



SARS-CoV-2 genetic diversity in South America: demographic history and structuration signals

Online resource 2.

Table S1. The lineages identified at each country

Argentina		Brazil		Chile		Colombia		Ecuador		Peru		Suriname	
L	%	L	%	L	%	L	%	L	%	L	%	L	%
B.1	0,333	A.2	0,007	A	0,006	A.1	0,028	A.1	0,015	A.1	0,010	B.1.219	0,953
B.1.1	0,212	B	0,005	A.1	0,006	A.2	0,019	B.1	0,328	A.2	0,033	N.2	0,047
B.1.1.1	0,091	B.1	0,087	A.2	0,062	A.5	0,028	B.1.1	0,313	A.5	0,023		
B.1.220	0,030	B.1.1	0,063	A.5	0,043	B	0,009	B.1.1.1	0,090	B	0,007		
B.1.499	0,121	B.1.1.28	0,305	B	0,031	B.1	0,514	B.1.1.10	0,015	B.1	0,155		
C.22	0,030	B.1.1.33	0,500	B.1	0,389	B.1.1	0,093	B.1.223	0,104	B.1.1	0,201		
N.3	0,182	B.1.195	0,002	B.1.1	0,173	B.1.1.231	0,009	B.1.225	0,015	B.1.1.1	0,135		
		B.1.212	0,014	B.1.1.10	0,012	B.1.1.388	0,019	B.1.308	0,015	B.1.1.110	0,020		
		B.1.9	0,002	B.1.1.33	0,043	B.1.104	0,009	B.1.371	0,015	B.1.1.220	0,003		
		B.3	0,002	B.1.110	0,179	B.1.111	0,168	B.1.67	0,075	B.1.1.370	0,003		
		B.39	0,005	B.1.111	0,012	B.1.314	0,009	B.1.9	0,015	B.1.1.381	0,010		
		B.40	0,002	B.1.355	0,006	B.1.420	0,065			B.1.13	0,003		
		B.59	0,002	B.29	0,006	B.1.610	0,009			B.1.205	0,086		
		B.6	0,002	B.40	0,006	B.1.8	0,009			B.1.547	0,003		
				C.11	0,019	B.29	0,009			B.1.8	0,007		
				N.4	0,006					B.3	0,003		
										C.13	0,043		
										C.14	0,162		
										C.22	0,003		
										C.25	0,026		



C.32	0,030
C.33	0,010
C.4	0,023

Table S2. Zns, SSD, Raggedness and Neutrality tests for South American populations

	Zns	SSD ¹	Raggedness index ¹	SSD ²	Raggedness index ²	Arlequin	
						Tajima's D	Fu's Fs
Argentina	0.055	0.0017	0.0058	0.0027	0.0058	-1.65*	-13.51 ⁺⁺
Brazil	0.004	0.0007	0.0035	0.0014	0.0035	-2.81 ⁺⁺	-24.39 ⁺⁺
Chile	0.002	0.0066	0.0128	0.0026	0.0128	-2.38**	-24.72 ⁺⁺
Colombia	0.023	0.0120	0.0207	0.0071	0.0207	-2.40 ⁺⁺	-24.72 ⁺⁺
Ecuador	0.061	0.0041	0.0116	0.0033	0.0116	-1.78**	-5.202
Peru	0.007 ⁺	0.0010	0.0013	0.0016	0.0013	-2.69 ⁺⁺	-23.90 ⁺⁺
Suriname	0.086	0.0233	0.0181	0.0253	0.0181	-1.60*	-21.91 ⁺⁺

*: $p < 0.05$; **: $p < 0.02$; +: $p < 0.01$; ++: $p < 0.001$; ¹: Expansion model; ²: Spatial model. Tajima's D and Fu's Fs were computed by using both, DnaSP (Table 1, in the main manuscript) and Arlequin software.

Table S3: Neutrality tests by each SARS-CoV-2 loci for South American populations

Whole Genome	N	Gene	H	Tajima			Fu's Fs
				D	D*	F*	
Argentina	33	ORF1a	16	-1.82615 ⁺	-2.21071	-2.45823	-8.832
		ORF1b	15	-1.98094*	-3.31391 ⁺	-3.39523 ⁺	-10.215 ⁺
		S	5	-1.33955	-1.01364	-1.28968	-2.647
		ORF3a	8	-1.67588*	-2.57558 ⁺	-2.68828 ⁺	-4.441 ⁺
		E	2	0.37079	0.58366	0.60399	0.811
		M	4	-1.55202 ⁺	-1.52312	-1.77563	-2.867 ⁺
		ORF6	3	-0.50667	-0.7684	-0.80206	-0.47
		ORF7a	1	-	-	-	-
		ORF7b	1	-	-	-	-
		ORF8	1	-	-	-	-
		N	8	0.2108	-0.42566	-0.26753	-0.53
ORF10	1	-	-	-	-		
Whole Genome	n	Gene	H	Tajima			Fu's Fs
				D	D*	F*	
Brazil	426	ORF1a	178	-2.84952 ⁺⁺	-14.48328 ⁺⁺	-9.79754 ⁺⁺	-32.610 ⁺⁺
		ORF1b	114	-2.80588 ⁺⁺	-12.0294 ⁺⁺	-8.72919 ⁺⁺	-297.323 ⁺⁺
		S	71	-2.63997 ⁺⁺	-11.78005 ⁺⁺	-8.80706 ⁺⁺	-141.103 ⁺⁺
		ORF3a	34	-2.49335 ⁺⁺	-7.34023 ⁺⁺	-6.3084 ⁺⁺	-67.776 ⁺⁺
		E	7	-1.78625*	-4.54335 ⁺⁺	-4.2941 ⁺⁺	-16.410 ⁺⁺
		M	16	-2.26224 ⁺⁺	-5.86568 ⁺⁺	-5.39059 ⁺⁺	-38.413 ⁺⁺
		ORF6	7	-0.76934	-3.43331*	-2.99937 ⁺⁺	-2.273
		ORF7a	9	-2.06792 ⁺⁺	-5.46773 ⁺⁺	-5.07322 ⁺⁺	-19.695 ⁺⁺
		ORF7b	4	-1.40288 ⁺⁺	-4.06054 ⁺⁺	-3.79475 ⁺⁺	-9.086 ⁺⁺
		ORF8	7	-1.75763*	-3.43331 ⁺⁺	-3.41748 ⁺⁺	-14.363 ⁺⁺
		N	36	-2.08013 ⁺⁺	-8.31804 ⁺⁺	-6.68319 ⁺⁺	-32.001 ⁺⁺
ORF10	5	-1.56346 ⁺⁺	-4.66408 ⁺⁺	-4.32413 ⁺⁺	-11.825 ⁺⁺		



Whole Genome	n	Gene	H	Tajima		Fu & Li		Fu's Fs
				D	D*	F*	F*	
Chile	162	ORF1a	36 ⁺⁺	-2.54704 ⁺	-7.87474 ⁺⁺	-6.67628 ⁺⁺	-38.208 ⁺⁺	
		ORF1b	34 ⁺⁺	-2.53828 ⁺⁺	-6.15586 ⁺⁺	-5.55625 ⁺⁺	-44.112 ⁺⁺	
		S	15 [*]	-2.01238 ⁺⁺	-4.63578 ⁺⁺	-4.37553 ⁺⁺	-15.692 ⁺⁺	
		ORF3a	9	-1.73012 [*]	-2.22104 [*]	-2.43953 [*]	-8.354 ⁺⁺	
		E	1	-	-	-	-	
		M	4 ⁺	-1.50083 ⁺⁺	-5.988 ⁺⁺	-2.16857 ⁺⁺	-2.3041 ⁺⁺	
		ORF6	3	-0.98497	-1.17946	-1.31525	-2.034	
		ORF7a	6 ⁺⁺	-1.83752 ⁺⁺	-4.61284 ⁺⁺	-4.36356 ⁺⁺	-10.81 ⁺⁺	
		ORF7b	3	-1.21636 ⁺⁺	-1.17946	-1.4011	-3.472 ⁺⁺	
		ORF8	4	-0.9269	-2.16857 [*]	-2.08562	-1.947	
		N	14	-1.06193	-1.79193	-1.81509	-3.772	
ORF10	1	-	-	-	-			
Colombia	107	ORF1a	37 ⁺⁺	-2.65837 ⁺⁺	-7.41057 ⁺⁺	-6.56523 ⁺⁺	-52.184 ⁺⁺	
		ORF1b	22	-2.39023 ⁺⁺	-4.92508 ⁺⁺	-4.72866 ⁺⁺	-26.040 ⁺⁺	
		S	19 ⁺⁺	-2.41607 ⁺⁺	-4.84516 ⁺⁺	-4.70056 ⁺⁺	-26.205 ⁺⁺	
		ORF3a	9 ⁺⁺	-2.02204 ⁺⁺	-2.00493 [*]	-2.38353 [*]	-11.256 ⁺⁺	
		E	1	-	-	-	-	
		M	5 [*]	-1.62741 ⁺⁺	-1.49413	-1.80914	-5.615 ⁺⁺	
		ORF6	2	-0.9115	0.48816	0.07724	-1.546	
		ORF7a	4 ⁺	-1.54213 ⁺⁺	-2.02337	-2.19642 ⁺⁺	-5.085 ⁺⁺	
		ORF7b	1	-	-	-	-	
		ORF8	2	-0.30254	0.48816	0.29131	0.048	
		N	10 [*]	-1.589 [*]	-1.70712	-1.98174	-4.426	
ORF10	2	-1.02032 [*]	-2.0485 [*]	-2.02738 [*]	-2.276			



Whole Genome	n	Gene	H	Tajima	Fu & Li		Fu's Fs
				D	D*	F*	
Ecuador	67	ORF1a	20	-1.81305 ⁺	-2.82049 ⁺	-2.92156 ⁺	-9.91 ⁺
		ORF1b	17	-2.10908 ⁺	-3.63705 ⁺	-3.66961 ⁺	-9.894 [*]
		S	3	-1.24375	-1.84225	-1.93658	-1.02
		ORF3a	4	-1.32189 [*]	-1.84225	-1.96469	-2.806 [*]
		E	1	-	-	-	-
		M	3	0.7115	-0.6539	-0.2375	1.7017
		ORF6	1	-	-	-	-
		ORF7a	1	-	-	-	-
		ORF7b	2	-1.0721	-1.92436	-1.94201	-1.882
		ORF8	2	-1.0721	-1.92436	-1.94201	-1.882
N	5	0.7115	-0.65392	-0.24926	1.702 [*]		
ORF10	1	-	-	-	-		
Whole Genome	n	Gene	H	Tajima	Fu & Li		Fu's Fs
				D	D*	F*	
Peru	303	ORF1a	130	-2.74537 ⁺⁺	-9.53654 ⁺⁺	-7.18273 ⁺⁺	-33.559
		ORF1b	97	-2.61136 ⁺⁺	-7.97334 ⁺⁺	-6.36766 ⁺⁺	-31.992 ⁺⁺
		S	58	-2.52994 ⁺⁺	-6.73142 ⁺⁺	-5.72069 ⁺⁺	-86.05 ⁺⁺
		ORF3a	32	-2.44302 ⁺⁺	-5.21523 ⁺⁺	-4.86163 ⁺⁺	-52.992 ⁺⁺
		E	2	-0.90963 [*]	-2.29533 [*]	-2.1619 [*]	-3.162 ⁺⁺
		M	11	-1.87433 ⁺⁺	-4.05035 ⁺⁺	-3.8966 ⁺⁺	-11.646 ⁺⁺
		ORF6	4	-1.65212 ⁺⁺	-0.24065	-0.86567	-4.617 [*]
		ORF7a	11	-1.94558 [*]	-0.96155	-1.59846	-13.291 ⁺⁺
		ORF7b	4	-1.44924 ⁺⁺	-3.92223 ⁺⁺	-3.69484 ⁺⁺	-8.259 ⁺⁺
		ORF8	11	-1.96005 [*]	-5.21868 ⁺⁺	-4.82929 ⁺⁺	-15.896 ⁺⁺
N	30	-1.79508 [*]	-7.40257 ⁺⁺	-5.99857 ⁺⁺	-18.273 ⁺⁺		
ORF10	5	-1.59521 ⁺⁺	-3.16082 ⁺⁺	-3.13979 ⁺⁺	-9.877 ⁺⁺		



Whole Genome	n	Gene	H	Tajima	Fu & Li		Fu's Fs
				D	D*	F*	
Suriname	43	ORF1a	22	-1.37246*	-2.68076 ⁺⁺	-2.64619 ⁺⁺	-12.907
		ORF1b	12	-1.4038	-1.5208	-1.74984	-4.401
		S	11	-1.74141 ⁺	-2.98719 ⁺⁺	-3.04059 ⁺⁺	-6.878 ⁺
		ORF3a	3	1.70713	0.76321	1.20403	1.625
		E	1	-	-	-	-
		M	1	-	-	-	-
		ORF6	3	-1.30235*	-0.8495	-1.13797	-2.119
		ORF7a	1	-	-	-	-
		ORF7b	1	-	-	-	-
		ORF8	4	-0.144	-0.37099	-0.35282	-0.34
N	9*	-1.98912 ⁺⁺	-1.88024	-2.2555	-5.291 ⁺⁺		
ORF10	2	-1.11747	-1.79614	-1.85123	-1.51		

*: $p < 0.05$; **: $p < 0.02$; +: $p < 0.01$; ++: $p < 0.001$. H: Haplotype-test