

COVID-19 as a worldwide selective event and bitter taste receptor polymorphisms: An ecological correlational study

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Abstract

Background: Given the observed olfactory and gustatory dysfunctions in patients with COVID-19 and recent findings on taste receptors possible important activities in the immune system, we elected to estimate the correlation between COVID-19 mortality and polymorphism of a particular type of bitter taste receptor gene called TAS2R38, in a worldwide epidemiological point of view.

Methods: Pooled rate of each of the rs713598, rs1726866, rs10246939, and PAV/AVI polymorphisms of the TAS2R38 gene was obtained in different countries using a systematic review methodology and its relationship with the mortality of COVID-19. Data were analyzed by the comprehensive meta-analysis software and SPSS.

Results: There was only a significant reverse Pearson correlation in death counts and PAV/AVI ratio, $p = 0.047$, $r = -0.503$. Also, a significant reverse correlation of PAV/AVI ratio and death rate was seen, $r = -0.572$, $p = 0.021$. rs10246939 ratio had a significant positive correlation with death rate, $r = 0.851$, $p = 0.031$. Further analysis was not significant. Our results showed that the higher presence of PAV allele than AVI, and a higher rate of G allele than A in rs10246939 polymorphism in a country, could be associated with lower COVID-19 mortality. While assessing all three polymorphisms showed a huge diversity worldwide.

Conclusion: Due to extraoral activities of bitter taste receptor genes, especially in mucosal immunity, this gene seems to be a good candidate for future studies on COVID-19 pathophysiology. Also, the high worldwide diversity of TAS2R38 genes polymorphism and its possible association with mortality raises concerns about the efficiency of vaccine projects in different ethnicities. (c) 2021 Elsevier B.V. All rights reserved.

Keywords

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