous disease outbreaks such as Ebola, climatic condition and strict measures such as prompt lockdown, early closure of borders and surveillance have helped the African countries in combating the Covid-19 pandemic. In all, there is still variability in coronavirus responses even among the Africans, therefore, the study of the genetic implications of the disease transmission, organism virulence and the host response still remain important. Also, there is also variation in treatment modality and patient response during the acute phase of the coronavirus disease. It is noted that diverse treatment modalities were instituted due to patient idiosyncrasies. Despite the multi-centre clinical trial of hydroxychloroquine across the globe, the scientific community witnessed sharp differences in the experimental outcome. For example, a leading U.K journal firstly published that hydroxychloroquine increases the chances of patients dealt and therefore should be avoided in the treatment regimen. This findings however is at variance to report of hydroxychloroquine clinical trial from other centres

outsides the U.K and the U.S. Interestingly, this created a further search and re-evaluation of the clinical methods. Consequently, a vaccine trial in Brazil demonstrated a genetic variability among the volunteers. Similarly, in the U.S, certain side effects and individual differences were reported following administration of vaccines. This shows that no two individuals are exactly the same, the reason why the knowledge of genetics and genomics is important to understand the dynamics of Covid-19 disease causation, spread and treatment regimen (Murray et al, 2020; LoPresti, Beck, Duggal, Cummings, Solomon, 2020; Hou, Zhao, Martin, Kallianpur, Chung, Jehi, 2020). Cutting edge precision medicine recognizes genetic link to the epidemiology of the novel coronavirus. One suggestion for scientists is to evaluate the core genetic makeup of diverse Covid-19 victims to uncover the clinical impediments related to Covid-19 pandemic. The review presented a systematic analysis of the variability in term of pattern of transmission, virulence and susceptible host responses to the novel coronavirus with particular reference to Africa. The effect of predictive factors of Covid-19 transmission such as temperature, atmospheric humidity and geographical location is not scientifically clear. The knowledge of human genetics and genomics is stressed to help in understanding the diverse variability about the novel coronavirus. Patient centered treatment modality that respect individual personality, gene, cultural background, race, geography need to be explore. The author also develop a letter-seal-envelop model to explain the dynamics of infection transmission with particular reference to the genetic core, the host defensive ability and the host environment. Consequently, molecular basis of Covid-19 strains required a re-assessment and documentation.



**Letter – Seal - Envelope model (Ogundeji, 2021)**

### **Letter –Seal- Envelope Model**

The letter seal envelope model is conceptualized to understand the relationship between the individual, the environmental factors and the genetic make up about disease transmission and the host responses to infection. The LSE is developed from the author primary understanding of the host lines of defense and resistance against the stressor as explained in Betty Newman’s model. The LSE model is particularly critical to genetic core of individual to build up resistance to overcome the virulence of the organism. The central theme of Letter- Seal-Envelope Model are the genetic core- host defensive ability- environment. The LSE model view man’s survival of diseases as being ultimately determined by the individual genetic underwritten. Similar to the Newman’s idea, the genetic core is the innermost component which will be invaded by the offending organism for infection transmission to occur. In LSE model, the ‘letter’ is the individual gene which must be protected to prevent infection transmission. The letter therefore must be protected by the seal and the envelope. Diseases such as polycystic kidney disease, sickle cell anemia, haemophilia including the novel coronavirus occurred due to exposure of the hidden ‘letter’, the

genetic make-up of the individual. Genetic mutation further open the envelope and exposes the “life letter”, the DNA and the immune system which fight invading microorganisms.

The author see the seal in the envelope as the host defensive ability. It is the gate way to the envelope and the letter. The letter is expose when the seal wipe away or faded away. The author opined that the seal is more critical to protecting the letter as the envelope itself. In reality, the host defensive ability is critical to transmission of infection to the genetic core. The individual with certain comorbidities are less likely to resist the invading organism than individual without any underlying secondary disease condition. The host defensive ability relates to factors such as nutrition and vaccination which can prevent the onward transmission into the genetic core. The model explained that the envelope is the individual environment. The envelope is the outermost part covering the important letter. From the model, the environment is the first exposure to contacting the infection. The microorganism lives and thrive on surfaces and transmit infection within the physical environment. This is the gate way to the important host defensive mechanism and the genetic core.

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