

Genética Médica Populacional

CENISO –Censo Nacional de Isolados – Brasil

CELAISO – Censo Latino Americano de Isolados



INa**G**e**M**P
INa**G**e**M**P

Genetic Drift

On Being a Medical Geneticist

Eduardo E. Castilla*

ECLAMC, Genetica, Fiocruz, Rio de Janeiro RJ, Brazil

Unlike other medical specialties, medical genetics deals with families, rather than with individual persons, as patients.

venous return (TAPVR) (# 106700 OMIM), and although some familial cases with this form, as well as with the perhaps unrelated partial anomalous pulmonary venous return, or

stating: "In 2 brothers and a male paternal first cousin, Paz and Castilla [1971] observed total anomalous pulmonary venous return."

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**Thus,
as a person is the object of Medicine, and
a family is the object of Medical Genetics,
a population must be the object of Population Medical
Genetics.**

banding. Therefore, the normal karyotypes of the brother and sister who had fathered and mothered the three affected infants, and, as such, were presumable carriers, did not exclude the existence of a small, undetectable chromosome translocation segregating in this family. A second possible genetic mechanism was then hypothesized, namely, two loci

Thus, the updated knowledge indicates a not unexpected genetic heterogeneity for TAPVR.

These reports prompted me to recontact our patient family 30 years later, to offer them the eventual benefit of new technologies. At that time I was already living in another country, but the colleague in charge of the Department of



- Angra dos Reis 1
- Assis Brasil 2
- Aracati 3
- Belém 4
- Campinas 5
- Cândido Godói 6
- Fortaleza 7
- Guaporé 8
- Tabuleiro do Norte 9
- Juazeiro do Norte 10
- Monte Negro 11
- Monte Santo 12
- Porto Alegre 13
- Porto Velho 14
- Pouso Alegre 15
- Rio de Janeiro 16
- Salvador 17
- São Gabriel 18
- São Paulo 19
- Triunfo 20



12

Monte Santo – BA

This group develops a comprehensive population medical genetics program in a remote area of Bahia State, which center is the town of Monte Santo [600 km far from Salvador]. On this area several genetic diseases [Mucopolysaccharidosis VI, phenylketonuria and others] seem to be more frequent than in other places, possibly due to the combination of founder effect and endogamy. Prevalent mutations were identified and a customized newborn screening scheme associated to early management program is in progress, among other actions.



11

Monte Negro – RO

This group is devoted to multidisciplinary studies on infectious diseases that are endemic in the Amazon region [Malaria, Leishmaniasis, Chagas disease, Hepatitis, filariasis]. Together with classical epidemiological surveys, research on genetic mechanisms associated with these diseases are being pursued, employing modern methods of molecular genetics and powerful statistical tools of genetic epidemiology.

6

Cândido Godoy – RS

Cândido Godói (CG) is a small municipality in South Brazil with approximately 6,000 inhabitants, and it is known as the "Twins' Town" due to its high rate of twin births. Recently this village has got attention from the international press after a journalist claimed that this high frequency of twinning could be connected to experiments performed by the german nazi doctor Joseph Mengele. After a call from the mayor of CG, INAGEMP started there a project to investigate the possible explanations for this twin phenomenon in this small village.

Health facts: positive

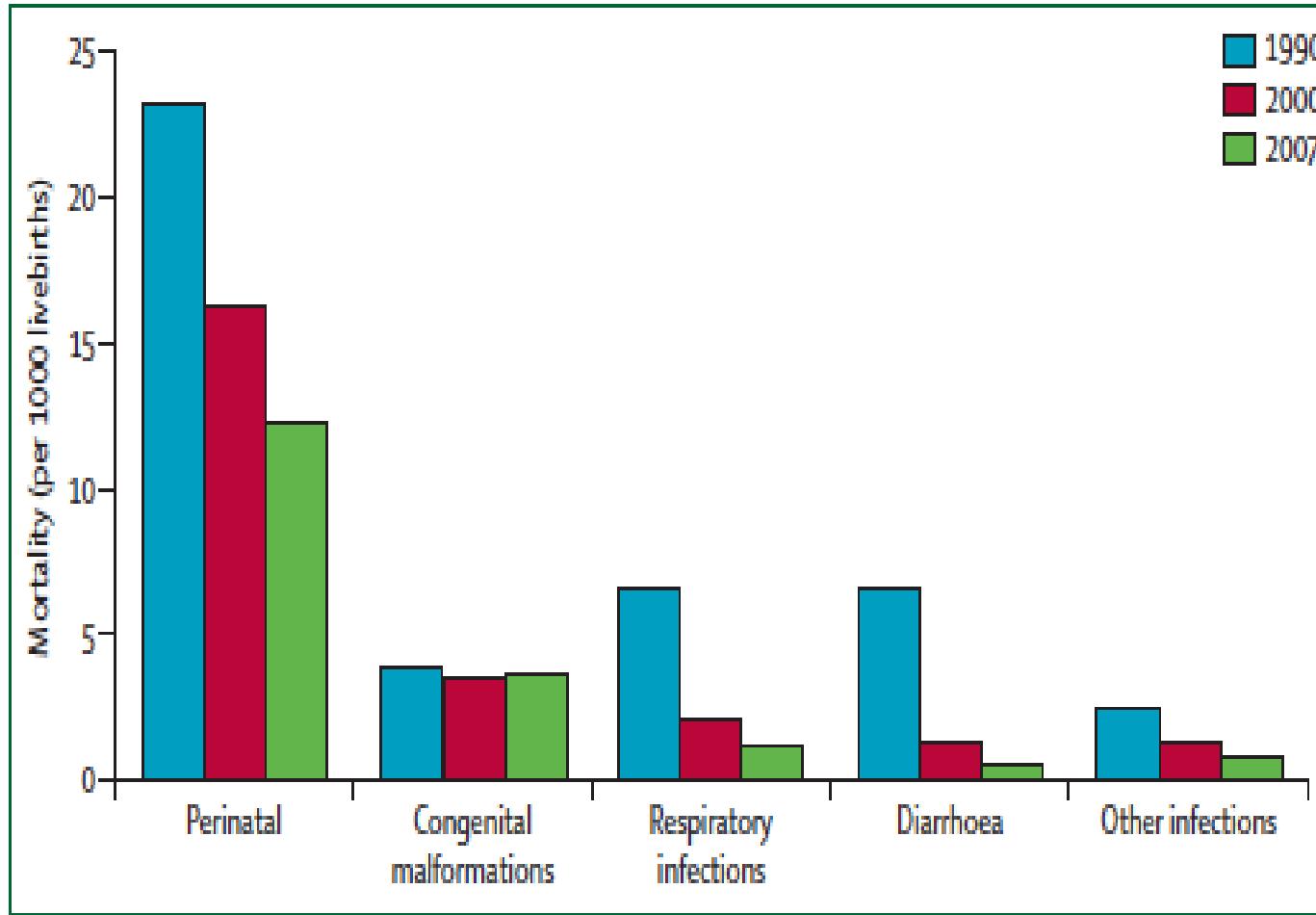


Figure 3: Infant mortality by cause and year

Victora et al.,

Lancet 2011; 377: 1863-76

SAÚDE BRASIL 2018

Uma análise da situação de saúde e das doenças e agravos crônicos: desafios e perspectivas



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Secretaria de Vigilância em Saúde
Departamento de Vigilância de Doenças e
Agravos não Transmissíveis e Promoção da Saúde

PARTE I – ANÁLISE DA SITUAÇÃO DE SAÚDE	15
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2 Evolução e principais causas da mortalidade na infância e componentes nas regiões brasileiras entre 2010 e 2016	33
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Tabela 6 – Percentual de mortalidade por Causa GBD e componente – Brasil, 2000 e 2016

Ordem	Causa GBD	Percentual							
		0 a 6 dias		7 a 27 dias		28 a 364 dias		Menor de 1 ano	
		2000	2016	2000	2016	2000	2016	2000	2016
1	Complicações neonatais no parto pré-termo	48,3%	31,2%	26,2%	19,4%	4,4%	8,6%	35,2%	25,0%
2	Anomalias congênitas	10,7%	18,9%	17,9%	24,8%	22,1%	39,9%	14,3%	23,7%
3	Encefalopatia neonatal devido à asfixia e ao trauma no nascimento	19,5%	19,8%	8,4%	10,6%	2,5%	4,5%	14,0%	15,3%
4	Outros transtornos do período neonatal	10,0%	17,6%	9,8%	16,1%	2,1%	4,6%	8,2%	15,0%
5	Sepse neonatal e outras infecções neonatais	9,3%	9,4%	30,7%	23,6%	4,1%	6,2%	11,4%	11,6%
6	Corpo estranho	0,1%	0,1%	0,5%	0,8%	4,9%	7,2%	1,2%	1,5%
7	Doenças diarreicas	0,1%	0,0%	1,8%	0,4%	24,1%	5,4%	5,7%	1,0%
8	Doenças sexualmente transmissíveis, exceto HIV	0,2%	0,7%	0,2%	0,6%	0,1%	0,5%	0,2%	0,7%
9	Doença hemolítica e outra icterícia neonatal	0,7%	0,8%	1,2%	0,7%	0,1%	0,2%	0,7%	0,7%
10	Infeções de vias aéreas inferiores	0,0%	0,0%	0,1%	0,1%	2,6%	3,2%	0,6%	0,6%

continua

- **Population Genetics and Medical Genetics**
 - Demographic factors: migration, founder effect, isolation, inbreeding, consanguinity
 - Major predisposition gene

Geographic isolates



Cultural or Religious Isolates

- Jewish Populations
- Amish
- Romanis (ciganos)
- Menonitas (Brasil)



Signatures of founder effects, admixture, and selection in the Ashkenazi Jewish population

Steven M. Bray^a, Jennifer G. Mulle^a, Anne F. Dodd^a, Ann E. Pulver^b, Stephen Wooding^c, and Stephen T. Warren^a

16222–16227 | PNAS | September 14, 2010 | vol. 107 | no. 37



The Ashkenazi Jewish (AJ) population has long been viewed as a genetic isolate, yet it is still unclear how population bottlenecks, admixture, or positive selection contribute to its genetic structure. Here we analyzed a large AJ cohort and found higher linkage disequilibrium (LD) and identity-by-descent relative to Europeans, as expected for an isolate. However, paradoxically we also found higher genetic diversity, a sign of an older or more admixed population but not of a long-term isolate. Recent reports have reaffirmed that the AJ population has a common Middle Eastern origin with other Jewish Diaspora populations, but also suggest that the AJ population, compared with other Jews, has had the most European admixture. Our analysis indeed revealed higher European admixture than predicted from previous Y-chromosome analyses. Moreover, we also show that admixture directly correlates with high LD, suggesting that admixture has increased both genetic diversity and LD in the AJ population. Additionally, we applied extended haplotype tests to determine whether positive selection can account for the level of AJ-prevalent diseases. We identified genomic regions under selection that account for lactose and alcohol tolerance, and although we found evidence for positive selection at some AJ-prevalent disease loci, the higher incidence of the majority of these diseases is likely the result of genetic drift following a bottleneck. Thus, the AJ population shows evidence of past founding events; however, admixture and selection have also strongly influenced its current genetic makeup.

Panorama

GENÉTICA DE POBLACIONES

La historia de los gitanos europeos

El estudio de su genoma indica que migraron a Europa desde la India hace unos 1500 años



LOS GITANOS migraron del subcontinente indio a Europa hace unos 1500 años (rojo). Tras una rápida travesía por Oriente Próximo, en la que se produjo un escaso intercambio genético con las poblaciones autóctonas que encontraban en el camino, se asentaron en los Balcanes (verde). Empezó entonces, hace unos 900 años, la fragmentación que dio lugar a la diversidad de grupos actual.

—Isabel Mendizabal y David Comas
Instituto de Biología Evolutiva
CSIC-Universidad Pompeu Fabra

Americas – colonial period



Isolados Genéticos e Consanguinidade no Brasil.



[Ann Hum Genet. 1977 Jul;41\(1\):99-102.](#)

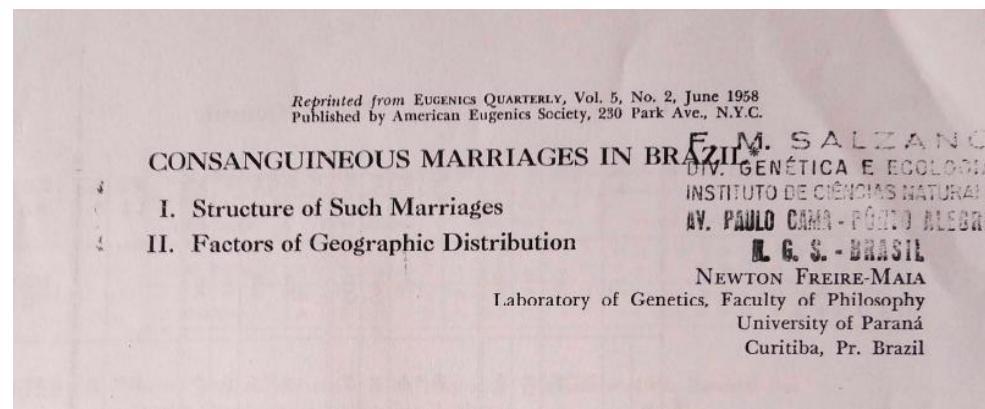
Inbreeding effect on precocious mortality in Japanese communities of Brazil.

[Freire-Maia N, Takehara N.](#)

Abstract

Data on precocious mortality (from abortions up to the age of 20) are presented for three Japanese communities in Brazil. The inbreeding load (B) approximately 1-5) is estimated on the basis of these data. B/A lies between 7 and 30. Three general working hypotheses are presented.

PMID: 921222 [PubMed - indexed for MEDLINE]



[Am J Med Genet. 1990 Jan;35\(1\):115-7.](#)

Genetic effects in Brazilian populations due to consanguineous marriages.

[Freire-Maia N.](#)

Author information

Abstract

Estimates of "relative risks" and "attributable risks" are presented for two Brazilian regions with the lowest ($F = 0.00030$) and the highest ($F = 0.00395$) inbreeding levels of the country, and for the whole country ($F = 0.00088$). The abolition of all consanguineous marriages (from second cousins up to and including uncle-niece/aunt-nephew marriages) in Brazil would eliminate only about 0.22, 3.05, and 0.65% of the "total damage," respectively. "Total damage" is defined as including abortions, miscarriages, stillbirths, infant-juvenile mortality (up to the age of 20 years), and anomalies in the survivors. The reduction of prenatal damage would be 0.11, 1.46, and 0.31%, and that of postnatal damage would be 0.49, 6.65, and 1.36%, respectively.

PMID: 2301460 [PubMed - indexed for MEDLINE]

[Ann Hum Genet. 1964 Jun;27:329-39.](#)

THE GENETICAL LOAD IN THE BAURU JAPANESE ISOLATE IN BRAZIL.

[FREIRE-MAIA N, GUARACIABA MA, QUELCE-SALGADO A.](#)

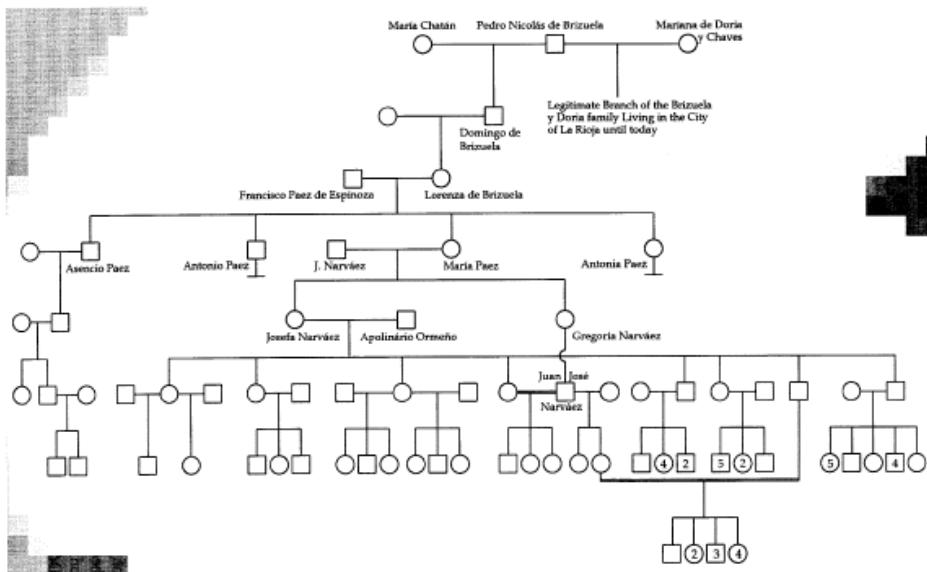
PMID: 14175198 [PubMed - OLDMEDLINE]



Consanguinity in South America: Demographic Aspects

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**Human
Heredity****Original Paper**

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Revision rece
Accepted: De

Correlation between Molecular and Conventional Genealogies in Aicuña: A Rural Population from Northwestern Argentina

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Key Words

Mitochondrial genealogy · Y chromosome genealogy · Aicuña genealogy

Abstract

Aicuña is a village in the northwest of Argentina, located about 300 km south of La Rioja city, in the province of La Rioja. The population of Aicuña derives from a founder couple established in the uninhabited Aicuña valley in the early years of the 17th century. Due to land ownership litigation, the descendants maintained a well-documented genealogy that extends for 12 generations, comprising more than 8,000 individuals. From the historical pedigree of Aicuña, we selected 14 males with direct molecular genealogies, with mtDNA haplotypes A or B, and Y chromosome haplotypes 1, 3, or 4. We performed Y chromosome and mtDNA analysis on 11 males and found that all 11 males had the same Y haplotype (Y3). All 11 males also had the same mtDNA haplotype (haplotype B). The Y3 haplotype was shared by 6 males and the mtDNA B haplotype by 3 males. Three males selected as Ormeño patrilineal ancestors showed a different Y haplotype (Y3), probably due to erroneous paternity registration during the genealogy compilation. The remaining case (haplotype Y4), a male belonging to the Ormeño lineage, was probably an erroneously registered paternity. Two males showed an association of mtDNA marker B and Y chromosome haplotype 4. The Y4 haplotype could be traced back for many generations. The haplotype B of one remaining male did not correspond with the historical pedigree, due to an error in the genealogy registration. This male showed an 85% agreement between conventional and molecular genealogies, with mtDNA haplotype A and Y chromosome haplotype 1.

which were shared by 6 and 3 donors, respectively. Three males selected as Ormeño patrilineal ancestors showed a different Y haplotype (Y3), probably due to erroneous paternity registration during the genealogy compilation. The remaining case (haplotype Y4), a male belonging to the Ormeño lineage, was probably an erroneously registered paternity. Two males showed an association of mtDNA marker B and Y chromosome haplotype 4. The Y4 haplotype could be traced back for many generations. The haplotype B of one remaining male did not correspond with the historical pedigree, due to an error in the genealogy registration. This male showed an 85% agreement between conventional and molecular genealogies, with mtDNA haplotype A and Y chromosome haplotype 1.



American Journal of Medical Genetics 9:31–41 (1981)



Acheiropodia



American Journal of Medical Genetics 2:321–330 (1978)

LMBR1

Am. J. Hum. Genet. 68:38–45, 2001

Genetics of Acheiropodia (the Handless and Footless Families of Brazil). VII. Population Dynamics

ADEMAR FREIRE-MAIA,¹ WEN-HSIUNG LI,² AND TAKEO MARUYAMA³

Under the title “Hereditary Absence of Hands and Feet,” *Eugenical News* [1] published in 1929 a note and picture about a “remarkable family” from Brazil. This was the first of a series of notes published on “the handless and footless family of Brazil.” For a long time, this family has been cited in a number of papers and textbooks, sometimes incorrectly.



Genetics and Molecular Biology, 37, 1 (suppl), 186-193 (2014)
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www.sbg.org.br

Research Article

From rumors to genetic isolates

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ORIGINAL ARTICLE

Clusters of genetic diseases in Brazil

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Genealogical data in population medical genetics: Field guidelines

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Rio de Janeiro, RJ, Brazil.*

Abstract

This is a guide for fieldwork in Population Medical Genetics research projects. Data collection, handling, and analysis from large pedigrees require the use of specific tools and methods not widely familiar to human geneticists, unfortunately leading to ineffective graphic pedigrees. Initially, the objective of the pedigree must be decided, and the available information sources need to be identified and validated. Data collection and recording by the tabulated method is advocated, and the involved techniques are presented. Genealogical and personal information are the two main components of pedigree data. While the latter is unique to each investigation project, the former is solely represented by gametic links between persons. The triad of a given pedigree member and its two parents constitutes the building unit of a genealogy. Likewise, three ID numbers representing those three elements of the triad is the record field required for any pedigree analysis. Pedigree construction, as well as pedigree and population data analysis, varies according to the pre-established objectives, the existing information, and the available resources.

Keywords: medical genetics, population medical genetics, geographic clusters, isolates, rare diseases.

- ‘*Rumor*’ is the systematic and scientific evaluation of any account of unusual occurrence of a given congenital anomaly or risk factor exposure.
- A lay person’s anecdotal description of many cases of a given malformation in a given village is a rumor; a newspaper reporting dioxin contamination of the soil in a given area is a rumor.



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PERGUNTA:

VOCÊ SABE DE ALGUMA
POPULAÇÃO COM
PROBLEMAS GENÉTICOS ?

CENISO Censo Nacional de Isolados
INAGEMP Instituto Nacional de Genética Médica Populacional



<https://www.surveymonkey.com/r/Rumor-LatinoAmericano>

Usted sabe de alguna población con problemas genéticos?

El INAGEMP, Instituto Nacional de Ciencia y Tecnología, el CNPq, es un grupo de investigación dedicado a la Genética Médica de Poblaciones (www.inagemp.bio.br). Desde 2009 desarrolla un censo nacional de poblaciones brasileñas con alta frecuencia de enfermedades o características mono u oligogénicas o expuestas a factores de riesgo genético (ej.:endogamia), ambiental (ej.: talidomida), o factores desconocidos, para el ocurrencia de cualquier trastorno del desarrollo físico o mental.

Este censo está especializado en poblaciones aisladas y grupos de enfermedades llamadas “genéticas” y constituye el primer paso para un centro especializado en investigación y normativas de atención médica de este tipos de patologías, ofreciendo servicios de soporte técnico y metodológico tanto a genetistas como a las comunidades afectadas.

Ahora se busca realizar un censo similar para las poblaciones aisladas de América Latina. En esta etapa inicial del censo estamos interesados en cualquier “rumor” o información exacta sobre poblaciones que usted considere pertinente para ser incluidas.

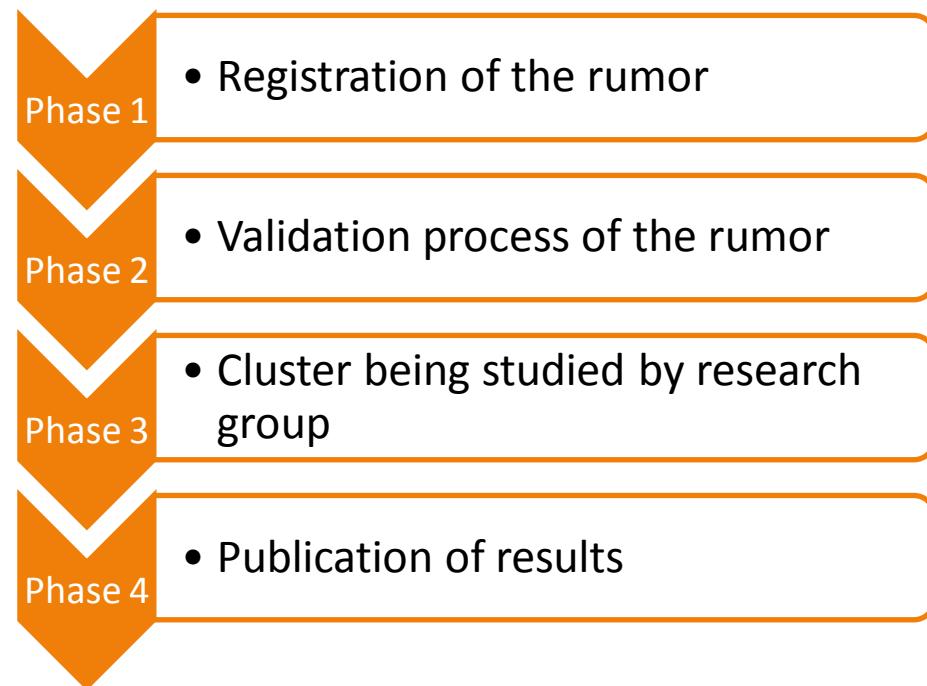
En caso de que se conozca más de una población afectada, favor diligenciar el formulario para cada una de ellas.

Agradecemos su interés y participación

Equipo Rumor-Latinoamericano



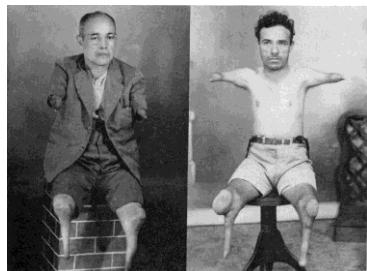
Keywords:
founder effect OR consanguineous marriages OR isolated population genetic diseases OR consanguinity marriage AND Brazil.



Results



Gaucher Disease, Tabuleiro do Norte – CE
DOI: [10.1007/s9004_2011_19](https://doi.org/10.1007/s9004_2011_19)



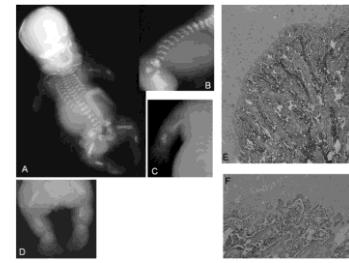
Acheiropodia, Minas Gerais
PMCID: [PMC1762812](https://pubmed.ncbi.nlm.nih.gov/1762812/)



Fraser Syndrome, Vinhedo - SP
DOI: [10.1002/ajmg.a.31426](https://doi.org/10.1002/ajmg.a.31426)



Fig 1. Rumors and clusters identified by CENISO.



Short Rib Polidactily, Gameleira – PE
DOI: [10.1136/jmg.2009.069468](https://doi.org/10.1136/jmg.2009.069468)



Aniridia, Água Branca – AL
DOI: [10.1111/cge.12329](https://doi.org/10.1111/cge.12329)



Xeroderma Pigmentosum, Araras - GO
<http://g1.globo.com/goias/noticia/2014/05/povoado-em-goias-tem-maior-taxa-mundial-de-doenca-rara-pele.html>

www.inagemp.bio.br



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O INAGEMP, Instituto Nacional de Ciéncia e Tecnologia do CNPq, dedicado à Genética Médica Populacional desde 2008 está iniciando um censo nacional de populações brasileiras com alta freqüência de doenças ou características mono ou oligogénicas ou expostas a fatores de risco genéticos (Ex.: endocruzamento), ambientais (Ex.: mercúrio), ou desconhecidos, sobre a ocorrência de algum transtorno do desenvolvimento físico ou mental.

Este censo, complementado com uma biblioteca virtual especializada em isolados populacionais e "clusters" de doenças chamadas "genélicas", é o primeiro passo em direção a um centro especializado na pesquisa e normativas de atenção médica deste tipo de patologias, oferecendo serviços de suporte técnico e metodológico aos geneticistas e às comunidades afetadas.

Nesta etapa inicial do censo o INAGEMP está interessado em qualquer "rumor" ou certeza sobre grupos populacionais que você achar conveniente nos informar.

Este primeiro contato seu com o INAGEMP iniciará um relacionamento de longo prazo desde sua incorporação no mailing list eletrônico do instituto, até possíveis colaborações em projetos de pesquisa específicos, convite a cursos especializados e outras atividades do INAGEMP.

Para informar uma população

(PDF) Para ver populações já registradas

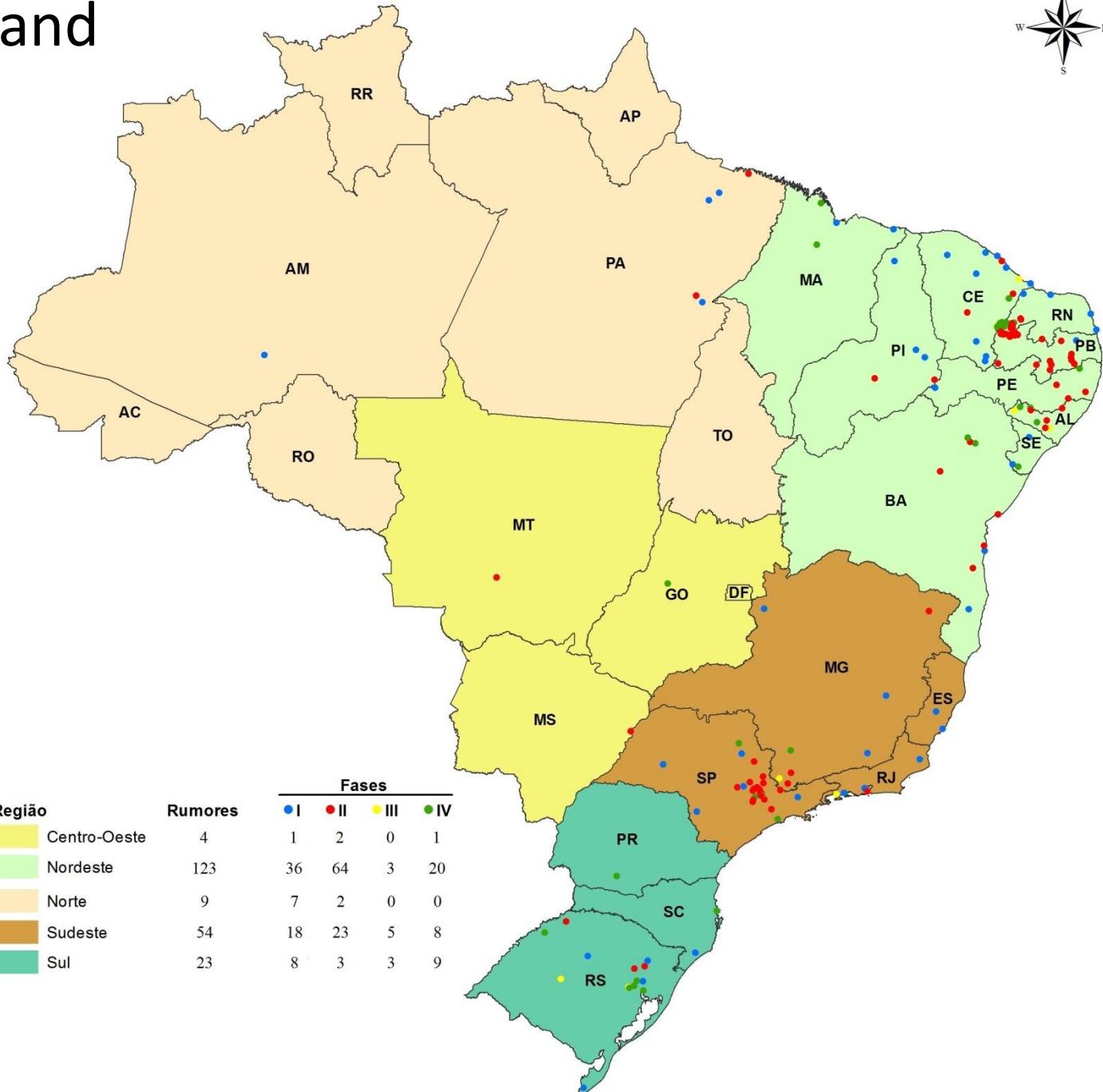
Ver Mapa (Q)

CNPq CAPES INCT Ministério da Ciéncia, Tecnologia e Inovação SISTEMA FEDERAL BRASIL PAIS RICO E PAIS SEM PÓRTEA



ID	DOENÇA	MIM	LOCALIDADE	ESTADO	LAT S	LONG W	REFERÊNCIA BIBLIOGRaFICA
1	Doença de Stargardt	600110#	Sobral	CE	3° 41'	40° 21'	
2	Li-Fraumeni	151623#	Sul e Sudeste do Brasil				Achatz, MI et al., Highly prevalent TP53 mutation predisposing to many cancers in the Brazilian populations: case for newborn screening?, Lancet Oncol., 2009, 10:920-5.
3	Fendas orais	11953%	Alfenas	MG	21° 25'	45° 56'	Aquino, S et al., Estudo de pacientes com fendas labio palatinas com pais consanguíneos., Braz. j. otorhinolaryngol., 2011, 77:19-23.
4	Sarcoma precoce	190030*	Marabá	PA	5° 22'	49° 7'	
5	SPOAN	609541%	Serrinha dos Pintos	RN	06°06'	37°57'	Macedo-Souza, LI et al., Spastic paraplegia, optic atrophy, and neuropathy is linked to chromosome 11q13., Ann Neurol., 2005, 57(5): 730-7. / Macedo-Souza, LI et al., Spastic paraplegia, optic atrophy, and neuropathy: new observations locus refinement, and exclusion of candidate genes., Ann Hum Genet., 2009, 73(Pt 3): 382-7.
6	Huntington	143100#	Feira Grande	AL	9° 54'	36° 40'	
7	Albinismo cutâneo, sem problemas visuais	203200#	Santana do Mundaú	AL	9° 10'	36° 13'	
8	Doença de Minamata		Rio Tapajós	AM	2° 26'	54° 42'	
9	Malformações		Angra dos Reis	RJ	23° 0'	44° 19'	
10	Acondrogênese de Grebe	200700#	Sul da Bahia	BA			Quelce-Salgado, A et al., A new type of dwarfism with various bone aplasias and hypoplasias of the extremities., Acta Genet Stat Med., 1964, 14:63-6.
11	Gaucher I	230800#	Tabuleiro do Norte	CE	5°15'	38°07'	
12	Tricoepitelioma familiar	601606#	Aracati	CE	4° 33'	37° 46'	
13	Malformações		Jetibá	ES	20° 1'	40° 44'	

Rumors and clusters



CODIGO	ENFERMEDAD	DONDE	Estado/Região/Província	PAÍS
ARG001	Albinismo	Acuña	La Rioja	Argentina
ARG001	Albinismo	Acuña	La Rioja	Argentina
ARG002	Ellis van Creveld	San Luis del Palmar.	Corrientes	Argentina
ARG002	Ellis van Creveld	San Luis Del Palmar	Corrientes	Argentina
ARG002	Ellis van Creveld	San Luis Del Palmar	Corrientes	Argentina
ARG003	Gemelaridade (gemelos)	-	Tucumán	Argentina
ARG004	Doença de Huntington	San Lorenzo e Rosario	Santa Fé	Argentina
ARG005	Doença de Sandhoff	Córdoba	Córdoba	Argentina
ARG006	Retardo mental/ autismo	Santa Fè	Santa Fé	Argentina
ARG007	Fissura palatina e anomalias urogenitais	Posadas	Misiones	Argentina
ARG008	anomalias urogenitais		Misiones	Argentina
ARG009	Alta frequência de doenças raras		Misiones	Argentina
ARG010	metabolopatias, anomalias lisossômicas		Misiones	Argentina
ARG011	neuromusculares e cerebrais com defeitos associados		Misiones	Argentina
ARG012	deficit familiar de OC		Chaco	Argentina
ARG013	Distrofia muscular de Duchenne		Chaco	Argentina
ARG014	Síndrome de Bloom	San Luis del Palmar.	Corrientes	Argentina
ARG015	Endogamia	Guatrache	La Pampa	Argentina
ARG016	Doença de Gaucher	Recreo	Santa Fe	Argentina
ARG017	Fissura oral		El Bolson	Argentina

CODIGO	ENFERMEDAD	DONDE	Estado/Região/Província	PAÍS
CHL001	Síndrome de Nijmejn	Arca Maule (Maule)	Talca	Chile
CHL002	Acromatopsia			Chile
CHL002	Acromatopsia	-	Rigião de Valparaiso	Chile
CHL003	MSUD	-	Região O'Higgins	Chile
CHL004	Colelitíase	Isla de Chiloé		Chile
CHL005	MPS	Isla de Chiloé		Chile

CODIGO	ENFERMEDAD	DONDE	Estado/Região/Província	PAÍS
COL001	Albinismo	-	Antioquia	Colombia
COL002	Alzheimer	-	Antioquia	Colombia
COL005	Doença de Huntington	-	-	Colombia
COL005	Doença de Huntington (Corea de Huntington)	Juan de Acosta	Atlântico	Colombia
COL006	MPS		Cauca	Colombia
COL006	MPS IV (Morquio)	-	Boyacá	Colombia
COL006	MPS	-	Cauca	Colombia
COL006	MPS IV (Morquio)	-	Boyacá	Colombia
COL007	MPS IV	-	Cauca	Colombia
COL008	MPS VI	Resguardo, Totoro	Cauca	Colombia
COL008	MPS VI	-	Cauca	Colombia
COL009	Fenilcetonuria (PKU)	-	Boyacá	Colombia
COL010	MPS IV A	Pereira, Manizales e Armenia	Departamentos de Risaralda, Caldas e Quindío. Região de Eje Cafeteno.	Colombia
COL011	X Frágil	Ricaurte e Bolívar	Cundinamarca(Depa- rtamento)	Colombia
COL012	Neurofibromatose tipo 1		Atlântico (departamento)	Colombia
COL013	Síndrome de Lesch Nyhan)	Meta	região Orinoquia	Colombia
COL014	Fissura oral: labio e palato	Meta	região Orinoquia	Colombia
COL015	câncer de estomago	Tuquerres	Nariño	Colombia
COL016	X Frágil	Ricaurte		Colombia
COL016	X Frágil	Ricaurte	Vale del Cauca	Colombia
COL017	Endogamia	Eje Cafetero (Risaralda, Quindío y Caldas)	Risaralda	Colombia
COL018	Transtorno Bipolar		Antioquia	Colombia
COL019	Acidose Renal Tubular Distal		Antioquia	Colombia
COL020	Parkinson de inicio precoce		Antioquia	Colombia
COL021	Sickle Cell Disease		Antioquia	Colombia

CODIGO	ENFERMEDAD	DONDE	Estado/Região/Província	PAÍS
CRC001	MSUD	Turrialba		Costa Rica
EQU001	Síndrome de Laron	Loja	Manabí (provincia)	Equador
EQU002	Fissura oral	região central de la serraria	Cotopaxi, Tungurahua e Chimborazo	Equador
EQU003	Ictiosis		Manabí (provincia)	Equador
EQU004	Labio leporino		sierra equatoriana	Equador
GUA001	Surdez		Huehuetenango	Guatemala
GUA002	Inflamações cutâneas		Huehuetenango	Guatemala
GUA003	Xeroderma Pigmentoso		Huehuetenango	Guatemala
MEX001	Coloboma de Iris (visão preserrada, pode ser uni ou bilateral)	Emilio Carranza	centro de Veracruz	México
MEX002	Síndrome de Van der Woude	Cintalapa	Chiapas	México
MEX003	Fibrose cística	Base en Monterrey	Nuevo León	México
NIC001	Albinismo	Matagalpa		Nicaragua
PAR001	Problemas mentais e convulsão		Chaco	Paraguay
PAR002	Ellis-van-Creveld		Gravidas paraguaias na Argentina	Paraguay
PER001	Consanguinidade	Pirua		Peru
PER002	Problemas de visão na infância	Serra do Peru		Peru
PER003	Doença de Huntington	Cañete - Lima		Peru
PER004	Lipodistrofia congénita de Berardinelli Seip	Piura		Peru
VZL001	Doença de Huntington	Rosario de Perija (Barranquita)	Lago Maracaibo	Venezuela

<http://www.inagemp.bio.br/videos/quatro-herancas-genetica-medica-populacional/>

Genética Médica Populacional



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GENÉTICA MÉDICA NA AMÉRICA LATINA

