

Supplementary data for Clonal reproduction and low genetic diversity in Northern Australian *Santalum lanceolatum* (*Santalaceae*) populations highlights the need for genetic rescue of this commercially significant species

Table S1. List of 22 *Santalum* sp. microsatellite markers (primers) screened for cross-amplification with *Santalum lanceolatum*.

Primer Name	Forward Sequence	Reverse Sequence	Species	Source
mSiCIR39	AGTGACCCGTAGTTTGAC	GGAGAGATTGTATTGGAAC	<i>S. insulare</i>	LHullier et al., (2006)
mSiCIR42	CGCACAACTAAAAACCCT	TCGTAATGGATGGCTTCTA	<i>S. insulare</i>	LHullier et al., (2006)
mSiCIR44	GCCTTTTTCACTTTTCGC	ACACCTCACACAGTTCCT	<i>S. insulare</i>	LHullier et al., (2006)
mSiCIR139	GTGCTACTTGATACCCAGG	GGACAACCAGAGGAGAAC	<i>S. insulare</i>	LHullier et al., (2006)
mSiCIR148	CATAGAAGTAGTTGGGTTTA	TTTAGGTAGGATGTTGG	<i>S. insulare</i>	LHullier et al., (2006)
mSiCIR153	ATGCTTTTGTGGTGATTC	GCTTGGAGTATCTTGTGG	<i>S. insulare</i>	LHullier et al., (2006)
mSiCIR185	ACAACAACGCATAACCCT	AAAACAATGGCACTGAGAA	<i>S. insulare</i>	LHullier et al., (2006)
mSaCIRH09	GCCTCTGCTTCCTCCCATGTAG	AACTCCATTGTGATTCTCCCA	<i>S. austrocaledonicum</i>	Bottin et al., (2005)
mSaCIRH11	AGTCACGGAACAGCCAAGC	CTTCCCTGTGCCTTGTGTA	<i>S. austrocaledonicum</i>	Bottin et al., (2005)
mSaCIRG01	GCTCAACCCATTTTATCC	ACACAGCAGAACTCCAACA	<i>S. austrocaledonicum</i>	Bottin et al., (2005)
mSaCIRG10	GTGCTACCTGCTACCTTTTT	CCAATAACGGCTTCAACTCA	<i>S. austrocaledonicum</i>	Bottin et al., (2005)
mSaCIRF04	TCATTACACAGGCATCAGAAA	CTACCATCCACCACCGACAT	<i>S. austrocaledonicum</i>	Bottin et al., (2005)
mSaCIRF10	TTAGGAAAAACATAGCACACT	GAGCACTTCACCACCATTAC	<i>S. austrocaledonicum</i>	Bottin et al., (2005)

SsA004	AGCTTGTTCCAATTAACCTGTC	AAGGGACGGTAACTTGATGAG	<i>S. spicatum</i>	Millar et al., (2011)
SsA103	ATTGCATAAGCATGATCTTCC	GCAGAACTTGGTTGGCTACT	<i>S. spicatum</i>	Millar et al., (2011)
SsA105	TCGCAATTAGAGAAATTCCTC	GCAGAACTTGGTTGGCTACT	<i>S. spicatum</i>	Millar et al., (2011)
SsA106	AAGGTTGGTTTTTAGTGTGC	CATTCTATGGGGGAAATCTC	<i>S. spicatum</i>	Millar et al., (2011)
SsA119	TTCCTAGACATTGGCACATTG	GCCCCTAAAGAATTACAGAC	<i>S. spicatum</i>	Millar et al., (2011)
SsB112	GGAGCAAGCTAAGCACAC	GCAGCCAAGAAAAATTACTAC	<i>S. spicatum</i>	Millar et al., (2011)
SsB122	AGGTGCGTCTCTTTCATACTA	CAGTCGTTTCGGTCACA	<i>S. spicatum</i>	Millar et al., (2011)
SsB126	ACCGCCCGGTTGTATA	GTGGGTATTCGCTGAGTATG	<i>S. spicatum</i>	Millar et al., (2011)
SsB128	CCCAAAGCCATTCTTAAAGGT	CTAAGGGACGAAGCGAAATC	<i>S. spicatum</i>	Millar et al., (2011)

Table S2. Summary of Micro-checker and ML_NULLFREQ analysis across 13 loci and eight population of *Santalum lanceolatum*.

Locus	Null Present	Oosterhout	Chakraborty	Brookfield 1	Brookfield 2	ML_NULLFREQ
mSiCIR42	yes	0.1496	0.2521	0.0771	0.2183	0.006
mSiCIR44	no	0.0577	0.0632	0.0394	0.0394	0.142
mSiCIR153	yes	0.2086	0.3018	0.1886	0.3408	0.000
mSaCIRH11	no	-0.0583	-0.05	-0.0458	0.0243	0.884
mSaCIRF10	no	0.054	0.0502	0.0349	0.1112	0.300
SsA106	no	0.0485	0.0707	0.0129	0.0129	0.187
Lanc03	yes	0.2479	0.6387	0.1555	0.2894	0.000
Lanc07	no	0.0566	0.0737	0.0386	0.0962	0.005
Lanc08	yes	0.1809	0.5285	0.0831	0.1423	0.000
Lanc09	no	0.0287	0.0228	0.0187	0.0868	0.334
mSiCIR33	yes	0.0584	0.0635	0.0531	0.0832	0.036
mSaCIRE09	yes	0.0626	0.0706	0.0566	0.0889	0.027
mSaCIRH10	no	0.0334	0.0236	0.0171	0.0981	0.200

Table S3. Characterization of twelve microsatellite loci isolated from 135 unique multilocus genotypes of *Santalum lanceolatum* from the Northern Peninsula Area (NPA) of Cape York (Queensland, Australia).

Locus - GenBank	Size range (bp)	PIC	N _A	H _O	H _E	F _{IS}
mSiCIR44 AM113981	114-116	0.374	2	0.499	0.35	- 0.424
mSiCIR153 AM113981	282-296	0.625	5	0.326	0.431	0.244
mSaCIRH11 AJ831404	233-243	0.686	6	0.723	0.516	- 0.403
mSaCIRF10 AJ831398	138-160	0.610	6	0.55	0.462	- 0.19
SsA106 EU287765	204-218	0.235	3	0.108	0.11	0.017
mSiCIR42 AM113980	210-222	0.273	6	0.23	0.243	0.051
Lanc07 HM448039	137-161	0.384	6	0.422	0.351	-0.203
Lanc08 HM448040	112-128	0.085	4	0.052	0.098	0.467
Lanc09 HM448041	166-184	0.680	8	0.557	0.489	- 0.14
mSiCIR33 AM113978	200-234	0.756	12	0.685	0.616	- 0.112
mSaCIRE09 AJ831397	154-172	0.741	10	0.759	0.649	- 0.168
mSaCIRH10 AJ831403	217-237	0.555	8	0.577	0.507	- 0.139
<i>mean</i>		0.500	6.33	0.457	0.402	- 0.083

PIC - Polymorphic information content, N_A - number of alleles; H_O - observed heterozygosity; H_E - expected heterozygosity; F_{IS} - inbreeding coefficient.

Table S4. Summary of clonal measures between adult and juvenile *Santalum lanceolatum* populations across the Northern Peninsula Area (NPA), Cape York (Queensland, Australia).

Population - age class	N	G	G/N	% Clones	N _{CE}	N _{RA}	P _{sex}	P _{sex} N _{gen}
<i>Adults</i>								
Bamaga	25	19	0.76	24.00	2	6	<0.0001	<0.0001
Injinoo	19	7	0.37	63.16	2	12	<0.0001	<0.0001
Muttee Heads	12	5	0.42	33.33	1	7	<0.0001	<0.0001
Seisia	25	21	0.84	16.00	2	4	<0.0001	<0.0001
Somersset West	15	7	0.47	53.33	3	8	<0.0001	<0.0001
Somersset East	21	15	0.71	28.57	3	6	<0.0001	<0.0001
<i>mean</i>	19.20	12.33	0.57	37.96	2.17	7.17		
<i>Juveniles</i>								
Bamaga juveniles	19	11	0.58	42.10	4	12	<0.0001	<0.0001
Injinoo juveniles	20	10	0.50	50.00	3	13	<0.0001	<0.0001

Seisia juveniles	21	18	0.86	14.28	4	7	<0.0001	<0.0001
mean	20	13.00	0.65	35.46	3.67	10.67		

N – number of sampled trees; G – number of unique multilocus genotypes; G/N , mean proportion of distinguishable genotypes; N_{GE} – number of genets, N_{RA} – number of ramets; P_{sex} – probability of encountering genotype more than once by chance; $P_{sexN_{gen}}$ – probability of finding the MLG in the N sampling units collected and analysed.

Table S5. Summary of private alleles from Cape York (Queensland, Australia) *Santalum lanceolatum* populations.

	Locus	Private allele count
<i>Adult subpopulation</i>		
Bamaga	n/a	0
Injinoo	mSaCIRF10	1
Muttee Heads	n/a	0
Seisia	Lanc07, Lanc09, mSiCIR33 (x3), mSaCIRE09	6
Somerset East	mSiCIR42, mSaCIRF10, Lanc08, mSiCIR153	3
Somerset West	mSaCIRH11, Lanc08	2
Rocky Creek	mSiCIR42, mSiCIR33, mSaCIRE09 (x2)	4
Price Creek	mSiCIR44, mSaCIRF10, Lanc07 (x2), Lanc09, mSiCIR33 (x2), mSaCIRH10	8

Table S6. Summary of Wrights F-statistics between all combined age class populations and adult v juvenile Cape York (Queensland, Australia) populations of *Santalum lanceolatum*.

	Among population variation	Among individual variation	Within individual variation	F_{ST}	F_{IS}	F_{IT}
All populations	24%	12%	64%	0.242	0.163	0.365
Adult v Juvenile populations	11%	15%	74%	0.110	0.167	0.259

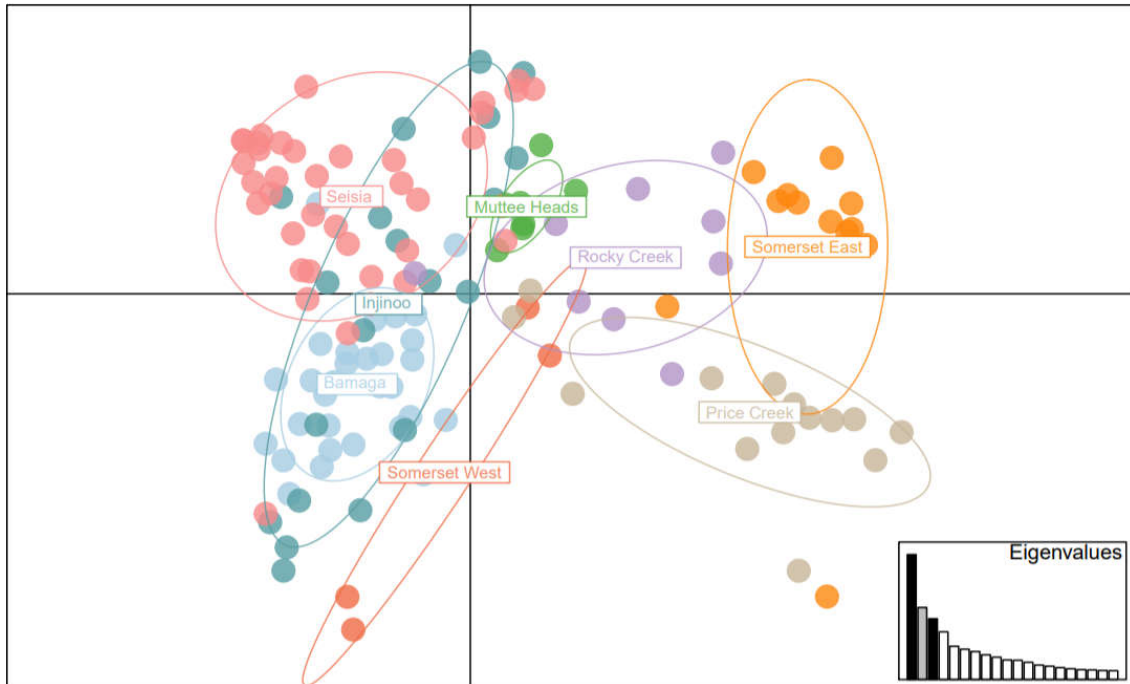


Figure S1. Principal coordinates analysis (PCoA) of eight *Santalum lanceolatum* populations using the axes 1 and 3 of genetic distance matrices. Eigenvalues at axes 1 and 3 shown explains 26.77% of variation.

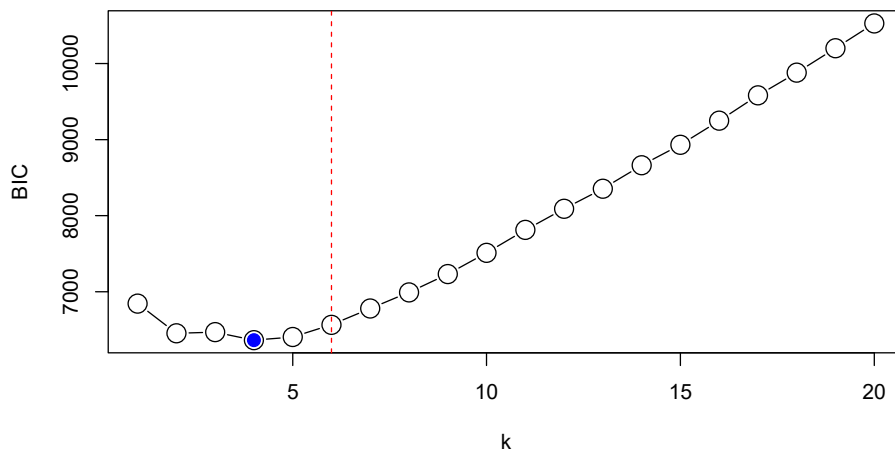


Figure S2. Bayesian Information Criterion (BIC) plot from the snapclust command (Adegent, R) displaying BIC values for increasing values of K for eight *Santalum lanceolatum* populations. The blue dot indicates 'optimal k', dashed red line indicates 'true k'.

K	Reps	Mean LnP(K)	Stdev LnP(K)	Ln'(K)	Ln''(K)	Delta K
1	20	-5556.095000	0.336350	—	—	—
2	20	-4932.540000	88.074164	623.555000	164.460000	1.867290
3	20	-4473.445000	82.675653	459.095000	186.030000	2.250118
4	20	-4200.380000	39.030765	273.065000	133.855000	3.429474
5	20	-4061.170000	143.412457	139.210000	28.685000	0.200017
6	20	-3893.275000	108.607991	167.895000	110.280000	1.015395
7	20	-3835.660000	191.086876	57.615000	—	—

Figure S3. Output of STRUCTURE validation for increasing values of K for optimal group selection for eight *Santalum lanceolatum* populations.

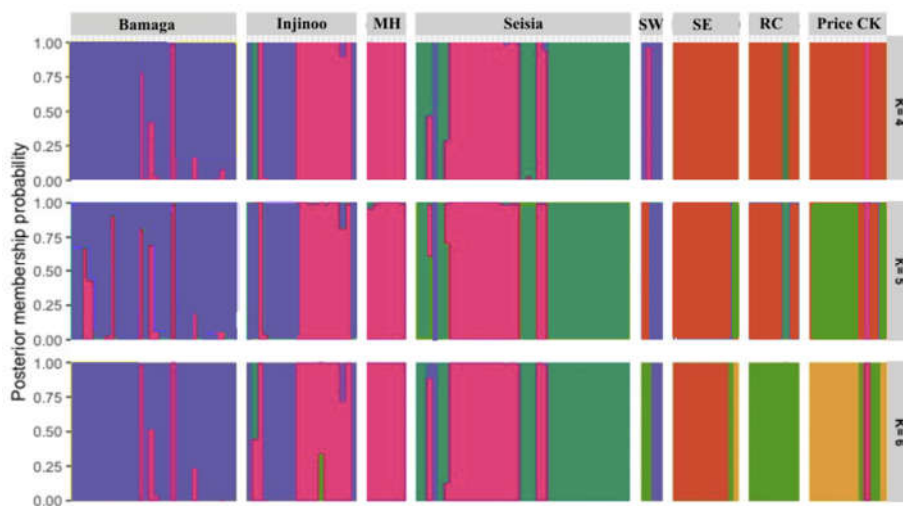


Figure S4. Individual admixture coefficients at $K = 4 - 6$ within and between eight *Santalum lanceolatum* populations from Cape York (Queensland, Australia) inferred using a discriminant analysis of principal components (DAPC). MH = Muttee Heads; SW = Somerset West; SE = Somerset East; RC = Rocky Creek.