Review of: "A population-based model for rationing COVID-19 vaccine"

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SARS-CoV-2 clinical symptoms and signs range from mild to moderate-severe with different stages that can lead to a severe and in some cases to death. After the incubation period, there are 3 phases: a purely 'virologic' phase, which lasts 7-10 days where viral replication predominates and is characterized by mild, nonspecific respiratory symptoms ; a 'pulmonary' phase, which possesses the characteristics of interstitial pneumonia and depends on the host immune response, often associated with respiratory symptoms that can lead to progressive clinical instability; and the " 'inflammatory cytokine storm' phase that can evolve into 'ARDS (Acute Respiratory Distress Syndrome) characterized by a dysregulated host immune response, even in the absence of the viral trigger, which can lead to multi-organ failure and exitus.

Since the beginning of the pandemic in 2020, it has been clear that evolution into more severe disease is related in most cases to patient comorbidities.

For this reason, at the beginning of the vaccination campaign, it was crucial to identify the most fragile individuals, who were predisposed to severe pneumonia.

This article shows a valid and cost-effective approach to identify those individuals predisposed to develop severe viral pneumonia. This approach is useful in identifying individuals that should be early vaccinated.

Data from other scientific and governative reports comparing the clinical impact of different variants certainly point out that, the Omicron variant has a lower clinical severity than its predecessors. However, there is no doubt that the presence of comorbidities still influences the clinical course of the disease.

This article shows a practical, useful, and inexpensive approach to identify the categories of patients most at risk of developing severe SARS-CoV-2 disease. These categories should be protected first with vaccine and treated early with antiviral drugs and/or monoclonal antibodies in the case of SARS-CoV-2 infection. This approach probably should be implemented with data on the genetics of individual patients. Indeed, the last 3 years have taught how patients of the same age, with the same comorbidities may still have different disease evolution.