

Ceinge, Omicron multiplies, 3 versions in Italy

There are three 'sisters' of the Omicron variant (B.1.1.529) of the SarsCoV2 virus currently in circulation in Italy, where the presence of Delta or variants other than Omicron are no longer detected. This is what the advanced Ceinge-Biotechnology analyzes, based on data from the Gisaïd international bank indicate. (HANDLE)

There are three 'sisters' of the Omicron variant (B.1.1.529) of the SarsCoV2 virus currently in circulation in Italy, where the presence of Delta or variants other than Omicron are no longer detected.

The latter now represents 100% of the circulating virus, but its first version, BA.1 is contracting due to the pressure of BA.1.1, present for 36%, and BA.2, equal to 5%. A third sub-variant, BA.3, is currently very little present.

This is what the advanced Ceinge-Biotechnology analyzes, based on data from the Gisaïd international bank indicate.

"We used to talk about BA.1, which at the moment constitutes 53% of the virus circulating in our country, but in reality the 'new Omicron' are new variants", observes geneticist Massimo Zollo, coordinator of the Covid Task Force- 19 of the Ceinge.

The Gisaïd data were processed by Angelo Boccia, of the center's Bioinformatics group, coordinated by Giovanni Paoletta.

"The Omicron BA.1 sub-variant is the most prevalent, if we consider all cases of infection in the last 60 days, but it is gradually thinning, while BA.2 and BA.1.1 are progressively expanding," notes Boccia.

Then analyzing the mutations accumulated by the sub-variants, it emerges that it is possible to speak of family similarities only up to a certain point.

"The sub-variant BA.1.1 is very similar to BA.1, from which it derives.

BA.2, on the other hand, has mutations that differentiate it from BA.1," notes Boccia.

"New mutations are also being observed, which it is not known if they will catch on," says Zollo.

What we are seeing, continues the geneticist, is that in all the sub-variants of Omicron "most of the mutations are found in the Spike (S) protein, with which the virus attacks human cells".

A phenomenon, notes Zollo, which "could make us think that the virus is looking for new entry keys and ways out to escape the antibodies.

However, concluded Zollo, “consolidated data is needed to prove this hypothesis”.

As for the other mutations observed, these are found above all on the Nucleocapsid (N) protein, which is important because it helps the virus to replicate, and on which no selective pressure is noticeable at the moment ”.

[Ceinge, Omicron multiplies, 3 versions in Italy - The Limited Times \(newsrd.com\)](https://www.newsrd.com/ceinge-omicron-multiplies-3-versions-in-italy/)

