

## Whole genome sequencing typing suggests multiple *P. brasiliensis* dispersion events into endemic areas of paracoccidioidomycosis in Argentina and Paraguay

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Paracoccidioidomycosis (PCM) is a deep systemic mycosis endemic to South America that affects both health and immunocompromised mammals, including humans. The disease is caused by the thermo-dimorphic fungal species: *Paracoccidioides lutzii*, *P. brasiliensis* (S1), *P. americana* (PS2), *P. restrepiensis* (PS3) and *P. venezuelensis* (PS4). Paraguay and Argentina are included in the endemic area of PCM. Argentina has two well-defined areas; the north-western and the more extensive in the north-eastern. South-eastern Paraguay is considered the endemic region of this disease.

Genomes of 13 isolates from Argentina (10) and Paraguay (3) were sequenced “*de novo*” and analyzed. Phylogenomics analysis suggests that two different *P. brasiliensis* genotypes are endemic to Argentina: *P. brasiliensis* S1a and S1b. In contrast, paraguayana isolates clustered only with S1b.

Isolates that clustered within S1b are close related with the reference strain Pb18 and other distributed within the Brazilian territory. The second genetic cluster is composed by *P. brasiliensis* from S1a lineage and the Argentinian strains and two from Mato-Grosso state of Brazil form a monophyletic clade that is separated from the isolated collected in São Paulo state, showing a high level of geographic isolation within this genetic cluster. We concluded that there were two main events of introduction of *P. brasiliensis* in Argentina that was potentially originated from Brazil.

Keywords: endemic, S1a, S1b