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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Letter to the Editor: Can the seasonal influenza vaccine for 2019/2020 have cross reactivity with some of the SARS-CoV-2 proteins?

Dear Editor,

Since December 2019, when severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerged, several studies have examined the similarities and differences between SARS-CoV-2 and influenza viruses. In a recent study by Ilic et al., which was published in *International Journal of Infectious Diseases*, the authors stated that SARS-CoV-2 has an hemagglutinin-esterase (HE) glycoprotein. This study also suggested that the seasonal influenza vaccine for 2019/2020, which contained three or four strains of influenza A and B viruses, may have had cross reactivity with some SARS-CoV-2 proteins (Ilic et al., 2021); however, the proteins of these two different viruses are not the same.

The SARS-CoV-2 and influenza viruses are both enveloped with an encapsulated single-stranded RNA genome. However, their genomes vary in terms of polarity and segmentation. Influenza viruses have 7-8 segmented, negative-sense, single-stranded RNA genomes, while the SARS-CoV-2 genome comprises a non-segmented, positive-sense, single-stranded RNA (Pormohammad et al., 2020).

The *Orthomyxoviridae* family contains three major viruses: influenza types A, B and C. Influenza C carries seven encapsulated segments of negative-sense genomes encoding its structural proteins and non-structural proteins. It can encode a single envelope glycoprotein, named hemagglutinin-esterase-fusion factor (HEF), which is a single multifunction protein and plays a key role in attachment, fusion and receptor destruction. Influenzas A and B comprise eight encapsulated genomic segments and can encode two membrane glycoproteins: haemagglutinin (HA) and neuraminidase (NA). HA plays a key role in attachment and fusion, and NA plays an important role in receptor destruction and release of virions (Wang and Veit, 2016).

SARS-CoV-2 is a member of the *Coronaviridae* family; this viral family has four genera: alpha-coronavirus, beta-coronavirus, gamma-coronavirus and delta-coronavirus (Hosseini et al., 2021). The beta-coronavirus genus comprises five sub-genera: *Embecovirus* or lineage A (OC43-CoV, HKU1-CoV); *Sarbecovirus* or lineage B (SARS-CoV-2, SARS-CoV); *Merbecovirus* or lineage C (MERS-CoV-); *Nobecovirus* or lineage D; and *Hibecovirus* (Decaro and Lorusso, 2020). Among beta-coronaviruses, only beta-coronaviruses lineage A, such as OC43-CoV, encodes HE (Kim, 2020). The HE gene has been transferred to beta-coronavirus lineage A through horizontal gene transmission from an HEF of influenza C (Kim, 2020).

In conclusion SARS-CoV-2, like SARS-CoV, lacks the HE gene (Kumar et al., 2020, To et al., 2021, Chan et al., 2020) and it has four structural proteins: spike (S), envelope (E), nucleoprotein (N) and membrane (M) (Troyano-Hernáez et al., 2021); therefore, the seasonal influenza vaccine for 2019/2020 could not have had cross-reactivity with some of the SARS-CoV-2 proteins.

Conflict of Interest

None.

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None.

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