

# Discussion on correlations between population genetic diversity of *Bombax malabaricum* and its adaptability to dry-hot valleys in Yunnan

Shuli Wang, Qiaoming Li\*

Xishuangbanna Tropical Botanical Garden, CAS, 88 Xuefu Road, Kunming, Yunnan 650223, P. R. China

Email: [lqm@xtbg.ac.cn](mailto:lqm@xtbg.ac.cn)

**Abstract:** In order to discuss the correlations between genetic diversity of *Bombax malabaricum* and the dry-hot environment, we surveyed the genetic diversity of 4 populations (YJ, YM, QJ, DJ) in dry-hot valleys of Yunnan province, 2 populations (GX, HN) in dry-hot regions and 1 population (BN) in wet-hot region using ISSR markers. Based on 10 primers, 142 clear and reproducible DNA fragments were generated. The percentage of polymorphic loci *PPB* was 90.14%, and Shannon's Information index *I* was 0.3864. Moreover, the coefficient of genetic differentiation (*G<sub>ST</sub>*) equaled 0.1870 and the  $\Phi_{st}$  equaled 0.177(AMOVA). The results showed high level of genetic diversity and low level of genetic differentiation among its populations. Furthermore, there were positive associations between genetic and geographic distance among *B. malabaricum* populations. We tested the associations between the five ecological factors (Annual relative humidity, Annual average temperature, Annual  $\geq 10^{\circ}\text{C}$  accumulated temperature, Annual precipitation, Altitude) and the genetic diversity (observed number of alleles *N<sub>a</sub>*, effective number of alleles *N<sub>e</sub>*, *PPB*, Nei's gene diversity *H* and Shannon's Information index *I*) of *B. malabaricum*. The results revealed that there were no significant correlations between the five ecological factors and genetic diversity. We inferred that the high level of genetic diversity and effective gene flow of *B. malabaricum* may play an important role in its adaptability to dry-hot adversity, and dry-hot environment has neutral effect on its genetic diversity. Considering the introduction of *B. malabaricum* in dry-hot regions, we need to sample abundantly within populations and involve different populations.

**Key words:** *Bombax malabaricum*, dry-hot valleys, ISSR, genetic diversity, genetic differentiation



Population code	Location	Sample size	No. of samples for experiments	Latitude	Longitude
QJ	Qionjiang, Yunnan	48	19	28°54'N	102°33'E
YM	Yunnan, Yunnan	68	14	23°40'N	103°30'E
YJ	Yuanjiang, Yunnan	40	16	23°36'N	102°00'E
DJ	Dianjiang, Yunnan	40	15	23°04'N	98°30'E
GX	Guangxi	42	14	23°18'N	109°37'E
HN	Hunan	66	16	18°40'N	109°00'E
BN	Xishuangbanna, Yunnan	40	16	21°38'N	101°28'E
Total		352	110		

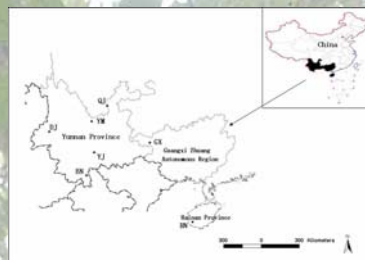


Fig. 1 Map showing sampled *Bombax malabaricum* populations

Population codes	Altitude(m)	Annual $\geq 10^{\circ}\text{C}$ accumulated temperature(°C)	Annual precipitation(mm)	Annual relative humidity(%)	Annual average temperature(°C)
QJ	1400	7253.9	823.0	90.8	20.9
YM	1206	7817.4	642.2	87.0	21.5
YJ	411	8073.4	796.4	89.0	23.7
DJ	960	5112.4	986.2	74.8	15.9
GX	382	7060.0	1260.0	80.0	21.0
HN	1429	8580.0	1279.5	83.0	25.4
BN	1080	7800.6	1520.5	84.0	21.3

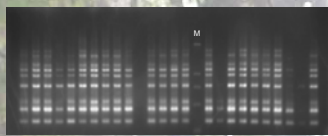


Fig. 2 The amplification products of *Bombax malabaricum* individuals of DJ population using primer 991

Primer	Sequence(5'-3')	Annealing temperature(°C)	No. of amplifying loci
810	GAGT	54	6
811	GAGC	54	15
816	GCAT	54	11
826	CACG	56	17
827	CACG	56	17
861	CACC	58	12
888	HBR(CA)	52	17
890	HBR(CA)	52	16
890	HVB(TG)	52	17
891	HVB(TG)	52	12

D:A,G or T:B,C; G or T:A,C or T; A,C or G

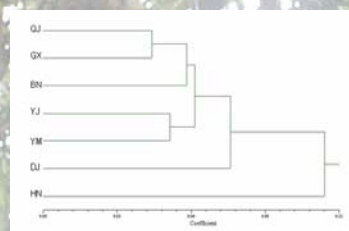


Fig. 3 Dendrogram of UPGMA cluster analysis among *Bombax malabaricum* populations based on Nei's(1978) genetic distance

Population code	No. of total loci	No. of polymorphic loci	<i>PPB</i> (%)
QJ	109	85	95.86
YM	104	76	83.52
YJ	100	80	86.54
DJ	102	79	85.43
GX	114	93	85.49
HN	100	75	82.82
BN	111	80	80.86
Mean	105.714	82.571	86.149
At species level	142	128	90.14

Population code	<i>N<sub>a</sub></i>	<i>N<sub>e</sub></i>	<i>H</i>	<i>I</i>
QJ	1.9986±0.4939	1.3772±0.3832	0.2179±0.2081	0.3232±0.2921
YM	1.5352±0.8005	1.3271±0.3754	0.1898±0.2037	0.2824±0.2915
YJ	1.5634±0.4977	1.3517±0.3907	0.2021±0.2078	0.2998±0.2969
DJ	1.5363±0.4986	1.2300±0.3801	0.1914±0.2039	0.2366±0.2969
GX	1.4549±0.4771	1.4494±0.3799	0.2429±0.2006	0.3804±0.2848
HN	1.2582±0.3820	1.2869±0.3738	0.1737±0.1997	0.2809±0.2846
BN	1.6376±0.4839	1.3807±0.3872	0.2223±0.2042	0.3311±0.2863
Mean	1.5815±0.4829	1.3461±0.3815	0.2089±0.2036	0.3062±0.2845
At species level	1.9014±0.2902	1.4302±0.3717	0.2210±0.1874	0.3864±0.2816

*N<sub>a</sub>*, Observed number of alleles; *N<sub>e</sub>*, Effective number of alleles; *H*, Nei's (1975) gene diversity; *I*, Shannon's information index.



Source of variance	SSD	MSD	Variance component	Variance (%)	<i>P</i> *
Among groups	1.6847	0.842	0.040359	1.76	<0.001
Among populations/groups	2.8837	0.721	0.034854	15.88	<0.001
Within populations	1.4833	0.179	0.179158	82.35	<0.001

SSD, Sum of squared deviations; MSD, Mean of squared deviations; *P*-values, The probabilities of having a more extreme variance component than the observed values above.

	QJ	GX	HN	YJ	DJ	BN	YM
QJ	****	0.9848	0.9287	0.9440	0.9235	0.9490	0.9480
GX	0.0084	****	0.9163	0.9358	0.9341	0.9162	0.9420
HN	0.0740	0.0885	****	0.9126	0.8724	0.8724	0.9041
YJ	0.0871	0.0857	0.0915	****	0.9449	0.9424	0.9540
DJ	0.0779	0.0862	0.1160	0.0867	****	0.9363	0.9213
BN	0.0609	0.0489	0.1160	0.0668	0.0635	****	0.9247
YM	0.0576	0.0397	0.1009	0.0471	0.0820	0.0579	****