Journal of Research in Health Sciences
ISSN: 2228-7809 | https://jrhsjournal.com

Evaluating the Association Between Transmission and Severity in SARS-CoV-2

Dr. Jeroen van Dijk[1]*, Dr. Sophie de Vries[2]

[1]Department of Biomedical Sciences, University of Amsterdam, Amsterdam, Netherlands

[2]Erasmus Medical Center, Rotterdam, Netherlands

Abstract.

An understanding of the origin, evolution and biochemistry (molecular biology) of SARS-COV-2 is a prerequisite to its control. There is no definitive answer as to the origin of SARS-COV-2. The evolution of SARS-COV-2 can be gleaned from a comparative study of its Infectivity and Virulence in different populations and environments. A method for measuring the Infectivity and Virulence at the population level has been designed. IP 10000 defined as the Number of Individuals Infected with SARS-COV-2 Per 10000 Population and DP 10000 defined as the Number of Deaths Per 10000 Individuals Infected with SARS-COV-2 measure the Infectivity and Virulence of SARS-COV-2 respectively. There is no correlation between IP 10000 (Infectivity) and DP 10000 (Virulence). Based on their associated IP 10000 and DP 10000, one Group in Asia Pacific (Group A), two Groups in Europe (Group B and Group C), and one Group in North America (Group X) can be identified. Group A countries are also associated with high temperature, high humidity and high Far Infrared Irradiation. Group B countries are associated with low Temperature, low Far Infrared Irradiation but high Humidity whereas Group C countries are associated with low Temperature, low Humidity and low Far Infrared Irradiation. Group X countries are associated with low Temperature, relative low Humidity and relatively low Far Infrared Irradiation.

Introduction.

SARS-COV-2, the etiologic agent of COVID-19 [1-4] has been ravaging the

entire world causing much suffering, deaths in the hundreds of thousands (still counting) and economic upheaval costing trillions of dollars (still counting). Currently, the only effective means of avoiding morbidity due to infections by SARS-COV-2 is through population control and contact restriction which appear to be quite effective in some parts of the world and not others. However, the number of deaths in various populations and regions of the world are not uniform [5,6] (See below). Although the medical infrastructure, medical response strategy and medical protocol play an important role in mitigating illnesses and deaths as a result of SARS-COV-2 infection, other factors, including environmental factors cannot be ruled out and must not be ignored.

In order to study the effects of various factors on the Infectivity and Virulence of SARS-COV-2 in various populations and locations, measures of Infectivity and Virulence of SARS-COV-2 are necessary. Here, we have developed a method for determining the Infectivity and Virulence of SARS-COV-2 at the population level in various countries. IP 10000 Number and DP-10000 Number which are defined as Number of Individuals Infected with SARS-COV-2 Per 10000 Population and Number of Deaths Per 10000 Individuals Infected with SARS-COV-2, are calculated from total number of individuals infected with SARS-COV-2, total population, and total number of deaths and total number of individuals infected with SARS-COV-2 respectively. Here, we show that IP 10000 Number (Infectivity) and DP 10000 Number (Virulence) provide a means to compare Infectivity and Virulence in various populations and locations around the world.

Methods.

Data for the total number of individuals infected with SARS-COV-2 and total number of deaths due to SARS-COV-2 infections for each country was curated from the World Health Organization, the United States Center For Disease Control and Prevention, and Department of Health of each countries. IP 10000, a measure of Infectivity is defined as the Number of Individuals Infected with SARS-COV-2 Per 10000 Population. DP 10000, a measure of Virulence is defined as the Number of Deaths Per 10000 Individuals Infected with SARS-COV-2. IP 10000

and DP 10000 were calculated based on the total number of individuals infected with SARS-COV-2, population and total number of deaths due to SARS-COV-2 infections.

Temperature, Humidity and Far Infrared Irradiation values were curated from the Meteorological Readings and forecasts of each country.

Data was analyzed for correlations by the Pearson method [7,8]. Differences between groups were determined by the student t-test [9,10] or one way Anova test [11,12] with $p < 0.05$ accepted as statistically significant.

Results.

As a first step in determining whether Infectivity and Virulence of SARS-COV-2 may be changing and different in various populations and locations, the number of Individuals Infected with SARS-COV-2 Per 10000 Population or IP 10000, and the number of Deaths per 10,000 individuals infected with SARS-COV-2 or DP10000 in a given population were calculated based on the available data curated from the World Heath Organization (WHO), the United States Center for Disease Control and Prevention (CDC) and the Departments of Health Services from each country. Figure 1 shows that IP 10000 (Infectivity) and DP 10000 (Virulence) varied quite considerably in different populations and regions of the world. The lowest IP 10000 Numbers (Infectivity) (~2) and lowest DP 10000 Numbers (Virulence) (~193) were recorded for countries in Asia and Pacific, including Taiwan, Hong Kong, Bangladesh, China, India, Malaysia, Australia, New Zealand, Sri Lanka, and Singapore, respectively. The highest IP 10000 Numbers (Infectivity) (~26) and highest DP10000 Numbers (Virulence) (~1242) were obtained for countries in Europe, including Spain, Italy, France, United Kingdom, Belgium, Netherlands and Sweden. Although part of Europe, Finland and Germany had average IP 10000 Numbers (Infectivity) and DP 10000 Numbers (Virulence) of ~12 and ~283 respectively. United States, New York City and Canada were associated with intermediate average IP 10000 Numbers (Infectivity) and DP 10000 Numbers (Virulence) of ~89 and ~652 respectively. Figure 2 shows that there is no correlation between Infectivity and Virulence.

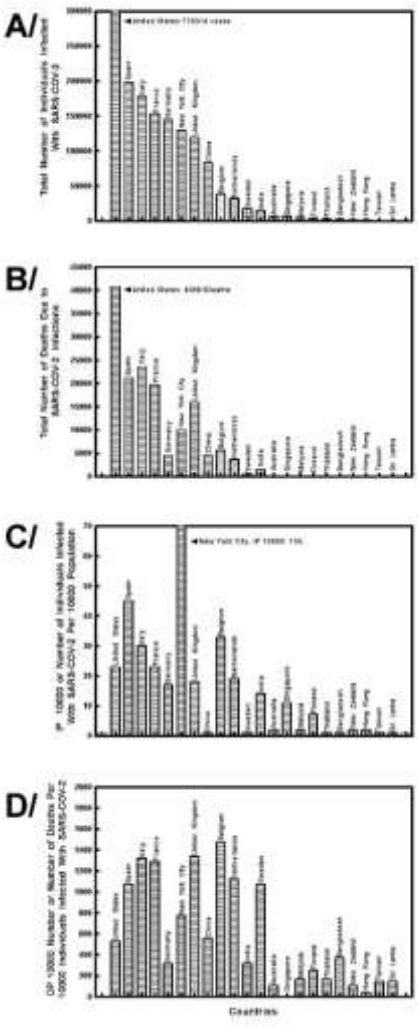


Figure 1. Comparision of the Total Number of Individuals Infected with SARS-COV-2 (Panel A), Total Number of Deaths due to SARS-COV-2 (Panel B), IP 10000 or Number of Individuals Infected with SARS-COV-2 Per 10000 Population (Panel C) and DP 10000 Number or Number of Deaths Per 10000 Individuals Infected with SARS-COV-2 (Panel D) in different countries, including Hong Kong, Taiwan, Thailand, Sri Lanka, Malaysia, Bangladesh, Australia, Finland, China, Netherlands, Sweden, Germany, India, United Kngdom, Singapore, Italy, France, Belgium, Spain, USA (NYC), USA and Canada. The data is for April 18, 2020.

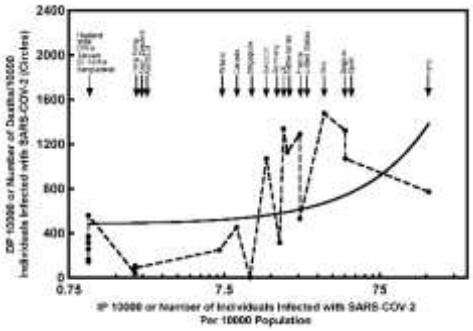


Figure 2. No Correlation between IP 10000 (Infectivity) and DP 10000 (Virulence). (p = >0.05).

Based on their associated IP Numbers (Infectivity) and DP Numbers (Virulence) for SARS-COV-2, countries can be classified into four groups (Figure 3). Group A countries are located in Asia Pacific Region and have low IP Numbers (Infectivity) and DP 10000 Numbers (Virulence) for SARS-COV-2. Group B countries are European countries and have intermediate IP Numbers (Infectivity) and DP 10000 Numbers (Virulence) for SARS-COV-2. Group C countries are European countries and have very high IP Numbers (Infectivity) and DP 10000 Numbers (Virulence) for SARS-COV-2. Group X countries are North American countries and have relatively high IP Numbers (Infectivity) and DP 10000 Numbers (Virulence) for SARS-COV-2 (Figure 3).

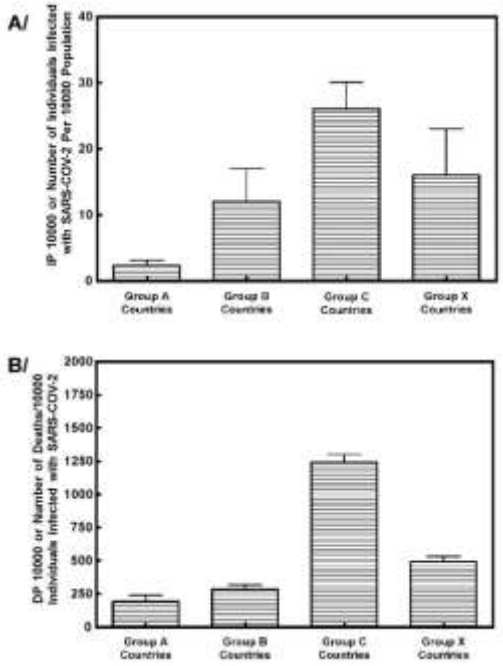


Figure 3. Identification of 4 groups of countries based on their associated IP 10000 (Infectivity) and DP 10000 (Virulence) for SARS-COV-2. Group A countries include Australia, Singapore, Malaysia, Thailand, Bangladesh, New Zealand, Hong Kong, Taiwan, Sri Lanka, India, and China. Group B countries include Finland and Germany. Group C countries include Spain, Italy, France, Sweden, United Kingdom, Belgium and Netherlands. Group X countries include United States and Canada. Means of Groups were significantly different ($p < 0.0001$); Means of Group A and Group B were significantly different ($p = 0.004$); Means of Group A and Group C were significantly different ($p < 0.001$). Means of Group A and D were significantly ($p < 0.001$). Means of Group B and C were significantly different ($p < 0.001$). Means of Group B and D were significantly different ($p < 0.001$). Means of Group C and D were significantly different ($p = < 0.001$).

Group A countries are also associated with high Temperature, high Humidity and high Far Infrared Irradiation. Group B countries are associated with low Temperature, low Far Infrared Irradiation but high Humidity. Group C countries are associated with low Temperature, low humidity and low Far Infrared Irradiation. Group X countries are associated with low Temperature, relatively low Humidity and relatively low Far Infrared Irradiation (Figure 4).

Discussion.

In the present work, a method for comparative study of Infectivity and Virulence of SARS-COV-2 in different populations and locations is present. IP 10000 is defined as the Number of Infected Individuals Per 10000 Population and DP 10000 is defined as the Number of Deaths per 10000 Individuals Infected with SARS-COV-2. IP 10000, a measure of Infectivity and DP 10000, a measure of Virulence can be calculated from the total number of individuals infected with SARS-COV-2, population and total number of deaths due to SARS-COV-2 infections. IP 10000 Numbers and DP 10000 Numbers allow comparative studies across the board irrespective of the number of individuals infected with SARS-COV-2, number of deaths of individuals infected with SARS-COV-2 and size of population.

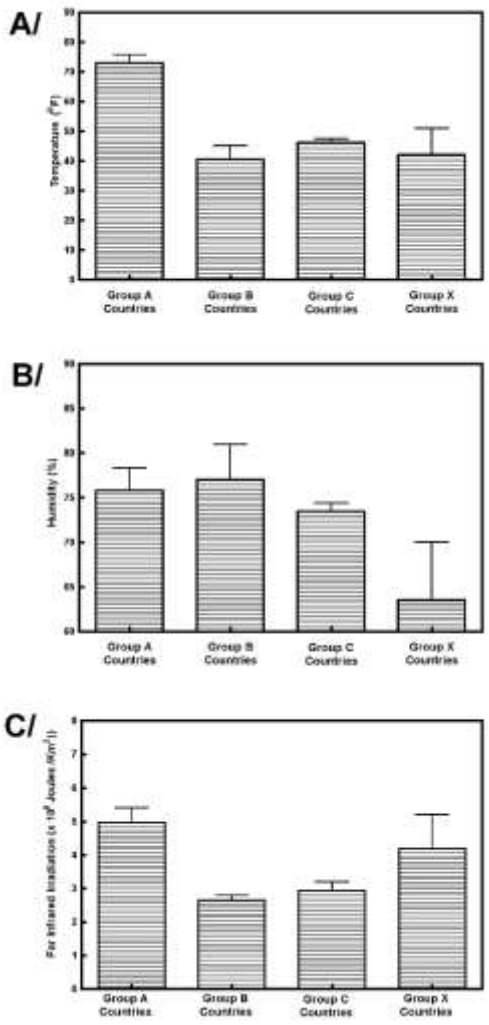


Figure 4. Identification of 4 groups of countries based on their associated Temperature, Humidity and Far Infrared Irradiation during the months of December 2019, January 2020, February 2020, March 2020 and April 2020. Panel A, Means of Groups were significantly different ($p < 0.0001$); Panel B, Means of Groups were not significantly different ($p = 0.14$); Panel C, Means of Groups were were significantly different ($p = 0.007$).

Discussion.

In the present work, a method for comparative study of Infectivity and Virulence of SARS-COV-2 in different populations and locations is present. IP 10000 is defined as the Number of Infected Individuals Per 10000 Population and DP 10000 is defined as the Number of Deaths per 10000 Individuals Infected with SARS-COV-2. IP 10000, a measure of Infectivity and DP 10000, a measure of Virulence can be calculated from the total number of individuals infected with SARS-COV-2, population and total number of deaths due to SARS-COV-2 infections. IP 10000 Numbers and DP 10000 Numbers allow comparative studies across the board irrespective of the number of individuals infected with SARS-COV-2, number of deaths of individuals infected with SARS-COV-2 and size of population.

The present work shows that there is great variability of IP 10000 Numbers (Infectivity) and DP 10000 Numbers (Virulence) of SARS-COV-2 in various populations and locations. There was no correlation between Infectivity and Virulence indicating that many factors determine the Infectivity and Virulence of SARS-COV-2 within a population and

deaths due to SARS-COV-2 infections can be prevented. In Europe, Finland and Germany registered relatively low IP 10000 Numbers (Infectivity) (~12) and relatively low DP 10000 Numbers (Virulence) (~283) for SARS-COV-2 while other European countries, including Spain, Italy, France, United Kingdom, Belgium, Netherlands and Sweden experienced the highest IP 10000 (~26) and highest DP 10000 Numbers (Virulence) (~1242) for SARS-COV-2 (Figure 3). It is difficult to explain why countries, including Spain, Italy, France, United Kingdom, Belgium, Netherlands and Sweden, all members of the European Union with very similar Healthcare System and fairly sophisticated Medical Infrastructure that is comparable to that of Finland and Germany, and relatively high degree of competence of their Healthcare Professionals, were not able to counteract the effects SARS-COV-2 with respect to their DP 10000 Numbers (or Deaths Per 100000 Individuals Infected with SARS-COV-2). The DP 10000 Numbers for Spain, Italy, France, United Kingdom, Belgium, Netherlands and Sweden were 1069, 1322, 1289, 1388, 1476, 1128 and 1071 respectively representing ~378%, 467%, 455%, 490%, 521%, 399% and 378% of that of Finland and Germany (DP 10000 = ~283). These data suggest that the Medical Infrastructure, and Response Strategy and Protocol to SARS-COV-2 infections in Finland and Germany were better suited to mitigate the effects of SARS-COV-2 on mortality. Incompetence of the leaderships of their Medical Research Establishments, Response Agencies and Governments may also explain in part these abominable DP10000 Numbers but it is submitted that there may be explanations that have to do with SARS-COV-2 itself, in particular the biochemistry (or molecular biology) of SARS-COV-2 due to mutational events that may have affected and changed its Virulence.

New York City deserves a special mention because in comparison to any of the other countries, its associated IP 10000 Number (Infectivity) is extremely high and its DP 10000 Number (Virulence) is also very high. It is not clear why. Further investigation is necessary. At this point in time, it appears that the New York City and the New York State Governmental leaderships were caught off-guard and were inadequately prepared in their Response Strategy. As there is no

correlation between Infectivity and Virulence of SARS-COV-2, there is no justifiable reasons to account for the distressing figures that are being recorded for New York City and the State of New York. Failure to pay attention to details, and to repertory and analyze small chaotic events will lead to irreversible and complete chaotic events in the forms of deaths [13].

In this work, it has also been shown that countries can be classified based on their associated IP 10000 Numbers (Infectivity) and DP 10000 Numbers (Virulence) SARS-COV-2. Thus, Group A countries are located in Asia Pacific Region and have low IP Numbers (Infectivity) and DP 10000 Numbers (Virulence) for SARS-COV-2. Group B countries are European countries and have intermediate IP Numbers (Infectivity) and DP 10000 Numbers (Virulence) for SARS-COV-2. Group C countries are European countries and have very high IP Numbers (Infectivity) and DP 10000 Numbers (Virulence) for SARS-COV-2. Group X countries are North American countries and have relatively high IP Numbers (Infectivity) and DP 10000 Numbers (Virulence) for SARS-COV-2 (Figure 3). The method of classification of countries described here is further supported by the fact that they have distinct environmental features that distinguish the different groups from one another. Group A countries are also associated with high Temperature, high Humidity and high Far Infrared Irradiation. Group B countries are associated with low Temperature, low Far Infrared Irradiation but high Humidity. Group C countries are associated with low Temperature, low humidity and low Far Infrared Irradiation. Group X countries are associated with low Temperature, relatively low Humidity and relatively low Far Infrared Irradiation (Figure 4). The analysis presented here may be useful in the development of Response Strategy for the control SARS-COV-2 that take into account factors that are specific for each population and location.

There has not been any studies of the Virulence of SARS-COV-2 in different populations and environments. Such studies are greatly anticipated. However, current available data points to differential Virulence of SARS-COV-2 in different populations and environments. These results strongly suggest that there may be different SARS-COV-2 strains within

different populations and environments. The sequences of several SARS-COV-2 strains have been determined [1-4,14,15]. Liu et al. [14] reported that they sequenced SARS-COV-2 genomes from nine individuals from the same location and found that they had 99.98 sequence identity. However, analysis of the sequences of SARS-COV-2 in different populations and environments must be made in order to determine differences in Virulence that are populations and environments specific. There is some evidence that SARS-COV-2 is a highly mutating virus and that mutations affecting key functions of SARS-COV-2 encoded proteins have taken place in various populations and locations [Tung, H.Y.L. and Limtung, P, manuscript in preparation]. Pursuant to the Theory of Chaos [13], small but significant changes can in principle have tremendous impact that can lead to Irreversible and Complete Chaos in the form of death as seen in SARS-COV-2 infections.

Medical Infrastructure, Preparedness and Response Strategy alone cannot explain the lack of correlation between Infectivity as measured by IP 10000 Number and Virulence as measured by DP 10000 Number. Other factors, including Temperature, Humidity and Far Infrared Irradiation associated with each country, prior health status of individuals infected with SARS-COV-2 and Mutations of SARS-COV-2 encoded proteins also play important roles in determining the Infectivity and Virulence of SARS-COV-2. At the population level, all these factors must be considered together when devising and implementing a specific response strategy.

References.

1. Zhu, N., Zhang, D., Wang, W., Li, X., Yang, B., Song, J., Zhao, X., Huang, B., Shi, W., Lu, R., Niu, P., Zhan, F., Ma, X., Wang, D., Xu, W., Wu, G., Gao, G.F. and Tan, W. (2019) N. Engl. J. Med., Vol. 382, pp727-733.
A novel coronavirus from patients with pneumonia in China, 2019.

2. Lu, R., Zhao, X., Li, J., Niu, P., Yang, B., Wu, H., Wang, W., Song, H., Huang, B., Zhu, N., Bi, Y., Ma, X., Zhan, F., Wang, L., Hu, T., Zhou, H., Hu, Z., Zhou, W., Zhao, L., Chen, J., Meng, Y., Wang, J., Lin, Y., Yuan, J., Xie, Z., Ma, J., Liu, W.J., Wang, D., Xu, W., Holmes, E.C., Gao, G.F., Wu, G., Chen, W., Shi, W. and Tan, W. (2020) Lancet, Vol. 395, pp565-574.
Genomic characterization and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding.

3. Zhou, P., Yang, X.L., Wang, X.G., Hu, B., Zhang, L., Zhang, W., Si, H.R., Zhu, Y.,

Li, B., Huang, C.L., Chen, H.D., Chen, J., Luo, Y., Guo, H., Jiang, R.D., Liu, M.Q., Zhao, K., Chen, Q.J., Deng, F., Liu, L.L., Yan, B., Zhan, Q.J., Deng, F., Liu, L.L., Yan, B., Zhan, F.X., Wang, Y.Y., Gao, G.F. and Shi, Z.L. (2020) Nature, Vol. 579, pp270-273.
A pneumonia outbreak associated with a new coronavirus of probable bat origin.

4. Wu, F., Zhao, S., Yu, B., Chen, Y.-M., Wang, W., Song, Z.-G, Hu, Y., Tao, Z.-W., Tian, J.-H., Pei, Y.-Y., Yuan, M.-L., Zhang, Y.-L., Dai, F.-H., Liu, Y., Wang, Q.-M., Zheng, J.-J., Xu, L., Holmes, E.C. and Zhang, Y.Z. (2020) Nature, Vol., 579, pp265-269.
A new coronavirus associated with human respiratory disease in China.

5. Tung, H.Y.L. and Limtung, P. (2020) ResearchGate,
DOI: 10.13140/RG.2.2.14741.55522.
SARS-COV-2 infection and virulence: reverse correlations with temperature, humidity and far infrared radiation. elevated temperature, humidity and far infrared irradiation will significantly lower the Viability, Infectivity and Virulence of SARS-COV-2.

6. Tung, H.Y.L. and Limtung, P. (2020) ResearchGate,
DOI: 10.13140/RG.2.2.25358.38723.
SARS-COV-2 infection and virulence: comparision between United Kingdom and Germany, and other European countries.

7. Pearson, K. (1920) Biometrika, Vol. 13, pp25-45.
Notes on the history of correlations.

8. Lindeman, R.H., Morenda, P.F. and Gold, R.Z. (1980) Introduction to bivariate and multivariate analysis, Foresman & Company, Glenview, Illinois, U.S.A.

9. Student or Gosset, W.S. (1908) Biometrika, Vol. 6, pp1-25.
The Probable Error of a Mean.

10. Armitage, P. and Berry, G. (1994) Statistical methods in medical research, 3rd Edition, Blackwell Scientific, Oxford, UK.

11. Welch, B.L. (1951) Biometrika, Vol. 38, pp330-336.
On the comparison of several means values.

12. Mc Donald, J.H. (2009) Handbook of biological statistics, 3rd Edition, Sparky House Publishing, Baltimore, Maryland, U.S.A

13. Tung, H.Y.L. (2020) A new theory of chaos, an introduction and its application in the study of climate change, diabetes, life and death, and SARS-COV-2, Cactoa Scientific Publishers, Inc., Astoria (NYC), New York, U.S.A.

14. Liu, Z., Xiao, X., Wei, X., Li, J., Yang, J., Tan, H., Zhu, J., Zhang, Q., Wu, J. and Liu, L. (2020) J. Med. Virol., DOI: 10.1002/jmv.
Composition and divergence of coronovirus spike proteins and host ACE2 receptors predict potential intermediate hosts of SARS-CoV-2.

15. Wei, J., Wang, W., Zhao, X., Zai, J. and Li, X. (2020) J. Med. Virol., DOI: 10.1002/jmv.25682.
Cross-species transmission of the newly identified coronavirus 2019-nCov.

NEW BIOMEDICAL SCIENCES
EDITED BY H.Y. LIM TUNG, Ph.D.
(www.newbiomedicalsciences.net)
(editorialoffice1@newbiomedicalsciences.net)
VOLUME ONE, ISSUE ONE (JULY 2020),

CALL FOR SUBMISSION OF MANUSCRIPTS IN THE FORM OF ARTICLES AND REPORTS.

1. New Biomedical Sciences is pleased to accept manuscripts in the form of Articles (long or short) with maximum of 6 figures plus 2 tables and Review Articles that describe news ways of thinking, new ideas, new theories and new ways of doing biomedical sciences.

2. New Biomedical Sciences will not be peer-reviewed by so-called pundits and scientific experts who have no idea what biomedical sciences are and how biomedical sciences are practiced at the bench, and who have long ago stopped working at the bench with their brains and hands. It is an aberration, tragic and comical that the direction of biomedical sciences are now being dictated by so-called top scientific journals (and also most scientific journals) that are run by ex-post-docs who could not make it in the highly competitively world of research universities and other research institutions, and by other arm-chair scientists who have long ago stopped doing biomedical sciences at the bench with their brains and hands.

3. New Biomedical Sciences will only publish papers with significant new ideas, new theories, and new results that have or will have relevance in understanding and curing disease states that afflict humans. Review Articles must contain new ideas, new concepts and new theories, and not just replicas (rehash) of published scientific articles (Scientific Researchers who work at the bench with their brains and hands know how to read the scientific literature. There is no need for arm-chair scientists to summarize the boring scientific literature for them).

4. New Biomedical Sciences will only publish papers that are simple but illuminates a high degree of new knowledge, ideas and theories. At New Biomedical Sciences, we believes that the purpose of a scientific paper is not to inundate and confuse the reader with irrelevant and mundane facts that cannot be reproduced in most cases even by the people who generated them in the first place but to illuminate the reader with new knowledge, ideas and theories.

4. New Biomedical Sciences is not for tricksters who resort to Data Fabrication, Data Falsification and Dishonest Scientific Reporting, and violate Scientific Ethics Rules.

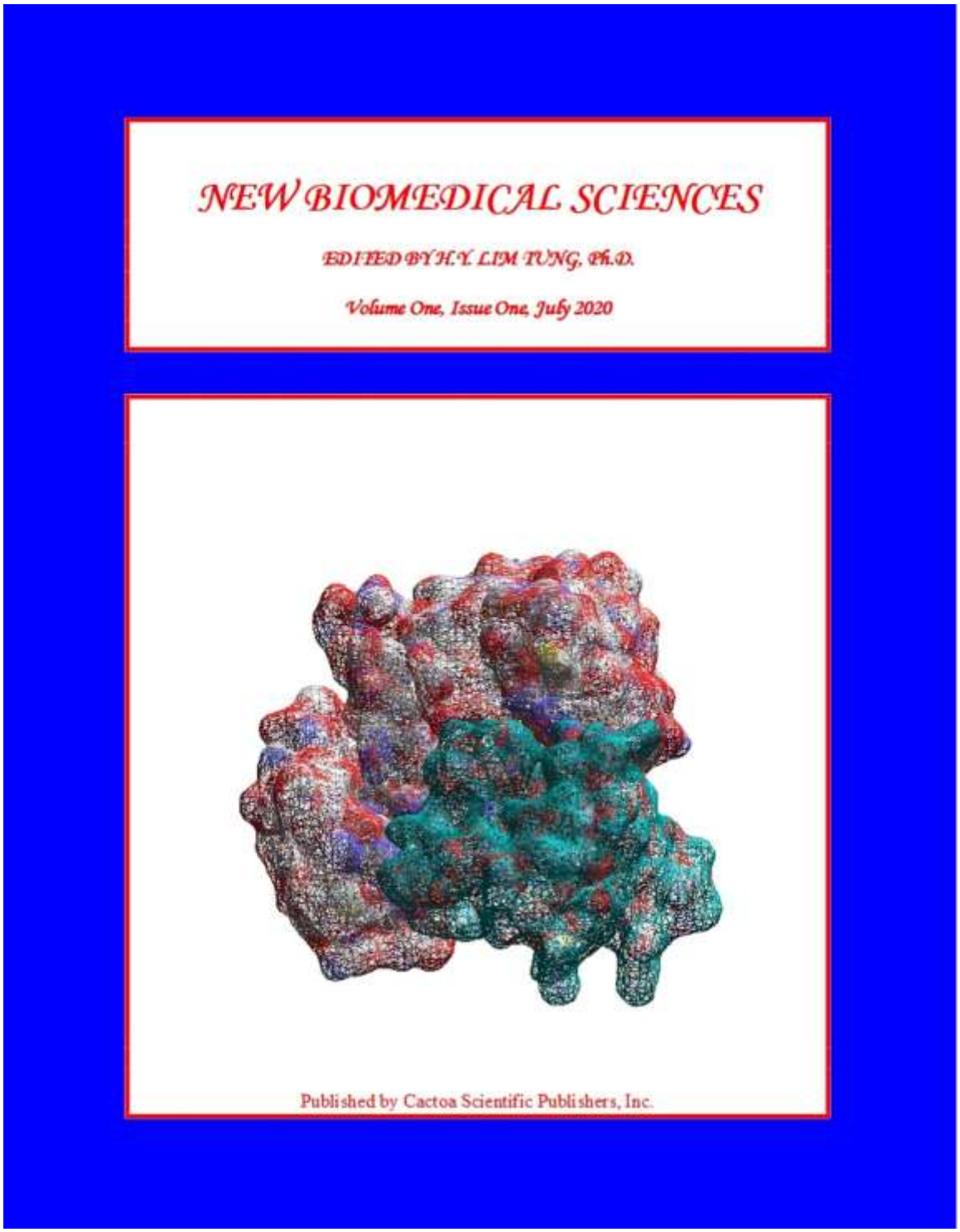
5. New Biomedical Sciences challenges the so-called pundits and scientific experts to spend a few months in the laboratory at the bench doing some simple experiments on their own without the help of post-docs and research associates and see how hard it is to come up with an original experiment, do the experiment, collect the results, analyze the results, and write the paper without resorting to Data Fabrication, Data Falsification and Dishonest Scientific Reporting.

5. Please submit your Manuscript (pdf or doc format) to: editorialoffice1@newbiomedicalsciences.net.

8. The Editor of New Biomedical Sciences reserves the right to accept or not to publish submitted manuscripts.

9. The Corresponding Author of papers accepted for publication in New Biomedical Sciences will be asked to pay a small processing and publishing fee of US $300. (Compare to the enormous and gouging Open Access fee that other scientific journals charge!). Abstracts of accepted manuscripts will be posted online at www.newbiomedicalsciences.net. Accepted manuscript will be edited to conform to the editorial style of New Biomedical Sciences and published in a paperback version. At New Biomedical Sciences, we do not believe that scientific articles should be available free of charge and that the authors should pay for others to read their papers. No authors in the literary world would pay so that others can read their books for free. At New Biomedical Sciences, we do not believe in Communism. We only believe in free enterprise and the market economy.

10. Each Paperback Issue New Biomedical Sciences shall contain no more than eight (8) Articles.


NEW BIOMEDICAL SCIENCES
EDITED BY H.Y. LIM TUNG, PH.D.
Volume One, Issue One, July 2020
Published by Cactoa Scientific Publishers, Inc.