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Evaluation of combining ability and genetic variance for growth traits in *Bauhinia variegata* L.

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Abstract

The present investigation was undertaken to study the combining ability and genetic variance for growth traits in *Bauhinia variegata*. In this study 6 lines (female) genotypes (P_3, P_8, P_{16}, P_{24}, P_{27} and P_{32}) and 4 testers (male) genotypes (P_{12}, P_{13}, P_{14} and P_{17}) were crossed using line x tester mating design and their 24 F_1 hybrids were raised in the mist chamber of the Department of Tree Improvement and Genetic Resources, Dr. Y S Parmar University of Horticulture and Forestry, Nauni, Solan (H.P.) during 2017-2018. After 6 months the resulting progenies were evaluated for growth traits in a randomized complete block design with three replications at nursery stage. ANOVA suggested significant differences among lines and testers on most studied characters. Among lines P_{16} followed by P_{32}, P_{27} and P_3 were identified as promising good general combiners for growth traits with significant positive general combining abilities (GCA). Among testers P_{17} followed by P_{14} provided good GCA for most of the traits studied. Crosses $P_{16} \times P_{14}$, $P_{32} \times P_{17}$ and $P_3 \times P_{17}$ exhibited best specific combining ability (SCA) for the majority of growth and biomass traits. The ratio of $\sigma^2 gca/\sigma^2 sca$ which was less than unity in most of the traits and more than unity in others suggested the important role of both additive and non-additive gene actions in the inheritance of these characters with preponderance of non-additive gene actions.

Keywords: Line x tester, combining ability, progenies, GCA, SCA, gene action

Introduction

Bauhinia variegata (Fabaceae) commonly known as Kachnar in Hindi and Mountain Ebony in English is a small to medium-sized deciduous tree with a short bole and spreading crown, attaining a height of up to 15 m. It is planted in garden, park and roadsides as ornamental plant in many warm temperate and sub-tropical regions. The species is native to Southeast Asia and grows from India to China in tropical and sub-tropical climate (Hocking, 1993; Sinha and Verma, 2012) [21]. It commonly grows in the sub-Himalayan tract and outer Himalaya from the Indus River eastwards across Assam and also in dry forests of east, central and south India (Anonymous, 1983) [1]. It is also distributed in most tropical countries, including Africa and South America (Anonymous, 1995) [2]. In India it is one of the important fodder species on which farmers bank up during the winter lean period when the grasses are dry, less digestible and unpalatable. Its leaves are rich in mineral and proximate composition which makes it highly nutritious and palatable (Thakur, 2010) [23].

The genus *Bauhinia* consists of about 500 species grown in the tropical regions of the world (Larson, 1974) [15]. The genus includes trees, vines and shrubs that are frequently planted for their showy flowers and ornamental foliage (Bailey, 1941) [5]. *Bauhinia variegata* grows well in soils of medium fertility that are either droughty or moist. It commands a good reputation of wind firmness, wide adaptability, frost and drought resistance, coppicing and high aesthetic value (Anonymous, 1983) [1]. While the species is most frequently planted for its ornamental qualities other properties are utilized: the bark is used as an astringent in tanning and dyeing and the leaves and flower buds as a vegetable (Bailey, 1941) [5]. The various parts of the plant *viz.*, flower buds, flowers, stem, stem bark, leaves, seeds and roots are practiced in various indigenous systems of medicine and popular among the various ethnic groups in India for the cure of variety of ailments (Arvind *et al.*, 2012) [4].

Materials and Methods

The experiment was conducted in mist chamber condition of the Department of Tree Improvement and Genetic Resources, Dr. Y S Parmar University of Horticulture and Forestry,

Nauni, Solan (H.P.) from 2017 to 2018. The experimental site is located at an elevation of 1200 m above mean sea level in north-west of Himalayas and lies between 30º51' N latitude and 76°11' E longitude. The experimental area is hilly, marked with elevations, depressions and has a gentle slope towards the southeastern aspect. The genotypes involved in this study were originated from seeds of plus trees collected from different states *viz*; Himachal Pradesh, Haryana, Jammu and Kashmir and Uttarakhand and maintained as seedling seed orchard in the research farm field of the Department of Tree Improvement and Genetic Resources. The materials were crossed using Line x Tester Mating Design (Comstock and Robinson, 1948, 1952) [10, 11]. Line x tester is a modified nested design where each male is mated to a number of same females in a set. It can be used to estimate genetic variance components that is additive and dominance variances and narrow-sense heritability. In addition combining ability effect can also be evaluated. The progenies were created by crossing each of the 4 male *B. variegata* genotypes [P_{12} (Mandi), P_{13} (Nahan), P_{14} (Kunihar) and P_{17} (Paonta Sahib)] with one set of 6 female genotypes [P_3 (Kathua), P_8 (Giripul), P_{16} (Solan), P_{24} (Narag), P_{27} (Dhaulakuan) and P_{32} (Sahastradhara)].

Statistical Analysis
The data collection was based on five plants per replication and was computed using IBM SPSS Statistics V24.0 program. Simple statistics for each trait such as Mean, Standard Error (SE), and Standard Deviation (SD) were determined. Analyses of variance (ANOVA) among traits were also carried out. GCA and SCA and standard errors of the estimates were determined by the following formula (Singh and Chaudhary, 1985) [22]:

GCA (lines) = Yi../rt – Y…/rlt
GCA (testers) = Y.j./rl – Y…/rlt
SCA= Yij./r – Yi../rt – Y.j./rl + Y…/rlt
SE (GCA for lines) = $(Me/rt)^{1/2}$
SE (GCA for tester) = $(Me/rl)^{1/2}$
SE (SCA) = $(Me/r)^{1/2}$
SE (GCAi – GCAi') line= $(2Me/rt)^{1/2}$
SE (GCAj – GCAj') tester= $(2Me/rl)^{1/2}$
SE (SCAij – SCAi'j') = $(2Me/r)^{1/2}$

where, Yi..= Total of the ith line, Y.j. = Total of the jth tester, Y…= Grand total, r, l and t = number of replications, lines and testers, respectively, SE= Standard error of the estimate and Me= Error mean square.
The significance of GCA and SCA effects were tested by dividing the corresponding GCA and SCA values by their respective standard error and comparing the obtained t with tabular t-value at error degree of freedom. The genetic components were determined as follows:

Cov H.S. (female) = (Ml – Ml x t) / r x t
Cov H.S. (male) = (Mt – Ml xt) / r x l
Cov H.S. (average) = 1/r(2lt-l-t){[((l-t)Ml + (t-1)Mt) / (l + t – 2)] – Ml x t}
Cov F.S. = {[(Ml – Me) + (Mt – Me) + (Ml x t – Me)]/3r} + [6r Cov HS (average) –r (l- CovHS (average)] /3r

Additive genetic variance (σ^2A), dominance genetic variance (σ^2D and average degree of dominance were estimated as below (Singh and Chaudhary, 1985) [22]:

σ^2A= [4/(1 +F)] σ^2gca = [4/(1 +F)] Cov HS (average)
σ^2 D= [4/(1 +F)^2] σ^2sca =[4/(1 +F)^2] Cov HS (average)
Average degree of dominance= $(\sigma^2$ D/ σ^2A)$^{1/2}$

where, σ^2gca= Estimate of GCA variance, σ^2sca= Estimate of SCA variance, σ^2 P= Estimate of phenotypic variance (plot basis) and F= Inbreeding coefficient, which was considered as zero because both lines and testers were non-inbred. In addition it was assumed that the epistasis variance is negligible.

Results and Discussion
Combining ability
The ANOVA for growth traits showed significant differences between tested crosses for all of the traits under study (Table 1). High significant differences were observed among lines (female) parents for all the studied traits except for leaf area. Significant differences were also observed among testers (male) parents for all the studied traits except for plant height and collar diameter indicating the existence of ample genetic variability among parents used as experimental materials in this study. This observation was sufficient evidence for breeding and selection of improved fodder parent candidates for these characters.

Table 1: Analysis of variance for combining ability for growth traits in *B. variegata*

Sources of Variation	DF	Mean sum squares							
		Plant height	Collar diameter	No. of branches	No. of leaves	Leaf area	Petiole length	Internodal length	Root length
Replication	2	71.43	0.15	0.28	0.66	18.01	0.74	0.37	70.37
Crosses	23	85.97*	0.50*	1.76*	92.35*	48.72*	1.13*	0.78*	199.50*
Lines	5	122.40*	1.20*	2.89*	140.30*	42.28	2.90*	1.17*	294.27*
Testers	3	62.97	0.52	5.56*	37.21*	38.25*	0.50*	1.31*	228.58*
Line x Tester	15	8.43*	0.26*	0.62*	87.40*	27.93	0.67*	0.54	162.09*
Error	46	21.17	0.24	6.93	1.15	10.63*	0.09	0.36	8.32

*Significant at 0.05 level

General combining ability effects
General combining ability (GCA) estimates for growth traits revealed that among lines P_3 showed significant positive GCA effect for plant height, collar diameter, number of branches, petiole length and root length; P_{24} for leaf area; P_{16} for plant height, number branches, number of leaves, internodal length and root length; P_{27} for number of branches and number of leaves; P_{32} for plant height, number of leaves, internodal length and root length (Table 2). Among testers P_{12} recorded significant and positive GCA effect for plant height, collar diameter, internodal length and root length; P_{13} for leaf area; P_{14} for petiole length and root length and P_{17} for number of branches, number of leaves, and root length indicating that they were good general combiners for these traits (Table 2). High magnitude of GCA with respect to growth, physiological and wood traits have been reported by (Li and

Li, 1999) [17] on Chinese fir, (Cameron *et al.,* 2008) [9] on willows, (Vijayan *et al.,* 2008) [24] on mulberry, (Arna *et al.,* 2013) [3] on Sesame and (Zhao *et al.,* 2014) [26] on *Betula platyphylla*. Constantin *et al*. (2016) [12] also reported positive and negative GCA effects from yield components of oil palm population using North Carolina Mating Design II. The GCA estimates for a character such as height increment was negative and non-significant for most of *Dura* female and *Tenera* male parents: DA787D, DA507D, LM7899D and LM9175T, LM9927T. They opined that negative values of combining abilities are preferred by breeders when only considering the selection criteria of this height character in plant breeding.

Table 2: General combining ability estimates for growth traits in *B. variegate*

| General combining estimates | | | | | | | |
Females	Plant height	Collar diameter	No. of branches	No. of leaves	Leaf area	Petiole length	Internodal length	Root length
P$_3$	2.44*	0.45*	0.22*	-3.39*	0.44	0.62*	-0.16*	2.03*
P$_8$	-1.71	0.04	-0.43*	-2.23*	-1.62	-0.18	-0.12*	-4.33*
P$_{16}$	2.30*	0.13	0.62*	2.64*	-1.24	-0.05	0.31*	4.68*
P$_{24}$	-5.69*	-0.52*	-0.72*	-3.62*	1.95*	-0.17	-0.44*	-6.58*
P$_{27}$	0.67	-0.1	0.26*	2.99*	-1.07	-0.21	-0.43*	-1.48*
P$_{32}$	1.99*	-0.01	0.04	3.60*	1.53	-0.01	0.84*	5.68*
SEgi	1.06	0.14	0.09	0.31	0.98	0.14	0.06	0.66
CD$_{0.05}$	1.75	0.23	0.15	0.52	1.62	0.24	0.09	1.09
Males								
P$_{12}$	1.82*	0.19*	-0.37*	-0.97*	1.03	0.18	0.17*	0.01*
P$_{13}$	-2.36*	-0.17	-0.38*	-0.90*	1.42*	-0.15	0.04	-4.43*
P$_{14}$	1.13	0.1	-0.05	-0.23	-0.84	0.27*	0.02	0.12*
P$_{17}$	-0.59	-0.11	0.80*	2.10*	-1.61*	-0.30*	-0.23*	4.30*
SEgi	0.82	0.11	0.07	0.24	0.76	0.11	0.05	0.51
CD$_{0.05}$	1.36	0.18	0.12	0.4	1.26	0.18	0.08	0.85

*Significant at 0.05 level

Specific combining ability effects
The specific combining ability (SCA) estimates and their significant levels (tested at 5%) of crosses for growth traits are presented in Table 3.
Both negative and positive significant estimates of SCA effects were observed among the family crosses. For plant height, full sib families of P$_8$ × P$_{12}$, P$_8$ × P$_{14}$, P$_{16}$ × P$_{13}$, P$_{27}$ × P$_{13}$ and P$_{32}$ × P$_{17}$; for collar diameter P$_8$ × P$_{12}$; for number of branches per plant P$_3$ × P$_{14}$, P$_3$ × P$_{17}$, P$_8$ × P$_{17}$, P$_{16}$ × P$_{12}$, P$_{16}$ × P$_{13}$, P$_{24}$ × P$_{12}$, P$_{27}$ × P$_{14}$; P$_{27}$ × P$_{17}$ and P$_{32}$ × P$_{17}$; for number of leaves per plant P$_3$ × P$_{14}$, P$_8$ × P$_{12}$, P$_8$ × P$_{17}$, P$_{16}$ × P$_{13}$, P$_{24}$ × P$_{14}$, P$_{27}$ × P$_{12}$, P$_{27}$ × P$_{17}$, P$_{32}$ × P$_{13}$ and P$_{32}$ × P$_{17}$; for leaf area P$_3$ × P$_{12}$, P$_3$ × P$_{17}$, P$_8$ × P$_{13}$, P$_{16}$× P$_{14}$, P$_{24}$ × P$_{12}$, P$_{27}$ × P$_{13}$, P$_{27}$ × P$_{17}$, and P$_{32}$ × P$_{14}$; for petiole length P$_8$ × P$_{14}$; for internodal length P$_3$ × P$_{12}$, P$_3$ × P$_{17}$, P$_8$ × P$_{13}$, P$_{16}$ × P$_{14}$, P$_{24}$ × P$_{14}$, P$_{27}$ × P$_{12}$ and P$_{32}$ × P$_{12}$; for root length P$_3$ × P$_{12}$, P$_8$ × P$_{14}$, P$_{16}$ × P$_{13}$, P$_{24}$ × P$_{14}$, P$_{27}$ × P$_{14}$ and P$_{32}$ × T$_{17}$ with significant specific combining abilities were found to be the best cross combinations (Table 3).

Table 3: Specific combining ability estimates for growth traits in *B. variegata*

| Specific combining ability estimates | | | | | | | |
Crosses	Plant height	Collar diameter	No. of branches	No. of leaves	Leaf area	Petiole length	Internodal length	Root length
P$_3$ × P$_{12}$	-1.62	-0.30	-0.42*	-1.20*	4.12*	0.39	0.22*	15.86*
P$_3$ × P$_{13}$	-1.72	0.03	-0.17	-2.32*	-3.00*	-0.47*	-0.25*	-4.75*
P$_3$ × P$_{14}$	1.27	0.10	0.28*	2.67*	-4.83*	0.21	-0.57*	-9.33*
P$_3$ × P$_{17}$	2.06	0.17	0.32*	0.85	3.72*	-0.13	0.60*	-1.78
P$_8$ × P$_{12}$	5.49*	0.41*	-0.08	4.15*	1.64	0.05	-0.32*	-3.26*
P$_8$ × P$_{13}$	-8.73*	-0.16	-0.04	-4.42*	1.78*	-0.30	0.78*	-0.66
P$_8$ × P$_{14}$	7.71*	0.06	-0.41*	-1.20*	0.04	0.61*	-0.11	3.40*
P$_8$ × P$_{17}$	-4.46*	-0.30	0.53*	1.47*	-3.46*	-0.36	-0.36*	0.52
P$_{16}$ × P$_{12}$	-3.01	-0.21	0.42*	-1.45*	-4.85*	0.03	-0.24*	-9.87*
P$_{16}$ × P$_{13}$	6.02*	0.27	0.45*	5.93*	-2.62	0.42	-0.44*	7.63*
P$_{16}$ × P$_{14}$	-3.15*	-0.08	-0.11	0.70	4.71*	-0.76*	0.57*	1.08
P$_{16}$ × P$_{17}$	0.14	0.02	-0.75*	-5.18*	2.76	0.32	0.12	1.17
P$_{24}$ × P$_{12}$	1.82	0.23	0.37*	-1.52*	3.20*	0.19	-0.27*	0.09
P$_{24}$ × P$_{13}$	2.72	-0.39	0.17	-2.42*	-2.18	-0.26	-0.20*	1.70
P$_{24}$ × P$_{14}$	-2.26	0.17	0.09	8.63*	2.35	-0.17	0.68*	4.64*
P$_{24}$ × P$_{17}$	-2.29	0.00	-0.64*	-4.69*	-3.37*	0.24	-0.21*	-6.44*
P$_{27}$ × P$_{12}$	-1.65	0.18	-0.52*	4.43*	-0.97	-0.43*	0.22*	-0.62
P$_{27}$ × P$_{13}$	5.72*	0.36	-0.10	-4.08*	4.34*	0.38	-0.04	0.89
P$_{27}$ × P$_{14}$	-1.39	-0.30	0.35*	-2.82*	-6.66*	-0.14	-0.33*	4.10*
P$_{27}$ × P$_{17}$	-2.68	-0.25	0.27*	2.47*	3.29*	0.19	0.15	-4.37*
P$_{32}$ × P$_{12}$	-1.03	-0.30	0.23	-4.41*	-3.14*	-0.22	0.39*	-2.21*
P$_{32}$ × P$_{13}$	-4.02*	-0.10	-0.30*	7.31*	1.69	0.23	0.16	-4.81*
P$_{32}$ × P$_{14}$	-2.19	0.05	-0.20	-7.98*	4.40*	0.25	-0.23*	-3.89*
P$_{32}$ × P$_{17}$	7.23*	0.35	0.28*	5.08*	-2.95	-0.26	-0.31*	10.90*
SEsi	1.84	0.24	0.16	0.54	1.71	0.25	0.10	1.15
CD$_{0.05}$	3.04	0.40	0.26	0.89	2.82	0.41	0.17	1.90

*Significant at 0.05 level

High significant SCA effects of the crosses indicate the extent of deviation in performance of the considered cross combinations from that predicted on the basis of the general combining abilities of parents involved in crosses. Thus these crosses with high positive and significant estimates of SCA effect could be selected for their specific combining ability and exploited for fodder improvement in *Bauhinia* breeding programmes.

Our findings are in conformity with the findings of Li and Wu (1996) [16] in Aspen, Yanchuk (1996) [25] in Douglas-fir, Miyashita and Nakada (2010) [19] in *Cryptomeria japonica*, Biabani *et al*. (2012) [7] in Jatropha, Constantin *et al*. (2016) [12] in Oil palm and Beniwal *et al*. (2018) [6] in Sesame. The existence of both positive and negative SCA effects has also been reported by Noh *et al*. (2012) [20] in oil palm crosses. However, high general combining ability for one trait will not always produce high SCA for the same trait in the same parent (Hossein and Aziz, 1998) [13].

Gene action and degree of dominance
The results on specific combining ability variance (σ^2sca) and the general combining ability (σ^2gca) estimates as well as their ratio (σ^2gca / σ^2sca) for growth components (Tables 4) indicated that the general combining ability variance estimate (σ^2gca) was lower than the estimate of variance due to the specific combining ability variance (σ^2sca) for the majority of the characters studied. This emphasized that non-additive gene action is possibly controlling these characters. With

regards to collar diameter and number of branches σ^2gca was slightly greater than specific combining ability variance (σ^2sca), indicating that additive gene actions were important in controlling these traits in the studied population. Dominance genetic variance was larger than additive genetic variance except for collar diameter and number of primary branches. These results are confirmed by the ratio of the general combining ability variance to the specific combining ability variance (σ^2gca/σ^2sca) from which smaller values than unity were recorded and by the degree of dominance which produces values greater than unity for collar diameter and number of branches (Table 4). Therefore, it can be assumed that the inheritance of these studied characters was controlled by the main role of non-additive gene effects. This suggests that the base population of this study was a heterozygote *Bauhinia variegata* breeding population. In addition selection for improved performance of hybrids can be operated by the breeding program.

It was observed that the gene action process for component characters was more controlled by non-additive gene effects. Thus potential presence of heterosis in the studied population to release superior improved intraspecific hybrid in *Bauhinia variegata* can also be found. However, the results showed negative additive genetic variance for some studied traits. The estimates of the genetic components of variance for these characters were set to be zero based on expected mean squares.

Table 4: Estimates of genetic components for growth traits in *B. variegata*

Variance components	Plant height	Collar diameter	No. of branches	No. of leaves	Leaf area	Petiole length	Internodal length	Root length
σ^2gca	0.95	0.04	0.24	0.09	-1.64	0.05	0.07	6.62
σ^2sca	20.73	0.01	0.17	28.66	14.6	0.08	0.21	51.92
σ^2A	3.8	0.16	0.96	0.36	-6.57	0.19	0.27	26.49
σ^2D	82.92	0.03	0.68	114.65	58.39	0.32	0.83	207.69
σ^2gca/ σ^2sca	0.05	4.00	1.41	0.00	-0.11	0.63	0.33	0.13
σ^2A/ σ^2D	0.05	5.33	1.41	0.00	-0.11	0.59	0.33	0.13

Negative estimates of genetic components of variance for some characters were reported by Mather and Jinks (1982) [18]. Although additive genetic variance was present for some characters under study, dominance genetic variance was much larger than additive genetic variance for all of the traits except for collar diameter and number of branches indicating that dominance gene effects were more important than additive gene effects in controlling growth traits. Thus a favorable *Bauhinia* hybrid breeding program can be established for this studied breeding population.

Conclusion
The results of this study revealed that several crosses are highly promising to breed new *Bauhinia* cultivars possessing genetic factors for growth characters to improve fodder yield potential. The results also indicated that among female parent families (lines) P$_3$ (Kathua) was a good general combiner for plant height, collar diameter, number of branches, petiole length and root length whereas P$_{16}$ (Solan) was a good general combiner for plant height, number of branches, number of leaves, internodal length and root length. P$_{27}$ (Dhaulakuan) was a good general combiner for number of branches and number of leaves while P$_{32}$ (Sahastradhara) was a good

general combiner for plant height, number of leaves, internodal length and root length.

Among male parent families (testers) P$_{12}$ (Mandi) was recorded as a good general combiner for plant height, collar diameter and internodal length while P$_{13}$ (Nahan) was a good general combiner for leaf area. P$_{14}$ (Kunihar) was a good general combiner for petiole length and root length whereas P$_{17}$ (Paonta Sahib) was a good general combiner for number of branches, number of leaves and root length. Thus these female and male parent families possess the potential to be utilized in seed production programmes for fodder improvement and for other breeding purposes. Crosses P$_{16}$ × P$_{13}$ and P$_{32}$ × P$_{17}$ showed the best specific combiner effects for the majority of growth components. These crosses with highly positive and significant estimates of SCA effect could be selected for use in fodder improvement breeding programs in *Bauhinia variegata*. The σ^2gca / σ^2sca estimates supported the involvement of both additive and non-additive gene effects with preponderance of non-additive gene actions.

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