

Table S1. Number of individuals/populations and genetic markers used, obtained through a literature review of studies that tested the Amazon, Doce, and São Francisco rivers, or that included occurrence data from nearby regions.

Sampling site	Article	Authors	Year	Group	Specie	No. fo individuals/pops	Marker
Rio Amazonas	Evaluation of the Amazon River delta as a barrier to gene flow for the regional malaria vector, <i>Anopheles aquasalis</i> (Diptera: Culicidae) in northeastern Brazil	Fairley, TL; Póvoa, MM; Conn, JE	2002	Insecta	<i>Anopheles aquasalis</i>	52/5	mtDNA (COI)
	Implications of headwater contact zones for the riverine barrier hypothesis: a case study of the Blue-capped Manakin (<i>Lepidothrix coronata</i>)	Moncrieff, AE; Faircloth, BC; Remsen, RC; Hiller, AE; Felix, C; Capparella, AP; Aleixo, A; Valqui, Thomas; Brumfield, Robb T	2023	Ave	<i>Lepidothrix coronata</i>	706/83	SNP
	Genomic differentiation with gene flow in a widespread Amazonian floodplain-specialist bird species	Luna, LW; Ribas, CC; Aleixo, A	2021	Ave	<i>Xiphorhynchus obsolentus</i>	59/3	SNP
	Geographic variation in mitochondrial DNA sequences of an Amazonian nonpasserine: The Black-spotted Barbet complex	Armentia, JK; Weckstein, JD; Lane, DF	2005	Ave	<i>Capito niger</i> ; <i>C. auratus</i> , e <i>C. brunneipectus</i> .	21/2	mtDNA (Cyt-B)
	Integrating phylogeography and ecological niche modelling to test diversification hypotheses using a Neotropical rodent	Machado, AP; Nunes, MS; Silva, CR; dos Santos, MA; Farias, IP; da Silva, MNF; Anciães, M	2019	Manífero	<i>Hylocichla megaloccephalus</i>	146/4	mtDNA (Cyt-B)
	Recent lineage diversification in a venomous snake through dispersal across the Amazon River	Gibbs, HL; Sovic, M; Amazonas, D; Chalkidis, H; Salazar-Valenzuela, D; Moura-Da-Silva, AM	2018	Réptil	<i>Bothrops atrox</i>	25/4	mtDNA (Cyt-B)
	Phylogeography of a Typical Forest Heliothermic Lizard Reveals the Combined Influence of Rivers and Climate Dynamics on Diversification in Eastern Amazonia	Cronemberger, AA; Werneck, FP; avila-Pires, TCS	2022	Réptil	<i>Kentropyx calcarata</i>	223/9	mtDNA (Cyt-B)
	Phylogeography of the teiid lizard <i>Kentropyx calcarata</i> and the sphaerodactylid <i>Gonatodes humeralis</i> (Reptilia: Squamata): testing a geological scenario for the lower Amazon-Tocantins basins, Amazonia, Brazil	Avila-Pires, TCS; Mulcahy, DG; Werneck, FP; Sites, JW	2012	Réptil	<i>Gonatodes humeralis</i> , <i>Kentropyx calcarata</i>	<i>K. calcarata</i> (67/20); <i>G. humeralis</i> (56/17)	mtDNA (Cyt-B)
	Phylogeography, population history and conservation genetics of jaguars (<i>Panthera onca</i> , Mammalia, Felidae)	Eizirik, E; Kim, J; Menotti-Raymond, M; Crawshaw Jr, PG; O'Brien, SJ; Johnson, WE	2000	Manífero	<i>Panthera onca</i>	44	mtDNA (Cyt-B)
	Spatial expansion and population structure of the neotropical malaria vector, <i>Anopheles darlingi</i> (Diptera: Culicidae)	Pedro MP; Sallum, MAM	2009	Insecta	<i>Anopheles darlingi</i>	40	mtDNA (COI)
	The Role of Vicariance and Paleoclimatic Shifts in the Diversification of <i>Uranoscodon superciliosus</i> (Squamata, Teiidae) of the Amazonian Floodplains	Santos, MV; Prudente, ALC; Rodrigues, MT; Sturaro, MJ	2022	Réptil	<i>Uranoscodon superciliosus</i>	95	mtDNA (12S)
	Morphological and molecular discordance in the taxonomic rearrangement of the Marmosops pinheiroi complex (Marsupialia: Didelphidae)	Guimarães, RR; Rocha, RG; Loss, AC; Mendes-Oliveira, AN; Patterson, BD; Costa, LP	2021	Manífero	<i>Marmosops pinheiroi</i> , <i>M. woodalli</i> and <i>M. marina</i>	109	mtDNA (Cyt-B)
	Concordant Phylogeographies of 2 Malaria Vectors Attest to Common Spatial and Demographic Histories	Pedro, MP; Uezu, A and Sallum, MAM	2010	Insecta	<i>Anopheles triannulatus</i>	72	mtDNA (COI)
	Population history, phylogeography, and conservation genetics of the last Neotropical mega-herbivore, the lowland tapir (<i>Tapirus terrestris</i>)	De Thoisy, B; Silva, AG; Ruiz-Garcia, M; Tapia, A; Ramirez, O; Arana, M; Quise, V; Paz-y-Miño, Tobler, M; Pedraza, C; Lavergne, A	2010	Manífero	<i>Tapirus terrestris</i>	48/4	mtDNA (Cyt-B)
	Hidden in the DNA: How multiple historical processes and natural history traits shaped patterns of cryptic diversity in an Amazon leaf-litter lizard <i>Loxopholis osvaldoi</i> (Squamata: Gymnophthalmidae)	Marques-Souta, Sergio; Pellegrino, KCM; Brunes, TO; Carnaval, AC; Damasceno, RP; Borges, MLO; Gallardo, CC; Rodrigues, MT	2019	Réptil	<i>Loxopholis osvaldoi</i>	157/47	nuDNA (NT3)
	Evolutionary history of the Pectoral Sparrow <i>Arremon taciturnus</i> : evidence for diversification during the Late Pleistocene	Moura, CCM; Fernandes, AM; Aleixo, A; Araújo, HFP; Mariano, EF; Wink, M	2020	Ave	<i>Arremon taciturnus taciturnus</i> , <i>Arremon taciturnus</i>	107/67	mtDNA (Cyt-B)
Rio Doce	Neither barriers nor refugia explain genetic structure in a major biogeographic break: phylogeography of praying mantises in the Brazilian Atlantic Forest	Bernardo F. Santos; Marcus V. Scherrer & Ana Carolina Loss	2018	Insecta	<i>Mobantia fuscata</i>	102/25	mtDNA(ND4)
	Deep Genomic Divergence and Phenotypic Admixture of the Treefrog <i>Dendropsophus elegans</i> (Hylidae: Amphibia) Coincide With Riverine Boundaries at the Brazilian Atlantic Forest	Renata M. Piani; João F. R. Tonini; Andréa T. Thomaz; Marcelo F. Napoli; Laís C. Encarnação; L. Lacey Knowles; Fernanda P. Werneck	2022	Anfibio	<i>Dendropsophus elegans</i>	36/2	mtDNA (Cyt-B)
	Multilocus Phylogeography of the Treefrog <i>Scinax eurydice</i> (Anura, Hylidae) Reveals a Plio-Pleistocene Diversification in the Atlantic Forest	Menezes, L; Canedo, C; Batalha, H; Garda, AA; Gehara, M; Napoli, MF	2016	Anfibio	<i>Scinax eurydice</i>	94/4	mtDNA (NAD2)
	Phylogeography and species limits in the <i>Gymnodactylus darwini</i> complex (Gekkonidae, Squamata): genetic structure coincides with river systems in the Brazilian Atlantic Forest	Pellegrino, KCM; Rodrigues, MT; Waite, AN; Morando, M; Yassuda, YY; Sites, JWJ	2005	Anfibio	<i>Gymnodactylus darwini</i> complex	42/3	mtDNA (Cyt-B)
Rio São Francisco	Dwarf geckos and giant rivers: the role of the São Francisco River in the evolution of <i>Lygodactylus klugei</i> (Gekkonidae: Gekkonidae) in the semi-arid Caatinga of north-eastern Brazil	Lanna, FM; Gehara, M; Werneck, FP; Fonseca, EM; Colli, GR; Sites, JW; Rodrigues, MT; Garda, AA	2020	Réptil	<i>Lygodactylus klugei</i>	124/19	mtDNA (Cyt-B)
	The Role of Historical Barriers in the Diversification Processes in Open Vegetation Formations during the Miocene/Pliocene Using an Ancient Rodent Lineage as a Model	Nascimento, FF; Lazar, A; Menezes, AN; Durans, AD; Moreira, JC; Salazar-Bravo, J; D'Andrea, PS; Bonvicino, CR	2013	Manífero	<i>Thrichomys apereoides</i> ; <i>T. laurentius</i> ; <i>T. inermis</i>	48/12	mtDNA (ND2)
	Phylogeography of Muller's termite frog suggests the vicariant role of the Central Brazilian Plateau	Oliveira, EF; Gehara, M; Sao-Pedro, VA; Costa, GC; Burbink, FT; Colli, GR; Rodrigues, MT; Garda, AA	2018	Anfibio	<i>Dermatonotus muelleri</i>	179/66	mtDNA (Cyt-B)
	Biogeographic determinants of genetic diversification in the mouse opossum <i>Gracilinanus agilis</i> (Didelphimorphia: Didelphidae)	Faria, MB; Nascimento, FF; Oliveira, JA; Bonvicino, CR	2013	Manífero	<i>Gracilinanus agilis</i>	59/19	mtDNA (Cyt-B)
	Diversification with gene flow and niche divergence in a lizard species along the South American "diagonal of open formations	Fonseca, EM; Gehara, M; Werneck, FP; Lanna, FM; Colli, GR; Sites Jr, JW; Rodrigues, MT; Garda, AA	2018	Réptil	<i>Polychrus acutirostris</i>	68/33	mtDNA (Cyt-B)
	Evidence for the Pleistocene Arc hypothesis from genome-wide SNPs in a Neotropical dry forest specialist, the Rufous-fronted Thornbird (<i>Furnariidae</i> : <i>Phacelodomus rufifrons</i>)	Corbett, EC; Bravo, GA; Schunk, L; Naka, LN; Silveira, LF; Edwards, SV	2020	Ave	<i>Phacelodomus rufifrons</i>	74/4	mtDNA (Cyt-B)
	Biogeographic history and cryptic diversity of saxicolous Tropiduridae lizards endemic to the semiarid Caatinga	Werneck, FP; Leite, RN; Geurgas, SR; Rodrigues, MT	2015	Réptil	<i>Tropidurus semitaeniatus</i>	138/2	mtDNA (Cyt-B)
	Colonization Process of the Brazilian Common Vesper Mouse, <i>Calomys expulsus</i> (Cricetidae, Sigmodontinae): A Biogeographic Hypothesis	Do Nascimento, FF; Pereira, LG; Geise, L; Bezerra, AMR; D'Andrea, PS; Bonvicino, CR	2011	Manífero	<i>Calomys expulsus</i>	58/3	SNP
	Lutzomyia longipalpis s.l. in Brazil and the impact of the São Francisco River in the speciation of this sand fly vector	Coutinho-Abreu, IV; Sonoda, IV; Fonseca, JA; Melo, MA; Balbino, VQ; Ramalho-Ortigao, M	2008	Insecta	<i>Lutzomyia longipalpis</i> s.l.	5/5	mtDNA(12S)
	Rapid identification of mitochondrial cytochrome B haplotypes by single strand conformation polymorphism in <i>Lutzomyia longipalpis</i> (Diptera: Psychodidae) populations	Hodgkinson, VH; Birungi, J; Haghighanah, M; Joshi, S; Munstermann, LE	2002	Insecta	<i>Lutzomyia longipalpis</i> s.l.	20/2	ND2
	Mitochondrial cytochrome b variation in populations of the visceral leishmaniasis vector <i>Lutzomyia longipalpis</i> across eastern Brazil	Hodgkinson, VH; Birungi, J; Quintana, M; Deitz, R; Munstermann, LE	2003	Insecta	<i>Lutzomyia longipalpis</i> s.l.	78/30	mtDNA (Cyt-B)
	Genomic data from the Brazilian sibilator frog reveal contrasting pleistocene dynamics and regionalism in two South American dry biomes	Thomé, MTC; Carstens, BC; Rodrigues, MT; Alexandrino, J; Haddad, CFB	2021	Anfibio	<i>Leptodactylus troglodytes</i>	159/61	mtDNA (Cyt-B)
	Speciation with gene flow in whiptail lizards from a Neotropical xeric biome	Oliveira, EF; Gehara, M; Sao-Pedro, VA; Chen, X; Myers, EA; Burbink, FT; Mesquita, DO; Garda, AA; Colli, GR; Rodrigues, MT; Arias, FJ; Zaher, H; Santos, RML; Costa, GC	2015	Réptil	<i>Cnemidophorus ocellifer</i>	398/79	mtDNA (Cyt-B)
					<i>C. brasiliensis</i> (34); <i>Phaethornis margaritae camargoi</i> ; <i>Thalaurania watertoni</i> ; <i>Picumnus pernambucensis</i> , <i>Platyrinchus mystaceus niveigularis</i> ; <i>Henithraupis flavicollis melanoxantha</i> ; <i>Tangara cyanocapilla aff. corallina</i> ; <i>Caryothraustes brasiliensis</i> .	<i>Henithraupis flavicollis melanoxantha</i> (17); <i>Phaethornis</i> (54); <i>Picumnus</i> (29); <i>Platyrinchus</i> (107); <i>Tangara</i> (31); <i>Thalaurania</i> (158)	mtDNA (COI)
	Comparative phylogeographic and demographic analyses reveal a congruent pattern of sister relationships between bird populations of the northern and south-central Atlantic Forest	Bocalini, F; Bolívar-Legunizamón, SD; Silveira, LF; Bravo, GA		Ave		25/10	mtDNA (COI)
	Species limits in Wiedomys (Cricetidae: Sigmodontinae) reinforce the South American São Francisco River as a biogeographic barrier	Di-Nizo, CB; Lazar, A; Cunha-Filho, CA; Silva, MJJ; Bezerra, AMR; Suárez-Villota, EY; Bonvicino, CR; Pessoa, LM; Gonçalves, PR	2024	Manífero	<i>Wiedomys pyrrhorhinos</i> e <i>Wiedomys cerradensis</i>	282	SNP
	Phylogeny, species limits, and biogeography of the Brazilian lizards of the genus <i>Eurolophosaurus</i> (Squamata: Tropiduridae) as inferred from mitochondrial DNA sequences	Passoni, JC; Benozzati, ML; Rodrigues, MT	2008	Réptil	<i>Eurolophosaurus divaricatus</i> , <i>Eurolophosaurus an</i>	25/10	mtDNA (28S)
	Genetic structure, phylogeny, and biogeography of Brazilian cycloid-less lizards of genera <i>Calyptommatus</i> and <i>Nothobachia</i> (Squamata, Gymnophthalmidae) as inferred from mitochondrial DNA sequences.	Siedschlag, AC; Benozzati, ML; Passoni, JC; Rodrigues, MT	2010	Réptil	<i>Calyptommatus sinebrachiatum</i> , <i>C. leirolepis</i> , <i>C. confusioibis</i> , <i>C. nicturus</i>	<i>Calyptommatus sinebrachiatum</i> (53); <i>C. leirolepis</i> (10/6); <i>C. confusioibis</i> (2/1); <i>C. nicturus</i> (2/1)	mtDNA (Cyt-B)