

Wellcome Genome Campus | Mariana viegas_PAIS project coordinator

Good morning, good afternoon, good evening. My name is Mariana Viegas. I'm a virologist. I work at the virology laboratory of the Ricardo Gutierrez Childrens' Hospital in Buenos Aires City, Argentina, and I am the coordinator of the SARS-CoV-2 Genomics Consortium in Argentina.

First of all, I would like to tell you how the Argentine SARS-CoV-2 genomic consortium is made up of. We are more than 100 researchers and health care professionals working in a coordinated and collaborative way throughout the country. We work sequentially in different nodes with different functions, but with a common objective. That is to perform the genomic epidemiological surveillance of SARS-CoV-2 in Argentina.

As you can see on this slide and this map, all this work is carried out at the federal level. The PAIS Project began in March 2020 with the objective that I just mentioned, which is based on genomic evolutionary studies performed by NGS. But in December 2020, in view of the global concern due to the emergence of variants, we proposed an alternative line of surveillance. We decided to use all the sequencing technologies that we had available to be able to respond in real time. That we put forward by gene sequencing the spike protein gene by Sanger to confirm whether or not we were in the presence of a variant of concern.

As you can see on this image, the blue lines represent the spike gene of each variant, and the region analysed is highlighted. Thus, by monitoring this constellation of mutations, we can confirm a variant of concern or a variant of interest, or we can monitor the emergence of a new variant. We also continue to perform or to carry out surveillance of evolution for evolutionary studies.

This is the time span of the two waves of SARS-CoV-2 in Argentina. In this example of our first strategy, in which we performed whole genome sequencing by NGS and evolutionary analysis, the phylogenetic tree on the left allowed us to assign lineages to the Argentine genomic sequences. In the pie chart on the right, you can see the distribution of SARS-CoV-2 lineages of the first wave in Argentina.

As you can see, the B.1.499 lineage was the most prevalent one during the first wave, and together with the B.1, N.5, N.3, B.11, and B.111 constituted the 94% of all circulating lineages in Argentina during the first wave. Lineages N.3, N.5, and B.1.499 are distinctly Argentine lineages.

B.1.499 was established as a lineage derived from B.1 in March 2020 in Argentina. It first circulated a lot in vulnerable neighbourhoods of the city of Buenos Aires. And afterwards, it has spread throughout the country. On the other hand, M.3 and M.5 lineages derived from the B.1133 from Brazil.

But as I told you before, our second strategy-- which started in December 2020-- allowed us to analyse the distribution of variants in the second wave in Argentina. As you can see in this area chart, through the active surveillance of variants, we have seen from the end of 2020 when we started with this strategy, until epidemiological week 41 of 2021, the variants of first wave, as I told you before, highlighted in grey in this area chart have been replaced by the new variants, and even the variants of concern as Gamma and Delta, which have increased significantly since the epidemiological week 8 in the Metropolitan Area of Buenos Aires, which is the most populated area of our country.

At the country level, the second wave was driven mainly by the Gamma variant that is represented in this area chart-- although, we did recognise its distribution all over the country. Currently, in the epidemiological week 49, an increase in Delta is observed in all the analysed regions of the country, being 100% of all the variants circulating in the Metropolitan Area of Buenos Aires. And so far, the Omicron variant has not been detected in local transmission.

With this presentation, I have tried to summarise all our work in this moment. If I had to highlight the benefits of this project, I would mention the human capital, always willing to work collaboratively in teams, the know-how acquired along this last two years, and the generosity and cooperation among peers. On the other hand, the challenges presented in this project were the low budget we had, the import restrictions, the bureaucratic procedures at the customs, and, finally, the scarce availability of laboratory reagents from the high-income countries' companies.

Finally, I would like to show you this, that these are pictures of the researchers and health professionals part of this big project. Thank you very much for your attention.