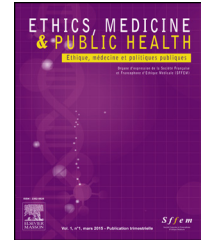




Available online at
ScienceDirect
www.sciencedirect.com

Elsevier Masson France
EM|consulte
www.em-consulte.com/en



LETTER TO THE EDITOR

Comment on “Could health only be defined by an equilibrated microbiome? A COVID-19 reappraisal” by P. Charlier



Keywords COVID-19; Dysbiosis; Immunology; Infections; Microbiota; Public Health

Dear Editor,

In his interesting editorial “*Could health only be defined by an equilibrated microbiome? A COVID-19 reappraisal*” P. Charlier expresses some concerns about the current view of the human microbiota. Issues of both quantitative and qualitative variation of the microbiota leading to dysbiosis are exposed and its relationship with the diet, the environment, and with the new lifestyle due to the current pandemic, such as the use of the masks, disinfectants and new eating habits are reported.

I want to emphasize that microbial communities vary in different parts of a single individual, but the microbes of a specific body area of different subjects share multiple common ecosystems. Furthermore, this diversity of microbial cells also refers to the microbiome, or the whole microbial genetic material that, due to its biological importance for humans, should be considered a part of the entire human genome [1]. Indeed, microbiota not only in healthy people is like a fingerprint but it can also be different when sick. However, microbes are in constant interaction with their host, in a dynamic balance that results in their harmonious coexistence and mutual benefits. But, several studies have shown that the microbial composition can change, as in the case of the new viral pandemic infection, mainly that of gut microbiota when for some reason these conditions change (dysbiosis) by diet, lifestyle, age, the state of the immune system, infections, drugs intake (moreover antimicrobials) [2,3]. Therefore, it is difficult to predict the course of a local or systemic pathological variation of all body microbiotas. In the case of the current COVID-19 pandemic the variation of gut microbiota composition and the C reactive protein may predict the clinical course on this viral infection [4,5]. Provocatively, Charlier asks if “*So, can health only be defined by an equilibrated microbiome?*” answering “*Reasonably no*”. I agree with him because today, when no one disputes its importance in human physiology and pathology, our knowledge remains limited, since it is impossible

to identify the action and relationship of all the microorganisms that make up the human microbiota. On the other hand, some members of the normal microbiota belong to the category of potential pathogens, that under certain conditions (e.g., immunosuppression, infections, etc.) can cause infections and sepsis, and their role in SARS-CoV-2 infection may be crucial [1,6].

The use of the protective masks can potentially be the cause of both these quantitative and qualitative variations for the contact of the tissue with the skin. Also, the mask can create a local microclimate in the oral cavity and nostrils because altering the temperature and humidity of the mucous membranes. In fact, the oral microbiota requires specific environmental conditions to grow in the oral cavity, such as the O₂ presence (aerobic or anaerobic areas), temperature, and pH. Although the oral cavity is rich in oxygen (most of it dissolved in saliva) and the main factor responsible for depleting oxygen levels is the presence of bacteria in saliva that use to metabolizes carbohydrates and nitrogenous substrates [7]. The new condition in the airways tract creates a “confined territory” that could alter the biology of certain bacteria such as that of *Porphyromonas gingivalis* [7]. We must remember that in the mouth the normal temperature is 35–36 °C and affects the growth rate of microorganisms, as well as the pH, solubility of gases in saliva, adhesion of microbes to tooth surfaces, and the ionic activity. We may suppose that these new conditions could therefore cause or aggravate local diseases such as the periodontitis through the development of dental plaque and tartar. This leads to a continuous local inflammatory reaction which could aggravate dysbiosis with several consequences for the health. It could easily induce effects on other organs with or without systemic consequences, including lichen planus, candidiasis, mucositis, cardiovascular diseases, lower respiratory tract infections, IBDs, and others [7,8].

Finally, the administration of probiotic formulas for oral bacteriotherapy in COVID-19 patients seems to be useful to prevent or reduce this dysbiosis on the microbiota or contribute to restore eubiosis (such as reducing the translocation of pathogens avoiding overlapping infections), and lead to a normal function of the immune-microbial cross-talking axes between intestine/lung, intestine/brain, intestine/skin, and bladder/intestine/brain [9,10].

According to these considerations and literature data, in the next future we can prospectively consider our microbiota and its manipulation as one of the main health

features, always in close relationship with the individual's characteristics and environment, but not the only one.

Human and animal rights

The author declares that the work described has not involved experimentation on humans or animals.

Informed consent and patient details

The author declares that this report does not contain any personal information that could lead to the identification of the patient(s) and/or volunteers.

Funding

This work did not receive any grant from funding agencies in the public, commercial, or not-for-profit sectors.

Disclosure of interest

The author declares that he has no competing interest.

References

- [1] Santacroce L, Man A, Charitos IA, Haxhirexa K, Topi S. Current knowledge about the connection between health status and gut microbiota from birth to elderly. A narrative review. *Front Biosci (Landmark Ed)* 2021;26:135–48, <http://dx.doi.org/10.52586/4930>.
- [2] Wu Y, Cheng X, Jiang G, Tang H, Ming S, Tang L, et al. Altered oral and gut microbiota and its association with SARS-CoV-2 viral load in COVID-19 patients during hospitalization. *NPJ Biofilms Microbiomes* 2021;7:61, <http://dx.doi.org/10.1038/s41522-021-00232-5>.
- [3] Iebba V, Zanotta N, Campisciano G, Zerbato V, Di Bella S, Cason C, et al. Profiling of oral microbiota and cytokines in covid-19 patients. *Front Microbiol* 2021;12:671813, <http://dx.doi.org/10.3389/fmicb.2021.671813>.
- [4] Zhou Y, Zhang J, Zhang D, Ma WL, Wang X. Linking the gut microbiota to persistent symptoms in survivors of COVID-19 after discharge. *J Microbiol* 2021:1–8, <http://dx.doi.org/10.1007/s12275-021-1206-5>.
- [5] Moreira-Rosário A, Marques C, Pinheiro H, Araújo JR, Ribeiro P, Rocha R, et al. C. Gut microbiota diversity and c-reactive protein are predictors of disease severity in covid-19 patients. *Front Microbiol* 2021;12:705020, <http://dx.doi.org/10.3389/fmicb.2021.705020>.
- [6] Carretta DM, Silva AM, D'Agostino D, Topi S, Lovero R, Charitos IA, et al. Cardiac involvement in covid-19 patients: a contemporary review. *Infect Dis Rep* 2021;13:494–517, <http://dx.doi.org/10.3390/idr13020048>.
- [7] Mangini F, Santacroce L, Bottalico L. Parodontopatie e patologie sistemiche [Periodontitis and systemic diseases]. *Clin Ter* 2006;157:541–8.
- [8] Schirinzi A, Cazzolla AP, Lovero R, Lo Muzio L, Testa NF, Ciavarella D, et al. New insights in laboratory testing for covid-19 patients: looking for the role and predictive value of human epididymis secretory protein 4 (HE4) and the innate immunity of the oral cavity and respiratory tract. *Microorganisms* 2020;8:1718, <http://dx.doi.org/10.3390/microorganisms8111718>.
- [9] Santacroce L, Inchingolo F, Topi S, Del Prete R, Di Cosola M, Charitos IA, et al. Potential beneficial role of probiotics on the outcome of COVID-19 patients: an evolving perspective. *Diabetes Metab Syndr* 2021;15:295–301, <http://dx.doi.org/10.1016/j.dsx.2020.12.040>.
- [10] Zhang L, Han H, Li X, Chen C, Xie X, Su G, et al. Probiotics use is associated with improved clinical outcomes among hospitalized patients with COVID-19. *Therap Adv Gastroenterol* 2021;14, <http://dx.doi.org/10.1177/17562848211035670> [17562848211035670].

L. Santacroce

*Department of Interdisciplinary Medicine,
University of Bari, Microbiology and Virology Unit,
Policlinico University Hospital of Bari, p.zza G.
Cesare 11, 70124 Bari, Italy*

E-mail address: luigi.santacroce@uniba.it

Received 29 August 2021;

accepted 30 August 2021

Available online 6 September 2021

<https://doi.org/10.1016/j.jemep.2021.100720>

2352-5525/© 2021 Elsevier Masson SAS. All rights reserved.