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Supplementary data

Genomic sequencing using 454 pyrosequencing and development of an SSR primer database for *Lagerstroemia indica* L.

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Table S1. Detailed information on different crape myrtle samples used in this study

	Accession no.	**Cultivar**	**Origin**
1	B8	*Lagerstroemia indica* Linn.	Baokang, Hubei Province, China
2	B16	*Lagerstroemia indica* Linn.	Baokang, Hubei Province, China
3	B78	*Lagerstroemia indica* Linn.	Baokang, Hubei Province, China
4	B91	*Lagerstroemia indica* Linn.	Baokang, Hubei Province, China
5	B11	*Lagerstroemia indica* ‘Ewei 1’	Baokang, Hubei Province, China
6	ZX2	*Lagerstroemia indica* Linn.	Zhongxiang, Hubei Province, China
7	ZX4	*Lagerstroemia indica* Linn.	Zhongxiang, Hubei Province, China
8	ZX6	*Lagerstroemia limii* Merr	Zhongxiang, Hubei Province, China
9	HY1	*Lagerstroemia indica* Linn.	Hanyang, Hubei Province, China
10	HY2	*Lagerstroemia indica* Linn.	Hanyang, Hubei Province, China
11	HF1	*Lagerstroemia indica* Linn.	Hefeng, Hubei Province, China
12	HF2	*Lagerstroemia indica* Linn.	Hefeng, Hubei Province, China
13	HF5	*Lagerstroemia indica* Linn.	Hefeng, Hubei Province, China
14	SC1	*Lagerstroemia indica* Linn.	Sichuan Province, China
15	HN2	*Lagerstroemia indica* Dynamite	Hunan Province, China
16	HN3	*Lagerstroemia indica* Red Rocket	Hunan Province, China
17	ZK1	*Lagerstroemia* 'Biloxi'	Beijing Botanical Garden, China
18	ZK8	*Lagerstroemia* 'Wichita'	Beijing Botanical Garden, China
19	ZK13	*Lagerstroemia indica* Linn.	Beijing Botanical Garden, China
20	ZKM4	*Lagerstroemia indica* Linn.	Beijing Botanical Garden, China
21	M2	*Lagerstroemia indica* Linn.	America
22	M5	*Lagerstroemia indica* Linn.	America
23	M8	*Lagerstroemia indica* Linn.	America
24	ME6	*Lagerstroemia indica* Linn.	America
25	M1-1	*Lagerstroemia indica* Linn.	America

Table S2 Sequences and characterization of the primers screened using 24 crape myrtle samples.

Locus	**Primer sequences (5'-3')**	**Repeat motif**	**Size(bp)**	**Tm(°C)**
ZW1	F: GTCGGGATGAAAACCAAT R: GTAGGGGAGCAAGCGTAG	(AAGA)3	283	50.2
ZW3	F: CGTTCTAACACTGCCTTTT R: AACCAACTCATTGCTTCG	(TTTC)3	247	46.3
ZW4	F: CGCCAGACTTTGCTTATC R: ATCGTTCCACCTCCTTTC	(AG)11	214	48.6
ZW5	F: AAGGAGTTGGTGAGGGAA R: AGAAGGAAGCAAGGCAGA	(TC)9	208	50.1
ZW7	F: AAAATACGGACGGGAGAT R: AGGAGGAGGGTGCTAAAA	(AT)7	264	49.1
ZW8	F: CGGGACTCGCTCAGAGGACA R: CTTCGCCGCTGCGTTTCA	(TCT)5	248	57.3
ZW9	F: CCTCCGACTTGAGCACTG R: CTTTTACCCATCCACCGA	(AAT)4	277	46.9
ZW10	F: AGTGGCAGTAGGTAAGTG R: TAGTGTTTGATGGTCTCC	(ACAA)3	283	45.9
ZW11	F: CCACTGTCTGGTCCTTGC R: GTTTCTGTCCTCGGCTTG	(TTCT)3	276	50
ZW12	F: GGACTGTGAAGGGCTGTG R: ACGGAAGTAGGGACCAAA	(GGA)5	297	53.5
ZW14	F: TGCTTCAAAGTTCATTCT R: AAAACCATTATTCTCCCT	(AAG)4	282	46.7
ZW15	F: AAGTCAAGTAGTTAGCAAGT R: AACATAAACAGCCAGAGT	(TC)6	282	46.2
ZW16	F: CCTTTCAACCCTCCCTTCC R: CCGCCTATGACCCCAGAT	(CT)7	168	51.6
ZW17	F: CTATCTTATTATGTGGTG R: ACTTGGTATGTATCTGTC	(TAAT)3	217	40.8
ZW18	F: AAAACCGTCAATCATCAC R: AACTCCACCCTGCTCTGT	(TTC)8	202	49
ZW20	F: CTTTGTCAAGCCTTTCGG R: CACTCCTTCGGTGGTCGT	(AG)6	287	49.8

ZW21	F:	CTTCGGTTCTTTCTTAGTG	(AG)6	200	48.5
	R:	GTGATTTGCTTGCCTTGA			
ZW23	F:	GGTTGACTTTCACCGACA	(CAAT)3	198	45.2
	R:	CTAAGCCAGTAATCTCCA			
ZW24	F:	GGGGAGTAATACAAAGCA	(AACA)3	275	48.3
	R:	TGGGATTGAAGTAGAGGC			
ZW25	F:	GCCATCCATCATTATCAA	(AG)7	250	45.8
	R:	TTACGGCTGCTTATCTAC			
ZW26	F:	GACCGACCACATCCTTCT	(AGAC)3	255	49.2
	R:	CTTTCACGCACCTTCCCT			
ZW29	F:	CGAATGGAAGCATAGAGC	(TG)6	272	46.6
	R:	GCATAGATACAGGGTTTG			
ZW30	F:	CCTCCCAATCTTCAATCC	(GGAA)3	235	48.4
	R:	AACCGTGACTAACACCTCTA			
ZW32	F:	CTTCCTCGTCCTTCTCCA	(TGGG)3	250	48.3
	R:	GCCACTTTCCAGGTAGCC			
ZW34	F:	CTAATCCTGCGGTTCAAG	(TA)9	170	44.7
	R:	ACATCATAGCACAAGCGT			
ZW36	F:	GGCTAAAATGGTTGGACA	(TGA)4	292	49.9
	R:	TTGGATAATAAACGAGGA			
ZW38	F:	TCACTGCCAAGAATACGA	(AG)7	273	51.8
	R:	GTTACAGGTCCCACATCC			
ZW39	F:	CACATTCTTTCGCCATAC	(AG)7	184	48.6
	R:	AGTTCCCTCCGACTACAA			
ZW42	F:	TTGAACCACTTCCCTTTG	(ACAT)3	286	47.8
	R:	TCGGCTCAGACTTAGACC			
ZW45	F:	CGTCATCCCAACCAAGAA	(TAAT)3	187	48.9
	R:	CATAACCAAAGCCAGTCA			
ZW46	F:	ATGCCCGACTTCCACCAA	(CT)7	169	50.8
	R:	CAACGGATGTCCTTCACC			
ZW48	F:	ACCAAGAATACCAGTCGT	(TAA)4	177	46.7
	R:	TCAGTCGCTCGCTACAAC			