

Table S2: Population sizes and historical migration rate estimates among *Cryptococcus gattii* populations. The population sizes and migration rates were estimated using Migrate v2.3 (<http://popgen.scs.fsu.edu>) based on the five nuclear SCAR-MLST loci. The centre column shows the mean N_m value, while the left flanking values represents the lower (left value) and upper (right value) 95% confidence interval values.

Population	Population size (θ)			2Nm [+receiving population]											
				Lower	Mean	Upper	Lower	Mean	Upper	Lower	Mean	Upper	Lower	Mean	Upper
	[2Nm _μ]			SA,+	SA,+	SA,+	AFR,+	AFR,+	AFR,+	AUS,+	AUS,+	AUS,+	EUR,+	EUR,+	EUR,+
South America (n = 76)	0,0121	0,0224	0,0485				0,0000	0,0000	1,1954	2,8948	6,3345	11,7904	0,1631	2,8550	12,5672
Africa (n = 10)	0,0030	0,0094	0,0568	0,0000	0,0000	2,9298				0,0000	0,0000	1,5210	0,1631	2,8550	12,5672
Australasia (n = 38)	0,0024	0,0062	0,0249	6,5686	12,2932	20,6754	0,0000	0,0000	1,1954				0,1631	2,8550	12,5672
Europe (n = 6)	0,0022	0,0098	0,1712	0,7640	3,0733	7,9845	0,0000	0,0000	1,1954	0,0000	0,0000	1,5210			
North America (n = 48)	0,0061	0,0089	0,0137	6,1579	11,9553	20,5466	1,9000	4,3769	8,3399	1,8882	4,7509	9,6257	3,5451	11,4201	26,5310