

SARS-CoV-2 Recombination event

17 March 2022

Situation Summary

On 8 February 2022, a recombination event between the variants of concern (VOC) Delta and Omicron was reported in Europe. Although the event was described for the first time in France, it is not clear yet where the emergence of the recombinant has occurred. The virus sequence indicates mainly Delta genes (sublineage AY.4) with most of the Spike protein gene (S) corresponding to Omicron (sublineage BA.1).

Similar recombinants were documented in clusters reported by Denmark and the Netherlands, as well as in isolated cases in Belgium and Germany. It is not yet clear if these viruses derive from a common ancestor or if they correspond to different recombination events.

So far, about 50 sequences have been confirmed between January and March 2022, in which the cut and splice sites (breakpoints) that define the recombination event have been demonstrated.

Genetic recombination is a natural phenomenon already described in different viruses as a mutation mechanism to exchange genomic material (which is different from the reassortment mechanism observed in segmented genomes such as that of influenza).

A recombination event can occur when two (2) viruses of the same species but that are genetically different simultaneously infect the same cell in the same individual. Therefore, the current recombination event likely occurred in late 2021 (mid-November to December) when the incidence of both Delta and Omicron was high in some countries of western Europe, increasing the chances of a co-infection to happen.

Although a recombination event can occur in any infected cell, specific signals (cut/splice or breakpoint sites) within the genome are required for the recombination process to occur; likewise, a recombination event can lead to the generation of non-viable viral particles or infectious particles that can be transmitted from one individual to another.

Note from PAHO/WHO

- Currently, there is no evidence that indicates an increased transmission capacity, or changes in the clinical form or severity of the disease due to infection with this recombinant virus.
- To date, no specific name has been assigned to this recombinant virus and it is advised to refer to it as BA.1 x AY.4 recombinant virus.

- The confirmation of a recombinant virus must be carried out carefully, considering not only inconsistencies during the assembly of the genomes and the reconstruction of the phylogenetic trees, but also through the analysis and comparison of sequences obtained from viruses isolated in cell culture. Both the occurrence of individuals with co-infections, or cross-contamination in the laboratory, can lead to results that may be misinterpreted as a genetic recombination event.
- The recommendation to maintain and enhance genomic surveillance for the early detection of any change in viral sequences and viral behavior is reiterated.

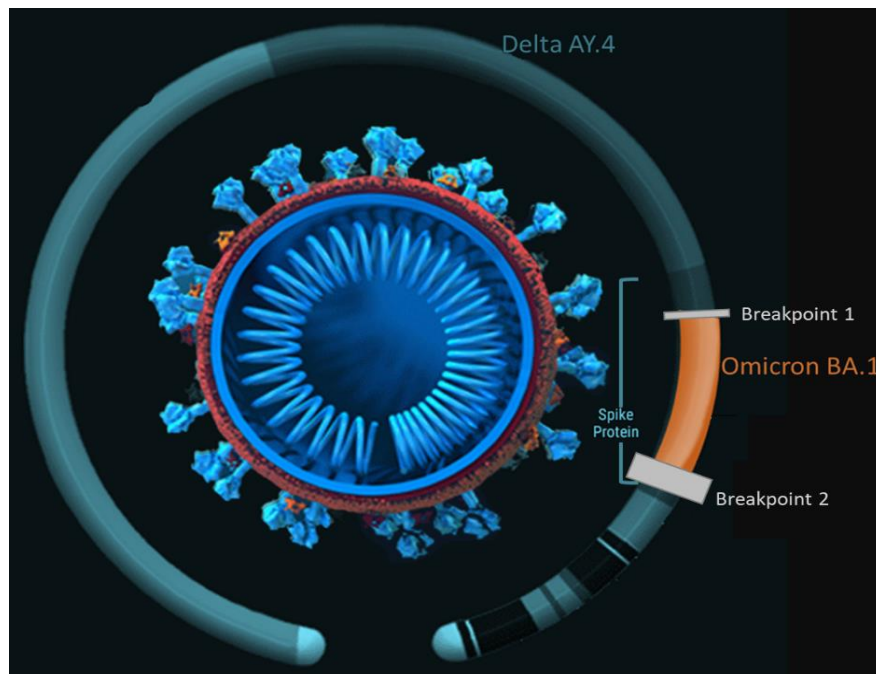


Figure 1. Diagram of the viral genome of the BA.1 x AY.4 recombinant virus, indicating the cut and splice sites (breakpoints) within the *S* protein gene.

This note is shared in order to keep Member States informed.