







PAIS project: Argentine SARS-CoV-2 Genomics Consortium "Evolutionary analyses"

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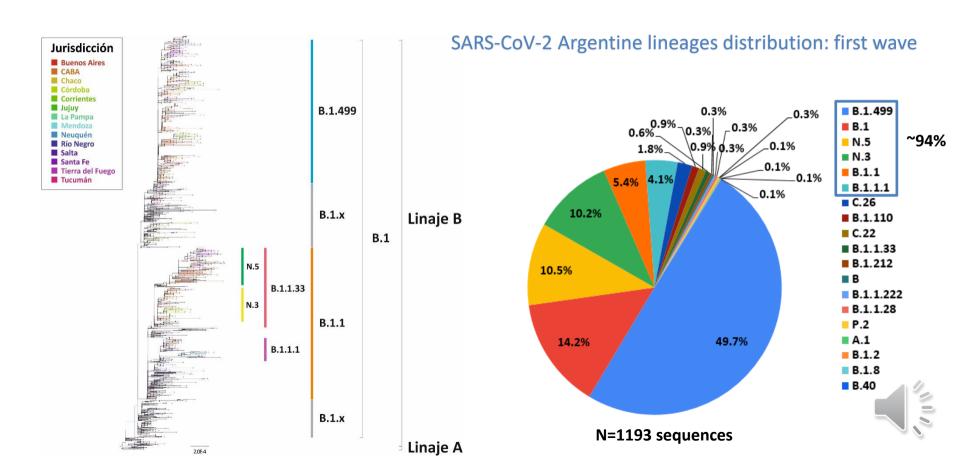


@CaroTorr



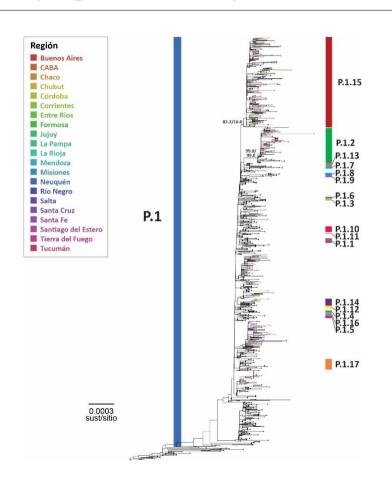
Phylogenetic analyses: confirmation of lineage assignment





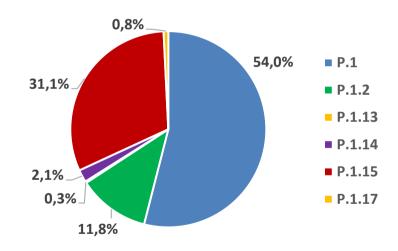
Phylogenetic analyses: confirmation of lineage assignment





GAMMA

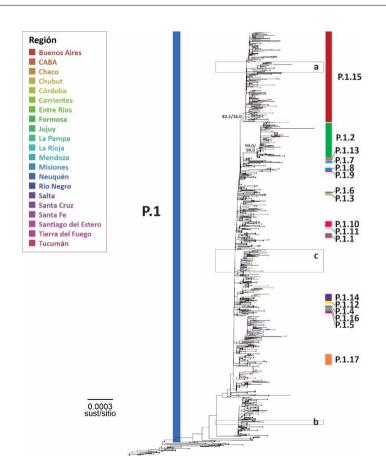
Lineage P.1 and its derived lineages





Phylogenetic analyses: introduction and transmission chains





GAMMA

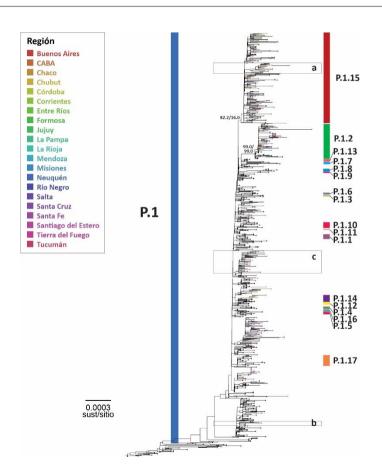
- Multiple introductions and clusters of Argentine sequences with no epidemiological link were observed, indicating introduction, establishment, and local transmission.
- Monophyletic groups were observed, suggesting transmission chains circumscribed to one or a few areas, dispersed regionally or between distant provinces:





Phylogenetic analyses: introduction and transmission chains

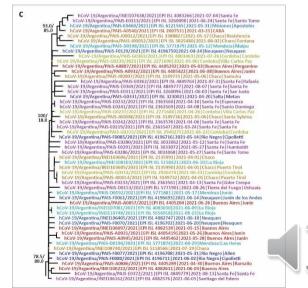




GAMMA

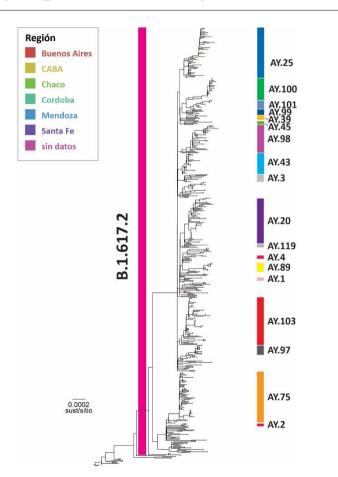
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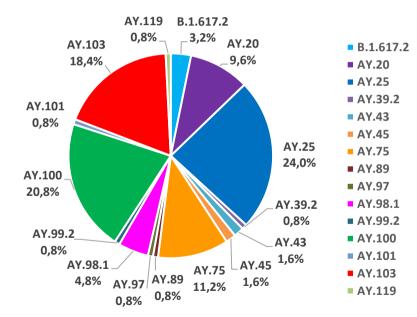
Phylogenetic analyses: confirmation of lineage assignment





DELTA

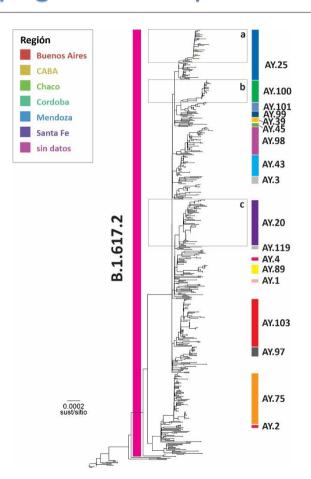
Lineage B.1.617.2 and its derived lineages





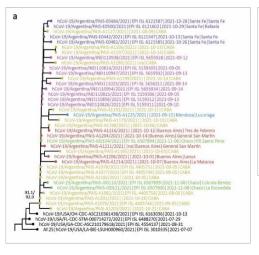
Phylogenetic analyses: introduction and transmission chains

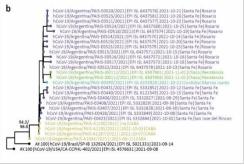




DELTA

- As for other variants, multiple introductions and groupings of Argentine sequences with no epidemiological link were observed, indicating introduction, establishment, and local transmission.
- Groups were observed suggesting transmission chains circumscribed to one or a few areas, dispersed regionally or between distant provinces:

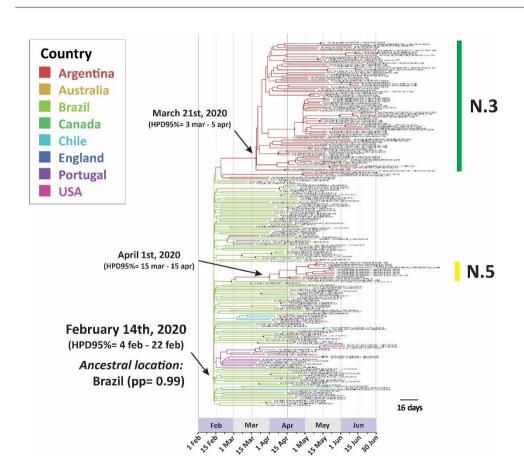






Phylodynamics: dating, evolutionary rate and phylogeography



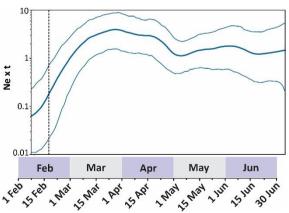


B.1.1.33 and its derived lineages

Evolutionary rate= 6.0×10^{-4} (s/s/y) (HPD95%= $4.8 \times 10^{-4} - 7.2 \times 10^{-4}$)

~ 18 subs/year

Demographic reconstruction











http://pais.qb.fcen.uba.ar



