Acta Scientific Pharmacology

Volume 4 Issue 1 January 2023

Conceptual Paper

# Probability of SARS-CoV-2 Infections for Future Cancer Incidence in World Population - A Commentary

**K Ramalingam[1]*, P Karnan[2] and A Anbarasu[3]**

*[1]Mediclone Biotech Research Centre, Chennai, Dr. Rai Memorial and Medical Centre (Cancer Treatment and Research), I.E.C Member, India*

*[2]Associate Professor, GRT College of Education, Tiruttani, Tiruallur, India*

*[3]PG Assistant in Biology, Government Higher Secondary School, Chithathur, Tiruvannamalai, India*

***Corresponding Author:** K Ramalingam, Mediclone Biotech Research Centre, Chennai, Dr. Rai Memorial and Medical Centre (Cancer Treatment and Research), I.E.C Member, India.

**Received:** January 17, 2023

**Published:** December 31, 2022



In the event of the fortuitous emergence and outbreak of corona virus in 2019 and the great toll of human life in millions by COVID-19 next to Spanish flu syndrome in the world (1918), the probability of cancer incidence and its increase in human population may not be ruled out by the thinking that the corona virus outbreak since 2019 and its phenotype modifications into variants to date will not be a worldwide cancer burden in view of the WHOs (GENEVA) statement that 50 percent of world population are the would be sufferers of cancer disease in the near future due to multifarious factors. The above hypothesis may be considered as conceivable in view of the generalization that viruses are causative agents for malignant cancers. John B Leo., *et al*. [1].

The etiology of viral infections to cancer disease and the tenable hypothesis that COVID-19 Corona virus may also be viewed in the line as causative agent to future outbreaks of cancers is based on the following evidences Viz.,

- The infections of certain viruses like human papilloma bring directly the carcinogenesis in both the animals and human either alone and/or along with others chemical carcinogens i.e. syncarcinogenesis.
- The second point is that some RNA viruses may contribute indirectly to the emergence of human cancers by reducing their host immune potentials and functions. For example herpes simplex virus and cytomegalo viruses have been demonstrated to help the persisting tumour viruses like papilloma and polyoma by amplifying their genomes in the infected organs/cells/tissues in the manifestation of cancer.
- The third mechanism for the viral etiology of human cancers is the induction of chronic inflammation and the synthesis of carcinogenic free radicals which is an invariable event even in normal tissue metabolism.

The probability of viral infection will account for the future cancer incidence in world population is also based on the feasibility of the following major reasons. Every individual is prone to cancer disease as he/she is endowed with built in latent cancer cells innately. The ubiquitous presence of carcinogenic viruses and their metamorphosis (change of forms) into different morphological types or variants by mutations.

The persistence of new viruses which made an outbreak alongside already existing viruses for decades and the coincidence of the latent period for the cancer emergence being the same i.e. two to three decades.

The downgrading mode of human nutrition endowed with mutagenic substances, devoid of anti-oxidants combined with a stressful environment with concurrent congenial environmental niches have proven unequivocally without doubt, the prospective

future for the infecting viruses and preemptive human population scrambling to cancers.

As infectious viruses and chemical carcinogens can synergistically cause cancer, the prevalence and persistence of environmental carcinogens (chemical) as well as the physical carcinogens (Radiations) may increase in future, the probability of more cancers in the world.

The present commentary delineates the new concept in cancer origin i.e., the synergism of immune depression and genomic instability due to viral infections alongside promotor/starter chemical carcinogens. In this context, it is of interest to mention that the immunological landscape among individuals of the world population is different due to multifarious factors such as

- Deficiency of antioxidants
- High intake of sugars and fats in the diet which could induce the latent cancer cells into active malignant cells by their inflammatory potentials.
- The severity and transmissibility of novel COVID-19 variants. Pearson., *et al*. [2]
- The capability of the variants to reduce antibody neutralization Xie., *et al*. [3] by their spike protein mutations.
- The escape of SARS-COV-2 variants from the immune surveillance i.e. the vaccine induced humoral immunity. Garcia., *et al*. [4].

It is also elucidated that combination of a physical agent and multiple viruses infections can bring cancer. In a rare human condition called epidermo dysplasia verruciformes Orth., *et al*. [5] within the cervical cancer mass besides specific HPVs ViZ., HPV-5, HPV-8, HPV15, additional types of papilloma viruses (Variants) have been revealed. Considering the potential of undergoing changes to produce variant forms of COVID-19 Corona Virus since its origin in 2019, it may not be unexpected that more variants may be persisting passively in humans. SARs -CoV-2 the interagency group (SIG) established by the US department of Health and Human Services, HHS, NIH, FDA, BARDA and DOD have enumerated variants of SARs CoV-2 since 2020 December to 2021 September COVID-19 [6]. In the former the interactions of viruses (HPV) and physical carcinogens namely the ultraviolet rays of the sunlight has been construed to have caused cancers. The HPVs syngenic variants, so far identified in the genital tract in situ is about 14. These HPVs which produced cervical dysplasia has been attributed as etiological agents for the premalignant condition of women's cervical cancers. The malignant and the range of HPV infection on organs are not strictly restricted to genital region alone but also in other organs. For instance HPVs DNA has been identified in vulvar cancer, penile cancers, oral cancer, tongue cancer, laryngeal and lung carcinoma, perianal and anal cancers etc.

Putative proteins have been identified in HPVs. These proteins were demonstrated to show some distant relationship to the cancer epidermal growth factors. Studies have also revealed in the case of HPVs the development of human cancer is due to failure of host cell control of the persisting viral genes.

Thus the existence of intracellular surveillance mechanism that controls HPV infection may also be expected for other human tumour viruses. The above intracellular control has been ascribed to an ancestral defense mechanism which alongside immune cells protects the host at the cellular level against potentially lethal functions of co evolving viruses.

How these defense mechanisms are threatened by the persisting oncogenic viruses and the infecting non-oncogenic counterparts remains obscure to be delineated in research. The fact that the functional oncogenes (V-sis; Erb-b; src and ras; mye; myb; and fos) etc., which encode malignant cell growth by affecting the regulations of other cellular genes gives a cue to the understanding of carcinogens by viral infections. Devita., *et al*. [7].

## Oncogenes encoding proteins for malignant cells growth.

| | |
|---|---|
| V-SIS | Encodes the hormone platelet derived growth factor(PDGF) |
| Erb-b | Encodes the hormone receptors for epidermal growth factor(EGE) |
| Sre&ras | Encodes proteins involved in second signaling within in cell |
| Mye,myb and fos | Encode proteins that control differentiation. |

**Table 1**

Moreover Allison Greaney., *et al*. [8] have made a comprehensive mapping of mutations in the SARS-CoV-2 receptor binding domain which reduced the host humoral immunity. Towards this end ACE-2 receptor and binding of SARS-CoV-2 in the lung alveolar epithelial cells and endothelial cells have enabled their multiplication ending in lung pathology and death. The above binding specific of SARS-CoV-2 the infection world over was made severely aweful. In the same way, non specific binding of virus proteins may not be unexpected with others organs or cells.

Recently Oscar., *et al*. [9] have revealed that SARS CoV-2 spike protein binds and modulates estrogen receptors in the alveolar cells and MCF-7 cells (Breast Cancer Cells). It is already known that estrogen in systemic circulation when binds to ER in breast cells, ovarian and cervical tissue cells may enhance multiplication of cells i.e metaplasia and further their transformation into premalignant cells and/or malignant cells. According to Oscar., *et al*. [9], the interaction of ERα and S protein of SARS virus is responsible for the lung lesion and pathology. The same may not be rule out for the non-specific induction of hormone responsive cancers like breast, ovary, cervix etc. The study of Montopoli., *et al*. [10] that SAR-CoV-2 infection and ER modulation in ovarian and breast cancer patients was protected by anti-estrogenic treatment, also strengthens the contention that SARS-CoV-2 infection of its variants of the category Viz., Variants of concern i.e. omicron may became a cause for concern in cancer incidence of future in the world.

The feasibility of mutations in the COVID viruses genome and their frequent occurrence may not be an un common event, as such an event could change the characteristics of the above virus. A new variant of SARS-CoV-2 may also be formed by recombination in which the genomes of two SARS-CoV-2 variants that infected an individual simultaneously could combine during their replication. The new recombinant virus may also differ from the parent lineages. Such an incidence has been reported in the case of SARS-CoV-2 by the interagency group (SIG) in USA. They have classified the SARS-CoV-2 variants based on the number and locations of the spike proteins; the antibody neutralization, capacity of the spike proteins to polyclonal antibodies; their susceptibility to monoclonal antibodies; their virulence disease severity and their risk to public health; their capacity/efficiency of transmissibility; etc., (Table 2).

| Abr | Variants of SARS—CoV-2 |
|---|---|
| VBM | Variants Monitored = Alpha, Beta… Lineage |
| VOL | Variants of Interest = Omicron Lineage |
| VOC | Variants of Concern = Omicron Lineage |
| VOHC | Variants of High Consequence = None |

**Table 2**

## Bibliography

1. John B Liao. "Viruses and Human Cancer". *Yale Journal of Biology and Medicine* 79.3-4 (2006): 115-122.
2. Pearson CAB., *et al*. "Estimates of severity and transmissibility of novel South Africa SARS-CoV-2 Variants 501Y.V2". Centre for Mathematical Modelling of Infectious Diseases, London School of Hygiene and Tropical Medicine.
3. Xie X., *et al*. "SARS-CoV-2 spike E484K mutation reduces antibody neutralization". *The Lancet* 2.7 (2021): 283-284.
4. Garcia Beltran W., *et al*. "Multiple SARS-CoV-2 Variants escape neutralization". *Cell* 184.9 (2021): 2372-2383.
5. Orth G., *et al*. "Characterization of two types of human papilloma viruses in lesions of epidermo dysplasia verruciformis"". *Proceedings of the National Academy of Sciences of the United States of America* 75 (1978): 1537-1541.
6. COVID-19. SARS-CoV-2 Variant Classifications and Definitions, Centers for diseases control Prevention, USA (2022).
7. DeVita, Hellman, and Rosenberg's. Cancer: Principles and Practice of Oncology (Cancer Principles and Practice of Oncology) Twelfth Edition, Wolters Kluwer (2022).
8. Allison J Greaney., *et al*. "Comprehensive mapping of mutations in the SARS-CoV-2 receptor-binding domain that affect recognition by polyclonal human plasma antibodies". *Cell Host Microbe* 29.3 (2021): 463-476.e6.
9. Oscar Solis., *et al*. "The SARS-CoV-2 spike protein binds and modulates estrogen receptors". *BioRxiv* (2022).
10. Montopoli M., *et al*. "Androgen-deprivation therapies for prostate cancer and risk of infection by SARS-CoV-2: a population-based study (N = 4532)". *Annals of Oncology* 31 (2020): 1040-1045.