

## Wellcome Genome Campus | Carolina Torres\_Evolutionary node Coordinator

---

Hello, my name is Carolina Torres. I'm going to present you some evolutionary analyses that we have performed in the SARS-CoV-2 Genomics Consortium in Argentina, the PAIS project. As Dr. Mariana Viegas already told you, we used phylogenetic analyses to confirm the lineage assignment in the Pango system. This is the result for the first wave analysis, showing this particular distribution of SARS-CoV-2 lineages in Argentina, prevailing the lineages B.1.499, B.1, and N.3, and N.5 lineages.

In the same way, we confirmed the assignment of the derived lineages from the variant of interest and concern that prevail in our second wave. In this case, I show you the result for the phylogenetic analyses for Gamma sequences from different regions of Argentina.

And also, we studied the introduction and the transmission chains for this variant. And we found, for example, for Gamma variant, that multiple introductions and cluster of Argentine sequences with no epidemiological links were observed, indicating introduction, establishment, and local transmission of this variant. And also, monophyletic groups were observed, suggesting transmission chains circumscribed to one or few areas dispersed regionally, or between distant provinces. And this is the same analysis performed for Delta variant and its derived lineages, finding similar results for the analysis of the introduction and transmission chains.

And finally, we have performed phylodynamic analyses, such as this one carried out for lineage B.1.1.33 and its derived lineages, N.3, and N.5, important in our first wave. We could date and locate the initial diversification event for this lineage in South America, and estimate the evolutionary rate, and the viral demographic reconstruction for this lineage in the first month of the COVID-19 pandemic in South America. Thank you very much.