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Assessment of genetic variability, heritability, genetic advance and correlation for pod and seed traits in *Bauhinia variegata* L.

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Abstract

Bauhinia variegata L. belongs to family 'Fabaceae' and sub family Caesalpinioideae and is commonly known as Kachnar. It is one of the important fodder species on which farmer during the winter period rely on. In the present investigation pod and seed parameters were analyzed to determine the relative performance of 25 progenies of *Bauhinia variegata*. Analysis of variance for different pod and seed characters of important crosses and parents revealed significant variations among full-sibs families. The highest magnitude of PCV was recorded for seed weight per pod (23.85%) and number of seeds per pod (20.13%) whereas the lowest PCV were recorded for seed width (6.65%), seed length (6.69%). The moderate GCV was observed for seed weight per pod (17.69%) while, lowest GCV were found for pod width (4.95%), seed width (5.50%), seed length (5.53%), pod length (6.27%) and number of seeds per pod (9.58%). The highest heritability estimates were observed for seed width (68.38%), seed length (68.32%) and seed weight per pod (55.03%). The moderate genetic advance as percentage of mean was observed for seed weight per pod (27.04%). The high heritability coupled with moderate genetic advance as percentage mean was recorded for seed weight per pod exhibiting additive gene action and selection may be effective in this character. The genotypic and phenotypic correlation showed that all the characters were significant and positively correlated to all other characters at both level. Pod length showed maximum significant and positive correlation with pod width at genotypic levels and pod length showed maximum significant and positive phenotypic correlation with seed weight per pod at phenotypic level.

Keywords: Variability, heritability, genetic advance, correlation, pod and seed characters

Introduction

Bauhinia variegata L. is one of the important fodder species on which farmers rely during the winter lean period when the grasses are dry, less digestible and unpalatable. It belongs to family 'Fabaceae' and sub family Caesalpinioideae and is commonly known as Kachnar. It has lush green foliage and excels to other tree fodder in a comprehensive nutritive value and collates with cultivated green leguminous fodder (Negi, 1986) [17]. It is widely cultivated throughout the country for its leaf fodder and for its beautiful flowers. It is a multipurpose agroforestry tree species producing fodder, fiber, fuel and small timber. With the increase in demand for fodder, there is a need to strengthen the tree improvement programme in the species with a view to develop new varieties/ hybrids suiting to different agro-climatic zones with improved yield, fodder value and growth characters which may also meet the present day need of tree breeders for developing superior genotypes. Therefore, it is essential to understand the genetic architecture of this species which provides useful guidelines to determine the source population and from which it is possible to derive appropriate genotypes with desired characters. Effective tree breeding depends on an understanding of tree variation in nature and preserving such variation for future use. Information on the genetic variation and inter relationships of plant characters with tree volume end use and its component characters themselves is of great importance to a breeder in selecting a desirable genotype.

Knowledge of nature and magnitude of variability before starting any selection programme are helpful in carrying out a successful breeding programme because breeding techniques generally exploit the availability of genetic variability present in the germplasm for tree improvement. Thus, determining genetic variability and partitioning the observed variability into its heritable and non-heritable components with the help of suitable genetic parameters such as phenotypic variance, genotypic variance, heritability etc. is essential for understanding the genetic nature of traits. The heritability of the traits determines the extent of its transmission from one generation to the next. The response to selection will be higher if the heritability for the characters is higher (Sabu *et al.*, 2009) [26].

But the estimates of heritability alone fail to indicate the amount of progress expected from selection. Heritability coupled with high genetic advance would be more useful in predicting the resultant effect from selecting the best individuals (Johnson *et al.*, 1955a) [10]. The knowledge of these parameters is essential for proper understanding and their manipulation in any tree improvement programme. A wide range of genetic variability has been reported for quality traits earlier.

Zhao *et al.* (2012) [36] reported remarkable differences for coefficients of phenotypic variation for growth and morphological traits measured among 30 white poplar hybrid clones and also found significant phenotypic correlation among stem height, diameter, diameter at breast height, and volume per plant. Zhao *et al.*, 2014 [37] reported extremely significant correlations between tree height and diameter at breast height in *Betula platyphylla*. The results of the study carried out by Zeinab and Helal (2014) [35] in eight faba bean varieties in diallel crosses set revealed highly significant variations within parents and F₁ genotypes indicating a wide genetic variability for the studied characters and the possibility of genetic improvement using such genetic pools. Heritability in the broad sense (h_{bs}^2 %) estimates was generally high for all studied traits. High heritability values coupled with high genetic advance observed for 100-seed weight and number of pods per plant indicated that such traits would respond to selection. Dhixya Deve and Parthiban (2014) [5] studied the growth performance and variability of twenty *Dalbergia sissoo* clones. Among the traits studied height registered maximum heritability, followed by volume index. Heritability and genetic gain of all investigated traits were found to be high. Fakuta *et al.* (2015) [6] evaluated twelve *Acacia senegal* provenances to estimate mean effects, genetic variability, heritability and genetic advance in *Acacia senegal* provenances. Genetic component analysis showed that both genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for all the traits except bark thickness.

Keeping in view the above perspectives, the present investigation was thus carried out to estimate genetic variability, heritability and genetic advance of different pod and seed characters in *Bauhinia variegata* and to know the genotypic and phenotypic association between those traits.

Materials and Methods

The study was carried out in the Department of Tree Improvement and Genetic Resources, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan (H.P.) during 2015-17. The study site was located at an altitude of 1250m amsl in North-west Himalayas and lies between 30°51' N latitude and 76° 11' E longitude. The plant material *i.e.* flowering plant branches of five selected genotypes of the species were used for control crossing (hybridization) using full diallel (5×5) mating design. A set of 25 crosses including parents and reciprocals were produced by involving 5 selected parents (genotypes) (NA-7, PI-28, SU-11, JA-1, PI-28) in all possible combination. The sources of these selected plant material were *viz.*, Nauni (Himachal Pradesh) Pinjore (Haryana), Sundernagar (Himachal Pradesh), Jammu (Jammu & Kashmir), Dhaulakuan (Himachal Pradesh). The various pod and seed traits studied were; pod characters *viz.*, pod length, pod width, seed characters *viz.*, seed weight per pod, number of seeds per pod seed width and seed length.

Statistical analysis

The data obtained for all crosses including reciprocals F₁'s and parental F₁'s (progenies) were subjected to statistical analysis following randomized block design with three replications. The statistical analysis was carried out on mean values and the analysis of variance (ANOVA) was set up as explained by Gomez and Gomez (1983) [8].

Estimation of variability, correlation and genetic parameters Phenotypic, Genotypic and environmental variances

Coefficient of variability were worked out as suggested by Burton and De-vane (1953) [4] and Pillai and Sinha (1968) [20].

$$PCV (\%) = \frac{\sqrt{V_p}}{\bar{X}} \times 100; V_p = \text{Phenotypic variance}$$

$$GCV (\%) = \frac{\sqrt{V_g}}{\bar{X}} \times 100; V_g = \text{Genotypic variance}$$

$$ECV (\%) = \frac{\sqrt{V_e}}{\bar{X}} \times 100; V_e = \text{Environmental variance}$$

Where,

PCV = Phenotypic Coefficient of Variability

GCV = Genotypic Coefficient of Variability

ECV = Environmental Coefficient of Variability

\bar{X} = Population mean of character

Genotypic and phenotypic correlations were worked out as per Singh and Narayanam (2009) [31].

Genotypic correlation (r_g):

$$(r_g) = \frac{G \text{ Cov}_{xy}}{\sqrt{(V_{g_x} \cdot V_{g_y})}}$$

Phenotypic correlation (r_p):

$$(r_p) = \frac{P \text{ Cov}_{xy}}{\sqrt{(V_{p_x} \cdot V_{p_y})}}$$

Where,

G Cov_{xy} and P Cov_{xy} = Genotypic and Phenotypic covariance between x and y characters, respectively.

V_{g_x} and V_{p_x} = Genotypic and Phenotypic variance of x character

V_{g_y} and V_{p_y} = Genotypic and Phenotypic variance of y character

Heritability (Broad sense) ($h_{b.s}^2$):

Heritability in broad sense was calculated as suggested by Burton and De-Vane (1953) [4] and Johnson *et al.* (1955a) [10].

$$h_{b.s}^2 = \frac{V_g}{V_p} \times 100$$

Where,

$h_{b.s}^2$ = Heritability (broad sense)

Genetic Advance (GA):

The expected genetic advance at 5 per cent selection intensity was calculated by the formula suggested by Lush (1940) and further used by Burton and De-Vane (1953) [4] and Johnson *et al.* (1955a) [10].

$$GA = \left[\frac{Vg}{Vp} \right] \times (\sqrt{Vp}) \times K$$

K = Selection differential at 5 per cent selection intensity. The value of K= 2.06 (Allard, 1960).

GA was reported as percentage of mean and it was calculated as follows:

$$GA \text{ as percentage of mean} = \frac{GA}{\bar{X}} \times 100$$

Where, GA = Expected Genetic advance, \bar{X} = Mean of the character

Results and Discussion

The analysis of variance for all the characters under study showed significant differences among genotypes and thereby revealed sufficient variability among genotypes for all the characters.

Phenotypic and genotypic coefficient of variability

The PCV were marginally higher than the corresponding GCV. GCV and PCV are categorized as low (<10%), moderate (10-20%) and high (>20%) as suggested by Sivasubramanian and Madhavamenon (1973) [32]. The estimates of genotypic and phenotypic coefficient of variation for yield and its components have been presented in Tables 1 and discussed as follow:

Among pod and seed characters (Table 1), the highest magnitude of PCV was recorded for seed weight per pod (23.85%) followed by number of seeds per pod (20.13%). The moderate PCV was observed for pod width (10.76%) followed by pod length (10.68%) whereas the lowest PCV were recorded for seed width (6.65%) followed by seed length (6.69%).

The moderate GCV was observed for seed weight per pod (17.69%) while, lowest GCV were found for pod width (4.95%) followed by seed width (5.50%), seed length (5.53%), pod length (6.27%) and number of seeds per pod (9.58%).

Table 1: Estimates of variability and genetic parameters for pod and seed characters in *Bauhinia variegata*

Character	Mean	Range	Coefficient of variation (%)		Broad sense heritability (h ² bs) (%)	Genetic advance (GA)	Genetic advance as % of mean
			Phenotypic (PCV)	Genotypic (GCV)			
Pod length (cm)	19.05	16.90-22.10	10.68	6.27	34.48	1.45	7.59
Pod width (cm)	1.81	1.58-2.09	10.76	4.95	21.20	0.09	4.70
Seed weight per pod (g)	2.09	1.38-2.88	23.85	17.69	55.03	0.56	27.04
Number of seeds per pod	8.43	6.00-10.67	20.13	9.58	23.67	0.79	9.40
Seed width (mm)	12.91	11.60-14.67	6.65	5.50	68.38	1.21	9.37
Seed length (mm)	15.04	13.77-17.55	6.69	5.53	68.32	1.42	9.41

The magnitude of PCV was higher than the corresponding GCV for all the traits. This might be due to the interaction of the genotypes with the environment to some degree or environmental factor influencing the expression of these traits. Close correspondence between phenotypic and genotypic coefficient of variation were observed *i.e.* sufficient variability among the traits was present among the genotypes. Hence, there are enough scope of improvement of these traits. These results are in general accordance with the findings of Yadav (2007) [34], Showkat and Tyagi (2010) [27] and Reni and Rao (2013). The results are also in agreement with the findings of Fakuta *et al.* (2015) [6] where they found PCV was higher in proportion than GCV with respect to all the traits studied in *Acacia senegal*.

Heritability and genetic advance

The results on heritability and genetic advance in the present study are given in Table 1 and discussed as under.

In this study the heritability estimates in broad sense were classified into 3 groups such as high (>50%), moderate (50-30%) and low (<30%). The highest heritability estimates were observed for seed width (68.38%) followed by seed length (68.32%) and seed weight per pod (55.03%) indicating predominance of additive gene action in the expression of these traits. This being fixable in nature a considerable progress is expected through appropriate selection scheme to be adopted. The present findings are in agreement with the studies of Malik *et al.* (2006) [15] and Aditya *et al.* (2011) [1]. The moderate heritability was observed for pod length (34.48%) whereas the lowest heritability was observed for pod width (21.20%) followed by number of seeds per pod (23.67%).

The heritability values alone however provide no information of the amount of genetic improvement that would results from selection of superior genotypes. The heritability estimates would be more reliable if their limitation in a broad sense, additive and non-additive genes, where accompanied with high genetic advance (Ramanujam and Tirumalachar, 1967) [22]. Genetic advance in percentage of mean gives more precise result in comparison to only genetic advance. The magnitude of genetic advance as percentage of mean was categorized as high (> 30%), moderate (30% - 10%) and low (< 10%) (Johnson *et al.*, 1955a) [10]. The moderate genetic advance as percentage of mean was observed for seed weight per pod (27.04%) whereas, lowest genetic advance as percentage of mean was observed for pod width (4.70%) followed by pod length (7.59%), seed width (9.37%), number of seeds per pod (9.40%) and seed length (9.41%).

The high heritability coupled with moderate genetic advance as percentage mean was recorded for seed weight per pod. High heritability with low genetic advance as percentage of mean was shown for seed width followed by seed length. Pod length showed moderate heritability with low genetic advance as percentage of mean. Number of seeds per pod followed by pod width showed low heritability coupled with low genetic advance as percentage of mean. As per different interpretations suggested by Singh and Narayanam (2009) [31], seed weight per pod exhibited additive gene effect and selection may be effective in this character. Seed width, seed length and pod length was influenced by non-additive gene action and the high heritability was being exhibited due to favourable influence of environment rather than genotype and selection for these characters may not be rewarding. Pod width and number of seeds per pod were highly influenced by environmental effect and selection would be ineffective. The

high heritability coupled with high genetic advance in percentage of mean indicated that selection for these characters could be more effective due to additive gene action. Panse (1957)^[18] viewed that if a character is governed by non-additive gene action it may give high heritability but low genetic advance whereas, if it is governed by additive gene action heritability and genetic advance would be high. Higher estimates of heritability along with high genetic advance provide good scope for further improvement in advance generations if these characters are subjected to mass progeny and clonal selection. The characters *i.e.* pod width and number of seeds per pod showing low heritability coupled with low genetic advance are of less use in breeding programme due to poor transferability or transmission of genetic materials from one generation to another. Similar findings were also reported by Malik *et al.* (2006)^[15], Ramteke *et al.* (2010)^[23], Aditya *et al.* (2011)^[1], Reni and Rao (2013)^[24], and Ghodrati (2013)^[7]. In forest trees similar findings are reported by Singh (2002) in full-sib progenies of selected clones of Poplar (*Populus deltoides* Bartr.), Kadam

(2002)^[12] in full-sib progenies of selected clones of *Populus deltoides* and Huse (2004)^[9] on willow clones.

Correlation

The relationship and dependency of components characters provide a complex genetic system and as a result selection of one component character brings about the simultaneous change in the other traits. The complex genetic system of inter character correlation is of prime importance and always been given the due weightage in formulating the suitable selection criteria. The intensity and direction of association among characters may be measured by genetic coefficient of correlation depending upon the type of material and kind of design used. The knowledge of genotypic interrelationship between characters is of theoretical interest because genetic correlation may be derived from genetic linkage, pleiotropy or from developmentally induced relationship between components that are indirectly the consequences of gene action (Moll and Robinson, 1959; White *et al.*, 2007)^[16, 33]. The genotypic and phenotypic correlations between the various characters are presented in Table 2.

Table 2: Genotypical and phenotypical correlation matrix for pod and seed characters (ten months) in *Bauhinia variegata*

Character		Pod width (cm)	Seed weight per pod (g)	Number of seeds per pod	Seed width (mm)	Seed length (mm)
Pod length (cm)	G	0.99	0.93	0.88	0.94	0.91
	P	0.49 *	0.85 *	0.77 *	0.49 *	0.41 *
Pod width (cm)	G	1.00	0.97	0.98	0.98	0.98
	P	1.00	0.48 *	0.37 *	0.38 *	0.41 *
Seed weight per pod (g)	G		1.00	0.96	0.75	0.84
	P		1.00	0.84 *	0.50 *	0.45 *
Number of seeds per pod	G			1.00	0.82	0.96
	P			1.00	0.40 *	0.32 *
Seed width (mm)	G				1.00	0.93
	P				1.00	0.80 *
Seed length (mm)	G					1.00
	P					1.00

* Significance at the 5 per cent level of significance

The genotypic correlation showed that all the characters were significant and positively correlated to all other characters at genotypic level (Table 2). Pod length showed maximum significant and positive correlation with pod width at genotypic levels. It indicated that more the pod length more will be the pod width. Pod width showed strong correlation for number of seeds per pod, seed width and seed length indicating that if more the pod width more will be the number of seeds per pod, seed width and seed length. Positive correlations among different characters at genotypic level would be desired for better growth of the hybrids.

The phenotypic correlation also showed that all the characters were significant and positively correlated to all other characters at phenotypic level (Table 2). Among all characters, pod length showed maximum significant and positive phenotypic correlation with seed weight per pod. This indicated that more the pod length more will be the seed weight per pod.

Positive correlations among different characters at both genotypic and phenotypic levels would be desired for better growth of the hybrids. In general values of genotypic correlation coefficients were higher than phenotypic correlation coefficient values and are similar in direction. This indicated that there was strong inherent association among the various characters studied. The phenotypic correlation was lessened under the influence of environment. Similar results were found by Johnson (1955b)^[11]. Strong genetic correlation

of one character with other character suggested pleiotropy among these characters which means that any change in the gene locus of one character may affect the genetic expression of other.

The present investigations are in agreement with the findings of Zhongyo and Mingjian, 1992^[38]; Lin and Zsuffa, 1993^[13]; Ronnberg and Gulberg, 1999^[25]; Singh and Huse, 2004^[9] on willows, Pichot and Teissier, 1988^[19]; Rajora *et al.*, 1994^[21]; Bailian *et al.*, 1998^[3]; Kadam, 2002^[12] and Singh and Singh, 2004 in Poplars. A reasonable high genetic correlation for important characters as noticed in the results of present investigation may prove useful for early testing for determining juvenile mature correlation in the species.

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