Trends in the molecular epidemiology and population genetics of emerging *Sporothrix* species.

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Supplementary Table S1: Isolate, species, source, clinical form, and origin of 188 *Sporothrix* isolates used in this study.

Isolate	CBS code	Species	Source	Clinical Form	Origin	*MAT*	mtDNA
Ss05	CBS 132985	*S. brasiliensis*	Feline	LF	MG/Brazil	*MAT1-1*	1,157
Ss08	-	*S. brasiliensis*	Human	LF	MG/Brazil	*MAT1-1*	1,157
Ss09	-	*S. brasiliensis*	Human	LF	MG/Brazil	*MAT1-1*	1,157
Ss14	-	*S. brasiliensis*	Human	Disseminated	MG/Brazil	*MAT1-2*	1,157
Ss25	CBS 132988	*S. brasiliensis*	Human	Fixed	PR/Brazil	*MAT1-2*	1,157
Ss27	-	*S. brasiliensis*	Human	LF	PR/Brazil	*MAT1-1*	1,157
Ss33	-	*S. brasiliensis*	Human	LF	PR/Brazil	*MAT1-1*	1,157
Ss34	-	*S. brasiliensis*	Human	Fixed	PR/Brazil	*MAT1-1*	1,157
Ss37	-	*S. brasiliensis*	Human	Fixed	PR/Brazil	*MAT1-2*	1,157
Ss43	-	*S. brasiliensis*	Human	Fixed	CE/Brazil	*MAT1-1*	1,157
Ss53	CBS 132989	*S. brasiliensis*	Feline	LF	RS/Brazil	*MAT1-1*	1,157
Ss54	CBS 132990	*S. brasiliensis*	Feline	LF	RS/Brazil	*MAT1-1*	1,157
Ss55	-	*S. brasiliensis*	Human	LF	RS/Brazil	*MAT1-1*	1,157
Ss62	CBS 132991	*S. brasiliensis*	Human	LF	ES/Brazil	*MAT1-1*	1,157
Ss66	-	*S. brasiliensis*	Human	Fixed	RJ/Brazil	*MAT1-2*	1,157
Ss67	-	*S. brasiliensis*	Human	Fixed	RJ/Brazil	*MAT1-2*	1,157
Ss95	-	*S. brasiliensis*	Human	Fixed	RJ/Brazil	*MAT1-2*	1,157
Ss99	-	*S. brasiliensis*	Human	LF	RJ/Brazil	*MAT1-2*	1,157
Ss101	-	*S. brasiliensis*	Human	LF	SP/Brazil	*MAT1-2*	1,157
Ss104	-	*S. brasiliensis*	Human	LF	MT/Brazil	*MAT1-2*	1,157
Ss128	-	*S. brasiliensis*	Human	Fixed	SP/Brazil	*MAT1-1*	1,157
Ss149	-	*S. brasiliensis*	Human	LF	RS/Brazil	*MAT1-1*	1,157
Ss151	CBS 132994	*S. brasiliensis*	Canine	LF	RS/Brazil	*MAT1-1*	1,157
Ss152	CBS 132995	*S. brasiliensis*	Feline	LF	RS/Brazil	*MAT1-1*	1,157
Ss153	CBS 132996	*S. brasiliensis*	Feline	LF	RS/Brazil	*MAT1-1*	1,157
Ss154	-	*S. brasiliensis*	Feline	LF	RS/Brazil	*MAT1-1*	1,157
Ss171	CBS 132999	*S. brasiliensis*	Feline	N/A	PR/Brazil	*MAT1-1*	1,157
Ss172	CBS 133000	*S. brasiliensis*	Feline	N/A	PR/Brazil	*MAT1-1*	1,157
Ss174	CBS 133002	*S. brasiliensis*	Feline	N/A	PR/Brazil	*MAT1-1*	1,157
Ss177	IPEC 16919	*S. brasiliensis*	Human	N/A	RJ/Brazil	*MAT1-2*	1,157
Ss178	CBS 120339	*S. brasiliensis*	Human	N/A	RJ/Brazil	*MAT1-1*	1,157
Ss226	CBS 133003	*S. brasiliensis*	Feline	N/A	SP/Brazil	*MAT1-2*	1,157
Ss227	CBS 133004	*S. brasiliensis*	Canine	N/A	SP/Brazil	*MAT1-1*	1,157
Ss237	-	*S. brasiliensis*	Human	N/A	ES/Brazil	*MAT1-2*	1,157
Ss245	CBS 133005	*S. brasiliensis*	Feline	N/A	RJ/Brazil	*MAT1-2*	1,157
Ss246	CBS 133002	*S. brasiliensis*	Feline	N/A	RJ/Brazil	*MAT1-2*	1,157
Ss247	CBS 133006	*S. brasiliensis*	Feline	N/A	RJ/Brazil	*MAT1-2*	1,157
Ss248	CBS 133007	*S. brasiliensis*	Feline	N/A	RJ/Brazil	*MAT1-2*	1,157
Ss249	CBS 133008	*S. brasiliensis*	Feline	N/A	RJ/Brazil	*MAT1-2*	1,157
Ss250	CBS 133009	*S. brasiliensis*	Feline	N/A	RJ/Brazil	*MAT1-2*	1,157
Ss251	CBS 133010	*S. brasiliensis*	Feline	N/A	RJ/Brazil	*MAT1-2*	1,157
Ss252	CBS 133011	*S. brasiliensis*	Feline	N/A	RJ/Brazil	*MAT1-2*	1,157

Isolate	**CBS code**	**Species**	**Source**	**Clinical Form**	**Origin**	***MAT***	**mtDNA**
Ss256	CBS 133015	*S. brasiliensis*	Feline	N/A	RJ/Brazil	*MAT1-2*	1,157
Ss261	-	*S. brasiliensis*	Human	N/A	RS/Brazil	*MAT1-1*	1,157
Ss265	CBS 133020	*S. brasiliensis*	Human	N/A	MG/Brazil	*MAT1-1*	1,157
Ss292	-	*S. brasiliensis*	Feline	N/A	SP/Brazil	*MAT1-2*	1,157
Ss293	-	*S. brasiliensis*	Feline	N/A	SP/Brazil	*MAT1-2*	1,157
Ss294	-	*S. brasiliensis*	Feline	N/A	SP/Brazil	*MAT1-1*	1,157
Ss295	-	*S. brasiliensis*	Feline	N/A	SP/Brazil	*MAT1-1*	1,157
Ss319	-	*S. brasiliensis*	Feline	N/A	RS/Brazil	*MAT1-1*	1,157
Ss328	-	*S. brasiliensis*	N/A	N/A	RS/Brazil	*MAT1-2*	1,157
Ss330	-	*S. brasiliensis*	Feline	N/A	SP/Brazil	*MAT1-1*	1,157
Ss392	-	*S. brasiliensis*	N/A	N/A	RJ/Brazil	*MAT1-2*	1,157
Ss402	-	*S. brasiliensis*	N/A	N/A	RJ/Brazil	*MAT1-2*	1,157
Ss473	-	*S. brasiliensis*	N/A	N/A	RJ/Brazil	*MAT1-2*	1,157
Ss607	-	*S. brasiliensis*	Human	LF	PE/Brazil	*MAT1-2*	1,157
Ss608	-	*S. brasiliensis*	Human	LF	PE/Brazil	*MAT1-2*	1,157
Ss609	-	*S. brasiliensis*	Human	LF	PE/Brazil	*MAT1-2*	1,157
Ss610	-	*S. brasiliensis*	Human	LF	PE/Brazil	*MAT1-2*	1,157
Ss611	-	*S. brasiliensis*	Human	LF	PE/Brazil	*MAT1-2*	1,157
Ss612	-	*S. brasiliensis*	Human	LF	PE/Brazil	*MAT1-2*	1,157
Ss613	-	*S. brasiliensis*	Human	LF	PE/Brazil	*MAT1-2*	1,157
Ss614	-	*S. brasiliensis*	Human	LF	PE/Brazil	*MAT1-2*	1,157
Ss615	-	*S. brasiliensis*	Human	LF	PE/Brazil	*MAT1-2*	1,157
Ss616	-	*S. brasiliensis*	Human	LF	PE/Brazil	*MAT1-2*	1,157
Ss634	-	*S. brasiliensis*	Feline	N/A	SP/Brazil	*MAT1-2*	1,157
Ss654	-	*S. brasiliensis*	Feline	N/A	SP/Brazil	*MAT1-2*	1,157
Ss742	-	*S. brasiliensis*	N/A	N/A	MG/Brazil	*MAT1-1*	1,157
Ss743	-	*S. brasiliensis*	N/A	N/A	MG/Brazil	*MAT1-1*	1,157
26925	-	*S. brasiliensis*	Feline	N/A	PR/Brazil	*MAT1-2*	1,157
26926	-	*S. brasiliensis*	Feline	N/A	PR/Brazil	*MAT1-2*	1,157
27390	-	*S. brasiliensis*	Feline	N/A	PR/Brazil	*MAT1-2*	1,157
Ss289	CBS 110895	*S. brunneoviolacea*	Roots	N/A	Austria	-	-
Ss291	CBS 124561	*S. brunneoviolacea*	Soil	N/A	Spain	-	-
Ss469	CBS 139891	*S. chilensis*	Human	N/A	Chile	-	-
Ss470	CBS 139890	*S. chilensis*	Soil	N/A	Chile	-	-
Ss286	CBS 125442	*S. dimorphospora*	Soil	N/A	Spain	-	-
Ss288	CBS 125439	*S. dimorphospora*	Soil	N/A	United States	-	-
Ss06	CBS 132922	*S. globosa*	Human	Fixed	MG/Brazil	*MAT1-1*	557
Ss41	CBS 132923	*S. globosa*	Human	Fixed	CE/Brazil	*MAT1-2*	557
Ss49	CBS 132924	*S. globosa*	Human	LF	GO/Brazil	*MAT1-2*	557
Ss179	CBS 120340	*S. globosa*	Human	N/A	Spain	*MAT1-2*	557
Ss180	CBS 130104	*S. globosa*	Human	N/A	Spain	*MAT1-1*	557
Ss211	-	*S. globosa*	Human	N/A	SP/Brazil	*MAT1-1*	557
Ss236	CBS 132925	*S. globosa*	Human	N/A	MG/Brazil	*MAT1-2*	557
Ss376	-	*S. globosa*	Human	N/A	ES/Brazil	*MAT1-1*	557
Ss443	-	*S. globosa*	Human	N/A	Venezuela	*MAT1-1*	557

Isolate	CBS code	Species	Source	Clinical Form	Origin	*MAT*	mtDNA
Ss444	-	*S. globosa*	Human	N/A	Venezuela	*MAT1-2*	557
Ss445	-	*S. globosa*	Human	N/A	Venezuela	*MAT1-1*	557
Ss446	-	*S. globosa*	Human	N/A	Venezuela	*MAT1-1*	557
Ss448	-	*S. globosa*	Human	N/A	Venezuela	*MAT1-1*	557
Ss449	-	*S. globosa*	Human	N/A	Venezuela	*MAT1-1*	557
Ss456	-	*S. globosa*	Human	N/A	Venezuela	*MAT1-1*	557
Ss457	-	*S. globosa*	Human	N/A	Venezuela	*MAT1-1*	557
Ss460	-	*S. globosa*	Human	N/A	Venezuela	*MAT1-1*	557
Ss467	-	*S. globosa*	Human	N/A	SP/Brazil	*MAT1-1*	557
Ss471	-	*S. globosa*	Human	N/A	Chile	*MAT1-2*	557
Ss472	-	*S. globosa*	Human	N/A	Chile	*MAT1-2*	557
Ss489	-	*S. globosa*	Human	N/A	Mexico	*MAT1-1*	557
Ss492	-	*S. globosa*	Human	N/A	Argentina	*MAT1-1*	557
Ss520	-	*S. globosa*	Human	N/A	RJ/Brazil	*MAT1-1*	557
Ss521	-	*S. globosa*	Human	N/A	RS/Brazil	*MAT1-1*	557
Ss522	-	*S. globosa*	Human	N/A	RS/Brazil	*MAT1-2*	557
Ss524	-	*S. globosa*	Human	N/A	RS/Brazil	*MAT1-1*	557
Ss525	-	*S. globosa*	Human	N/A	RS/Brazil	*MAT1-1*	557
Ss545	-	*S. globosa*	Human	N/A	Mexico	*MAT1-1*	557
Ss583	CBS 140866	*S. globosa*	Human	N/A	Japan	*MAT1-1*	557
Ss584	CBS 140867	*S. globosa*	Human	N/A	Japan	*MAT1-1*	557
Ss585	CBS 140868	*S. globosa*	Human	N/A	Japan	*MAT1-1*	557
Ss586	-	*S. globosa*	Human	N/A	Japan	*MAT1-2*	557
Ss587	-	*S. globosa*	Human	N/A	Japan	*MAT1-1*	557
Ss588	-	*S. globosa*	Human	N/A	Japan	*MAT1-2*	557
Ss187	CBS 937.72	*S. luriei*	Human	N/A	Africa	*MAT1-1*	1,157
Ss132	CBS 132927	*S. mexicana*	Human	LF	PE/Brazil	-	-
Ss133	CBS 132928	*S. mexicana*	Human	LF	PE/Brazil	-	-
Ss181	CBS 120342	*S. mexicana*	Vegetal	Environmental	Mexico	-	-
Ss182	CBS 120341	*S. mexicana*	Soil	Environmental	Mexico	-	-
Ss184	FMR 8803	*S. pallida*	Insect	Environmental	China	-	-
Ss327	-	*S. pallida*	N/A	N/A	RS/Brazil	-	-
Ss589	-	*S. pallida*	N/A	N/A	Chile	-	-
Ss01	CBS 132961	*S. schenckii*	Feline	LF	SP/Brazil	*MAT1-2*	557
Ss03	CBS 132963	*S. schenckii*	Human	Fixed	RS/Brazil	*MAT1-2*	1,157
Ss04	-	*S. schenckii*	Human	Fixed	RS/Brazil	*MAT1-2*	1,157
Ss13	-	*S. schenckii*	Human	LF	MG/Brazil	*MAT1-2*	557
Ss16	-	*S. schenckii*	Human	LF	PI/Brazil	*MAT1-1*	1,157
Ss17	-	*S. schenckii*	Human	Fixed	PR/Brazil	*MAT1-2*	557
Ss36	-	*S. schenckii*	Human	LF	PR/Brazil	*MAT1-2*	557
Ss39	-	*S. schenckii*	Human	Fixed	PR/Brazil	*MAT1-2*	1,157
Ss40	-	*S. schenckii*	Human	Fixed	CE/Brazil	*MAT1-2*	557
Ss47	-	*S. schenckii*	Human	LF	GO/Brazil	*MAT1-2*	1,157
Ss50	-	*S. schenckii*	Human	LF	GO/Brazil	*MAT1-1*	1,157
Ss51	-	*S. schenckii*	Human	Fixed	PA/Brazil	*MAT1-1*	1,157

Isolate	CBS code	Species	Source	Clinical Form	Origin	*MAT*	mtDNA
Ss58	-	*S. schenckii*	Human	Fixed	SP/Brazil	*MAT1-2*	557
Ss61	-	*S. schenckii*	Soil	Environmental	SP/Brazil	*MAT1-1*	557
Ss63	CBS 132968	*S. schenckii*	Human	LF	ES/Brazil	*MAT1-2*	557
Ss90	-	*S. schenckii*	Human	Fixed	RJ/Brazil	*MAT1-1*	557
Ss105	-	*S. schenckii*	Human	LF	MG/Brazil	*MAT1-1*	1,157
Ss107	-	*S. schenckii*	Human	LF	MG/Brazil	*MAT1-2*	1,157
Ss110	-	*S. schenckii*	Human	Fixed	MG/Brazil	*MAT1-2*	1,157
Ss122	-	*S. schenckii*	Human	Fixed	SP/Brazil	*MAT1-1*	557
Ss126	-	*S. schenckii*	Human	Fixed	SP/Brazil	*MAT1-2*	557
Ss130	-	*S. schenckii*	Human	LF	PE/Brazil	*MAT1-1*	1,157
Ss137	-	*S. schenckii*	Human	LF	PE/Brazil	*MAT1-1*	557
Ss138	-	*S. schenckii*	Human	LF	PB/Brazil	*MAT1-2*	557
Ss141	CBS 132975	*S. schenckii*	Human	LF	DF/Brazil	*MAT1-1*	557
Ss143	-	*S. schenckii*	Human	LF	PA/Brazil	*MAT1-1*	557
Ss158	-	*S. schenckii*	Human	Fixed	AM/Brazil	*MAT1-2*	557
Ss159	CBS 132976	*S. schenckii*	Human	LF	Japan	*MAT1-2*	1,157
Ss160	-	*S. schenckii*	Human	LF	Mexico	*MAT1-1*	557
Ss161	-	*S. schenckii*	Human	LF	Mexico	*MAT1-2*	557
Ss162	CBS 132977	*S. schenckii*	Vegetal	Environmental	Mexico	*MAT1-2*	1,157
Ss163		*S. schenckii*	Human	Fixed	Peru	*MAT1-2*	1,157
Ss164	-	*S. schenckii*	Human	Fixed	Peru	*MAT1-2*	557
Ss167	CBS 132978	*S. schenckii*	Soil	Environmental	Peru	*MAT1-2*	1,157
Ss175	-	*S. schenckii*	Human	N/A	Italy	*MAT1-2*	557
Ss185	CBS 359.36	*S. schenckii*	Human	N/A	United States	*MAT1-1*	557
Ss192	-	*S. schenckii*	Human	N/A	SP/Brazil	*MAT1-1*	-
Ss193	-	*S. schenckii*	Human	N/A	SP/Brazil	*MAT1-2*	1,157
Ss194	-	*S. schenckii*	Human	N/A	SP/Brazil	*MAT1-2*	-
Ss200	CBS 132982	*S. schenckii*	Human	N/A	SP/Brazil	*MAT1-2*	557
Ss202	-	*S. schenckii*	Human	N/A	SP/Brazil	*MAT1-2*	557
Ss207	-	*S. schenckii*	Human	N/A	SP/Brazil	*MAT1-1*	557
Ss208	-	*S. schenckii*	Human	N/A	SP/Brazil	*MAT1-1*	557
Ss209	-	*S. schenckii*	Human	N/A	SP/Brazil	*MAT1-2*	557
Ss210	-	*S. schenckii*	Human	N/A	SP/Brazil	*MAT1-2*	557
Ss212	-	*S. schenckii*	Human	N/A	SP/Brazil	*MAT1-1*	557
Ss213	-	*S. schenckii*	Human	N/A	SP/Brazil	*MAT1-2*	557
Ss214	-	*S. schenckii*	Human	N/A	SP/Brazil	*MAT1-1*	-
Ss452	-	*S. schenckii*	Human	N/A	Venezuela	*MAT1-1*	557
Ss453	-	*S. schenckii*	Human	N/A	Venezuela	*MAT1-1*	557
Ss454	-	*S. schenckii*	Human	N/A	Venezuela	*MAT1-1*	557
Ss455	-	*S. schenckii*	Human	N/A	Venezuela	*MAT1-1*	557
Ss459	-	*S. schenckii*	Human	N/A	Venezuela	*MAT1-1*	557
Ss465	-	*S. schenckii*	Human	N/A	Venezuela	*MAT1-1*	557
Ss476	-	*S. schenckii*	Human	N/A	Mexico	*MAT1-1*	557
Ss479	-	*S. schenckii*	Human	N/A	Mexico	*MAT1-1*	557
Ss480	-	*S. schenckii*	Human	N/A	Mexico	*MAT1-2*	557

Isolate	**CBS code**	**Species**	**Source**	**Clinical Form**	**Origin**	***MAT***	**mtDNA**
Ss482	-	*S. schenckii*	Human	N/A	Mexico	*MAT1-2*	557
Ss493	-	*S. schenckii*	Human	N/A	Argentina	*MAT1-2*	1,157
Ss495	-	*S. schenckii*	Human	N/A	Argentina	*MAT1-2*	557
Ss496	-	*S. schenckii*	Human	N/A	Uruguay	*MAT1-2*	557
Ss499	-	*S. schenckii*	Human	N/A	Argentina	*MAT1-1*	1,157
Ss526	-	*S. schenckii*	Human	N/A	Mexico	*MAT1-2*	557
Ss527	-	*S. schenckii*	Human	N/A	Mexico	*MAT1-2*	557
Ss554	-	*S. schenckii*	Human	N/A	Mexico	*MAT1-2*	557
Ss597	-	*S. schenckii*	Human	N/A	ES/Brazil	*MAT1-2*	557
Ss696	-	*S. schenckii*	Human	N/A	ES/Brazil	*MAT1-2*	557
Ss329	-	*S. stenoceras*	Human	N/A	RS/Brazil	-	-

LF: Lymphocutaneous sporotrichosis. AM: Amazonas; CE: Ceará; DF: Federal District; ES: Espírito Santo; GO: Goiás; MG: Minas Gerais; MT: Mato Grosso; PA: Pará; PB: Paraíba; PE: Pernambuco; PI: Piauí; PR: Paraná; RJ: Rio de Janeiro; RS: Rio Grande do Sul; SP: São Paulo.

Supplementary Table S2. Cluster similarities among the three combinations evaluated for the isolates from clinical clade.

Species	**Subclade**	**AFLP combination #3**			**AFLP combination #5**			**AFLP combination #6**		
		N	**CC**	**Similarity**	**N**	**CC**	**Similarity**	**N**	**CC**	**Similarity**
S. brasiliensis	-	72	88	46.913% ± 4.43%	72	90	46.913% ± 4.43%	72	93	29.920% ±4.05%
	Ia	4	70	65.173% ± 2.63%	4	84	75.520% ± 2.91%	30	92	65.580% ± 2.70%
	Ib	28	86	74.840% ± 4.97%	24	89	74.193% ± 2.37%	18	92	68.687% ± 4.13%
	Ic	3	100	68.487% ± 0.56%	4	80	79.500% ± 3.19%	3	99	65.527% ± 1-14%
	Id	13	78	65.620% ± 6.87%	19	89	66.240% ± 5.23%	6	96	62.287% ± 1.94%
	Ie	4	98	91.320% ± 0.30%	3	97	67.506% ± 1.89%	2	99	63.247% ± 0.00%
	If	5	77	76.480% ± 2.76%	2	89	79.786% ± 0.00%	4	99	80.460% ± 0.93%
	Ig	2	88	68.253% ± 0.00%	6	98	63.606% ± 0.81%	2	100	67.840% ± 0.00%
	Ih	2	98	65.973% ± 0.00%	6	94	66.013% ± 3.58%	2	95	75.320% ± 0.00%
	Ii	2	98	89.200% ± 0.00%	2	88	70.313% ± 0.00%	-	-	-
	Ij	3	81	90.147% ± 1.31%	-	-	-	-	-	-
	Ik	2	88	78.247% ± 0.00%	-	-	-	-	-	-
S. schenckii	-	66	87	31.766% ±5.33%	66	83	31.766% ± 5.33%	66	87	26.747% ± 4.38%
	IIa	7	84	67.287% ± 4.63%	21	86	62.053% ± 3.25%	2	100	72.207% ± 0.00%
	IIb	6	78	80.533% ± 1-24%	4	70	73.620% ± 1.67%	5	66	67.727% ± 4.11%
	IIc	3	53	69.227% ± 5.27%	2	88	75.833% ± 0.00%	5	68	61.067% ± 3.86%
	IId	3	95	63.953% ± 2.12%	10	92	61.133% ± 4.16%	3	62	62.754% ± 3.27%
	IIe	5	83	62.140% ± 0.70%	2	91	77.180% ± 0.00%	6	85	63.880% ± 3.49%
	IIf	2	85	64.867% ± 0.00%	2	88	74.106% ± 0.00%	3	91	62.094% ± 1.57%
	IIg	2	93	65.873% ± 0.00%	3	71	65.680% ± 1.37%	2	90	63.380% ± 0.00%
	IIh	3	86	73.493% ± 1.35%	8	76	60.726% ± 3.89%	2	90	63.487% ± 0.00%
	IIi	2	75	76.167% ± 0.00%	4	85	60.206% ± 4.63%	4	95	63.167% ± 0.95%
	IIj	4	94	64.520% ± 1.31%	-	-	-	2	95	68.634% ± 0.00%
	IIk	2	71	65.287% ± 0.00%	-	-	-	3	88	61.547% ± 1-21%
	IIl	2	99	73.300% ± 0.00%	-	-	-	2	99	65.240% ± 0.00%
	IIm	10	92	62.620% ± 3.57%	-	-	-	2	99	90.120% ± 0.00%
	IIn	-	-	-	-	-	-	11	80	61.427% ± 8.63%
	IIo	-	-	-	-	-	-	2	86	70.794% ± 0.00%
S. globosa	-	34	97	38.780% ± 4.29%	34	93	38.780% ± 4.29%	34	93	42.007% ± 5.45%
	IIIa	24	87	76.373% ± 4.27%	24	83	65.726% ± 5.85%	27	87	58.040% ± 5.14%
	IIIb	2	94	78.753% ± 0.00%	2	88	75.680% ± 0.00%	2	98	80.180% ± 0.00%
	IIIc	6	99	69.027% ± 1.57%	6	91	63.673% ± 4.27%	-	-	-

N: number of isolates; CC: Cophenetic correlation coefficient.

Supplementary Table S3: Descriptive statistics of AFLP markers #3. #5 and #6 *in vitro*.

AFLP	**Genetic group/ species**	***S. brasiliensis***	***S. schenckii***	***S. globosa***	***S. chilensis***	***S. mexicana***	***S. pallida***	***S. dimorphos.***	***S. brunneo.***
#3 EcoRI- GA/MseI-TT	Number of isolates	72	67	34	2	4	3	2	2
	Minimum (fragment)	15	11	17	17	15	17	21	19
	10% Percentile (fragments)	21	15	20.5	17	15	17	21	19
	25% Percentile (fragments)	22.25	19	22	17	15.25	17	21	19
	Median (fragments)	26	21	23	20.5	16.5	19	21	22
	75% Percentile (fragments)	27.75	24	24	24	21.5	36	21	25
	90% Percentile (fragments)	29	27.2	30	24	23	36	21	25
	Maximum (fragments)	47	32	38	24	23	36	21	25
	Mean (fragments)	25.47	21.27	24.03	20.5	17.75	24	21	22
	Standard Deviation	4.615	4.273	4.232	4.95	3.594	10.44	0	4.243
	Standard Error of Mean	0.5438	0.5221	0.7257	3.5	1.797	6.028	0	3
	Lower 95% CI of mean	25	20	22	17	15	17	21	19
	Upper 95% CI of mean	27	22	24	24	23	36	21	25
	Coefficient of variation	18.12%	20.09%	17.61%	24.15%	20.25%	43.50%	0.000%	19.28%
	Geometric mean	25.08	20.84	23.71	20.2	17.5	22.66	21	21.79

AFLP	**Genetic group/ species**	***S. brasiliensis***	***S. schenckii***	***S. globosa***	***S. chilensis***	***S. mexicana***	***S. pallida***	***S. dimorphos.***	***S. brunneo.***
#5 EcoRI -GA/MseI-AG	Number of isolates	72	67	34	2	4	3	2	2
	Minimum (fragments)	15	12	16	31	19	23	17	20
	10% Percentile (fragments)	20	14.8	19	31	19	23	17	20
	25% Percentile (fragments)	22	18	20	31	19.25	23	17	20
	Median (fragments)	24	24	22	32	23	23	19	28
	75% Percentile (fragments)	26	27	24.25	33	26	26	21	36
	90% Percentile (fragments)	29.7	31	26.5	33	26	26	21	36
	Maximum (fragments)	39	33	30	33	26	26	21	36
	Mean	24.29	23.15	22.47	32	22.75	24	19	28
	Standard Deviation	3.686	5.666	2.977	1.414	3.775	1.732	2.828	11.31
	Standard Error of Mean	0.4345	0.6922	0.5106	1	1.887	1	2	8
	Lower 95% CI of mean	23	23	21	31	19	23	17	20

	Upper 95% CI of mean	24	25	24	33	26	26	21	36
	Coefficient of variation	15.18%	24.47%	13.25%	4.419%	16.59%	7.217%	14.89%	40.41%
	Geometric mean	24.03	22.39	22.28	31.98	22.51	23.96	18.89	26.83

AFLP	**Genetic group/ species**	***S. brasiliensis***	***S. schenckii***	***S. globosa***	***S. chilensis***	***S. mexicana***	***S. pallida***	***S. dimorphos.***	***S. brunneo.***
#6 EcoRI -TA/MseI-AA	Number of isolates	72	67	34	2	4	3	2	2
	Minimum (fragments)	9	8	8	13	11	14	19	19
	10% Percentile (fragments)	12	13	9	13	11	14	19	19
	25% Percentile (fragments)	12	16	10	13	11.25	14	19	19
	Median (fragments)	14	18	10.5	13	12.5	14	21.5	23.5
	75% Percentile (fragments)	15	20	12.25	13	13.75	16	24	28
	90% Percentile (fragments)	19	22	16	13	14	16	24	28
	Maximum (fragments)	23	25	19	13	14	16	24	28
	Mean	14.47	17.61	11.5	13	12.5	14.67	21.5	23.5
	Standard Deviation	2.793	3.357	2.766	0	1.291	1.155	3.536	6.364
	Standard Error of Mean	0.3292	0.4102	0.4744	0	0.6455	0.6667	2.5	4.5
	Lower 95% CI of mean	13	17	10	13	11	14	19	19
	Upper 95% CI of mean	15	19	12	13	14	16	24	28
	Coefficient of variation	19.30%	19.06%	24.05%	0.000%	10.33%	7.873%	16.44%	27.08%
	Geometric mean	14.23	17.27	11.22	13	12.45	14.64	21.35	23.07

Supplementary Table S4. Polymorphic statistics calculated for three combinations of selective primers for the subclades of *S. brasiliensis*, *S. schenckii*, and *S. globosa*.

#1 EcoRI-GA/MseI-TT										
Species	**Subclade**	**n**	**Fragments**	**H**	**PIC**	**E**	**Havp**	**MI**	**D**	**Rp**
S. brasiliensis	Ia	27	38	0.4292	0.3371	26.1481	0.0004	0.0109	0.5267	5.4074
	Ib	2	37	0.0526	0.0512	36.0000	0.0007	0.0256	0.0537	2.0000
	Ic	3	28	0.3084	0.2608	22.6667	0.0037	0.0832	0.3465	6.0000
	Id	8	31	0.3943	0.3166	22.6250	0.0016	0.0360	0.4681	5.2500
	Ie	2	19	0.2285	0.2024	16.5000	0.0060	0.0992	0.2489	5.0000
	If	2	26	0.2604	0.2265	22.0000	0.0050	0.1102	0.2866	8.0000
	Ig	5	30	0.1692	0.1549	27.2000	0.0011	0.0307	0.1785	4.0000
	Ih	5	28	0.2841	0.2437	23.2000	0.0020	0.0471	0.3145	4.4000
	Ii	2	24	0.1866	0.1692	21.5000	0.0039	0.0836	0.1995	5.0000
	Ij	2	28	0.0689	0.0665	27.0000	0.0012	0.0332	0.0708	2.0000
	Ik	3	26	0.0740	0.0712	25.0000	0.0009	0.0237	0.0759	2.0000
S. schenckii	IIa	2	16	0.1699	0.1555	14.5000	0.0053	0.0770	0.1815	3.0000
	IIb	4	30	0.3988	0.3192	21.7500	0.0033	0.0723	0.4761	8.5000
	IIc	6	23	0.2778	0.2392	19.1667	0.0020	0.0386	0.3066	4.3333
	IId	2	18	0.1975	0.1780	16.0000	0.0055	0.0878	0.2127	4.0000
	IIe	2	28	0.1626	0.1494	25.5000	0.0029	0.0741	0.1721	5.0000
	IIf	2	28	0.2449	0.2149	24.0000	0.0044	0.1050	0.2675	8.0000
	IIg	2	33	0.1896	0.1716	29.5000	0.0029	0.0848	0.2023	7.0000
	IIh	2	15	0.2778	0.2392	12.5000	0.0093	0.1157	0.3103	5.0000
	IIi	2	37	0.2531	0.2211	31.5000	0.0034	0.1077	0.2769	11.0000
	IIj	3	26	0.3550	0.2920	20.0000	0.0046	0.0910	0.4106	7.3333
	IIk	6	33	0.3921	0.3152	24.1667	0.0020	0.0479	0.4647	7.6667
S. globosa	IIIa	24	37	0.4610	0.3547	23.6667	0.0005	0.0123	0.5911	5.8333
	IIIb	2	37	0.1928	0.1742	33.0000	0.0026	0.0860	0.2058	8.0000
	IIIc	6	29	0.4324	0.3389	19.8333	0.0025	0.0493	0.5335	6.3333
#2 EcoRI-GA/MseI-AG										
Species	**Subclade**	**n**	**Fragments**	**H**	**PIC**	**E**	**Havp**	**MI**	**D**	**Rp**
S. brasiliensis	Ia	31	38	0.4775	0.3635	23.0323	0.0004	0.0093	0.6328	5.9355
	Ib	2	26	0.1087	0.1028	24.5000	0.0021	0.0512	0.1131	3.0000
	Ic	17	40	0.4657	0.3573	25.2353	0.0007	0.0173	0.6023	11.1765
	Id	2	33	0.1653	0.1516	30.0000	0.0025	0.0751	0.1748	6.0000
	Ie	2	25	0.1472	0.1364	23.0000	0.0029	0.0677	0.1551	4.0000
	If	5	26	0.1922	0.1737	23.2000	0.0015	0.0343	0.2045	2.0000
	Ig	3	29	0.3144	0.2650	23.3333	0.0036	0.0843	0.3545	6.6667
	Ih	4	32	0.2743	0.2367	26.7500	0.0021	0.0573	0.3023	5.5000
S. schenckii	IIa	3	30	0.2923	0.2496	24.6667	0.0032	0.0801	0.3256	6.0000
	IIb	10	36	0.4407	0.3436	24.2000	0.0012	0.0296	0.5487	7.6000
	IIc	2	28	0.1913	0.1730	25.0000	0.0034	0.0854	0.2045	6.0000
	IId	3	15	0.2923	0.2496	12.3333	0.0065	0.0801	0.3273	3.3333
	IIe	2	17	0.2076	0.1861	15.0000	0.0061	0.0916	0.2246	4.0000
	IIf	3	21	0.3457	0.2859	16.3333	0.0055	0.0896	0.3978	6.0000
	IIg	8	39	0.3782	0.3067	29.1250	0.0012	0.0353	0.4429	10.2500
	IIh	2	35	0.2449	0.2149	30.0000	0.0035	0.1050	0.2671	10.0000
	IIi	2	24	0.2188	0.1948	21.0000	0.0046	0.0957	0.2367	6.0000
	IIj	4	30	0.3394	0.2818	23.5000	0.0028	0.0665	0.3878	8.0000
S. globosa	IIIa	21	34	0.4499	0.3487	22.3810	0.0006	0.0141	0.5670	7.9048
	IIIb	2	28	0.2449	0.2149	24.0000	0.0044	0.1050	0.2675	8.0000
	IIIc	2	31	0.2248	0.1995	27.0000	0.0036	0.0979	0.2433	8.0000
	IIId	2	20	0.0950	0.0905	19.0000	0.0024	0.0451	0.0987	2.0000
	IIIe	2	26	0.2041	0.1833	23.0000	0.0039	0.0903	0.2195	6.0000

#3 *Eco*RI-TA/*Mse*I-AA

Species	**Subclade**	**n**	**Fragments**	**H**	**PIC**	**E**	**Havp**	**MI**	**D**	**Rp**
S. brasiliensis	Ia	24	22	0.4896	0.3698	12.5833	0.0009	0.0117	0.6733	1.8333
	Ib	3	26	0.3261	0.2729	20.6667	0.0042	0.0864	0.3703	6.0000
	Ic	6	18	0.3656	0.2987	13.6667	0.0034	0.0463	0.4252	4.0000
	Id	3	14	0.2449	0.2149	12.0000	0.0058	0.0700	0.2683	3.3333
	Ie	10	18	0.2778	0.2392	15.0000	0.0015	0.0231	0.3063	2.0000
	If	2	21	0.2778	0.2392	17.5000	0.0066	0.1157	0.3089	7.0000
	Ig	2	21	0.2098	0.1878	18.5000	0.0050	0.0924	0.2265	5.0000
	Ih	3	18	0.1372	0.1278	16.6667	0.0025	0.0423	0.1440	1.3333
	Ii	3	15	0.0000	0.0000	15.0000	0.0000	0.0000	0.0000	0.0000
S. schenckii	IIa	3	24	0.3299	0.2755	19.0000	0.0046	0.0870	0.3756	6.6667
	IIb	3	24	0.2778	0.2392	20.0000	0.0039	0.0772	0.3075	4.6667
	IIc	4	23	0.3639	0.2977	17.5000	0.0040	0.0692	0.4231	5.0000
	IId	2	19	0.2285	0.2024	16.5000	0.0060	0.0992	0.2489	5.0000
	IIe	2	15	0.2778	0.2392	12.5000	0.0093	0.1157	0.3103	5.0000
	IIf	2	12	0.0799	0.0767	11.5000	0.0033	0.0383	0.0833	1.0000
	IIg	6	22	0.4100	0.3260	15.6667	0.0031	0.0487	0.4944	5.3333
	IIh	4	22	0.2355	0.2078	19.0000	0.0027	0.0509	0.2555	4.0000
S. globosa	IIIa	12	14	0.4404	0.3434	9.4167	0.0026	0.0247	0.5489	2.1667
	IIIb	5	13	0.3011	0.2557	10.6000	0.0046	0.0491	0.3375	1.2000
	IIIc	8	16	0.3671	0.2997	12.1250	0.0029	0.0348	0.4272	3.7500
	IIId	2	21	0.2098	0.1878	18.5000	0.0050	0.0924	0.2265	5.0000

D: discriminating power; E: effective multiplex ratio; H: expected heterozygosity; Havp: mean heterozygosity; MI: marker index; PIC: polymorphism information content; Rp: resolving power.

Supplementary Table S5. Analysis of molecular variance (AMOVA) shows the partitioning of genetic variation within and between *Sporothrix brasiliensis* geographic populations.

Marker	**Source of variation**	**df**	**SS**	**MS**	**Est. var.**	**%**	***P*-value**
AFLP #3	Among Population	2	53.151	26.575	0.896	10%	0.0001
	Within Population	68	523.835	7.703	7.703	90%	0.0001
	Total marker #3	70	576.986		8.599	100%	
AFLP #5	Among Population	2	39.180	19.590	0.572	7%	0.002
	Within Population	68	511.890	7.528	7.528	93%	0.002
	Total marker #5	70	551.070		8.100	100%	
AFLP #6	Among Population	2	32.669	16.335	0.525	9%	0.0001
	Within Population	68	358.852	5.277	5.277	91%	0.0001
	Total marker #6	70	391.521		5.802	100%	

(df = degree of freedom, SS = sum of squares, MS mean squares, Est. var. = estimate of variance, %= percentage of total variation, *P*-value is based on 9,999 permutations). Geographic Population 1: *S. brasiliensis* isolates from South (n=22); Geographic population 2: *S. brasiliensis* isolates from Southeast (n=38); Geographic population 3: *S. brasiliensis* isolates from Northeast (n=11).

Supplementary Table S6. Summary of statistics calculated for mating-type of clinical clade isolates in the three combinations.

Species	**AFLP combination #3**						**AFLP combination #5**						**AFLP combination #6**					
	n	***MAT*-allele**		**χ^2 mating**			**n**	***MAT*-allele**		**χ^2 mating**			**n**	***MAT*-allele**		**χ2 mating**		
		1-1	***1-2***	**χ2**	**df**	***P*-value**		***1-1***	***1-2***	**χ2**	**df**	***P*-value**		***1-1***	***1-2***	**χ2**	**df**	***P*-value**
S. brasiliensis	72	30	42	2.000	1	0.1573	72	30	42	2.000	1	0.1572	72	30	42	2.000	1	0.157299
Subclade Ia	27	0	27	27.000	1	0.0001	31	3	28	20.161	1	0.0001	24	1	23	20.167	1	0.0001
Subclade Ib	2	0	2	2.000	1	0.1573	2	0	2	2.000	1	0.1573	3	0	3	3.000	1	0.0833
Subclade Ic	3	1	2	0.333	1	0.5637	17	12	5	2.882	1	0.0896	6	4	2	0.667	1	0.4142
Subclade Id	8	6	2	2.000	1	0.1573	2	0	2	2.000	1	0.1573	3	2	1	0.333	1	0.5637
Subclade Ie	2	1	1	0.000	1	10.000	2	2	0	2.000	1	0.1573	10	7	3	1.600	1	0.2059
Subclade If	2	1	1	0.000	1	10000	5	4	1	1.800	1	0.1797	2	0	2	2.000	1	0.1573
Subclade Ig	5	5	0	5.000	1	0.0253	3	2	1	0.333	1	0.5637	2	2	0	2.000	1	0.1573
Subclade Ih	5	4	1	1.800	1	0.1797	4	4	0	4.000	1	0.0455	3	2	1	0.333	1	0.5637
Subclade Ii	2	0	2	2.000	1	0.1573	-	-	-	-	-	-	3	3	0	3000	1	0.0833
Subclade Ij	2	2	0	2.000	1	0.1573	-	-	-	-	-	-	-	-	-	-	-	-
Subclade Ik	3	3	0	3.000	1	0.0833	-	-	-	-	-	-	-	-	-	-	-	-
S. schenckii	66	26	40	2.970	1	0.0848	66	26	40	2970	1	0.0848	66	26	40	2970	1	0.0848
Subclade IIa	2	2	0	2.000	1	0.1573	3	0	3	3000	1	0.0833	3	1	2	0.333	1	0.5637
Subclade IIb	4	0	4	4.000	1	0.0455	10	5	5	0.000	1	10000	3	1	2	0.333	1	0.5637
Subclade IIc	6	6	0	6.000	1	0.0143	2	1	1	0.000	1	10000	4	4	0	4000	1	0.0455
Subclade IId	2	1	1	0.000	1	10000	3	1	2	0.333	1	0.5637	2	1	1	0.000	1	10000
Subclade IIe	2	1	1	0.000	1	10000	2	2	0	2000	1	0.1573	2	0	2	2000	1	0.1573
Subclade IIf	2	1	1	0.000	1	10000	3	2	1	0.333	1	0.5637	2	0	2	2000	1	0.1573
Subclade IIg	2	1	1	0.000	1	10000	8	3	5	-	-	-	6	2	4	0.667	1	0.4142
Subclade IIh	2	0	2	2.000	1	0.1573	2	1	1	0.000	1	10000	4	4	0	4000	1	0.0455
Subclade IIi	2	2	0	2.000	1	0.1573	2	0	2	2000	1	0.1573	-	-	-	-	-	-

Species	**AFLP combination #3**						**AFLP combination #5**						**AFLP combination #6**					
	n	***MAT*-allele**		**χ^2 mating**			**n**	***MAT*-allele**		**χ^2 mating**			**n**	***MAT*-allele**		**χ2 mating**		
		1-1	***1-2***	**χ2**	**df**	***P*-value**		***1-1***	***1-2***	**χ2**	**df**	***P*-value**		***1-1***	***1-2***	**χ2**	**df**	***P*-value**
Subclade IIj	3	2	1	0.333	1	0.5637	4	1	3	1000	1	0.3173	-	-	-	-	-	-
Subclade IIk	6	2	4	0.667	1	0.4142	-	-	-	-	-	-	-	-	-	-	-	-
S. globosa	34	26	8	9.529	1	0.0020	34	26	8	9529	1	0.002022	34	26	8	9529	1	0.0020
Subclade IIIa	24	20	4	10.667	1	0.0011	21	17	4	-	-	-	12	12	0	12000	1	0.0005
Subclade IIIb	2	2	0	2.000	1	0.1573	2	2	0	2000	1	0.1573	5	1	4	1800	1	0.1797
Subclade IIIc	6	2	4	0.667	1	0.4142	2	2	0	2000	1	0.1573	8	7	1	4500	1	0.0339
Subclade IIId	-	-	-	-	-	-	2	0	2	2000	1	0.1573	2	2	0	2000	1	0.1573
Subclade IIIe	-	-	-	-	-	-	2	2	0	2000	1	0.1573	-	-	-	-	-	-

N: number of isolates; df: degree of freedom.

Supplementary Table S7: Search strategy: Phylogenetic trends in *Sporothrix*

Search #	Terms	Period covered	Number of articles
1	*Sporothrix* AND diagnosis	2007-2021	426
2	*Sporothrix* AND molecular diagnosis	2007-2021	44
3	Sporotrichosis AND molecular diagnosis	2007-2021	52
4	*Sporothrix* AND PCR	2007-2021	48
5	*Sporothrix* AND MLSA	2007-2021	0
6	*Sporothrix* AND barcoding	2007-2021	3
7	*Sporothrix* AND internal transcribed spacer	2007-2021	23
8	*Sporothrix* AND restriction fragment length polymorphism	2007-2021	8
9	*Sporothrix* AND restriction amplified polymorphic DNA	2007-2021	1
10	*Sporothrix* AND loop-mediated isothermal amplification	2007-2021	0
11	*Sporothrix* AND qPCR	2007-2021	6
12	*Sporothrix* AND microsatellites	2007-2021	1

A search of PubMed was undertaken in June 2021. The search terms used were: (1) *Sporothrix* AND diagnosis; (2) *Sporothrix* AND molecular diagnosis; (3) Sporotrichosis AND molecular diagnosis; (4) *Sporothrix* AND PCR; (5) *Sporothrix* AND MLSA; (6) *Sporothrix* AND barcoding; (7) *Sporothrix* AND internal transcribed spacer; (8) *Sporothrix* AND restriction fragment length polymorphism; (9) *Sporothrix* AND restriction amplified polymorphic DNA; (10) *Sporothrix* AND loop-mediated isothermal amplification; (11) *Sporothrix* AND qPCR; (12) *Sporothrix* AND microsatellites, and 426-44-52-48-0-3-23-8-1-0-6-1 results were returned, respectively. These articles were manually filtered to recover studies that describe the occurrence of medically relevant *Sporothrix* species (i.e., *S. brasiliensis*, *S. schenckii*, *S. globosa*, *S. luriei*, *S. mexicana*, *S. chilensis*, *S. pallida*, *S. stenoceras*) using molecular assays (e.g., DNA sequencing, DNA fingerprint, PCR, qPCR, etc.) to be included in the epidemiological trends of sporotrichosis. Due to the low frequency of species embedded in the environmental clade as agents of human and animal sporotrichosis, cases due to *S. mexicana*, *S. chilensis*, *S. pallida*, and *S. stenoceras* were counted as "Environmental clade." Isolates that appeared in multiple studies were computed a single time in our analysis.

The studies included in our analysis are listed below:

Arenas, R, Miller, D, and Campos-Macias, P. 2007. Epidemiological data and molecular characterization (mtDNA) of *Sporothrix schenckii* in 13 cases from Mexico. *Int J Dermatol* **46**: 177-179.

Boechat, JS, Oliveira, MME, Almeida-Paes, R, Gremião, IDF, Machado, ACS, Oliveira, RVC, Figueiredo, ABF, Rabello, VBS, Silva, KBL, Zancopé-Oliveira, RM, et al. 2018. Feline sporotrichosis: associations between clinical-epidemiological profiles and phenotypicgenotypic characteristics of the etiological agents in the Rio de Janeiro epizootic area. *Mem Inst Oswaldo Cruz* **113**: 185-196.

Borba-Santos, LP, Rodrigues, AM, Gagini, TB, Fernandes, GF, Castro, R, de Camargo, ZP, Nucci, M, Lopes-Bezerra, LM, Ishida, K, and Rozental, S. 2015. Susceptibility of *Sporothrix brasiliensis* isolates to amphotericin B, azoles, and terbinafine. *Med Mycol* **53**: 178-188.

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Córdoba, S, Isla, G, Szusz, W, Vivot, W, Hevia, A, Davel, G, and Canteros, CE. 2018. Molecular identification and susceptibility profile of *Sporothrix schenckii sensu lato* isolated in Argentina. *Mycoses* **61**: 441-448.

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de Oliveira, MM, de Almeida-Paes, R, de Medeiros Muniz, M, de Lima Barros, MB, Galhardo, MC, and Zancope-Oliveira, RM. 2010. Sporotrichosis caused by *Sporothrix globosa* in Rio De Janeiro, Brazil: case report. *Mycopathologia* **169**: 359-363.

de Oliveira, MM, Sampaio, P, Almeida-Paes, R, Pais, C, Gutierrez-Galhardo, MC, and Zancope-Oliveira, RM. 2012. Rapid identification of *Sporothrix* species by T3B fingerprinting. *J Clin Microbiol* **50**: 2159-2162.

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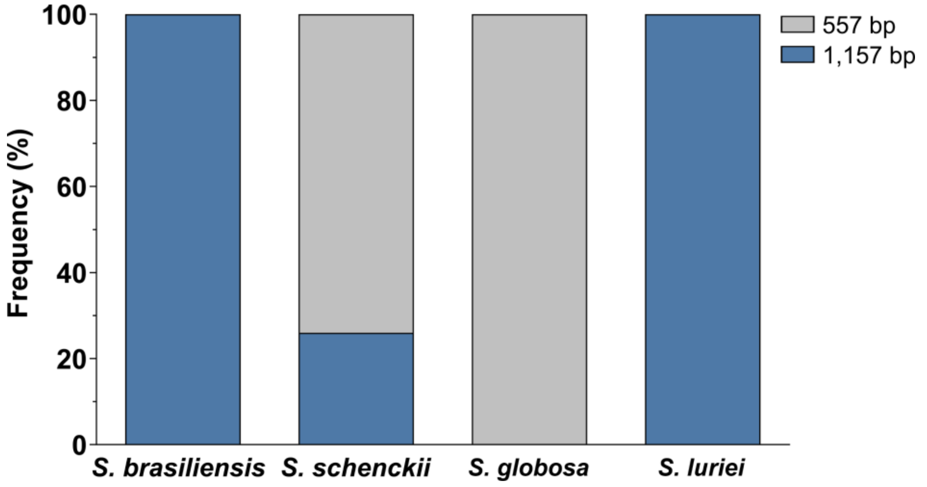
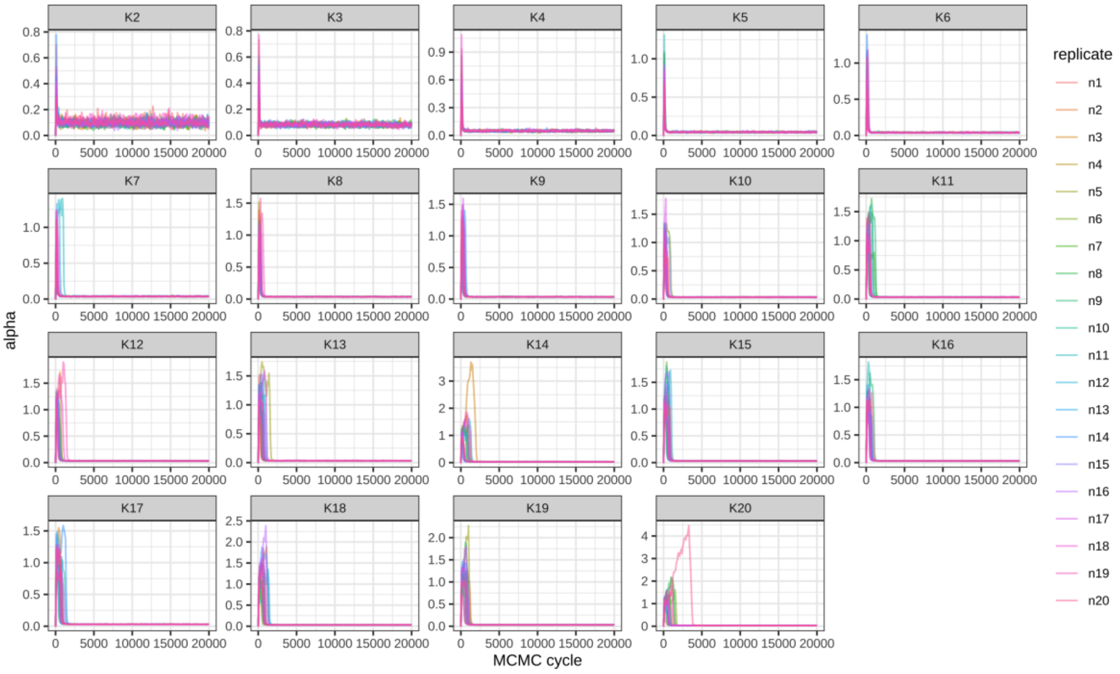
Supplementary Table S8: Simpson's diversity index and Shannon-Wiener diversity index of the Brazilian regions.

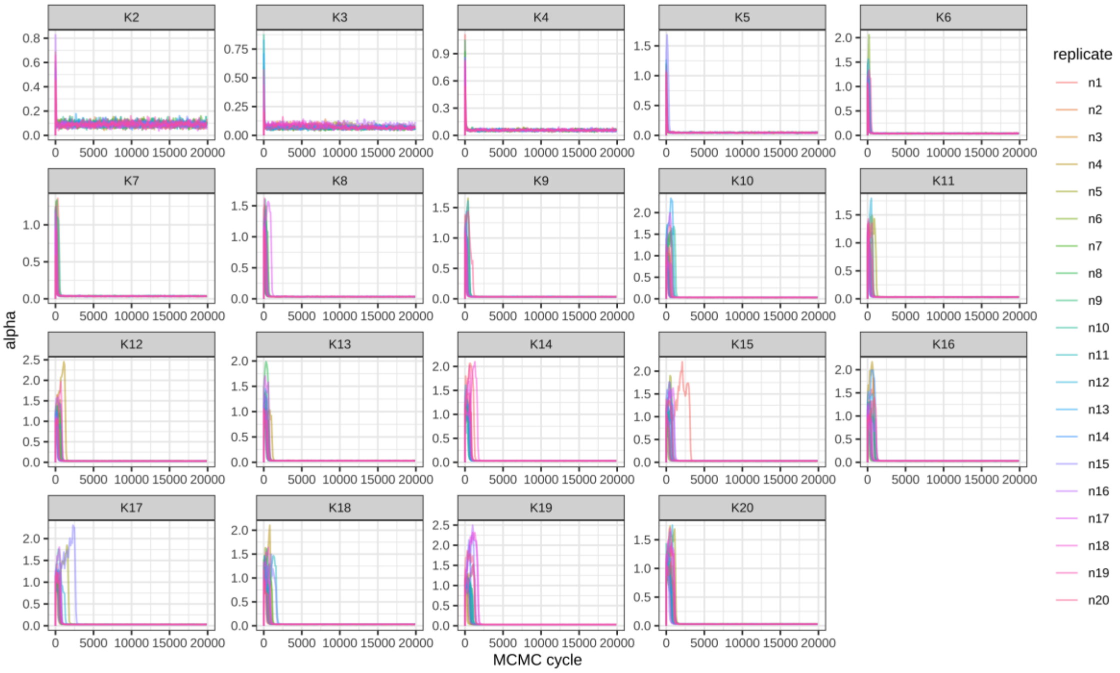
Brazilian Region	**Simpson's diversity index**		**Shannon-Wiener diversity index**	
	2007-2014	**2015-2021**	**2007-2014**	**2015-2021**
South	0.4613	0.7896	1.2300	0.5928
Southeast	0.5936	0.8042	0.9386	0.5507
Central west	0.4000	0.3333	1.2520	1.0000
Northeast	0.3896	0.3896	1.3950	1.3950
North	0.4613	0.7896	1.2300	0.5928



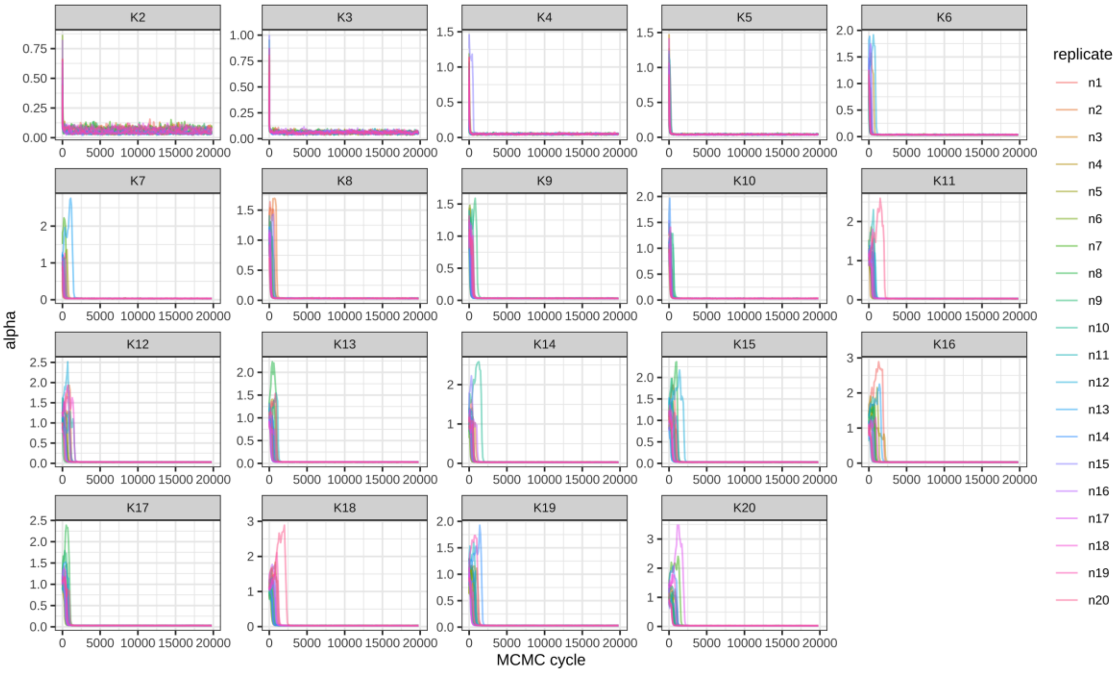
Supplementary Figure S1. Mitochondrial genotyping of *Sporothrix* spp. isolates revealed polymorphic amplicons, representing the variability of the intergenic region between *COX2* and *ATP9* in the mitochondrial genome of different isolates. The distribution of polymorphic amplicons (557 or 1,157) is represented according to the phylogenetic species.



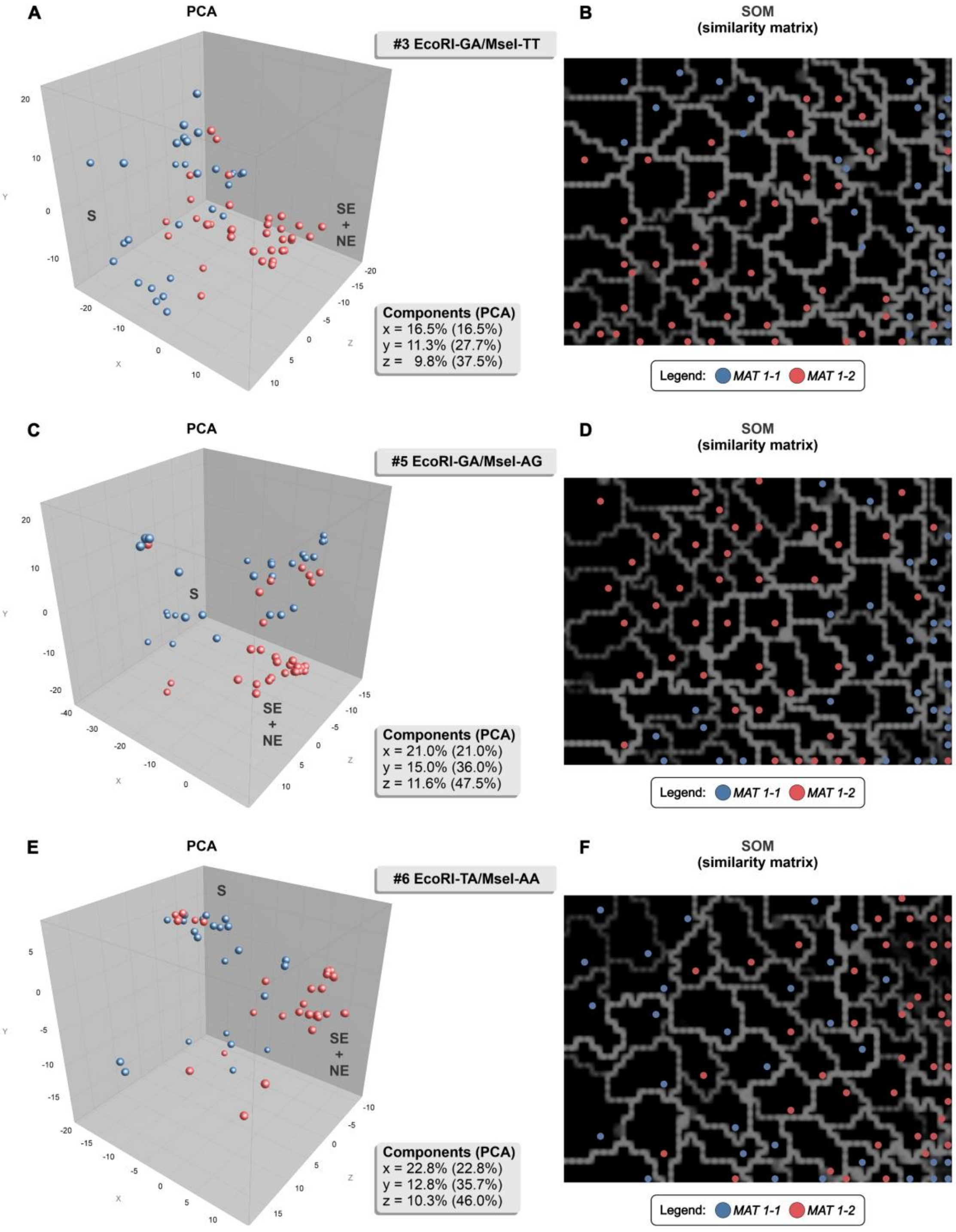
Supplementary Figure S2: Alpha values for 20 independent STRUCTURE MCMC chains at k values 1-20 show convergence for all k values apart from k=1 using combination #3 EcoRI-GA/MseI-TT.



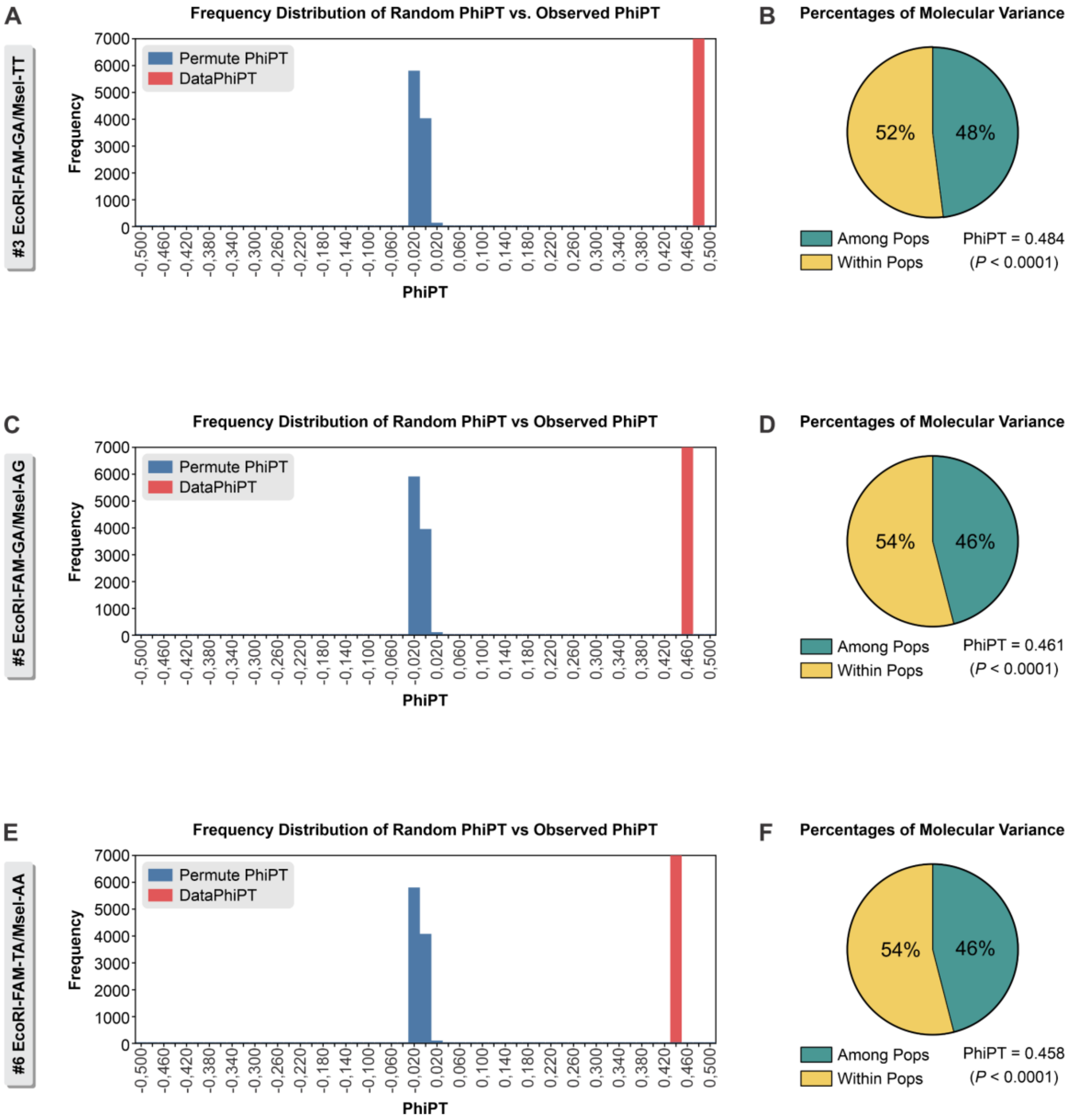
Supplementary Figure S3: Alpha values for 20 independent STRUCTURE MCMC chains at k values 1-20 show convergence for all k values apart from k=1 using combination #5 EcoRI-GA/MseI-AG.



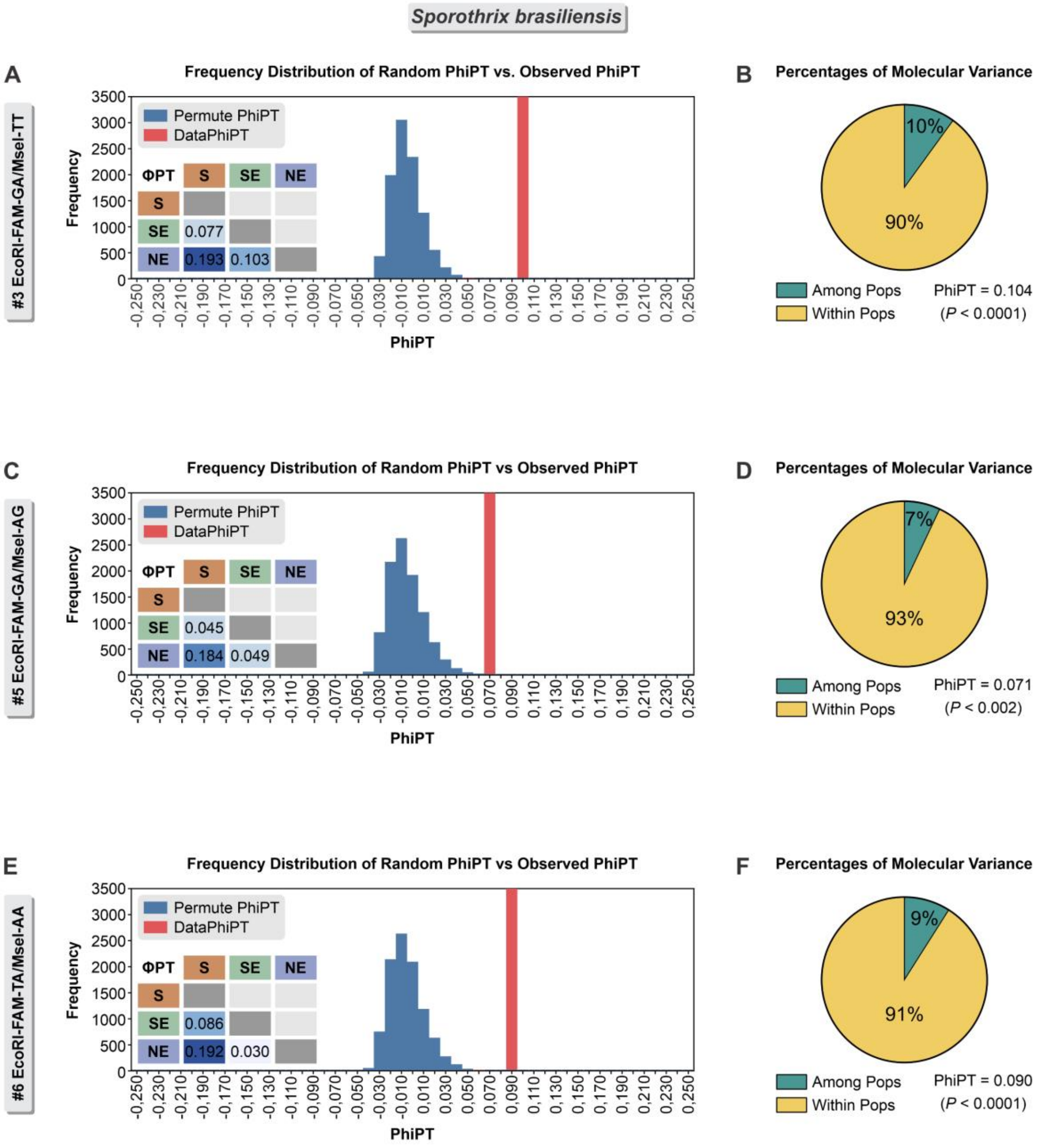
Supplementary Figure S4: Alpha values for 20 independent STRUCTURE MCMC chains at k values 1-20 show convergence for all k values apart from k=1 using combination #6 EcoRI-TA/MseI-AA.



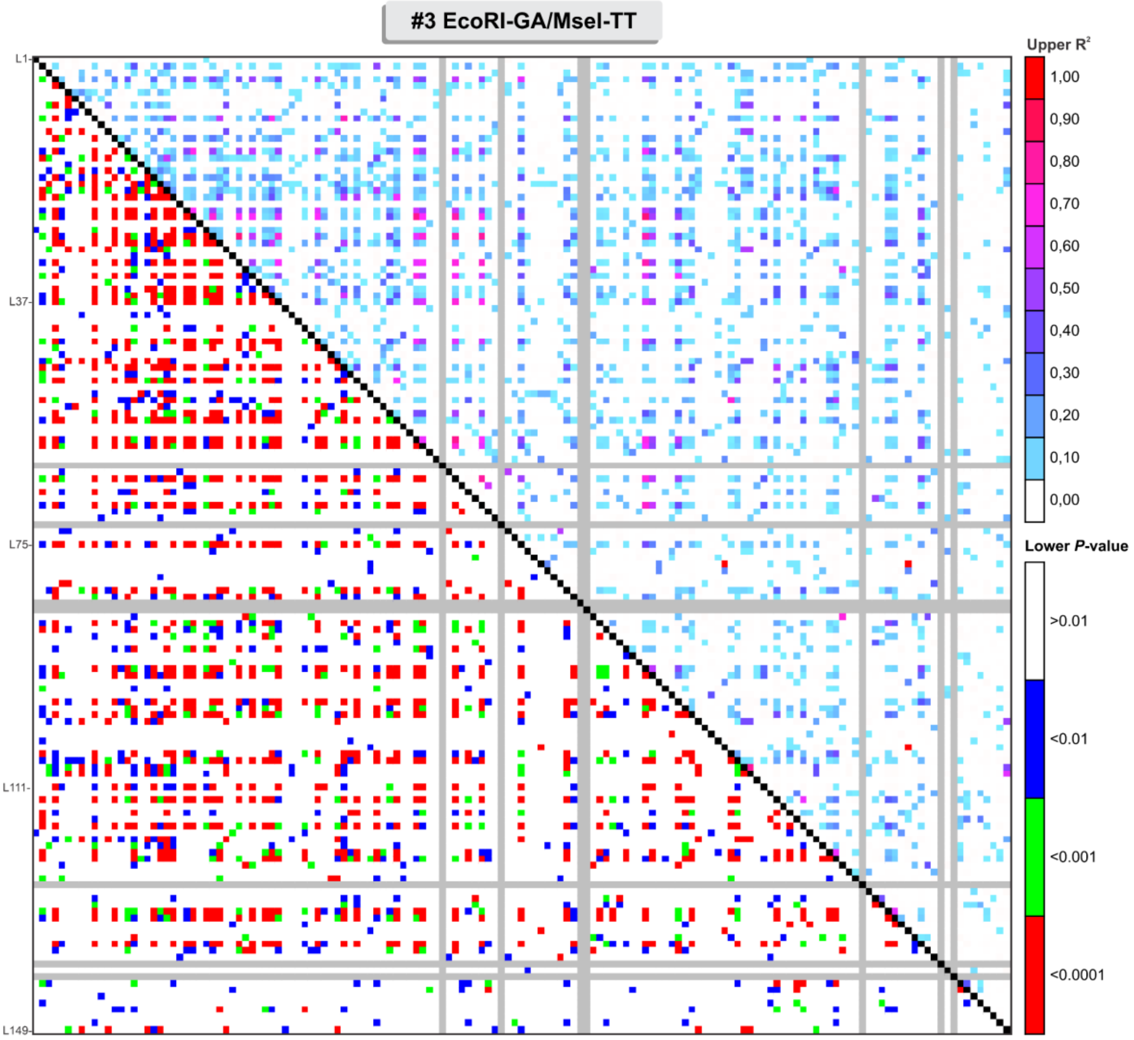
Supplementary Figure S5: Principal component analysis (PCA) and self-organizing mapping (SOM) analysis for *S. brasiliensis* isolates using the combinations #3 FAM-EcoRI-GA/MseI-TT (**A** and **B**), #5 FAM-EcoRI-GA/MseI-AG (**C** and **D**), and #6 FAM-EcoRI-TA/MseI-AA (**E** and **F**) plotted according to the mating-type groups. PCAs and SOMs were created in the software BioNumerics v.7.6. **S**: *S. brasiliensis* South isolates (n=22); **SE**: *S. brasiliensis* Southeast isolates (n=38); **NE**: *S. brasiliensis* Northeast isolates (n=11).



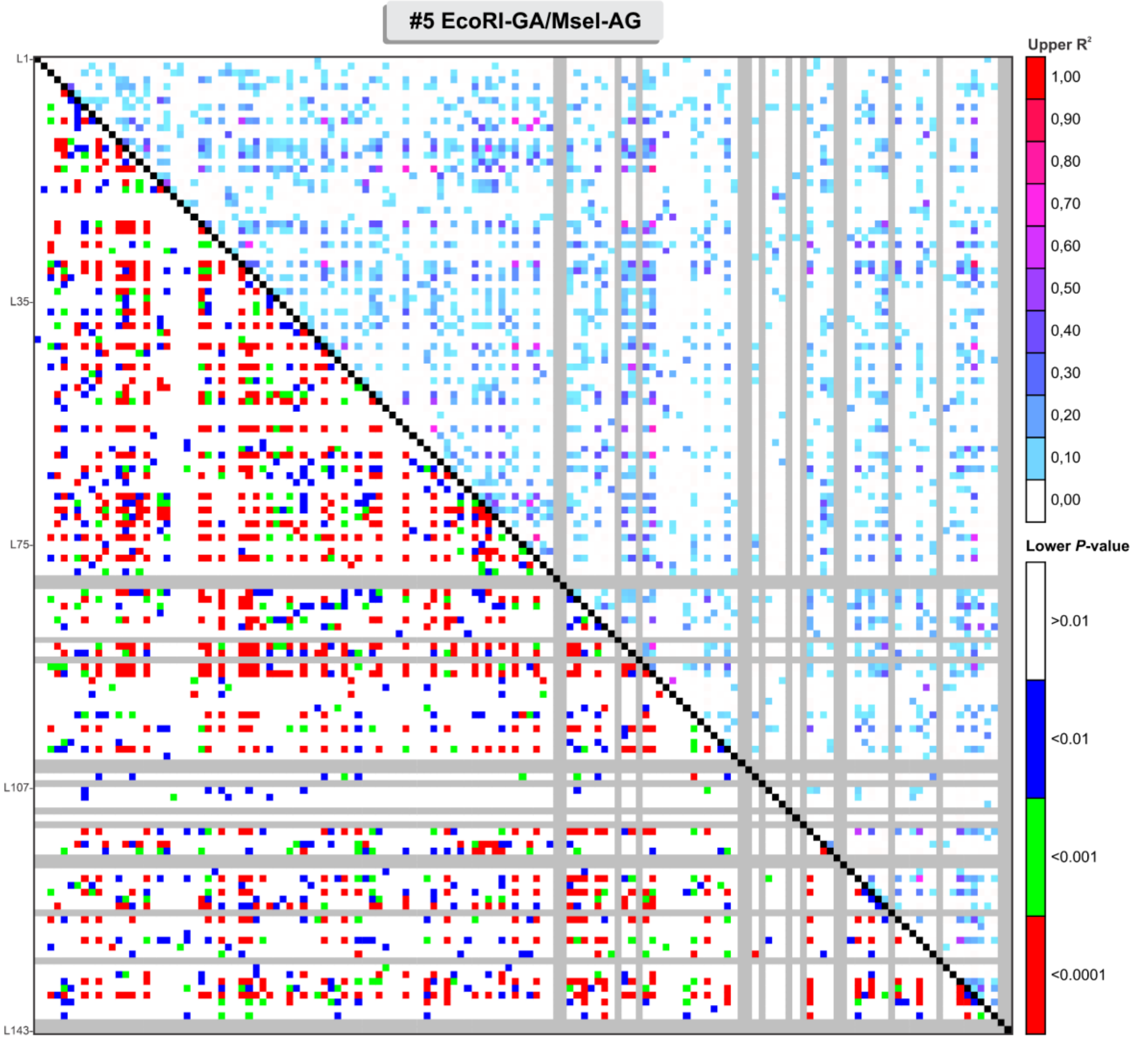
Supplementary Figure S6: PhiPT genetic distances among the studied populations for AFLP markers #3 EcoRI-GA/MseI-TT, #5 EcoRI-GA/MseI-AG, and #6 EcoRI-TA/MseI-AA. **A**, **C**, and **E**: Frequency Distribution of Random PhiPT vs. Observed PhiPT. **B**, **D**, and **F**: Percentages of molecular variance.



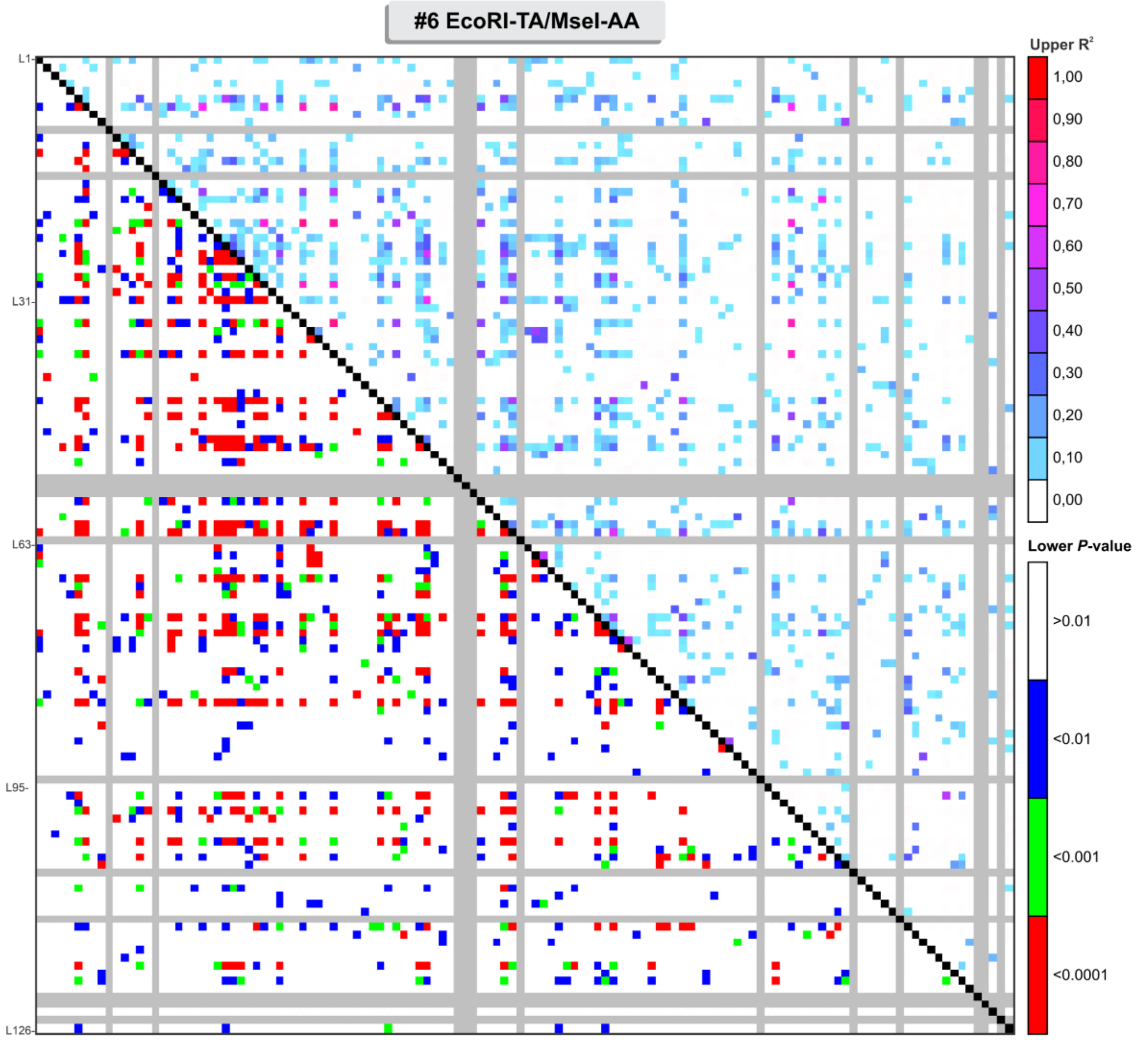
Supplementary Figure S7: PhiPT genetic distances among *S. brasiliensis* geographic populations for AFLP markers #3 EcoRI-GA/MseI-TT, #5 EcoRI-GA/MseI-AG, and #6 EcoRI-TA/MseI-AA. **A**, **C** and **E**: Frequency Distribution of Random PhiPT vs. Observed PhiPT. **B**, **D**, and **F**: Percentages of molecular variance. The most significant PhiPT values were found between the South (S) and Northeast (NE) isolates (PhiPT = 0.184–0.193). The lowest values were found in pairwise comparisons between the Southeast and Northeast, demonstrating the proximity of these isolates (PhiPT = 0.030–0.103). S: *S. brasiliensis* South isolates (n=22); SE: *S. brasiliensis* Southeast isolates (n=38); NE: *S. brasiliensis* Northeast isolates (n=11).



Supplementary Figure S8. Disequilibrium matrix for 149 polymorphic AFLP loci based on medically relevant *Sporothrix* species (*S. brasiliensis*, n=72; *S. schenckii*, n=67; *S. globosa*, n=34). Pairwise calculations (11,026 pairs) of linkage disequilibrium (LD) (r^2) are displayed above the diagonal, with the corresponding *P*-values for Fisher's exact test displayed below the diagonal. The colour legends indicate the level of significance (*P*-value) and the corresponding strength of LD (r^2). The locus position (L) is indicated on the left X-axis. Mean r^2 = 0.0379. Mean *D′* = 0.6729.



Supplementary Figure S9. Disequilibrium matrix for 143 polymorphic AFLP loci based on medically relevant *Sporothrix* species (*S. brasiliensis*, n=72; *S. schenckii*, n=67; *S. globosa*, n=34). Pairwise calculations (10,153 pairs) of linkage disequilibrium (LD) (r^2) are displayed above the diagonal with the corresponding *P*-values for Fisher's exact test displayed below the diagonal. The colour legends indicate the level of significance (*P*-value) and the corresponding strength of LD (r^2). The locus position (L) is indicated on the left X-axis. Mean r^2 = 0.0370. Mean *D'* = 0.6299.



Supplementary Figure S10. Disequilibrium matrix for 126 polymorphic AFLP loci based on medically relevant *Sporothrix* species (*S. brasiliensis*, n=72; *S. schenckii*, n=67; *S. globosa*, n=34). Pairwise calculations (7,875 pairs) of linkage disequilibrium (LD) (r^2) are displayed above the diagonal with the corresponding *P*-values for Fisher's exact test displayed below the diagonal. The colour legends indicate the level of significance (*P*-value) and the corresponding strength of LD (r^2). The locus position (L) is indicated on the left X-axis. Mean r^2 = 0.0271. Mean D' = 0.7111.