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Letter to the Editor

Efficacy and safety of tocilizumab in COVID-19 patients: a living systematic review and meta-analysis – Author's reply

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To the Editor,

We read with interest the letter by Koeckerling et al. [1] commenting on our meta-analysis on the efficacy and safety of tocilizumab in COVID-19 [2]. Koeckerling et al. [1] discussed the potential effect of immunomodulating therapies including tocilizumab on promoting SARS-CoV-2 evolution. Their argument was based on the observations of prolonged viral replication in severe COVID-19 disease and protracted viral shedding among immunocompromised patients, which could increase mutation rates and chance of emergence of new viral variants. The authors hypothesized that tocilizumab could enhance SARS-CoV-2 evolution by suppressing the immune system through blocking interleukin-6 (IL-6). We applaud the authors for raising this concern; however, we have several points to make in reference to this purported potential risk.

First, the inference that the authors made is an extrapolation from observations in immunocompromised patients. This population represent a chronic and more broad state of suppressed immunity in contrast with the more specific and short-term

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immunomodulatory effect of tocilizumab in the context of COVID-19 therapy. Further, Koeckerling et al. [1] postulated that IL-6 blockade by tocilizumab may dampen the host's antiviral responses and impair viral clearance. The authors guoted a study by Masiá et al. [3] in support of their hypothesis. In contrast to their claim, this study [3] not only revealed that IL-6 blockade was not associated with delayed viral clearance but also showed higher concentration of antiviral antibodies among tocilizumab-treated individuals [3]. Moreover, Guo et al. [4] reported that tocilizumab therapy was not associated with reduction in cytotoxic CD8⁺ and plasma B cell and suggested that tocilizumab may further promote the host's adaptive immune response [4]. In another intriguing study, Mazzoni et al. [5] showed that in severe COVID-19 disease, the impaired immune cell cytotoxicity was IL-6 dependent and that tocilizumab therapy restored the cytotoxic properties of the natural killer cells. Likewise, Giamarellos-Bourboulis et al. [6] demonstrated that COVID-19 patients with severe respiratory failure displayed very low expression of HLA-DR and marked reduction in CD4 and CD19 lymphocytes and natural killer cells. Tocilizumab partially restored HLA-DR in in vitro experiments [6]. These findings are reassuring that IL-6 blockade as a treatment strategy in severe COVID-19 disease is unlikely to broadly impair the immune response of patients against SARS-CoV-2 infection or cause delayed viral clearance.

Second, the authors correctly discussed the association between prolonged viral shedding and viral evolution in severe COVID-19. Indeed, tocilizumab use in COVID-19 is restricted to this group and several observational studies and randomized trials demonstrated that tocilizumab could lead to a reduction of disease severity in COVID-19 patients [2]. Reduction in disease severity and preservation of adequate immune response associated with tocilizumab therapy may theoretically shorten disease duration, shorten viral replication time and decrease viral mutation rate.

Third, similar to other RNA viruses, SARS-CoV-2 has been shown to have a high mutational rate. Emerging data report worldwide evolutionary changes of the SARS-CoV-2 virus [7-9]. In one study, the rate of SARS-CoV-2 mutation was estimated to be 4.133×10^{-4} substitutions/site/year [8], which is similar to the mutation rate of other

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coronaviruses [10]. Interestingly, the majority of documented SARS-CoV-2 mutations involve G-U and C-U substitutions with nearly 50% of all mutations involving C-U substitutions [10,11]. This type of mutation may represent host driven process through nucleotide deaminases [10,11] such as APOBEC proteins which are cytidine deaminases and represent one type of innate immune response against viruses [12]. This contention is supported by the findings of recent studies by Di Giorgio et al. [13] and Matyášek et al. [14]. APOBEC3 protein family is a target for induction by interferon type-I response and tocilizumab has been shown to upregulate interferon type-I response in rheumatoid arthritis patients [15]. These observations imply that the contribution of tocilizumab treated COVID-19 patients to SARS-CoV-2 evolution is unlikely.

Fourth, immunocompetent humans and animals represent the predominant reservoir for SARS-CoV-2 and could contribute to the ongoing evolution of the virus. For example, it has been well documented that SARS-CoV-2 virus continue to lurk within the gastrointestinal (GI) tract for a long time. In one systematic review, it has been shown that SARS-CoV-2 was detectable in GI tract up to 70 days from symptom onset and up to 33 days after complete clearance from the upper respiratory system [16]. This extra-pulmonary SARS-CoV-2 viral reservoir could be a more important source for continuing viral replication and evolution.

In conclusion, the evidence incriminating tocilizumab use in enhancing SARS-CoV-2 evolution is lacking. What potentially poses more risk of SARS-CoV-2 evolution is the ongoing spread of the virus among the chronically immunocompromised population, the indiscriminate use of convalescent plasma therapy [17] and the delay in vaccination worldwide. However, we agree with Koeckerling et al. [1] that ongoing and future studies should explore further whether tocilizumab or other immunomodulators use would have any impact on SARS-CoV-2 evolution.

Transparency declaration

The authors declare that there are no conflicts of interest.

References

 Koeckerling D, Pan D, Barker J. Re: Efficacy and safety of tocilizumab in COVID-19 patients: a living systematic review and meta-analysis by Tleyjeh et al. Clin Microbiol Infect 2021;27(8):1175–6. https://doi.org/10.1016/j.cmi. 2021.01.025.

- [2] Tleyjeh IM, Kashour Z, Damlaj M, Riaz M, Tlayjeh H, Altannir M, et al. Efficacy and safety of tocilizumab in COVID-19 patients: a living systematic review and meta-analysis. Clin Microbiol Infect 2020;27(2):215–27. https://doi.org/ 10.1016/j.cmi.2020.10.036.
- [3] Masiá M, Fernández-González M, Padilla S, Ortega P, García JA, Agulló V, et al. Gutiérrez, Impact of interleukin-6 blockade with tocilizumab on SARS-CoV-2 viral kinetics and antibody responses in patients with COVID-19: a prospective cohort study. EBioMedicine 2020;60:102999.
- [4] Guo C, Li B, Ma H, Wang X, Cai P, Yu Q, et al. Single-cell analysis of two severe COVID-19 patients reveals a monocyte-associated and tocilizumabresponding cytokine storm. Nat Commun 2020;11:3924.
- [5] Mazzoni A, Salvati L, Maggi L, Capone M, Vanni A, Spinicci M, et al. Impaired immune cell cytotoxicity in severe COVID-19 is IL-6 dependent. J Clin Invest 2020;130:4694–703.
- [6] Giamarellos-Bourboulis EJ, Netea MG, Rovina N, Akinosoglou K, Antoniadou A, Antonakos N, et al. Complex immune dysregulation in COVID-19 patients with severe respiratory failure. Cell Host Microbe 2020;27:992–1000. e3.
- [7] Sallam M, Ababneh NA, Dababseh D, Bakri FG, Mahafzah A. Temporal increase in D614G mutation of SARS-CoV-2 in the Middle East and North Africa. Heliyon 2021;7:e06035.
- [8] Motayo BO, Oluwasemowo OO, Bolusola BA, Akinduti PA, Arege OT, Obafemi YD, et al. Evolution and genetic diversity of SARS-CoV-2 in Africa using whole genome sequences. Int J Infect Dis 2020;103:282–7.
- [9] Maitra A, Sarkar MC, Raheja H, Biswas NK, Chakraborti S, Singh AK, et al. Mutations in SARS-CoV-2 viral RNA identified in Eastern India: Possible implications for the ongoing outbreak in India and impact on viral structure and host susceptibility. J Biosci 2020;45:76.
- [10] Simmonds P. Rampant C→U hypermutation in the genomes of SARS-CoV-2 and other coronaviruses: causes and consequences for their short- and long-term evolutionary trajectories. mSphere 2020;5. e405488–20.
- [11] De Maio N, Walker CR, Turakhia Y, Lanfear R, Corbett-Detig R, Goldman N. Mutation rates and selection on synonymous mutations in SARS-CoV-2. bio-Rxiv 2021. https://doi.org/10.1101/2021.01.14.426705. 2021.01.14.426705.
- [12] Harris RS, Dudley JP. APOBECs and virus restriction. Virology 2015;479–480: 131–45.
- [13] Di Giorgio S, Martignano F, Torcia MG, Mattiuz G, Conticello SG. Evidence for host-dependent RNA editing in the transcriptome of SARS-CoV-2. Sci Adv 2020;6:eabb5813.
- [14] Matyášek R, Kovařík A. Mutation patterns of human SARS-CoV-2 and bat RaTG13 coronavirus genomes are strongly biased towards C>U transitions, indicating rapid evolution in their hosts. Genes (Basel) 2020;11:761.
- [15] Sanayama Y, Ikeda K, Saito Y, Kagami S-i, Yamagata M, Furuta S, et al. Prediction of therapeutic responses to tocilizumab in patients with rheumatoid arthritis: biomarkers identified by analysis of gene expression in peripheral blood mononuclear cells using genome-wide DNA microarray. Arthritis Rheumatol 2014;66:1421–31.
- [16] van Doorn AS, Meijer B, Frampton CMA, Barclay ML, de Boer NKH. Systematic review with meta-analysis: SARS-CoV-2 stool testing and the potential for faecal-oral transmission. Aliment Pharmacol Ther 2020;52:1276–88.
- [17] Kemp SA, Collier DA, Datir RP, Ferreira IATM, Gayed S, Jahun A, et al. SARS-CoV-2 evolution during treatment of chronic infection. Nature 2021. https:// doi.org/10.1038/s41586-021-03291-y.