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Reading South American history in the native Brazilian genomes

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The contact with Europeans and the colonization of the New World led to the massive extermination of Native Americans, which concealed most of its pre-contact history. In this study, we uncovered ancient Brazilian native migrations, as well as aspects of the post-contact history of these populations using genomic data.

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The distribution of the present-day native Brazilian peoples considerably differs from the one found by Portuguese explorers in the 15th century. At the time, a third of the Brazilian native population (about 900,000) lived on the Atlantic coast and were part of complex societies. Most of these natives spoke a language derived from the Amazonian Tupí languages and were defined as the Tupí costal branch. Throughout the process of Brazilian colonization by the Portuguese, coastal populations went gradually extinct, leaving today only small self-declared indigenous communities that no longer speak any native language. In this work, we studied one of these populations to answer two main questions: Is this population, known as Tupiniquim, descendant of the coastal natives from the time of the European conquest? Which routes did the Amazonian Tupí take to reach the Atlantic coast and the southwest of the South American continent?

To answer these questions, we studied the genomic information of the Tupiniquim individuals to unravel some aspects of recent and ancient Brazilian history. Using genomic approaches, we retraced the main demographic and migratory events, as well as the relatedness between groups of speakers of some of

the most important native Brazilian language families. We also looked for post-Columbian dates when significant portions of the Tupiniquim and European or African populations mixed. Using this data, we were also able to estimate the number of individuals that initially formed the Tupiniquim population more than 500 years ago.

We then compared the genome of the Tupiniquim population with other worldwide populations. By examining the genetic variation of the Tupiniquim genomes in comparison to those of other Native Americans, as well as Europeans and Africans, we found that Tupiniquim genomes were predominantly Native American. The main post-Columbian miscegenation events were consistent with two key historical events: indigenous enslavement (Gold Cycle; 17th century), and the abolition of slavery with a consequent increase of the African and European populations in Brazil (19th century).

We estimated the Tupiniquim population size in 1500 at circa 100,000 individuals. Our genetic estimated date regarding the population collapse - the point of lowest population size - was seven generations ago, similar to data from the historic register from 1877 when only 55 Tupiniquim were counted in Brazil. Using only the native portion of the genomes of the Tupiniquim, we were able to show that they have not generated descendants of mixed ancestrywith the other Brazilian native groups studied. However, they are more genetically similar to present-day Tupí speakers of eastern Amazonia. Therefore, we could infer that the Tupiniquim group is part of the extinct coastal Tupí branch.

Finally, we tested different models for the history of the Tupí populations, corresponding to existing hypotheses about how the Tupí expansion unfolded from western Amazonia to Atlantic and Southwestern Brazil, which are mainly based on archeological and linguistic evidence. The best-fitted model relied on the hypothesis that the Tupí-speakers were incipient agriculturalists and expanded from Amazonia in search of new lands to cultivate, moving eastwards until the mouth of the Amazon River and then followed the Brazilian Atlantic coast. Independently, a different expansion went southwards and was the origin of the Guaraní people from Southwestern Brazil, Paraguay, and Argentina. Our results also pointed to a new genetic wave – or population migration and mixing - from Mesoamerica that differentiated the Southern Tupí from the other Tupí groups. This migration likely occurred around 1500 years ago.

Our study recovers the history of Brazilian native populations that were virtually extinct during the European colonization. By leveraging the genomic information from these individuals, we were able to reconstruct the recent and ancient history of these endangered populations.