Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

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SARS-CoV-2: Can sunlight exposure reduce the risk of developing severe consequences of COVID-19?

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ABSTRACT

Herein it is proposed that sufficient exposure to sunlight (UVB) modulates host gene expression, offering protection against severe consequences of COVID-19. This could be in addition to sunlight (UVB)-mediated protection by directly inactivating the virus and limiting the viral load. It is suggested that inhibition of CCR2, DPP9, HSPA1L, IFNAR2, OAS1, and TYK2 may, in part, explain UVB-mediated protection against severe consequences of COVID-19.

Dear Editor,

Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2)-induced coronavirus disease-2019, or commonly referred to as COVID-19, led to a global pandemic in an unusually short time. The fierce nature of COVID-19, which is evident by its high incidence and mortalities, remains only partly explained. COVID-19 effects are non-specific, ranging from severe forms that necessitate mechanical ventilation and/or lead to death, or completely asymptomatic. Although the health authorities have undertaken the strictest disease control measures, including 'stay home' restriction to partial or complete lockdown. These measures have led people to stay and work from home rendering total or less than optimal exposure to sunlight. Notably, people who are staying indoors appear to be affected by severe form of COVID-19 (Meo et al., 2020; Geddes, 2020). In part, this is suggested to be linked with Vitamin D deficiency (associated with limited sunlight UVB exposure) and reduced immune pathways activation leading to severe COVID-19 (Meo et al., 2020; Geddes, 2020; Ali, 2020). In contrast, it was reported that a higher duration of sunlight exposure was significantly correlated to health maintenance and speedy recovery in most of the COVID-19 patients (Asyary and Veruswati, 2020). Similarly, a highly significant and positive correlation was found between sunlight exposure and lower death rate due to COVID-19 (Whittemore, 2020). Another study as well, hinted towards protective effects of the sunlight exposure by assessing the relationship between COVID-19 mortality rate and the average annual hours of sunshine reported by country's national weather service agency (Lansiaux et al., 2020). Herein, we discuss the involvement of additional factors in sunlight (UVB)-mediated protection against severe COVID-19. Using *in silico* analysis, for the first time, we propose that UVB-induced genetic changes may also play a role in determining the disease severity in COVID-19 patients.

Severe COVID-19 outcomes in hospitalized patients have been linked with upregulation of *CCR2*, *DPP9*, *IFNAR2*, *OAS1*, and *TYK2*, while *HSPA1L* expression has been reported to promote SARS-CoV-2 survival in host cells through modulation of host epigenetic machinery (Muhammad et al., 2021; Pairo-Castineira et al., 2020). Along with these six genes, the upregulation of *ACE2* and *TMPRSS2* is also considered as a severity marker. The expression of aforementioned genes was searched in (i) lung autopsies of severe COVID-19 patients, (ii) lung autopsies of uninfected individuals, and (iii) UVB radiation-induced gene expression profiles in human cells. The publicly available transcriptomic datasets from National Center for Biotechnology Information Gene Expression Omnibus (https://www.ncbi.nlm.nih.gov/geo/) was used. The raw data of gene expression profiles were downloaded and processed using R statistical software. GSE150316 dataset was selected which included transcriptomic expression profile obtained from lung autopsies of severe COVID-19 patients. When lung autopsies of severe COVID-19 patients and uninfected individuals were compared, it was observed that all eight candidate genes showed a higher median expression in the lungs of severe COVID-19 patients (Fig. 1A).

Furthermore, the GSE157824 dataset was selected to identify UVB radiation-induced gene expression profiles in human cells. For UVB radiation-induced gene expression profiles, more than 5000

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differentially expressed genes (DEGs) were identified (Fig. 1B). The data were obtained from UVB-irradiation (91 mJ/cm^2) exposed to melanocytes using two UVB-lamps (each 9 W, at a distance of 21.7 cm) for 60 s before being cultivated for 2 h. Out of 5000 genes, it was observed that *CCR2*, *DPP9*, *HSPA1L*, *IFNAR2*, *OAS1*, and *TYK2* were significantly downregulated (Fig. 1C). Both *OAS1* and *HSPA1L* are associated with increased susceptibility to SARS-CoV-2 infection by promoting viral replication and survival in the host cells. Similar to these observations, an in vitro study reported inactivation and loss in viability of the SASR-CoV-2 virus upon simulated sunlight exposure for 37 min in culture media and 107 min in mucus (Sloan et al., 2021).

Furthermore, *IFNAR2, CCR2*, and *TYK2* are the key regulators of immune cell-mediated excessive inflammatory response in many viral infections including COVID-19. Hence inhibition of aforementioned genes may limit protection against severe consequences of COVID-19. The role of *DPP9* in COVID-19 is still uncharacterized, however it is known to encode for dipeptidyl peptidases involved in immune regulation (Ross et al., 2018), and its role in COVID-19 should be the subject of future studies. The expression of ACE2 and TMPRSS2 was not significantly different between UVB irradiated cells and severe COVID-19. Taken together, these findings suggest that inhibition of *CCR2*, *DPP9*, *HSPA1L*, *IFNAR2*, *OAS1*, and *TYK2* may, in part, explain UVB-mediated protection against severe consequences of COVID-19. Other than modulating host gene expression, it is likely that sunlight (UVB) offers protection by directly inactivating the virus and limiting the viral load.

A Chinese study conducted using a nonlinear dose-response relationship between ambient temperature and virus transmissibility suggested no significant associations of SARS-CoV-2 transmission with temperature or levels of UV radiation (Yao et al., 2020). However, we suggest that the association between COVID-19 severity and UVB exposure is more complex and might have been overlooked due to study limitations, such as a short study period and a nonlinear analytical framework. Based on the genetic correlations evidenced in this study, we propose that adequate exposure to sunlight may alleviate COVID-19-induced severity especially among vulnerable populations confined in long-term lockdown conditions. Also, creating an awareness regarding the importance of sensible exposure to sunlight, while adhering to other preventive measures such as face masks, and physical distancing, is of utmost importance.

Author contributions

RS and NAK conceptualized the concept amid critical discussions with JSM. JSM conducted literature review and prepared the first draft of the manuscript and the figures under the supervision of NAK. All authors contributed to the manuscript and will act as guarantors.

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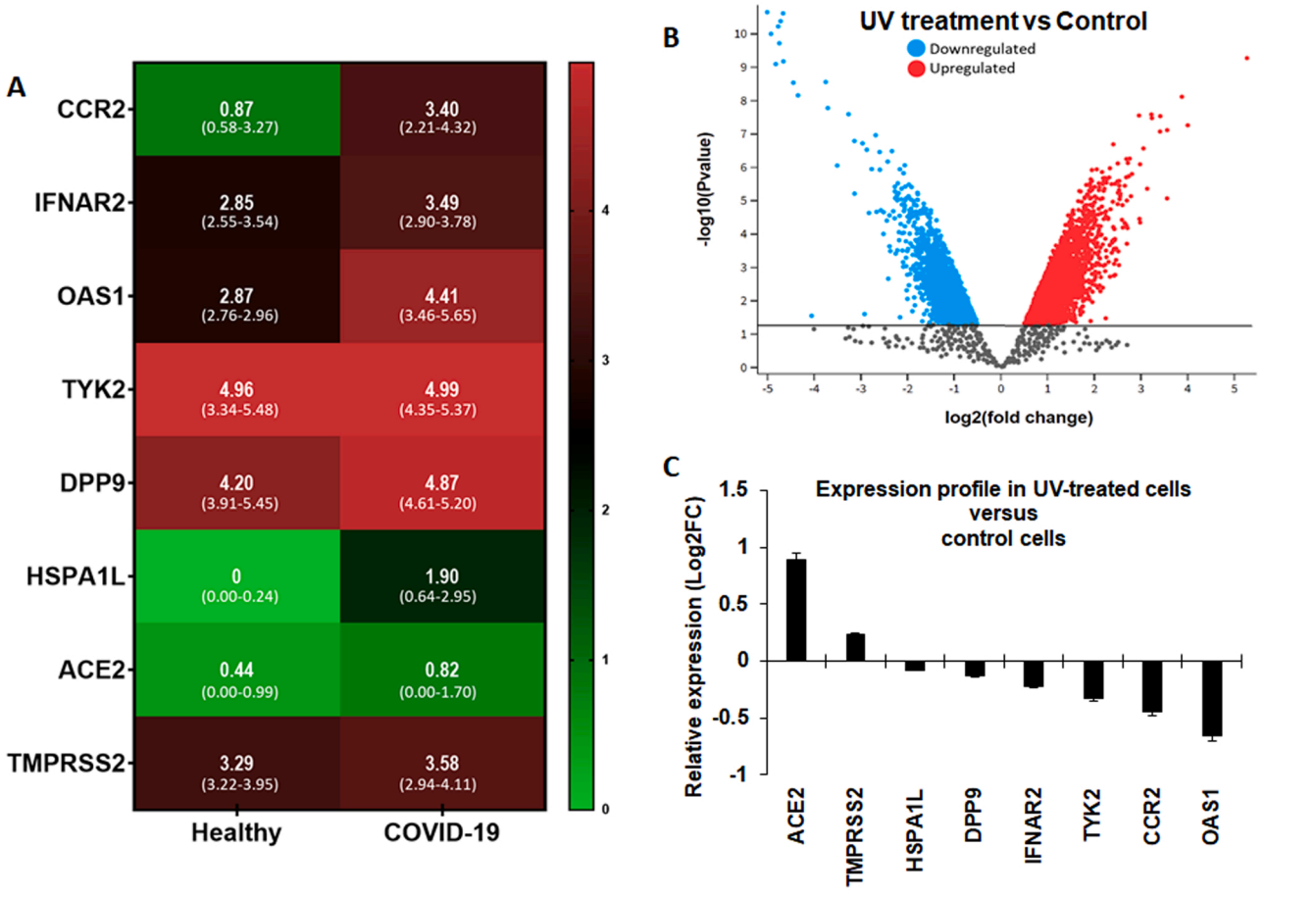

Fig. 1. *In silico* analysis of expression array obtained from publicly available NCBI GEO databases. A. Heatmap showing relative mRNA expression (Fold Change) from severe COVID-19 patients (n = 11) compared to healthy controls (n = 5), values shown represents "Median (Interquartile range)". B. Volcano plot showing the effect of UVB radiations on the genetic expression profile in human cells. C. Bar graphs showing relative mRNA expression of 8 candidate genes in UV-treated cell (n = 4), versus the controls cells (n = 5). Data is presented a mean ± SE in error bars.

Competing interests

The authors declare (1) no financial support for the submitted work from anyone other than their employer; (2) no financial relationships with commercial entities that might have an interest in the submitted work; (3) no spouses, partners, or children with relationships with commercial entities that might have an interest in the submitted work; and (4) no non-financial interests that may be relevant to the submitted work.

Declaration of Competing Interest

None

References

Ali, N., 2020. Role of vitamin D in preventing of COVID-19 infection, progression and severity. J. Infect. Public Health 13, 1373–1380.

Asyary, A., Veruswati, M., 2020. Sunlight exposure increased Covid-19 recovery rates: a study in the central pandemic area of Indonesia. Sci. Total Environ. 729, 139016.

Geddes, L. , 2020. How staying indoors affects your immune system. BBC Future. Retrieved October 27, 2021, from https://www.bbc.com/future/article/20200521-can-staying-inside-weaken-the-immune-system.

Lansiaux, É., Pébaÿ, P.P., Picard, J.L., Forget, J., 2020. Covid-19 and vit-d: disease mortality negatively correlates with sunlight exposure. Spat. Spatiotemporal Epidemiol. 35, 100362.

Meo, S.A., Abukhalaf, A.A., Alomar, A.A., AlMutairi, F.J., Usmani, A.M., Klonoff, D.C., 2020. Impact of lockdown on COVID-19 prevalence and mortality during 2020 pandemic: observational analysis of 27 countries. Eur. J. Med. Res. 25, 56.

Muhammad, J.S., Sharif-Askari, N.S., Cui, Z.G., Hamad, M., Halwani, R., 2021. SARS-CoV-2 infection-induced promoter hypomethylation as an epigenetic modulator of heat shock protein A1L (HSPA1L) gene. Front. Genet. 12, 622271.

Pairo-Castineira, E., Clohisey, S., Klaric, L., Bretherick, A.D., Rawlik, K., Pasko, D., Walker, S., Parkinson, N., Fourman, M.H., Russell, C.D., Furniss, J., Richmond, A., Gountouna, E., Wrobel, N., Harrison, D., Wang, B., Wu, Y., Meynert, A., Griffiths, F., Oosthuyzen, W., Kousathanas, A., Moutsianas, L., Yang, Z., Zhai, R., Zheng, C., Grimes, G., Beale, R., Millar, J., Shih, B., Keating, S., Zechner, M., Haley, C., Porteous, D.J., Hayward, C., Yang, J., Knight, J., Summers, C., Shankar-Hari, M., Klenerman, P., Turtle, L., Ho, A., Moore, S.C., Hinds, C., Horby, P., Nichol, A., Maslove, D., Ling, L., McAuley, D., Montgomery, H., Walsh, T., Pereira, A.C., Renieri, A., GenOMICC, I., Investigators, COVID- Human Genetics, I., Investigators, BRACOVID, I., Gen-COVID, I., Shen, X., Ponting, C.P., Fawkes, A., Tenesa, A., Caulfield, M., Scott, R., Rowan, K., Murphy, L., Openshaw, P., Semple, M.G., Law, A., Vitart, V., Wilson, J.F., Baillie, J.K., 2020. Genetic mechanisms of critical illness in COVID-19. Nature 591 (7848), 92–98.

Ross, B., Krapp, S., Augustin, M., Kierfersauer, R., Arciniega, M., Geiss-Friedlander, R., Huber, R., 2018. Structures and mechanism of dipeptidyl peptidases 8 and 9, important players in cellular homeostasis and cancer. Proc. Natl. Acad. Sci. USA 115 (7), E1437–E1445.

Sloan, A., Cutts, T., Griffin, B.D., Kasloff, S., Schiffman, Z., Chan, M., Audet, J., Leung, A., Kobasa, D., Stein, D.R., Safronetz, D., Poliquin, G., 2021. Simulated sunlight decreases the viability of SARS-CoV-2 in mucus. PLoS One 16 (6), e0253068.

Whittemore, P.B., 2020. COVID-19 fatalities, latitude, sunlight, and vitamin D. Am. J. Infect. Control 48 (9), 1042–1044.

Yao, Y., Pan, J., Liu, Z., Meng, X., Wang, W., Kan, H., Wang, W., 2020. No association of COVID-19 transmission with temperature or UV radiation in Chinese cities. Eur. Respir. J. 55 (5), 2000517.