Podcast in response to various doubts

Last week, some interesting questions were posed to the Difaem Health community by a colleague. They reflect doubts that many people have about whether it makes sense to get vaccinated with the currently available vaccines. Here we are particularly concerned with the effectiveness of the vaccines in the face of ever new variants of the Corona virus. We provide the answers to these questions here.

Question 1: If mutations alter the gene sequence of the spike protein, can antibodies formed by vaccination or infection still recognise and block the spike protein? In other words, does it still make sense to use vaccines developed against the original SARS-CoV-2 virus?

Antibodies formed by vaccination with the currently available vaccines or by infection do not just bind to a specific site on the spike protein. Rather, the antibodies match against the spike protein as a whole. If the spike protein changes due to mutation at individual sites, then the antibodies still fit as a whole, but perhaps not quite as well. This is reflected in a slight reduction of the protective effect.

So far, it has not happened that antibodies from a vaccination were no longer effective against a variant. The data after complete vaccination also speak for the good efficacy against the Delta variant which is now causing a new wave.

Question 2: Can the virulence of a new SARS-CoV-2 variant be predicted? Do these predictions take host factors into account?

The basic problem with predictive research is that science still does not understand and cannot predict with certainty how a linear genetic code becomes a three-dimensional protein. We know all the amino acids, we know how they are built, but we still cannot say what the product will look like in the end, especially how it will look spatially when the amino acids are assembled. Therefore, so far we can say little about how virulent a virus will become through a certain mutation. Research is being done on this, but the error rate is still very high.

Currently, virulence can only be deduced with reliable certainty from clinical trials. The variants are observed and after some time one knows whether a variant is dangerous on the basis of clinical data. Clinical data are data on the number of deaths among patients, the severity of symptoms, the number of people who have been infected by a patient, etc. Once these clinical observations are there, reliable simulations of virulence can be made.

Question3: Does this knowledge feed into the development of new vaccines?

All research and new knowledge is fed into vaccine research.

For example, we know the influenza virus for many years. Here, new vaccines are developed each year primarily on the basis of estimation and calculations of which mutations of the influenza virus are likely to occur that year. But as I said, this prediction is not really scientifically possible at 100%. Therefore, there are years in which the influenza vaccine works very well and others in which it works worse, because the probability calculations are just calculations and not facts.

Maybe one day we will be able to predictively develop vaccines for Sars-CoV-2, but at the moment we simply don't know this virus well enough. So we are very happy that it has nevertheless been possible to develop effective vaccines within such a short time. And adapted vaccines for the variants are already in clinical testing.

We will share with you several podcasts on vaccination in the coming four weeks to give you more background on this important topic. We are always happy to receive your feedback on the quality of our input.

Keep safe and healthy!