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

Tesfaye Ashine and IK Thakur

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 (P1, P6, P16, P24, P27 and P32) and 4 testers (male) genotypes (P12, P13, P14 and P17) were crossed using line x tester mating design and their 24 F1 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 P16 followed by P32, P27 and P3 identified as promising good general combiners for growth traits with significant positive general combining abilities (GCA). Among testers P12 followed by P14 provided good GCA for most of the traits studied. Crosses P16 × P12, P12 × P17 and P1 × P17 exhibited best specific combining ability (SCA) for the majority of growth and biomass traits. The ratio of gca/a+sc 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) [22].

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, copicing 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 30°51’ 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 are 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 \textit{B. variegata} genotypes \([P_{12} \text{ (Mandi)}, P_{13} \text{ (Nahan)}, P_{14} \text{ (Kunihar)} and P_{17} \text{ (Paonta Sahib)}]\) with one set of 6 female genotypes \([P_{3} \text{ (Kathua)}, P_{5} \text{ (Giripul)}, P_{16} \text{ (Solan)}, P_{24} \text{ (Narag)}, P_{27} \text{ (Dhaulakuan)} and P_{32} \text{ (Sahastradhara)}]\).

### 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 Chaudhury, 1985)\(^{(22)}\):

\[
\text{GCA (lines)} = \frac{Y_i.. - Y...}{r l}
\]

\[
\text{GCA (testers)} = \frac{Y.j. - Y...}{r l}
\]

\[
\text{SCA} = \frac{Yij. - Y_i.. - Y.j. + Y...}{r l}
\]

\[
\text{SE (GCA for lines)} = \frac{(\text{Me})}{\sqrt{r l} / 2}
\]

\[
\text{SE (GCA for tester)} = \frac{(\text{Me})}{\sqrt{r l} / 2}
\]

\[
\text{SE (SCA)} = \frac{(\text{Me})}{\sqrt{r l} / 2}
\]

where, Yi.. = Total of the i\textsuperscript{th} line, Y.j. = Total of the j\textsuperscript{th} 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:

\[
\text{Cov H.S. (female)} = \frac{(M - M \times t)}{r x t}
\]

\[
\text{Cov H.S. (male)} = \frac{(M - M \times t)}{r x l}
\]

\[
\text{Cov H.S. (average)} = \frac{1}{r(t-1)}\left[\frac{((l-0)\text{MI} + (t-1)\text{Mt}}{l(t-2)} - M \times t\right]
\]

\[
\text{Cov F.S.} = \frac{[\text{MI} - \text{Me} + \text{Mt} - \text{Me} + \text{Mt} - \text{Me}]}{3r} + \frac{6r}{3} \text{Cov HS (average) - r (l - Cov HS (average)) / 3r}
\]

Additive genetic variance \((\sigma^2 \text{A})\), dominance genetic variance \((\sigma^2 \text{D})\) and average degree of dominance were estimated as below (Singh and Chaudhury, 1985)\(^{(22)}\):

\[
\sigma^2 \text{A} = \frac{4}{(1 + F)} \sigma^2 \text{gca} = \frac{4}{(1 + F)} \text{Cov HS (average)}
\]

\[
\sigma^2 \text{D} = \frac{4}{(1 + F^2)} \sigma^2 \text{sca} = \frac{4}{(1 + F^2)} \text{Cov HS (average)}
\]

Average degree of dominance = \((\sigma^2 \text{D} / \sigma^2 \text{A})^{1/2}\)

where, \(\sigma^2 \text{gca}=\) Estimate of GCA variance, \(\sigma^2 \text{sca}=\) Estimate of SCA variance, \(\sigma^2 \text{P}=\) 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 \textit{B. variegata}

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

*Significant at 0.05 level

### General combining ability effects

General combining ability (GCA) estimates for growth traits revealed that among lines \(P_{13}\) 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...
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 P3 × P13, P8 × P14, P16 × P13, P23 × P13, P32 × P17, and P32 × P17; for collar diameter P8 × P12; for number of branches per plant P3 × P14, P3 × P17, P8 × P17, P16 × P15, P16 × P17, P16 × P17, P24 × P12, P27 × P17, and P32 × P17; for number of leaves per plant P3 × P14, P3 × P17, P8 × P17, P16 × P17, P24 × P14, P27 × P17, P32 × P17, P32 × P17; for collar diameter P8 × P12; for internodal length P3 × P12, P3 × P13, P8 × P14, P16 × P14, P16 × P15, P24 × P14, P27 × P14, and P32 × T17; for petiole length P3 × P14, P8 × P14, P16 × P14, P27 × P14, and P32 × T17; for petiole diameter P3 × P14, P8 × P14, P16 × P14, P27 × P14, and P32 × T17; 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

<table>
<thead>
<tr>
<th>Crosses</th>
<th>Plant height</th>
<th>Collar diameter</th>
<th>No. of branches</th>
<th>No. of leaves</th>
<th>Leaf area</th>
<th>Petiole length</th>
<th>Internodal length</th>
<th>Root length</th>
</tr>
</thead>
<tbody>
<tr>
<td>P3 × P13</td>
<td>-1.62</td>
<td>-0.30</td>
<td>-0.42*</td>
<td>-1.20*</td>
<td>4.12*</td>
<td>-0.39*</td>
<td>-0.22*</td>
<td>1.56*</td>
</tr>
<tr>
<td>P3 × P14</td>
<td>-1.72</td>
<td>0.03</td>
<td>-0.17</td>
<td>-2.52*</td>
<td>-1.00*</td>
<td>-0.47*</td>
<td>-0.25*</td>
<td>-4.75*</td>
</tr>
<tr>
<td>P3 × P17</td>
<td>2.06</td>
<td>0.17</td>
<td>0.32*</td>
<td>0.85</td>
<td>3.72*</td>
<td>-0.13</td>
<td>0.60*</td>
<td>-1.78</td>
</tr>
<tr>
<td>P8 × P13</td>
<td>5.40*</td>
<td>0.41*</td>
<td>-0.08</td>
<td>4.15*</td>
<td>1.64</td>
<td>0.05</td>
<td>-0.32*</td>
<td>-3.26*</td>
</tr>
<tr>
<td>P8 × P14</td>
<td>-8.73*</td>
<td>-0.16</td>
<td>-0.04</td>
<td>-4.42*</td>
<td>1.78*</td>
<td>-0.30</td>
<td>0.78*</td>
<td>-0.66</td>
</tr>
<tr>
<td>P8 × P17</td>
<td>7.71*</td>
<td>0.06</td>
<td>-0.41*</td>
<td>-1.20*</td>
<td>0.04</td>
<td>0.61*</td>
<td>-0.11</td>
<td>3.40*</td>
</tr>
<tr>
<td>P16 × P13</td>
<td>-4.46*</td>
<td>-0.30</td>
<td>0.53*</td>
<td>1.47*</td>
<td>-3.46*</td>
<td>-0.36</td>
<td>-0.36</td>
<td>-0.52</td>
</tr>
<tr>
<td>P16 × P14</td>
<td>-3.01</td>
<td>-0.21</td>
<td>0.42*</td>
<td>-1.45*</td>
<td>-4.85*</td>
<td>0.03</td>
<td>-0.24*</td>
<td>-9.87*</td>
</tr>
<tr>
<td>P16 × P17</td>
<td>6.02*</td>
<td>0.21</td>
<td>0.45</td>
<td>5.93*</td>
<td>-2.62</td>
<td>0.42</td>
<td>-0.44*</td>
<td>7.63*</td>
</tr>
<tr>
<td>P24 × P13</td>
<td>-3.15*</td>
<td>-0.08</td>
<td>-0.11</td>
<td>0.70</td>
<td>4.71*</td>
<td>-0.76*</td>
<td>0.57*</td>
<td>1.08</td>
</tr>
<tr>
<td>P24 × P14</td>
<td>0.14</td>
<td>0.02</td>
<td>-0.75*</td>
<td>-5.18*</td>
<td>2.76</td>
<td>0.32</td>
<td>0.12</td>
<td>1.17</td>
</tr>
<tr>
<td>P24 × P17</td>
<td>1.82</td>
<td>0.23</td>
<td>0.37*</td>
<td>-1.52*</td>
<td>3.29*</td>
<td>0.19</td>
<td>-0.27*</td>
<td>0.09</td>
</tr>
<tr>
<td>P27 × P13</td>
<td>2.72</td>
<td>-0.39</td>
<td>0.17</td>
<td>-2.42*</td>
<td>-2.18</td>
<td>-0.26</td>
<td>-0.20*</td>
<td>1.70</td>
</tr>
<tr>
<td>P27 × P14</td>
<td>-2.26</td>
<td>0.17</td>
<td>0.09</td>
<td>8.63*</td>
<td>2.35</td>
<td>-0.17</td>
<td>0.68*</td>
<td>4.64*</td>
</tr>
<tr>
<td>P27 × P17</td>
<td>-2.29</td>
<td>0.00</td>
<td>-0.64*</td>
<td>-4.69*</td>
<td>-3.37*</td>
<td>0.24</td>
<td>-0.21*</td>
<td>-6.44*</td>
</tr>
<tr>
<td>P32 × P13</td>
<td>-1.65</td>
<td>0.18</td>
<td>-0.52*</td>
<td>4.43*</td>
<td>-0.97</td>
<td>-0.43*</td>
<td>0.22*</td>
<td>-0.62</td>
</tr>
<tr>
<td>P32 × P14</td>
<td>5.72*</td>
<td>0.36</td>
<td>-0.10</td>
<td>-4.08*</td>
<td>4.34*</td>
<td>0.38</td>
<td>-0.04</td>
<td>0.89</td>
</tr>
<tr>
<td>P32 × P17</td>
<td>-1.39</td>
<td>-0.30</td>
<td>0.35*</td>
<td>-2.82*</td>
<td>-6.66*</td>
<td>-0.14</td>
<td>-0.33*</td>
<td>4.10*</td>
</tr>
<tr>
<td>P32 × T13</td>
<td>-2.68</td>
<td>-0.23</td>
<td>0.27*</td>
<td>2.47*</td>
<td>3.29*</td>
<td>0.19</td>
<td>0.15</td>
<td>-4.31*</td>
</tr>
<tr>
<td>P32 × T14</td>
<td>-1.03</td>
<td>-0.30</td>
<td>0.23</td>
<td>-4.41*</td>
<td>1.14*</td>
<td>-0.22</td>
<td>0.39*</td>
<td>-2.21*</td>
</tr>
<tr>
<td>P32 × T17</td>
<td>-4.02*</td>
<td>-0.10</td>
<td>-0.30*</td>
<td>7.31*</td>
<td>1.69</td>
<td>0.17</td>
<td>3.16</td>
<td>-4.81*</td>
</tr>
<tr>
<td>P32 × T14</td>
<td>-2.19</td>
<td>0.05</td>
<td>-0.20</td>
<td>-7.98*</td>
<td>4.40*</td>
<td>0.25</td>
<td>-0.23*</td>
<td>-3.89*</td>
</tr>
<tr>
<td>P32 × T17</td>
<td>7.23*</td>
<td>0.35</td>
<td>0.28*</td>
<td>5.08*</td>
<td>-2.95</td>
<td>-0.26</td>
<td>-0.31*</td>
<td>10.90*</td>
</tr>
<tr>
<td>SE &amp;i</td>
<td>1.84</td>
<td>0.24</td>
<td>0.16</td>
<td>0.54</td>
<td>1.71</td>
<td>0.25</td>
<td>0.10</td>
<td>1.15</td>
</tr>
<tr>
<td>CD (0.05)</td>
<td>3.04</td>
<td>0.40</td>
<td>0.26</td>
<td>0.89</td>
<td>2.82</td>
<td>0.41</td>
<td>0.17</td>
<td>1.90</td>
</tr>
</tbody>
</table>

*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.


**Gene action and degree of dominance**

The results on specific combining ability variance ($\sigma^2_{sca}$) and the general combining ability ($\sigma^2_{gca}$) estimates as well as their ratio ($\sigma^2_{gca} / \sigma^2_{sca}$) for growth components (Tables 4) indicated that the general combining ability variance estimate ($\sigma^2_{gca}$) was lower than the estimate of variance due to the specific combining ability variance ($\sigma^2_{sca}$) 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 $\sigma^2_{gca}$ was slightly greater than specific combining ability variance ($\sigma^2_{sca}$), 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 ($\sigma^2_{gca}/\sigma^2_{sca}$) 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

<table>
<thead>
<tr>
<th>Variance</th>
<th>Plant height</th>
<th>Collar diameter</th>
<th>No. of branches</th>
<th>No. of leaves</th>
<th>Leaf area</th>
<th>Petiole length</th>
<th>Internodal length</th>
<th>Root length</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\sigma^2_{gca}$</td>
<td>0.95</td>
<td>0.04</td>
<td>0.24</td>
<td>0.09</td>
<td>-1.64</td>
<td>0.05</td>
<td>0.07</td>
<td>6.62</td>
</tr>
<tr>
<td>$\sigma^2_{sca}$</td>
<td>20.73</td>
<td>0.01</td>
<td>0.17</td>
<td>28.66</td>
<td>14.6</td>
<td>0.08</td>
<td>0.21</td>
<td>51.92</td>
</tr>
<tr>
<td>$\sigma^2_A$</td>
<td>3.8</td>
<td>0.16</td>
<td>0.96</td>
<td>0.36</td>
<td>-6.57</td>
<td>0.19</td>
<td>0.27</td>
<td>26.49</td>
</tr>
<tr>
<td>$\sigma^2_D$</td>
<td>82.92</td>
<td>0.03</td>
<td>0.68</td>
<td>114.65</td>
<td>58.39</td>
<td>0.32</td>
<td>0.83</td>
<td>207.69</td>
</tr>
<tr>
<td>$\sigma^2_{gca}/\sigma^2_{sca}$</td>
<td>0.05</td>
<td>4.00</td>
<td>1.41</td>
<td>0.00</td>
<td>-0.11</td>
<td>0.63</td>
<td>0.33</td>
<td>0.13</td>
</tr>
<tr>
<td>$\sigma^2_{gca}/\sigma^2_{sca}$</td>
<td>0.05</td>
<td>5.33</td>
<td>1.41</td>
<td>0.00</td>
<td>-0.11</td>
<td>0.59</td>
<td>0.33</td>
<td>0.13</td>
</tr>
</tbody>
</table>

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) P₁₃ (Kathua) was a good general combiner for plant height, collar diameter, number of branches, petiole length and root length whereas P₁₆ (Solan) was a good general combiner for plant height, number of branches, number of leaves, internodal length and root length. P₂₇ (Dhaulakuan) was a good general combiner for number of branches and number of leaves while P₃₂ (Sahastradhara) was a good general combiner for plant height, number of leaves, internodal length and root length. Among male parent families (testers) P₁₂ (Mandi) was recorded as a good general combiner for plant height, collar diameter and internodal length while P₁₃ (Nahan) was a good general combiner for leaf area. P₁₄ (Kunihar) was a good general combiner for petiole length and root length whereas P₁₇ (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 P₁₆ × P₁₃ and P₃₂ × P₁₇ 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 $\sigma^2_{gca}/\sigma^2_{sca}$ estimates supported the involvement of both additive and non-additive gene effects with preponderance of non-additive gene actions.

**References**

15. Larson SS. Pollen morphology of Thai species of Bauhinia (Caesalpinioideae). Grana 1974; 14:114-131