Marcos Araújo Castro e Silva
Curriculum Vitae

Personal Information

Full name	Marcos Araújo Castro e Silva
Position	Postdoctoral fellow at the Human Genome Diversity Lab at the Institut de Biologia Evolutiva – Universitat Pompeu Fabra
Professional Address	Carrer del Dr. Aiguader, 88, Ciutat Vella, 08003 Barcelona
Nationality	Brazilian
E-mail	Contact e-mail: marcosaraujocastro@gmail.com Institutional e-mail: marcos.araujocastroesilva@upf.edu

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Research lines

1. Genetic history of Indigenous American peoples
2. Peopling of the Americas
3. Genetic diversity of admixed American populations
4. Human population genomics

CV Summary

I am currently working on a project I designed to investigate the fine-scale structure of European ancestry within admixed Latin American populations. Rather than treating continental and subcontinental ancestries as homogeneous, my work disentangles contributions from ancient lineages tracing how their proportions vary across Latin America. I am also studying the enrichment of these lineages in specific genomic regions, exploring functional relevance and associations with health traits. This research illuminates the impact of ancient admixture and deep demographic events on modern diversity, adaptation, and disease susceptibility in the Americas.

I also recently published a study featured on the cover of Nature that investigates the genetic history and diversity of Indigenous American populations. The study analyzes the most comprehensive dataset of Indigenous American whole genomes assembled to date, comprising 128 high-coverage genomes from 45 ethnic groups across eight Latin American countries. It aims to shed light on the peopling of South America, patterns of genetic continuity and population movement, the genetic structure of contemporary populations, and genetic adaptations, including those potentially introduced through archaic introgression or ancient admixture.

As part of my postdoctoral fellowship at IBE/CSIC, I contributed significantly to the *DNA do Brasil* project, a major national initiative led by Brazilian researchers to generate and analyze high-coverage whole-genome data from culturally and geographically diverse populations across Brazil. As co–first author of the project's first publication, now published in *Science*, I was responsible for the analysis of genetic structure and demographic history, working with a dataset of over 2,700 high-coverage genomes. Our findings revealed critical insights into the formation of Brazilian populations, including patterns of admixture, assortative-mating, subcontinental ancestry, demographic trajectories, adaptive variants, and genetic load. During this time, I was awarded two competitive and prestigious fellowships: the *EUTOPIA-SIF Marie Skłodowska-Curie COFUND Fellowship* and the *Juan de la Cierva Postdoctoral Fellowship*.

I am also currently involved in a research project focused on exploring the population history, genetic structure, and demographic dynamics of the European Roma. As part of this work, I co-supervised a Ph.D. student from Universitat Pompeu Fabra, who successfully defended his dissertation with cum laude honors in July 2025. The supervision was carried out in collaboration with Prof. David Comas, the project's principal investigator. This research has resulted in two publications to date: one in *Human Genetics*, which examines the autosomal genetic diversity of Iberian and broader European

Roma populations, and another in *BMC Genomics*, focusing on Y-chromosome lineages in European Roma groups.

Previously, as a *Research and Innovation Fellow with the Fundação Faculdade de Medicina*, I also worked on the *DNA do Brasil* project, focusing on inferring the genetic ancestry of Brazilian populations. Prior to that, as a *Technical Training Fellow*, I worked on the development of a machine learning approach to detect natural selection patterns in genomic data.

My Ph.D. research at the Universidade de São Paulo (Brazil) explored the genetic diversity and population histories of native Brazilians and South Americans, covering topics from the initial settlement of the continent to Late Holocene population expansions and the impact of European colonization. My thesis led to three high-impact publications: two in *PNAS* and one in *Molecular Biology and Evolution*, all widely covered by the media.

The paper “Genomic insight into the origins and dispersal of the Brazilian coastal natives” has received the *American Society of Human Genetics' Trainee Paper Spotlight*. The paper “Population histories and genomic diversity of South American natives” has received honorable mentions for *Best Graduate Student Paper*, from the *Society for Molecular Biology & Evolution*. My thesis won Best Thesis Awards from the Universidade of São Paulo and from the *Coordenação de Aperfeiçoamento de Pessoal de Nível Superior* (CAPES; Brazilian national funding agency), and I was awarded the *Young Geneticist Prize* by the *Brazilian Society of Genetics* for my contributions to the field.

During my M.Sc. at Universidade de São Paulo and undergraduate studies at Universidade Federal de Viçosa, my research focused on the molecular mechanisms of biotic and abiotic stress responses in plants, exploring signaling pathways through protein-protein interaction analysis. This work resulted in two co-authored publications in *Frontiers in Plant Science* and *Nature*.

In addition, I have over eight years of programming experience primarily with R, Shell script, as well as some experience with Python. During this period I have also been applying version control systems (Git and GitHub), Google Cloud Platform and institutional cloud computing systems.

Formal Education/Degree

30/01/2017–27/09/2021	PhD in Biology (Genetics) (41131). Universidade de São Paulo, USP, São Paulo, Brazil Project title: Genomic perspective on the origin, history, and diversity of indigenous peoples from South America: from the initial settlement to the European colonization Supervisor: Tábita Hunemeier Scholarship from: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)
20/02/2013–02/03/2015	MSc in Genetics and Plant Breeding Universidade de São Paulo, USP, São Paulo, Brazil Project title: Convergent evolution of *Arabidopsis thaliana* FtsH5 protease and its putative negative regulator FIP (FtsH5 interacting protein) Supervisor: Marcio de Castro Silva Filho Scholarship from: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq)
01/02/2008–18/02/2013	BSc in Biological Sciences Universidade Federal de Viçosa, UFV, Viçosa, Brazil Project title: Transcriptional expression analysis of *Arabidopsis thaliana* immune system genes related to response against geminivirus Supervisor: Elizabeth Pacheco Batista Fontes Scholarship from: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq)

Complementary Education

22–30/03/2022	EMBO virtual Practical Course Population genomics: background and tools. (60h) European Molecular Biology Organization, EMBO/EMBL, Germany
06–10/08/2018	PhD summer course in analyses of genotyping and sequencing data in medical and population genetics. (140h) University of Copenhagen, Copenhagen, Denmark

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Languages

Portuguese	Native
English	Fluent (TOEFL iBT® Total Score: 100)
Spanish	Upper-Intermediate proficiency - B2 (CEFR)

Professional experience

07/09/2022–present Postdoctoral fellow at the Institute of Evolutionary Biology at the Pompeu Fabra University (Barcelona, Spain)

As a postdoctoral fellow at the Institute of Evolutionary Biology (Pompeu Fabra University, Spain), I work on the "DNA do Brasil" project, analyzing over 2,700 genomes to study Brazilian population formation, admixture, and genetic diversity. I have also investigated the genetic diversity, demography, population structure and history, adaptive selection signatures of Indigenous Americans, focusing on 128 genomes from 45 groups across Latin America.

01/06/2022–30/08/2022 Innovation Research Fellowship at the Fundação Faculdade de Medicina (São Paulo, Brazil)

As an Innovation Research Fellow I was working at the project "DNA do Brasil: Establishment of a reference genome for the Brazilian population".

30/11/2021–31/05/2022 Technical Training Fellow at the Universidade de São Paulo (São Paulo, Brazil)

I was a Technical Training Fellow (TT5) and responsible for the project "Detecting Natural Selection Patterns in Native American Populations through the Machine Learning Approach".

20/02/2017–30/11/2021 PhD student/researcher at the at the Universidade de São Paulo (São Paulo, Brazil)

During my Ph.D. at the Universidade de São Paulo (Brazil), I investigated the genetic diversity and population histories of native Brazilians and South Americans, focusing on topics ranging from the continent's initial settlement to Late Holocene population expansions and the effects of European colonization.

01/02/2013–18/02/2015 MSc student/Researcher at the at the Universidade de São Paulo (Piracicaba, São Paulo state, Brazil)

I was the researcher responsible for the project “Convergent evolution of the *Arabidopsis thaliana* FtsH5 protease and its putative FIP negative regulator (FtsH5 interaction protein)”.

01/08/2011–01/07/2012 Scientific initiation fellow at the Universidade Federal de Viçosa (Viçosa, Minas Gerais state, Brazil)

I was the researcher responsible for the project “Convergent evolution of the *Arabidopsis thaliana* FtsH5 protease and its putative FIP negative regulator (FtsH5 interaction protein)”.

Coordination of academic research projects

01/01/2024–31/12/2025	**Juan de la Cierva-Formación (JCI-F) Fellowship** Project: Indigenous American Genomic Diversity Project Funding: Agencia Estatal de Investigación - AEI (JDC2022-049175-I) Institution: Universitat Pompeu Fabra, Spain.
07/09/2022–31/12/2023	**EUTOPIA-SIF Marie Sklodowska-Curie COFUND Fellowship** Project: The Impact Of Demography, Admixture, And Evolution On The Health Of Brazilian Populations Funding: European Union Horizon 2020 programme under the Marie Skłodowska-Curie grant agreement No 945380 Institution: Universitat Pompeu Fabra, Spain.

Participation in research projects

2023 - present	**Researcher associated with the research project** Project: Predição de Fenótipos de Comportamento Adaptativos em Primatas Usando Aprendizado de Máquina Funding: Conselho Nacional de Desenvolvimento Científico e Tecnológico - CNPq Institution: Universidade Federal do Rio Grande do Sul, Brazil Coordinator: Maria Cátira Bortolini
2023 - present	**Researcher associated with the research project** Project: Descifrando la Historia Poblacional de los Romani Americanos a Traves del Analisis de Diversidad Genomica Funding: Ministério de Ciência y Innovación, Espanha (PID2022-138755NB-I00) Institution: Universitat Pompeu Fabra, Spain Coordinator: David Comas
2019 - present	**Researcher associated with the research project** Project: Establishment of a Reference Genome of the Brazilian Population (DNA do Brasil) Funding: Health Ministry GRB/4 Coordinators: Tábita Hünemeier, Lygia da Veiga Pereira e Alexandre C. Pereira.
2020 - 2022	**Researcher associated with the research project** Project: Native American genomic diversity Funding: Fundação de Amparo à Pesquisa do Estado de São Paulo - FAPESP (FAPESP/2015/26875-9) Institution: Universidade de São Paulo, Brazil Coordinator: Tábita Hünemeier

Organization of academic events

24–27/11/2025	Symposium organizer **(**Genetic Histories and Evolutionary Landscapes of Indigenous and Admixed Americans), XXIII Coloquio Internacional Juan Comas / XVII Congreso Internacional de la Asociación Latinoamericana de Antropología Biológica, Ciudad de Cholula, Puebla, México (November 2025)
6–9/10/2022	Organizing Committee of the 16th Meeting of the Latin American Association of Biological Anthropology (ALAB), São Paulo, Brasil

Awards, Honors, and Distinctions

2026	Cover feature in Nature (May 7, 2026 issue) for the paper “The evolutionary history and unique genetic diversity of Indigenous Americans.”
2026	Seal of Excellence for my project proposal “Deep Population History of Admixed Americans” submitted under the Horizon Europe Marie Skłodowska-Curie Actions

	call HORIZON-MSCA-2025-PF-01-01 — MSCA Postdoctoral Fellowships 2025
2025	Young Investigator Attendance Award for the SMBE 2025, by the Society for Molecular Biology & Evolution
2025	Wiley Top Viewed Article, for the paper “A multidisciplinary overview on the Tupi-speaking people expansion”, by the American Journal of Biological Anthropology
2023	MBE Honorable Mentions - Best Graduate Student Paper, for the paper “Population Histories and Genomic Diversity of South American Natives”, by the Society for Molecular Biology & Evolution
2023	Young Geneticist Award “Francisco Mauro Salzano”, Sociedade Brasileira de Genética - SBG
2022	USP Highlight Thesis Award 11th Edition, University of São Paulo - USP
2022	CAPES Thesis Award, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - CAPES (Brazilian national funding agency)
2020	American Society of Human Genetics' Trainee Paper Spotlight, for the paper “Genomic insight into the origins and dispersal of the Brazilian coastal natives”, by the American Society of Human Genetics - ASHG
2013	Votes of praise for academic performance, Coordinating Committee of the Biological Sciences Course at the Universidade Federal de Viçosa - UFV

h index and citations of published articles

ORCID	https://orcid.org/0000-0002-9873-3717
MyCitations	https://scholar.google.com.br/citations?user=KkHCEkEAAAAJ&hl=en
h index	8
i-10 index	8
Citations	574

Articles Published in Scientific Journals († co-authorship; CA: Corresponding Author; * Highlighted research)

1. SENA, LUCAS; NUNES, KELLY; LEMES, RENAN; RODRIGUES, MAIRA; CANTÃO, HULLY; KIMURA, LILIAN; PASSARELLI, HEMANOEL; CÁTIRA BORTOLINI, MARIA; CADORE, NATHAN; VIANNA, FERNANDA; EDUARDO AMORIM, CARLOS; **CASTRO E SILVA, MARCOS**; PERERA DEL ROSARIO, SIMON; CALAFELL, FRANCESC; COMAS, DAVID; PEREIRA, ALEXANDRE; MILL, JOSÉ; PEREIRA, LYGIA; HÜNEMEIER, TÁBITA (CA). Clinically relevant drug-target genomic variation in Indigenous and admixed American populations. **Submitted to Nature Medicine.** (author position 12/19) DOI: Still does not have a DOI.

2. DE OLIVEIRA, LUIZA GOMES; NUNES, KELLY; BARBOSA, RENAN; **CASTRO E SILVA MARCOS**; BARQUERA, RODRIGO; MILL, JOSÉ GERALDO; SACUENA, PUTIRA; GUERREIRO, JOÃO; BORTOLINI, MARIA CÁTIRA; HÜNEMEIER, TÁBITA (CA). Subsistence-Driven Variation in Salivary Amylase Gene (AMY1) Copy Number Among Indigenous Populations of America. **Under review in Scientific Reports**. (author position: 4/10) DOI: Still does not have a DOI.

3. PATRICIO PEZO-VALDERRAMA, FLAVIO DE ANGELIS, MAÍRA R. RIBEIRO, **MARCOS ARAÚJO CASTRO E SILVA** … MARIA LAURA PAROLIN (CA), TÁBITA HÜNEMEIER (CA). Two Millennia of Demographic and Adaptive Shifts Revealed by Ancient Genomes from Atlantic Patagonia. **Under**

review in Cell. (author position: 4/15) DOI: Still does not have a DOI.

4. EPIFANÍA ARANGO-ISAZA (CA), PATRICK F. REILLY, ROMAN BRISKINE, **MARCOS ARAÚJO CASTRO E SILVA** … KENTARO K. SHIMIZU (CA), CHIARA BARBIERI (CA). Uncovering high levels of genomic diversity in the Southern Cone of South America. **Under review in Nature Communications**. (author position: 4/10) DOI: Still does not have a DOI.

*5. **CASTRO E SILVA, MARCOS ARAÚJO**; NUNES, KELLY; RODRIGUES RIBEIRO, MAÍRA; et al.; COMAS, DAVID; HÜNEMEIER, TÁBITA (CA). Indigenous American Genomes Harbor Unique Genetic Diversity and a Complex Evolutionary Past. **Nature, 2026**. (author position: 1/38) DOI: https://doi.org/10.1038/s41586-026-10406-w

Indigenous American populations remain markedly underrepresented in global genomic research, limiting our understanding of the evolutionary history and genetic diversity of the last continent settled by humans. To address this gap, we generated and analyzed 128 high-coverage whole-genome sequences from individuals representing 45 Indigenous ethnic groups across eight Latin American countries (Argentina, Bolivia, Brazil, Colombia, Ecuador, Mexico, Paraguay, and Peru), spanning 28 language families and a wide range of environments from the Arctic to the tropical lowlands and the Andes. These data were integrated with genomes from ancient individuals and worldwide populations to reconstruct the demographic history of the Americas while accounting for recent European and African admixture through local ancestry inference.

Our analyses uncovered more than one million previously undocumented genetic variants, highlighting the distinctive evolutionary history of Indigenous Americans and their persistent underrepresentation in global databases. We detected strong geographic structure in genetic variation, with patterns of similarity broadly reflecting geography over millennia. Comparisons with ancient DNA revealed evidence for multiple dispersals into South America, including a previously uncharacterized Late Holocene migration related to Mesoamerican populations that contributed to present-day South Americans and ancient Caribbean individuals. Despite these movements, several regions show long-term genetic continuity, indicating deep local ancestry maintained over thousands of years. We also identified signatures of natural selection, including adaptive introgression, affecting genes involved in immune response, metabolism, growth, and reproduction, consistent with adaptation to diverse environments across the American continent. In addition, our results support the hypothesis that the Australasian-like ancestry component (also known as “population Y” ancestry) reflects an ancient admixture event that contributed to the formation of the first Americans and was partly preserved by selection.

Together, these findings provide one of the most comprehensive views of Indigenous American genomic diversity to date, showing that the genetic landscape of the continent was shaped by multiple dispersals, regional continuity, and adaptation to highly diverse environments. The study also demonstrates that substantial human genetic variation remains undocumented, including variants with potential biomedical relevance, underscoring the importance of expanding genomic research in partnership with Indigenous communities to achieve a more complete and equitable representation of human diversity.

This research was recently accepted for publication in *Nature* (March 11, 2026), on which I am first author. The underlying dataset is publicly available through the European Genome-Phenome Archive (EGA) under controlled access (EGAS50000001664). To facilitate data exploration, we also developed an interactive genome browser that allows users to visualize variant-level and allele-frequency information specific to Indigenous American populations. The results have been presented at multiple international conferences and seminars, including the 2025 meeting of the Society for Molecular Biology and Evolution, where I delivered the presentation.

6. ENA, GIACOMO; GIMÉNEZ, AARON; CARBALLO-MESA, ANNABEL; **CASTRO E SILVA, MARCOS ARAÚJO**; COMAS, DAVID (CA). Demographic insights into paternal genetic diversity and regional substructure in the Spanish Roma. **BMC Genomics**. (author position: 4/5) DOI: https://doi.org/10.1186/s12864-025-12210-8 / High attention score, 91th percentile in Altimetrics.

7. CADORE, NATHAN A.; DE O FAM, BIBIANA S.; GIUDICELLI, GIOVANNA C.; … **SILVA, MARCOS A. C.**; … VIANNA, FERNANDA S. L. (CA). Carrying APOL1 G1 allele is associated with cardiovascular complications during COVID- 19 in an admixed population. **Human Genomics, 2025**. (author position: 6/17) DOI: https://doi.org/10.1186/s40246-025-00790-1

*8. ENA, GIACOMO; GIMÉNEZ, AARON; CARBALLO-MESA, ANNABEL; LIŠKOVÁ, PETRA; **CASTRO E SILVA, MARCOS ARAÚJO**; COMAS, DAVID (CA). The genetic footprint of the European Roma diaspora: Evidence from the Balkans to the Iberian Peninsula. **Human Genetics, 2025**. (author position: 5/6) DOI: https://doi.org/10.1007/s00439-025-02735-z / High attention score, 90th percentile in Altimetrics.

The Roma people, with South Asian origins, migrated westward about 1,000 years ago, settling in Europe, particularly the Iberian Peninsula, are the largest ethnic minority in Europe. This study is the most extensive genome-wide analysis of 181 Iberian Roma individuals, confirming their South Asian origins and revealing significant gene flow from populations encountered during migration. We found no genetic evidence supporting previous hypotheses of a North African migration route into Iberia or connections to Jewish populations. The Iberian Roma showed substantial genetic differentiation from non-Roma Iberians, as well as significant regional substructure. We also identified assortative mating within Roma groups, suggesting distinct mating patterns and increasing integration with non-Roma. These findings shed light on their complex demographic history, the influence of historical migrations, and the ongoing social dynamics shaping their genetic diversity, with potential implications for health risks in Roma and related populations.

This study has been published in *Human Genetics*, and as co-supervisor of the first author (Giacomo Ena), I contributed to the methodology, study design, writing, and editing of the manuscript. Our results have been presented by the first and corresponding authors at Spanish and international scientific conferences and seminars. This study was conducted under the project "El Camí del Poble Gitano: una història de diversitat" in collaboration with the Federation of Roma Associations of Catalonia. Preliminary findings were shared by the corresponding author with the local Roma community during a meeting at UPF in Barcelona, which was also streamed on YouTube (https://www.youtube.com/watch?v=JRP9So3bnwc). The newly sequenced data was made publicly available through a data access agreement on EGA (EGAS50000000746). Since the publication, the article has received widespread attention, already accumulating 4 citations on Google Scholar.

*9. NUNES, KELLY†; **CASTRO E SILVA, MARCOS ARAÚJO†**; RODRIGUES RIBEIRO, MAÍRA†; BARBOSA LEMES, RENAN†; … COMAS, DAVID; PEREIRA, ALEXANDRE (CA); PEREIRA, LYGIA (CA); HÜNEMEIER, TÁBITA (CA). Admixture's Impact on Brazilian Population Evolution and Health. **Science, 2025**. (author position: 2/24) DOI: https://doi.org/10.1126/science.adl3564 / High attention score, 99th percentile in Altimetrics.

Brazil, home to Latin America's largest population and the world's most extensive recently-admixed population, remains significantly underrepresented in global genomic research. As part of the Brazilian Ministry of Health’s DNA do Brasil project, we analyzed 2,723 high-coverage whole-genome sequences from individuals spanning the country's diverse ecoregions and ethnic backgrounds. Our study revealed an extraordinary level of genetic diversity compared to global reference datasets, identifying millions of novel variants—including thousands with potential deleterious effects. Notably, we observed a positive correlation between the number of deleterious variants and individual ancestry components.

Our findings portray the Brazilian population as a complex mosaic of global haplotypes, shaped by centuries of non-random mating, with peak admixture occurring in the 18th and 19th centuries. We uncovered fine-scale population structure both spatially and temporally, and identified candidate genes under selection both pre- and post-contact, particularly those related to fertility, immune function, and distinct metabolic traits. These insights highlight the profound influence of Brazil’s ancestral diversity on the genetic landscape and health of its admixed population.

This research was recently published as an Open Access article in Science (May 15, 2025), on which I am co-first author. The underlying dataset is publicly available through EGA (EGAS50000000730) under a data access agreement. To facilitate access for public health officials and clinicians, we also developed an interactive genome browser that enables users to explore variant-level and allele frequency data specific to the Brazilian population.

The DNA do Brasil project was funded by the Brazilian Ministry of Health. My contributions to this work were supported by the European Union’s Horizon 2020 programme (Marie Skłodowska-Curie grant No. 945380) and the Spanish Agencia Estatal de Investigación (AEI). The study’s results have been presented by the co-first and corresponding authors at numerous national and international scientific conferences and seminars. Since the publication, the article has received widespread attention, already accumulating 74 citations on Google Scholar, with over 40,000 downloads and media coverage by more than 30 international and Brazilian news outlets.

10. **CASTRO E SILVA, MARCOS ARAÚJO (CA)**; HÜNEMEIER, TÁBITA (CA). A multidisciplinary overview on the Tupi-speaking people expansion. **AMERICAN JOURNAL OF BIOLOGICAL ANTHROPOLOGY. p.1 - 12, 2023**. (author position: 1/2) DOI: https://doi.org/10.1002/ajpa.24876 / High attention score, 95th percentile in Altimetrics.

11. COUTO-SILVA, CAINÃ; NUNES, KELLY; VENTURINI, GABRIELA; **CASTRO E SILVA, MARCOS ARAÚJO**; PEREIRA, LYGIA; COMAS, DAVID; PEREIRA, ALEXANDRE; HÜNEMEIER, TÁBITA (CA). Indigenous people from Amazon show genetic signatures of pathogen-driven selection. **Science Advances, 9, eabo0234, 2023**. (author position: 4/8) DOI: https://doi.org/10.1126/sciadv.abo0234 / High attention score, 99th percentile in Altimetrics.

12. **SILVA, MARCOS ARAÚJO CASTRO E**; FERRAZ, TIAGO; HÜNEMEIER, TÁBITA (CA). A genomic perspective on South American human history. **GENETICS AND MOLECULAR BIOLOGY, v. 45, p. e20220078, 2022**. (author position: 1/3) DOI: https://doi.org/10.1590/1678-4685-GMB-2022-0078 / High attention score, 95 percentile in Altimetrics.

*13. **CASTRO E SILVA, MARCOS ARAÚJO**; FERRAZ, TIAGO; COUTO-SILVA, CAINÃ MAX; LEMES, RENAN BARBOSA; NUNES, KELLY; COMAS, DAVID; HÜNEMEIER, TÁBITA (CA). Population Histories and Genomic Diversity of South American Natives. **MOLECULAR BIOLOGY AND EVOLUTION, msab339, 2022**. (author position: 1/7) DOI: https://doi.org/10.1093/molbev/msab339 / High attention score, 96th percentile in Altimetrics.

This study examines the population history of South American Indigenous peoples, focusing on factors shaping their genetic diversity and geographic distribution. Using the largest genome-wide dataset of Indigenous Americans at the time, we analyzed 58 populations across the Amazon, Cerrado, Atlantic coast, Andes, Pacific coast, and Mexico, offering a broad view of the genetic landscape of the Americas. Our findings challenge the expected genetic divide between Andean and Amazonian populations, revealing a longitudinal genetic variation likely formed during the initial settlement of the continent. We also observed a west-to-east increase in inbreeding coefficient, shaped by geographical isolation and serial population bottlenecks. These results highlight the roles of isolation by distance and demographic history in shaping Indigenous genetic diversity. We further reconstructed the severe population collapse during European colonization, evidencing its devastating impact. Additionally, we uncovered a case of linguistic replacement in western Amazonia, emphasizing the complexity of pre-Columbian population interactions.

This research, published in *Molecular Biology and Evolution*, represented the most comprehensive chapter of my PhD thesis. Conducted in collaboration with an international team from multiple institutions, I was primarily responsible for performing the genomic analyses and writing the manuscript, with valuable input from coauthors. This research was supported by funding from the Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP, Brazil) with my personal funding provided initially by the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq; Brazil) and later through a competitive grant from FAPESP. The study is published as an Open Access article, and the datasets reported in this article have been deposited in EGA (EGAD00010002061 and EGAD00010001803).

As of now, the study has garnered 34 citations on Google Scholar, including significant contributions from independent research groups published in high-impact journals such as *MBE* and *Cell Genomics*. Furthermore, it has achieved a High Attention Score, ranking in the 96th percentile among publications of the same age, as reported by Altmetric. The findings were presented at multiple national and international scientific conferences and seminars and shared through a network of research collaborators who adapted their dissemination for local Indigenous communities. The study also attracted significant attention from prominent Brazilian and international media outlets.

*14. **CASTRO E SILVA, MARCOS ARAÚJO†**; FERRAZ, TIAGO†; BORTOLINI, MARIA CÁTIRA; COMAS, DAVID; HÜNEMEIER, TÁBITA (CA). Deep genetic affinity between coastal Pacific and Amazonian natives evidenced by Australasian ancestry. **PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, v. 118, p. e2025739118, 2021**. (author position: 1/4) DOI: https://doi.org/10.1073/pnas.2025739118 / High attention score, 99th percentile in Altimetrics.

Genetic evidence shows that all non-Arctic Native Americans share a common ancestor that entered the Americas via Beringia around 16,000 years ago. However, some Indigenous groups in the Amazon and Central Brazilian Plateau exhibit unexpected genetic similarities with populations from South Asia, Melanesia, and Australia. This unexpected affinity suggests previously unknown contributions to South American Indigenous ancestry.

Our research investigated this Australasian-like signal in South American populations, linked to a hypothesized and unsampled ancestral group, "Ypikuéra" or "Y." Using a genome-wide dataset, we found this signal extends beyond the Amazon to the Central Brazilian Plateau, southern Center-West, and Pacific coast, spanning both sides of the Andes. Our models suggest this ancestry spread along the Pacific coast during early dispersals, offering new insights into South America's genetic history.

This study, published in *PNAS*, was an integral part of my PhD. Project collaborators included my PhD supervisor, Tábita Hunemeier; Tiago Ferraz, another PhD student under her supervision specializing in archaeogenetics and affiliated with the Max Planck Institute for the Science of Human History (Jena, Germany); and Maria Catira Bortolini, a prominent authority on the study of Indigenous Americans in Brazil. Together with Tiago Ferraz, I was responsible for conducting the genomic analyses, while I wrote the paper with input from coauthors. This research received financial support from the FAPESP, while my personal funding came from the CNPq during part of the project and later from a competitive grant awarded by FAPESP. The publication is freely available through Open Access, and the newly generated genotypic data can be accessed via EGA under accession number EGAS00001005022.

As of now, the study has garnered 43 citations on Google Scholar, including significant contributions from independent research groups published in high-impact journals such as *Science* and *Nature*. Furthermore, it has achieved a High Attention Score, ranking in the 99th percentile among publications of the same age, as reported by Altmetric. The findings were presented at several national and international scientific conferences and seminars. Additionally, the results were communicated through a network of research collaborators, who tailored their dissemination to local Indigenous communities. The study also gained attention from important media outlets both Brazilian and international, as well as science communicators.

*15. **CASTRO E SILVA, MARCOS ARAÚJO**; NUNES, KELLY; LEMES, RENAN BARBOSA; HÜNEMEIER, TÁBITA (CA). Genomic insight into the origins and dispersal of the Brazilian coastal natives. **PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, v. 117, p. 2372-2377, 2020**. (author position: 1/12) DOI: https://doi.org/10.1073/pnas.1909075117 / High attention score, 96th percentile in Altimetrics.

Here we revealed the relationships among the Tupi from the Brazilian coast, Amazon, and Central-West Brazil human populations, as well as ancient individuals, retracing their dispersal routes from the Amazon to the Atlantic coast and Southern Brazil. Analyzing a small, admixed Tupiniquim community, we showed their descent from coastal Tupi groups with Amazonian origins. Our findings suggest the spread of Tupi-Guarani languages and culture was driven by population dispersal rather than cultural diffusion. We reveal that coastal Tupi (e.g., Tupinambá) and Guarani diverged and expanded from the Amazon via distinct routes. The Tupi expansion represents the most significant demographic event of the Holocene in eastern South America, shaping genetic diversity in Brazil and Latin America. By elucidating the dynamics of this dispersal, we contributed significantly to the comprehension of the complex Indigenous American genetic heritage of Brazil and its broader implications for the genetic composition of Latin American populations.

This scientific contribution was published in *PNAS* and was part of my PhD, involving an international team of collaborators from many institutions. I was responsible for conducting the genomic analysis and writing the paper, with input from coauthors. The study was funded by the FAPESP, with my own funding provided by the CNPq during one period, and a competitive grant from FAPESP during another period. The publication is available via Open Access, and all newly genotyped data can be accessed through a data access agreement in the European Genome-phenome Archive (EGA) under accession no. EGAS00001004036.

The study has currently received 49 citations according to Google Scholar, including notable studies from independent groups published in high-impact journals such as *PNAS* and *MBE*. Additionally, the publication has earned a High Attention Score, placing it in the 96th percentile compared to other outputs of the same age, according to Altmetric. This publication has also been awarded the American Society of Human Genetics' Trainee Paper Spotlight in 2020. The results were presented at national and international scientific conferences and seminars. Additionally, we shared a comprehensive summary of the findings with the Tupiniquim and Guarani-Mbya communities, the main focus of this study, in Aracruz (Espírito Santo state, Brazil), in collaboration with local researchers from the Universidade Federal do Espírito Santo. The publication has garnered attention from both Brazilian and international media.

16. LOPES, KARINA L.; RODRIGUES, RICARDO A. O.; **SILVA, MARCOS C.**; BRAGA, WILIANE G. S.; SILVA-FILHO, MARCIO C (CA). The Zinc-Finger Thylakoid-Membrane Protein FIP Is Involved With Abiotic Stress Response in Arabidopsis thaliana. **Frontiers in Plant Science, v. 9, p. 1/504-13, 2018**. (author position: 3/5) DOI: https://doi.org/10.3389/fpls.2018.00504 / Average attention score in Altimetrics.

17. ZORZATTO, CRISTIANE; MACHADO, JOÃO PAULO B.; LOPES, KÊNIA V. G.; … **SILVA, MARCOS A. C.**; … FONTES, ELIZABETH P. B (CA). NIK1-mediated translation suppression functions as a plant antiviral immunity mechanism. **Nature, p. 1-19, 2015**. (author position: 13/17) DOI: https://doi.org/10.1038/nature14171 / High attention score, 94th percentile in Altmetrics.

Scientific communication articles

1. **CASTRO-SILVA, MARCOS A.**; HÜNEMEIER, TÁBITA. Reading South American history in the native Brazilian genomes. The Science Breaker., v.07, p.1-2, 2021. (author position: 1/2) DOI: https://doi.org/10.25250/thescbr.brk472 (the link is broken, please see the one below) https://web.archive.org/web/20250203105040/https://thesciencebreaker.org/breaks/evolution-behaviour/reading-south-american-history-in-the-native-brazilian-genomes

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Books and book chapters

1. HÜNEMEIER, T., NUNES, K., **CASTRO E SILVA, M. A.** (2025). How did Evolutionary Processes Influence the Genetic Structure of Humans in the Neotropics?. In: BOHRER MONTEIRO SIQUEIRA, M.V., KONZEN, E.R., GALETTI JUNIOR, P.M. (eds) Population Genetics in the Neotropics. Springer, Cham. p. 377-417, chapter 18, 2025. (author position: 3/3) DOI: https://doi.org/10.1007/978-3-031-83685-5_18

Presentations in events

1. **CASTRO E SILVA, MARCOS A.** et al. Ancient origins and evolutionary legacies of the Eurasian ancestries in admixed American populations. **XXIII Colóquio Internacional Juan Comas / XVII Congreso Internacional de la Asociación Latinoamericana de Antropología Biológica (ALAB 2025).** 2025. Cholula, Mexico. (Symposium organizer and oral presentation)

2. **CASTRO E SILVA, MARCOS A.** et al. The Dynamic Genetic Landscape of Indigenous South Americans. **Society for Molecular Biology and Evolution Meeting (SMBE 2025)**. 2025. Beijing, China. (Oral presentation)

3. **CASTRO E SILVA, MARCOS A.** et al. Genomic Analysis Reveals Historical Assortative Mating and Sex-Biased Ancestry in Brazil. **EMBO | EMBL Symposium: Reconstructing the human past: using ancient and modern genomics**. 2024. Heidelberg, Germany. (Oral and poster presentation)

4. **CASTRO E SILVA, MARCOS A.** DNA do Brasil project: genomic insights into history, demography and evolution. **XXIII Jornada de Biologia Evolutiva**. 2024. Barcelona, Spain. (Oral presentation)

5. **CASTRO E SILVA, MARCOS A.** Uncovering the genetic history of American indigenous peoples. **Cycle of seminars BEEES (Behaviour, Ecology, Environment and Evolution Seminar) at the Department of Evolutionary Biology and Environmental Studies at the University of Zurich**. 2023. Zurich, Switzerland. (Invited speaker)

6. **CASTRO E SILVA, MARCOS A.** Untangling the threads of South America's Indigenous Diversity: Genomic Insights from Ancient Settlements to European Contact. **Congresso Brasileiro de Genética, 2023**. Ouro Preto, Brazil. (Presentation and poster for the Young Geneticist award)

7. **CASTRO E SILVA, MARCOS A. IBE/ICP SCIENTIFIC RETREAT 2022.** 2022. Barcelona, Spain. (Oral presentation)

8. **CASTRO E SILVA, MARCOS A.** Genomic perspective on the origin, history and diversity of the indigenous peoples of South America: from initial settlement to European colonization. **Seminars at the Department of Genetics and Evolutionary Biology at the USP Biosciences Institute**. 2022. São Paulo, Brazil. (Invited speaker)

9. **CASTRO E SILVA, MARCOS A.** The genomic landscape of Native American peoples. 92nd AABA Annual Meeting, 2023, Reno, EUA. **American Association of Biological Anthropologists**. 2023. Reno, USA. (Invited speaker)

10. **M. Castro e Silva**; C. M. Couto-Silva; R. B. Lemes; K. Nunes; D. Comas; T. Hünemeier. The genetic landscape of South Native American populations. **American Society of Human Genetics 2021 Annual Meeting**. 2021. (Poster presentation)

11. **M. Castro e Silva**; T. F. da Silva; C. M. Couto-Silva; T. Hünemeier. Genetic structure of the South American lowlanders. **American Society of Human Genetics 2020 Annual Meeting**. 2020. (Poster presentation)

12. **CASTRO E SILVA, MARCOS A.**; NUNES, KELLY; LEMES, RENAN BARBOSA; MAS-SANDOVAL, ÀLEX; GUERRA AMORIM, CARLOS EDUARDO; KRIEGER, JOSE EDUARDO; SALZANO, FRANCISCO MAURO; BORTOLINI, MARIA CÁTIRA; PEREIRA, ALEXANDRE DA COSTA; COMAS, DAVID; HÜNEMEIER, TÁBITA. Recovering a Native American lineage extinct during the Conquest Period from Admixed Genomes. **Society for Molecular Biology and Evolution Meeting (SMBE 2019)**. 2019. Manchester, England. (Poster presentation)

13. **CASTRO E SILVA, MARCOS A.** Reconstructing the History of the Native American Populations of the Brazilian Coast. **First Native American Studies Workshop (UFRGS)**. 2019. Porto Alegre, Brazil. (Invited speaker)

14. **CASTRO E SILVA, MARCOS A.**; NUNES, KELLY; HÜNEMEIER, TÁBITA. Genomic origins and admixture profile of Afro-Brazilians from Rio de Janeiro. **Brazilian International Congress of Genetics**. 2017. Águas de Lindóia, Brazil. (Poster presentation)

15. **CASTRO E SILVA, MARCOS ARAÚJO**; SILVA-FILHO, MARCIO C. Convergent evolution of Arabidopsis thaliana FtsH5 and its negative regulator FIP (FtsH5 interacting protein). **ISCB-Latin America x-Meeting on Bioinformatics with BSB and SoiBio**. 2014. Belo Horizonte, Brazil. (Poster presentation)

Academic or research stays in foreign centers

EUTOPIA-SIF fellowship external secondment at the University of Zurich (Switzerland), with the research group of Chiara Barbieri and Kentaro Shimizu, from November 27 to December 8 2023.

Short research stay at the California State University (USA), with the research group of Carlos Eduardo Guerra Amorim, from April 10 to April 18 2023.

Short research stay at University College London (UK), with the research group of Garrett Hellenthal, from July 29 to August 9 2019.

Postdoctoral fellowships

01/01/2024–present	**Postdoctoral Researcher Juan de la Cierva-Formación (JCI-F)** Funding: Agencia Estatal de Investigación - AEI (JDC2022-049175-I) Institution: Universitat Pompeu Fabra (Spain)
07/09/2022–31/12/2023	**Postdoctoral Researcher EUTOPIA-SIF Marie Sklodowska-Curie COFUND** Funding: European Union Horizon 2020 programme under the Marie Skłodowska-Curie grant agreement No 945380 Institution: Universitat Pompeu Fabra (Spain)

01/06/2022–30/08/2022 **Postdoctoral Researcher in Innovation Research at FFM, USP**
Funding: Fundação Faculdade de Medicina - FFM (Genoma de referência Brasileiro Ministério da Saúde GRB/4)
Institution: Universidade de São Paulo (Brazil)

Supervisions

2023 - 2025 Student: Giacomo Francesco Ena
Degree: PhD (defended with cum laude honors)
Project: **Fine-scale genetic structure of Roma in Iberia**
Universitat Pompeu Fabra

Competitive grants

01/01/2024–present **Postdoctoral Fellowship - Juan de la Cierva-Formación (JCI-F)**
Project: Indigenous American Genome Project
Funding: Agencia Estatal de Investigación - AEI (Espanha) (JDC2022-049175-I)
Institution: Universitat Pompeu Fabra, Spain

07/09/2022–31/12/2023 **Postdoctoral Fellowship - EUTOPIA-SIF Marie Sklodowska-Curie COFUND**
Project: The impact of demography, admixture, and evolution on the health of Brazilian populations
Funding: European Union Horizon 2020 programme under the Marie Skłodowska-Curie grant agreement No 945380
Institution: Universitat Pompeu Fabra, Spain

01/06/2022–30/08/2022 **Innovation Research Fellowship - FFM**
Project: Establishment of a Reference Genome of the Brazilian Population
Funding: Fundação Faculdade de Medicina - FFM (Convênio 888379/2019 - Projeto Genoma Biociências)
Institution: Universidade de São Paulo, Brazil

01/01/2019–30/11/2021 **PhD scholarship - FAPESP**
Project: Diversity and Evolution of Brazilian Populations
Funding: Fundação de Amparo à Pesquisa do Estado de São Paulo - FAPESP (FAPESP/2018/01371-6)
Institution: Universidade de São Paulo, Brazil

01/02/2017–01/01/2019 **PhD scholarship - CNPq**
Project: Genetic Structure and Ancestry of Brazilian Admixed Populations
Funding: Conselho Nacional de Desenvolvimento Científico e Tecnológico - CNPq (140155/2017-1)
Institution: Universidade de São Paulo, Brazil

01/02/2013–18/02/2015 **MSc scholarship - CNPq**
Project: Convergent evolution of Arabidopsis thaliana FtsH5 protease and its putative negative regulator FIP (FtsH5 interacting protein)
Funding: Conselho Nacional de Desenvolvimento Científico e Tecnológico - CNPq (130634/2013-1)
Institution: Escola Superior de Agricultura “Luiz de Queiroz” - Universidade de São Paulo, Brazil

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Non-competitive grants

30/11/2021–31/05/2022 **Technical Training Fellowship (TT5) - FAPESP**

Project: Detection of Natural Selection Patterns in Native American Population by Machine Learning
Funding: Fundação de Amparo à Pesquisa do Estado de São Paulo - FAPESP (FAPESP/2021/12238-8)
Institution: Universidade de São Paulo, Brazil

01/08/2011–01/07/2012 **Scientific Initiation Scholarship - CNPq**
Project: Transcriptional expression analysis of Arabidopsis thaliana immune system genes related to response against geminivirus
Funding: Conselho Nacional de Desenvolvimento Científico e Tecnológico - CNPq (160335/2012-4)
Institution: Universidade Federal de Viçosa, Brazil

Participation in thesis defense committees

1. Full Member of the monitoring committee of the student Gabriel Monteiro Lauria, at Master's level, held on June 17, 2025, on the Scientific Work entitled "**Evolutionary History of Ancient Domestic Dogs of Atlantic Patagonia**".

2. Full Member of the monitoring committee of the student Gabriel Monteiro Lauria, at Master's level, held on May 29, 2024, on the Scientific Work entitled "**Evolutionary History of Ancient Domestic Dogs of Atlantic Patagonia**".

3. Full Member of the Dissertation Defense of the student Ana Maria Barbosa Pessotti, at Master's level, held on May 10, 2024, on the Scientific Work entitled "**Analysis and comparison of the frequency of the main Alpha-1-AntiTrypsin variants using PCR and Genome-Wide Array**".

4. Full Member of the Qualification Exam of student Ana Maria Barbosa Pessotti, at Master's level, held on December 19, 2022, on the Scientific Work entitled "**Genotyping of Alpha-1-AntiTrypsin by PCR and Microarrays in a Population Sample from Ribeirão Black – SP**".

Teaching experience

1. Teaching Assistant – Bioinformatics (20428). Served as a teaching assistant for the Bioinformatics course in the Bachelor's program in Human Biology (3362) at the **Faculty of Health and Life Sciences, Universitat Pompeu Fabra**, during the first semester of the 2025/2026 academic year. Responsibilities included 12 hours of teaching support during practical sessions, under the supervision of Prof. Mireia Vallès Colomer.

2. Graduate Teaching – Evolutionary Biology (BIO0103). Completed the Teaching Improvement Program (Programa de Aperfeiçoamento de Ensino - PAE) during the Ph.D. in Genetics. This included a Pedagogical Preparation phase in the second semester of 2017, followed by a 120-hour supervised teaching internship in the undergraduate course BIO0103 – Evolutionary Biology, offered by the **Department of Genetics and Evolutionary Biology of the Universidade de São Paulo**. Teaching activities were conducted under the supervision of Prof. Sergio Russo Matioli.

Workshops and classes delivered

1. Class about population genomics of modern humans in the Masters of Genomes & Systems program at the Universitat Pompeu Fabra, Barcelona, Spain. (2025)

2. "Brief introduction to population structure and history inference from genetic data" in the IBE (Institut de Biologia Evolutiva) workshop at the **Universitat Pompeu Fabra, Barcelona, Spain**. (2025)

3. Class about population genomics of modern humans in the "Máster Universitario en Arqueología prehistórica" (módulo Osteoarqueología humana: análisis antropológico de grupos sociales), **Master in Prehistoric Archeology/UAB, Barcelona, Spain.** (2025)

4. Workshop "Avances en Genómica y Metagenómica: De la Microbiota Oral a las Poblaciones

Nativas Americanas” at the **Universitat Pompeu Fabra, Barcelona, Spain**. (2024)

5. “First Native American Studies” Workshop at the **Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil**. (2019)

Peer review

1. Journal: Genetics and Molecular Biology, ISSN: 1678-4685, Role: reviewer
2. Journal: BMC Biology, ISSN: 1741-7007, Role: reviewer (2 times)

Membership of scientific societies

Sociedade Brasileira de Genética (past)
Asociación Latinoamericana de Antropología Biológica (past)
Society for Molecular Biology and Evolution (current)
American Society of Human Genetics (past)
American Association of Biological Anthropology (past)

Scientific communication articles in blogs

1. **CASTRO E SILVA, MARCOS ARAÚJO**; HUNEMEIER, T. Lendo a história do Brasil nos genomas brasileiros, 2020. Blog Darwinianas.

Research impact on the media (examples)

International newspapers, magazines and blogs

- Unraveling the genomic roots of Indigenous peoples, Mapping the genome of the Brazilian population, with implications for healthcare, and Genetic adaptations help Amazonian populations resist Chagas infection - EurekAlert! AAAS.
- Ancient South Americans arrived in three waves—and had some surprising ancestry, Massive DNA sequencing effort reveals how colonization shaped Brazil’s genetic diversity, and Earliest South American migrants had Indigenous Australian, Melanesian ancestry - Science News.
- DNA study of nearly 200 Indigenous genomes reveals unknown Asian 'ghost' population contributed to American ancestry and 1st Americans had Indigenous Australian genes - Live Science.
- The Genetic Signal of Ancient Australians in South America Goes Deeper Than We Knew - Science Alert.
- Exploring Spanish Roma’s Genetic Diversity and Structure - Science Magazine.
- First humans who crossed the Bering Strait some 15,000 years ago had indigenous Australian DNA that is now found in the bloodline of South America tribes, study finds - Daily Mail
- The Peopling of South America - The Scientist.
- A New Big Database of DNA From Indigenous Americans Shakes Up Scientists’ Theories About Human Settlement of South America and Why Did Ancient Indigenous Groups in Brazil Hunt Sharks? - Smithsonian Magazine.
- New genetic database sheds light on Brazil’s ancestry and disease risks - The Medical News.
- De Asia a América: la genética desvela nuevos detalles de la migración más larga de la humanidad - El País.
- Colonización redujo la diversidad indígena a una fracción - Deutsche Welle
- La genética revela la extraordinaria historia de la población de Brasil and Los gitanos de la Península tienen diferencias genéticas respecto a los del resto de Europa - La Vanguardia.
- Genetic distinctions between Iberian Romas and other European Roma people found - Catalan News.

National newspapers, magazines and blogs (Brazil)

- Indígenas sul-americanos são diversos e descendem de terceira onda migratória, O brasileiro é ainda mais miscigenado do que você pensa, Defesa natural contra Chagas, Filhos de Ypykuéra and Os últimos Tupiniquim, - Pesquisa FAPESP.
- Indígenas da Amazônia possuem gene que protege contra a doença de Chagas, diz novo estudo - National Geographic Brasil.

- As descobertas sobre origem e história dos povos indígenas da América do Sul reveladas pela genética and O recém-descoberto gene que protege povos amazônicos da doença de Chagas e pode inspirar tratamentos - BBC Brasil.
- Nativos da América do Sul têm influência genética de povos da Oceania - Galileu.
- DNA de indígenas mostra elo com Oceania e três ondas de migração, Indígenas da América do Sul descendem, em parte, de povos do Pacífico, reforça novo estudo, and A partir do DNA, cientistas mapeiam 2.000 anos de rotas migratórias dos índios no Brasil - Folha de São Paulo.
- Estudo revela evolução e diversidade genética únicas dos indígenas americanos and DNA indica que tupiniquins são descendentes do grupo indígena que Cabral encontrou - Globo.
- Índios de Aracruz são descendentes diretos dos primeiros Tupiniquins - CBN Vitória Rádio.
- Evidência genética australo-melanésia em grupos nativos da américa do sul - Blog Arqueologia e Pré-História
- Genética conta história do colapso populacional de indígenas no Brasil and Genes de povos da Ásia e da Oceania estão em índios da América do Sul - Revista Planeta

YouTube creators

- Why do Amazonian people have some Australasian DNA? - Stefan Milo YouTube channel.
- The Tupinambá: From the Amazon to the Coast - Ancient Americas YouTube channel.

Podcasts

- The Long Walk South: Tracing the Longest Migration in Human History - Anthropology.net
- Lo que el ADN indígena revela sobre América - Principio de Incertidumbre – Canal Extremadura

Wikipedia pages (in English)

- Genetic history of the Indigenous peoples of the Americas
- Ancient Beringian

Wikipedia pages (in Portuguese)

- Estudos genéticos em brasileiros
- História genética dos povos indígenas da América
- Primeiras migrações humanas
- História do estado de São Paulo
- Rio de Janeiro (estado)
- Zona da Mata