

Omicron: Zollo (Ceinge), possible cause of serious illness

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"The contagiousness of the Omicron variant could not be serious in Africa due to the characteristics of the interaction with the host with a genome adapted to that environment, but in Europe - he notes - we begin to observe its ability to infect, to generate a serious illness and to escape vaccines".

The data on the diffusion are still very partial, so much so that the sequences of the Omicron genomes obtained in Italy and deposited in the international database Gisaid are 15, according to the elaboration made by the bioinformaticians of Ceinge, with Angelo Boccia: "I do not believe that this number represent the real situation". In fact, there could be many cases "hidden", ie not brought to light by means of sequencing. At an international level, the expert continues, the data allow us to say something more: for example in South Africa it is close to 100% as well as in Sierra Leone and Malawi and again in South Korea and Lebanon. "Delta prevails in Europe and the largest Omicron outbreak is in Great Britain."

What makes the difference between Omicron (B.1.1.529) and the variants that preceded it are the 32 mutations present on the Spike protein, which the virus uses to enter cells. "About a quarter of the 32 mutations were known to also be present in the Delta variant and three quarters are entirely new," notes Zollo.

"A very important thing - notes the geneticist - is that we must not only look at the Spike protein because the virus changes everywhere in its genome and could be pushed to make new mutations by the pressure exerted by vaccines, as the cases of infection that occur seem to indicate. in people who have had two doses of the vaccine. "

In fact, for the virus, mutating in sites of the genome other than the Spike protein means being able to continue to enter human cells and repropagate and mutate again: "the vaccine has protected, but to overcome this protection the virus has generated mutations that the antibodies do not cover. and the return to old vaccine concepts, such as the one that uses the attenuated virus, cannot be excluded: "in

these vaccines the entire genome of the virus is used and this would mean being able to have coverage also on the other areas of the virus genome subject to antibody response.

Working on innovative vaccines such as those with messenger RNA was an excellent choice, which allowed a rapid response to the pandemic, but perhaps now it is time to go back with heat inactivated vaccines and / or use cocktails of variants, with combined technologies. .

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