



Heritability and gene effects for plant architecture traits of crape myrtle using major gene plus polygene inheritance analysis



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ABSTRACT

Plant architecture is important for crape myrtle (*Lagerstroemia indica*) cultivation and breeding. To investigate the genetic inheritance of plant architecture traits in *Lagerstroemia*, a mixed major gene plus polygene inheritance model was employed to analyze three traits in six generations (P_1 , P_2 , F_1 , B_1 , B_2 and F_2), including plant height (PH), internode length (IL) and primary lateral branch height (PLBH). The three traits showed extensive coefficient of variation and high broad sense heritability (0.60–0.84). Though transgressive segregations were present, transgressive heterosis was not observed in all the generations. The results showed that the IL fitted the D-0 model, which was followed by a one additive-dominance major gene plus additive-dominance-epistasis polygene genetic model. In addition, the PH and PLBH were quantitative traits fitting the E-0 model, namely two additive-dominance-epistasis major genes plus additive-dominance-epistasis polygene genetic model. The highest heritability of the major gene (83.62%) for the IL was observed in F_2 population, indicating that the IL trait was mainly controlled by genetic factors with a low effect of environmental factors and should be selected in early generations. However, the highest heritabilities of the major genes for the PH and PLBH were 43.23% and 70.29% in B_1 population, indicating that the PH and PLBH should be selected in late generations due to the large effect of environmental factors. Therefore, these findings will provide a theoretical instruction for the QTL mapping and breeding of desirable plant architecture in crape myrtle.

1. Introduction

Lagerstroemia (Crape myrtle) is native to southeast Asia, including at least 50 species of deciduous shrubs or small trees (Brickell, 1996). It was firstly introduced in China, which took place approximately 1800 years ago (Byers, 1997). Species in this genus are valued in landscaping for their mild-climate habitat, graceful plant architecture, long-lasting flower period and diverse colors. Under natural conditions, crape myrtle exists as a diploid plant ($2n = 2x = 48$) (Wang et al., 2012). Most breeding programs focused on improving horticultural traits by inter-specific hybridization between *L. indica* and *L. fauriei*. These works resulted in the release of more than 20 inter-specific hybrids, which successfully combined the powdery mildew of *L. fauriei* with other ornamental traits from *L. indica* (Egolf, 1981, 1987, 1990; Pooler and Dix, 1999). Self-pollination is important to produce homozygous lines for traits such as plant architecture, flower color and pest resistance. The findings from decades of breeding programs at the U.S. National

Arboretum indicated that viable seeds can be produced by self-pollination of *L. indica* (Pooler, 2007). Crape myrtles possess high variabilities in the rate of growth, which had allowed to select a wide range of genotypes with height ranging from 20 cm to 10 m (Guidry and Einert, 1975). However, increased attention has been paid to breed new cultivars with peculiar plant type in America, Japan, Italy and China, especially dwarf or potted crape myrtle.

The first dwarf crape myrtle was introduced in 1960 by Otto Spring in Okmulgee, OK (Egolf and Andrick, 1978). These plants, characterized by low plant height, compact plant type, short internodes and abundant mini flowers, were pursued as container plants in the *Lagerstroemia* breeding programs. Although the dwarf crape myrtle was detailedly documented for the background and characteristic, the cause and genetic inheritance of this anomalous phenotype had not been further elucidated.

A number of studies have reported the inheritance of plant architecture such as compact dwarf plant pigeonpea (*Cajanus cajan*)

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Fig. 1. Plant materials used in this study. (a) female parent; (b) male parent; (c) individual in the F_1 population; (d) individuals in the B_1 population; (e) individual in the B_2 population; (f) individual in the F_2 population.

(Dhanasekar et al., 2007), pillar or dwarf plants in peach (*Prunus persica*) (Hu and Scorza, 2009; Dardick et al., 2013; Dardick et al., 2013), and basal branching type in guar (*Cyamopsis tetragonoloba*) (Liu et al., 2006). The genetic study in pigeonpea indicated the compact dwarf plant type was governed by a single recessive gene. In peach, the plant height and columnar (canopy angle) traits were each independently controlled by a single gene. The results in jatropha suggested that dwarfiness and erect growth habit were each controlled by independent genes with incomplete dominant action (Khin et al., 2014). For *Lagerstroemia* species, Ye et al. (2014, 2016) investigated the plant architecture using a F_1 population derived from *L. fauriei* (non-dwarf) \times *L.*

indica (dwarf), which showed that the dwarf trait was probably controlled by a major gene and modified by minor genes, and the plant height (PH) was determined by internode length (IL) and primary lateral branch height (PLBH). However, given the environmental factors, structure genes or other regulators, the speculation for the genetic inheritance of plant architecture should be confirmed using different methods or validated in various generations.

Various methods were used to investigate the genetic inheritance for quantitative traits. For example, Morton and Maclean (1974) identified the genetic hypotheses about quantitative characters using a mixed model of major locus, polygenic variation, and both common and

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