Gender narratives in Indian science publications

This is with regard to the article 'Gender dimensions in popular science writing in India'[1], which assesses the disparity between male and female authors of published scientific papers in notable Indian scientific journals. Though the paper is well researched and written, several points are raised.

While the authors investigate gender disparity, it is ironic that not a single female author has been involved in this study or acknowledged. One might assume that such a study was performed to create awareness and improve the current environment of male-dominated authors and reviewers, however, the absence of female investigators here leads one to believe that the efforts are half-willed or insincere.

The notion that only two genders exist is not only archaic but also unscientific. Even if there were not adequate trans/gender non-conformative authors in the sample, a simple mention of these would have increased the value and relevance of the paper. As scientists and people of influence in society, we must accept and promote inclusivity of all genders, especially in the field of science/scientific writing, where there is a lack of adequate representation, as has been shown by this study.

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Response

Agrima Thakur has correctly identified that the authors are males. However, the assumption that the absence of female investigators in carrying out the study reflects the 'insincere' and 'half-willed' efforts of the authors is entirely misplaced. The second point that the survey has mentioned only two genders is well-taken. As mentioned in the methodology, the gender was identified based on Mr/Ms/Mrs/Shri/Smt as given in the articles. And wherever the honorifics were not given, the gender was determined by the names. That there can be errors in gender determination in such cases is stated in the article. However, as correctly pointed out, we could have mentioned trans/third/other gender authors.

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Insight into possible adjuvant role of phytol to fight SARS-CoV-2

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Coronavirus disease 2019 (COVID-19) is a disease caused by the novel β-coronavirus (SARS-CoV-2), with the first case reported in Wuhan, China, in 2019 (ref. 1). It has become a global problem due to a large number of documented victims. Up until the end of January 2022, more than 511.7 million SARS-CoV-2 confirmed cases have been reported, leading to the death of more than 6.2 million people worldwide. COVID-19 has caused health emergencies all over the world, especially when complications associated with gastrointestinal infections, renal failure, heart diseases and diabetes were documented.

SARS-CoV-2 is a positive, single-stranded RNA virus, which has great genomic plasticity due to high propensity to errors during replication[1]. In addition, coronavirus strains can naturally present up to 20% of homologous RNA recombination when there are mixed infections with different viral strains belonging to the same taxon[2]. Such evidence may explain the diversity of human coronavirus strains of clinical interest disseminated throughout the world. In 2006, a prospective study using *in silico* predictions analysed 25 HCoV-229E (human coronavirus strain 229E) variants disseminated in Australia, reported during the years 1979–2004 (ref. 3). In the study, it was shown that the spike proteins and nucleoproteins play an important role during infection, and that these proteins have not mutated over the years. Non-synonymous substitution mutations in the spike protein are likely to be involved in a mechanism based on positive selection, thus resulting in near unchanged proteins in all-new coronavirus strains[3]. Although coronavirus strains were described nearly 100 years ago, clues suggest that they use the same molecular mechanisms for infection, in which the spike protein appears to be the main molecular tool used to enter target cells. Now it is known that the infection process also involves cleavage in the S_1/S_2 site by the transmembrane protease serine 2 (TMPRSS2) and by the cathepsin L. Data suggest that TMPRSS2 facilitates viral entry into the plasma membrane, while cathepsin L seems to activate the spike protein in endosomes compensating the TMPRSS2 absence for entrance into the cells. Then replicate components reorganize the endoplasmic reticulum into double-membrane vesicles that facilitate viral replication of genomic and subgenomic RNAs, where the subgenomic mRNAs are translated into structural and accessory proteins that facilitate the formation of viral particles[4,5].

Plants have been essential to humans for many centuries, being used as therapeutical agents, with reports of a significant number of potential antiviral compounds derived from plants. Among phytochemicals with antiviral properties, phytol stands out with recent evidence showing that this molecule plays an important role as an antiviral

agent[6]. Several epidemiological studies have demonstrated the relevance of green vegetables in diets improving immune responses and increasing resistance to infections of different origins. In this context, phytol is suitable for use as an immune adjuvant to be administered to diabetic patients with COVID-19 as both food and supplement due to its inherent ability to act as an efficient activator of antigen-presenting cells, upregulating costimulatory molecules and in the promotion of cellular crosstalk, besides the anti-inflammatory and antiviral activities mentioned previously. In addition, phytol is structurally simple, easily available and is relatively low-cost.

According to Carvalho *et al.*[7] phytol is a potent anti-inflammatory molecule. Interestingly, excessive inflammatory processes are among the most common clinical signs triggered after infection by the SARS-CoV-2 virus. In addition, the anti-inflammatory activity triggered by phytol can act by downregulating tumour necrosis factor-alpha (TNF-α), pro-inflammatory cytokines, and interleukin-6 through the regulation of the NF-kappa B pathway, which is also associated with insulin resistance[7]. Therefore, phytol may contribute to anti-inflammatory responses, and to an anti-diabetic effect as well. Assuming phytol as an antagonist to SARS-COV-2 and considering the several disorders and negative effects, the virus can cause in the more severe cases of COVID-19 which include antagonism of IFN-stimulated response elements[8,9], cleavage of the NF-κB essential modulator, and signal transducer and activator of transcription 2, resulting in the downregulation of IGSs[10], and interaction with E_3 ligase, of tripartite motif-containing protein 25, and interferon regulatory factor[9]. The use of phytol in conjunction with other therapeutics in the treatment of diabetic patients committed with COVID-19 could be a successful strategy.

COVID-19 has resulted in significant economic loss, especially in losing lives surpassing 5.6 million worldwide. Patients with chronic comorbidities, such as diabetes, usually show high risk of complications once infected by SARS-CoV-2 virus. Considering that diabetic patients with COVID-19 must be treated using more assertive therapeutic approaches, we hypothesize that such individuals can associate classic anti-diabetic agents with a diet rich in phytol, maximizing the response against SARS-CoV-2 and better controlling the side effects, given its high anti-inflammatory activity.

Conflict of interest: The authors declare no conflict of interest.

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