



Correction to: Sequence analysis of nucleoprotein gene reveals the co-circulation of lineages and sublineages of rabies virus in herbivorous in Rio Grande do Sul state, Brazil

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Discussion section, 9th paragraph. The paragraph should read: Co-circulation of two distinct RABV lineages in RS has already been reported by Fernandes [34] and Cargnelutti et al. [32] testing a smaller number of samples. Our data support and extend these findings indicating that these lineages are likely established in the RS ecosystem. Most of the sequences analyzed in the present study were grouped in cluster 1, which

presented a wide geographic distribution (Fig. 3), and were genetically related to viruses from a neighbor Argentine province. On the other hand, viruses belonging to cluster 2 showed a more restrict geographic pattern but were related to sequences from SC and from a neighbor Uruguayan province.

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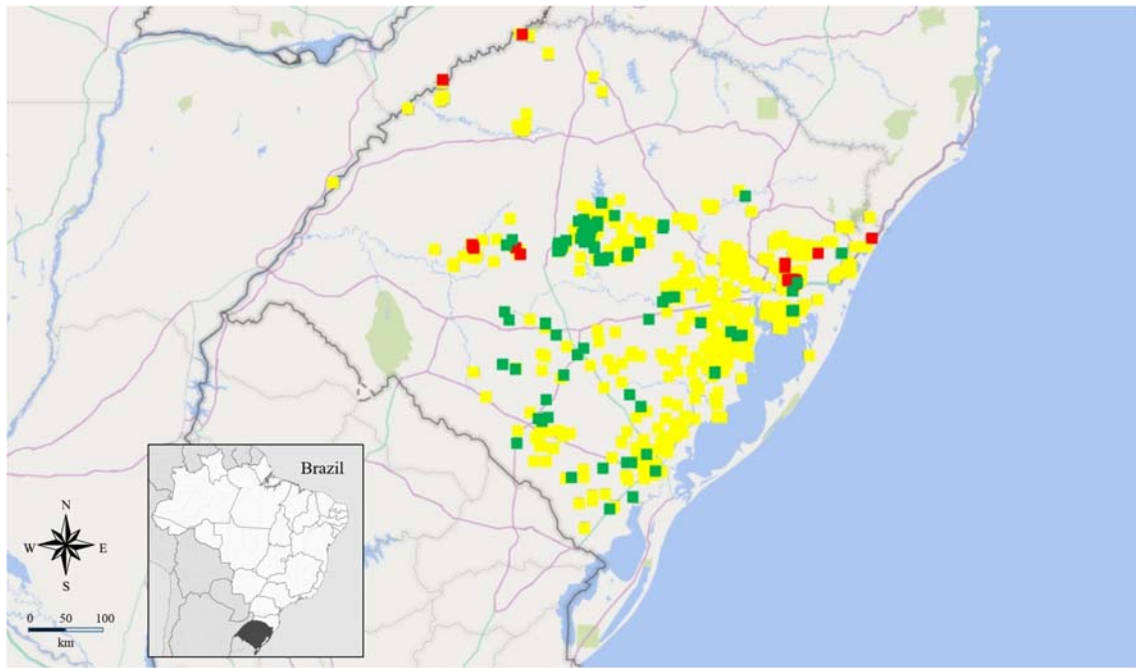


Fig. 3 Cases/outbreaks of herbivorous rabies in the state of Rio Grande do Sul, Brazil. Farms that had viruses grouped in cluster 1 in the phylogenetic tree are highlighted in green, and farms that had viruses in

cluster 2 are in red. Farms where the rabies diagnosis was performed by the immunofluorescence test, biological test, or RT-PCR from 2012 to 2017, but whose N sequences were not obtained are highlighted in yellow