

Supplementary Material

Table S1. *De novo* assembled and microsatellite containing contigs of *Amylostereum areolatum* strains.

Strains	<i>De novo</i> assembled contigs	Number of all microsatellite containing contigs					
		Dinucleotides	Trinucleotides	Tetranucleotides	Pentanucleotides	Hexanucleotides	Total
NZ_K17A	19 871	101	184	58	18	33	394
RSA_NK1	13 468	116	207	73	11	32	439
CMW6863	13 134	118	204	61	11	35	429
ARG8	18 657	118	204	61	11	35	429
CMW37110	12 101	99	173	58	11	36	377

Table S2. Microsatellite motifs isolated from the *Amylostereum areolatum* isolate NZ_K17A genome.

Microsatellite class	Total motif (% of all microsatellites)	Abundant motifs	Number of motifs	% of each microsatellite class	% of all microsatellites
Dinucleotides	66 (28.3%)	CG	12	18.2	5.2
		AT	11	16.7	4.7
		CT	13	19.7	5.6
		AG	16	24.2	6.9
		AC	9	13.6	3.9
		TG/GT	5	7.6	2.2
Trinucleotides	119 (51.1%)	CCG	3	2.5	1.3
		CGG/GGC	2	1.7	0.9
		GAT	2	1.7	0.9
		ATC	2	1.7	0.9
		AGG	22	18.5	9.4
		CCT	17	14.3	7.3
		GCT/CGT	19	15.9	8.2
		AGC/ACG	22	18.5	9.4
		CTT	2	1.7	0.9
		AAC	4	3.4	1.7
		GTT	1	0.8	0.4
		GGT	12	10.1	5.2
		ACC	11	9.2	4.7
		Tetranucleotides	32 (13.7%)	GGAT/AGGT	6
ATCC	2			6.3	0.9
ATCT	3			9.4	1.3
AGAT	7			21.9	3
CCGT	2			6.3	0.9
ACGG	1			3.1	0.4
ATGT	1			3.1	0.4
ACAT	2			6.3	0.9

		AAGG	1	3.1	0.4
		AACC	4	12.5	1.7
		GGTT	1	3.1	0.4
		AAAG	1	3.1	0.4
		TTTC	1	3.1	0.4
Pentanucleotide	5 (2.2%)	AAAGG	1	20	0.4
		AACCG/ACCAG	2	40	0.9
		GGATT	1	20	0.4
		AATGG	1	20	0.4
Hexanucleotide	11 (4.7%)	CCTCTT	1	9.1	0.4
		CATCCT	2	18.1	0.9
		GTCCTT	1	9.1	0.4
		CCTCGT	1	9.1	0.4
		GGACTION	1	9.1	0.4
		ACTGGG	1	9.1	0.4
		AAGACG	1	9.1	0.4
		AGCCCG	1	9.1	0.4
		ACCCGC	1	9.1	0.4
		ACCAGG	1	9.1	0.4
Total	233 (100%)	-	-	-	-

Table S3. Private alleles in *Amylostereum areolatum* microsatellite study.

Population	Isolates	Marker	# of Allele	Allele size
Western Cape	CMW11414	Aa3-7	1	218
	CMW29663	Aa3-7	1	218
Australia	CMW 40871	Aa3-23_Aa4-5_Aa3-24	3	244_182_225
USA 13028	CMW 40703	Aa3-24	1	228

Table S4. *Amylostereum areolatum* multilocus genotype (MLG) diversity.

Network	"poppr" MLG_label	Isolates	Population	Marker defining MLGs
1	MLG_6	CMW 13657 CMW 43945 CMW 43952 CMW 13832	KZN; EC; MP	
		CMW 13658 CMW 43946 CMW 46043 CMW 43955		
		CMW 13829 CMW 43948 CMW 47563 CMW 43958		
		CMW 13835 CMW 43950 CMW 43964 CMW 43962		
		CMW 29657 CMW 43951 CMW 10521 CMW 43963		
2	MLG_7	CMW 8901 CMW 11582 CMW 44291 CMW 44293	WC; EC	Aa3-24
	MLG_2	CMW 9894 CMW 40875 CMW 44965 CMW 44294		
		CMW 10300 CMW 44285 CMW 44966		
		CMW 11406 CMW 44286 CMW 44967		
		CMW 11411 CMW 44290 CMW 44292		
3	MLG_1	CMW 13656 CMW 43953	KZN; EC; MP	Aa3-4
		CMW 11315 CMW 43954		
		CMW 13653 CMW 43956		
		CMW 13836 CMW 43957		
		CMW 13838		
4	MLG_3	CMW 29659	KNZ; MP	Aa3-4
		CMW 43960		
		CMW 43961		
5	MLG_5	CMW 11414	WC	Aa3-7
		CMW 29663		
6	MLG_8	CMW 43947	KZN	Aa4-3
		CMW 43949		
7	MLG_9	CMW 8900	WC	Aa3-4 & Aa4-3
8	MLG_4	CMW 9745	WC	Aa3-4 & Aa4-3
9	MLG_10	CMW 40703	USA13028	Aa3-4 & Aa3-24
10	MLG_11	CMW 40871	Aus	Aa3-4, Aa3-23, Aa3-24, Aa4-4

MLG_2 included by poppr and excluded by Network

Table S5. *Amylostereum areolatum* multilocus genotypes (MLG)

MLG	Aa3-4	Aa3-5	Aa3-7	Aa3-8	Aa3-9	Aa3-23	Aa4-5	Aa4-3	Aa3-24	Aa3-25	Aa3-14
1	226 226	200 210	221 230	189 195	248 251	253 253	174 186	206 206	204 234	222 237	222 225
2	219 219	200 210	Missing	189 195	248 251	253 253	174 186	206 206	204 231	222 237	222 225
3	219 226	200 210	221230	189 195	248 251	253 253	174 186	206 206	204 234	222 237	222 225
4	226 226	200 210	221 230	189 195	248 251	253 253	174 186	222 222	204 231	222 237	222 225
5	219 219	200 210	218 218	189 195	248 251	253 253	174 186	206 206	204 231	222 237	222 225
6	219 219	200 210	221 230	189 195	248 251	253 253	174 186	206 206	204 234	222 237	222 225
7	219 219	200 210	221 230	189 195	248 251	253 253	174 186	206 206	204 231	222 237	222 225
8	219 219	200 210	221 230	189 195	248 251	253 253	174 186	206 222	204 234	222 237	222 225
9	219 226	200 210	221 230	189 195	248 251	253 253	174 186	222 222	204 231	222 237	222 225
10	226 226	200 210	221 230	189 195	248 251	253 253	174 186	206 206	204 228	222 237	222 225
11	226 226	200 210	221 230	189 195	248 251	244 244	174 182	206 206	204 225	222 237	222 225

Table S6. Vegetative compatibility group among *Amylostereum areolatum* isolates^a.

Isolates	CMW29659 ^c	CMW43961 ^c	CMW11414 ^e	CMW29663 ^e	CMW13658 ^f	CMW43962 ^f	CMW44294 ^g	CMW10300 ^g	CMW43949 ^h	CMW43947 ^h	CMW43956 ^b	CMW13656 ^b	CMW8900 ⁱ	CMW9745 ^d
CMW29659 ^c	+	+	+	+	+	+	+	+	+	+	+	+	+	+
CMW43961 ^c		+	+	+	+	+	+	+	+	+	+	+	+	+
CMW11414 ^e			+	+	+	+	+	+	+	+	+	+	+	+
CMW29663 ^e				+	+	+	+	+	+	+	+	+	+	+
CMW13658 ^f					+	+	+	+	+	+	+	+	+	+
CMW43962 ^f						+	+	+	+	+	+	+	+	+
CMW44294 ^g							+	+	+	+	+	+	+	+
CMW10300 ^g								+	+	+	+	+	+	+
CMW43949 ^h									+	+	+	+	+	+
CMW43947 ^h										+	+	+	+	+
CMW43956 ^b											+	+	+	+
CMW13656 ^b												+	+	+
CMW8900 ⁱ													+	+
CMW9745 ^d														+

^a Isolates were scored as compatible (+) and incompatible (-)

Multilocusgroup; ^bMLG1, ^cMLG3, ^dMLG4, ^eMLG5, ^fMLG6, ^gMLG7, ^hMLG8, ⁱMLG9

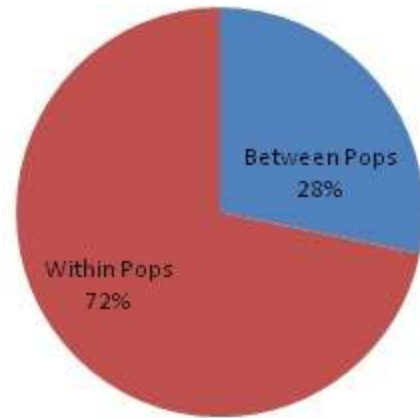


Figure S1. AMOVA illustrating the percentage of variation within and between populations of *Amylostereum areolatum* ($\Phi_{iPT} = 0.283$, $P = 0.001$) in South Africa. Most variation occurs within than between populations.