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VARIABILITY IN GROWTH AND BIOMASS OF *ROBINIA PSEUDOACACIA* L.: IMPLICATIONS FOR BREEDING

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ABSTRACT

Variability studies under various climatic conditions for a particular species is prerequisite and desirable for the genetic improvement and screening of the available variation for higher productivity and future breeding work. The assessment of tree-to-tree variation of candidate species is a process aimed at securing and increasing the production of food, flowers, barks and other useful plant products. The aim of this study was to estimate broad-sense heritability and G×E interactions in growth performance among nine seed sources of North Kashmir Himalayas. High heritability and high genetic gain was recorded in number of leaves (0.57), followed by seed germination (0.43). PCA for growth and biomass characters revealed six out of sixteen components contributed (78.78%) of total variation. The genotypes 10, 15, 16, 24 & 27 are categorized by cluster seventh having 52 per cent similarity with cluster 5 & 6. The cluster eight comprises of two genotypes *viz.*, 1 & 6 having 45 percent similarity with cluster 1 and 2. From the findings of this study, we summarize that these progenies are highly diverse and should be used for hybridization and improvement programmes.

Key words : *Robinia pseudoacacia*, Variation, Growth, Biomass, Heritability.

Introduction

Genetic variation is the basis for tree improvement. It cannot always be seen directly; it must be studied through well-designed tests. The study of variation is the first step for tree improvement and breeding programmes. Variability studies under various climatic conditions for a particular species is prerequisite and desirable for the genetic improvement and screening of the available variation for higher productivity and future breeding work. Variation within populations of tree species has been exploited in the selection of superior seed source for a given site and for evolving conservation strategies of genetic diversity within populations of tree species (Rawat *et al.*, 2006). A tree improvement programme involves all practices designed to produce genetically more desirable trees. The results of testing and evaluation form the basis of new selection. As the trials make it possible to distinguish genetic variation from other forms of variation, it is now possible to select the genetically best material for future use. Geographic variation exists in forest trees due to the genetic differentiation and the environmental divergence in which they have developed through ages. Basically, all the difference among trees is the result of three things that are: the different environments in which the trees are growing, the genetic differences among trees and the interactions between the tree genotypes and the environment in which they grow. Any attempt to examine the extent and pattern of genetic variation may help in early evaluation of criteria for selection of some prominent traits both in laboratory and nursery condition, which may be related to subsequent performance in the field (Nabi *et al.*, 2023; Ginwal *et al.*, 2004).

Materials and Methods

The study was carried out within the jurisdiction of three districts of North Kashmir *viz.*, Baramulla, Kupwara and Bandipora. From each district, three sites were selected based on distribution and abundance of the species i.e a total of nine (09) seed sources were selected

Table 1 : Description of seed sources of *Robinia pseudoacacia* Linn. in North Kashmir Himalayas under study.

S. no.	District	Source Name	Source No.	Altitude (m)	Latitude (N)	Longitude (E)
1	Baramulla	Sherabad Khore	S1	1585	34°08′	74°34′
		Palhallan Pattan	S2	1692	34°07′	74°54′
		Kunzer Tangmarg	S3	1814	34°04′	74°30′
2	Bandipora	Sumbal tangpora	S4	1589	34°23′	74°65′
		Chewa Bandipora	S5	1601	34°28′	74°65′
		Kanibathy Bediyaar	S6	1965	34°40′	74°53′
3	Kupwara	Nutnusa Kupwara	S7	1081	34°51′	74°37′
		Potushai Lolab	S8	1706	34°53′	74°35′
		Watyan Chandigam	S9	1596	34°40′	74°34′

in three districts. The geographical location of the seed sources is given in Table 1.

From each site, four middle aged trees having D.B.H equal to 15-25 cm have been randomly selected. These trees were marked for the collection of pods. The mature pods from the selected and marked trees were collected in the month of September, 2020 located 100 m apart from each other in order to avoid narrowing down of the genetic base due to inbreeding (Ginwal *et al*., 2004). The mature pods were then packed in gunny bags and brought to Faculty of Forestry for detailed study and analysis. Seeds were extracted from such pods and kept separately for each location with proper identity of site & individual tree.

Before sowing the seeds were pretreated with boiling water for one minute to break the dormancy. The seeds were sown in poly bags of the size 5″ × 7″ in month of February, 2021. The potting medium was soil, sand and FYM in the ratio of 1: 2: 1. Daily germination was recorded for 28 days following the procedure of ISTA. The raised seedlings were evaluated for one complete growing season and the whole data obtained was subjected to statistical analysis using RBD design employing R-studio. Genetic parameters were calculated in terms of mean, range, genotypic, phenotypic and environmental coefficient of variation, heritability (H), genetic advance and genetic gain as per cent of mean (Johnson *et al*., 1955). Genetic divergence was calculated by using non-hierarchical Euclidean cluster Analysis (Beale, 1969).

Results and Discussion

Variability estimates and Genetic evaluation

Sufficient variability in the material provides liberty to the breeder for the selection as per his objectives because of selection to be a mechanism of change. There must exist certain amount of observed genetic differences in a population amongst the individuals to be selected. A tree breeder doesn’t create genetic variations but uses the already existing variation as a tool for improvement through selection. Hence information on variation among the desirable parameters and their correlation is important for selection and breeding programme (Johnson *et al*., 1955).

Based on the analysis of variance the genetic components like genotypic, phenotypic and environmental coefficient of variation, heritability, genetic advance and genetic gain were computed.

The observed variation in a character is partly composed of genetic (heritable) variation and partly of non-heritable. The portion of total variation, which is heritable, is termed as heritability in broad sense (Johnson *et al*., 1955). Heritability and genetic advance provide the information of total variation present in the population and simultaneously gives an indication of the influence of environment on the character under study. The traits with higher heritability and higher genetic gain can be undertaken for further improvement programs, since they indicate the heritable additive component of variance.

Among growth and biomass characters wide range of values (Table 2) indicating the extent of variation existing in the genotypes. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation in all the characters which indicates that the traits were greatly influenced by the environment.

The number of leaves was found to have high heritability and high genetic gain followed by shoot dry weight and seed germination. Whereas, collar diameter and shoot dry weight had moderate heritability. Wide range (4.65-84.23%) was observed for genetic gain for different characters studied.

Higher values of heritability showed that these

Table 2 : Mean, range, GCV, PCV, heritability, genetic advance and genetic gain of growth and biomass characters of *Robinia pseudoacacia* Linn.

Characters	Mean	Range	Coefficient of Variance (%)		Heritability	Genetic Advance	Genetic gain (%)
			Genotypic	Phenotypic			
Seed germination	65.35	16.66-100	20.32	30.74	0.43	18.08	27.67
Number of leaves	8.42	1.6-36.67	53.79	70.77	0.57	7.09	84.23
Number of branches	1.68	0-3.60	18.99	34.76	0.29	0.36	21.37
Collar diameter	3.24	1.49-6.66	18.33	28.46	0.41	0.78	24.31
Survival percent	80.85	18.18-100	8.3	22.88	0.13	5.02	6.21
Seedling height	42.76	16.98-63.2	6.66	19.68	0.11	1.99	4.65
Root length	12.06	7.2- 17.26	6.21	14.9	0.17	0.64	5.33
Shoot fresh weight	3.62	0.89-14.54	33.37	54.04	0.38	1.53	42.46
Root fresh weight	2.6	0.5-5.72	13.22	38.23	0.11	0.24	9.41
Shoot dry weight	2.16	0.66- 6.97	32.43	47.7	0.46	0.98	45.44
Root dry weight	1.82	0.37-3.3	16.2	39.72	0.16	0.24	13.6
Root shoot ratio	1.01	0.17-4.36	27.12	74.6	0.13	0.20	20.3
Total fresh Biomass	6.23	2.51-20.08	21.77	38.07	0.32	1.59	25.64
Total Dry biomass	3.99	1.3-9.88	22.31	35.09	0.4	1.16	29.22
Sturdiness	14.18	5.44-37.91	21.52	35.89	0.35	3.77	26.59
Dicksons quality index	15.65	6.6-40.30	18.52	33.83	0.29	3.26	20.88

characters were under the strong influence of genetic control. The selection for traits would be quite effective and improvement would be through mass selection. High heritability indicates the effectiveness of selection based on good phenotypic performance but does not necessarily mean a high genetic gain for a particular trait. Heritability estimates in broad sense will be reliable if accompanied by high genetic gain (Burton and De Vane, 1953).

Johnson *et al*. (1955) reported that heritability estimates along with expected gain is more useful and realistic than the heritability alone predicting the resultant effect for selecting the best genotype. Higher genetic gain (84.23%) was recorded for number of leaves followed by shoot dry weight (45.44%), shoot fresh weight (42.46%) and total dry biomass (29.22%) in growth and biomass characters suggesting that additive genetic effects are important in the determination of these characters and therefore, selection would be effective for these traits.

A lowest value of genetic gain was recorded in root length (5.33%). Moderate genetic gain was observed for (26.59%) sturdiness. Low values of heritability and genetic gains indicated the expression of non-additive type of genetic gain and therefore simple selection will be a limiting factor for its improvement. Thus, the characters with higher heritability and genetic gain can be exploited well for advanced breeding programs.

Determination of phenotypic correlation coefficients among different growth and biomass parameters

Perusal of data in Table 3 revealed that seed germination had significant and positive phenotypic correlation with survival percent (0.621), root length (0.529), total fresh biomass (0.484), total dry biomass (0.478), Dicksons quality index (0.465), sturdiness (0.441), seedling height (0.409), shoot dry weight (0.326), root shoot ratio (0.279) and shoot fresh weight (0.205). However, it was found non-significantly correlated with all other combinations. that phenotypic correlation coefficients were lower than their corresponding genotypic values. This could be either due to the modifying effect of environment or the strong inherent association of characters at gene level.

Seed germination showed highly significant and positive genotypic correlation (0.997) accompanied by significant and positive phenotypic correlation (0.279) with root shoot ratio. Highly significant and positive genotypic (0.967) and significant phenotypic (0.890) correlation was exhibited by total fresh biomass with sturdiness.

Similarly seed germination showed highly significant genotypic (0.944) and significantly positive phenotypic (0.478) correlation with total dry biomass. Number of leaves showed highly significant and positive genotypic

Table 3 : Genotypic and Phenotypic correlation among growth and biomass characters of *Robinia pseudoacacia* Linn.

Characters		Seed germin-ation	No. of leaves	No. of branches	Collar diameter	Survival percent	Seedling height	Root length	Shoot fresh weight	Root fresh weight	Shoot dry weight	Root dry weight	Root shoot ratio	Total fresh Biomass	Total dry Biomass	Sturdi-ness	Dick-sons Quality index
Seed germination	**G**	**1**	0.683**	0.155	0.134	0.726**	0.409 **	0.773 **	0.345**	0.456 **	0.525**	-0.159	0.997**	0.792**	0.944 **	0.708 **	0.836**
	P		0.068	-0.030	0.192	0.621**	0.519**	0.529**	0.205*	0.199	0.326**	-0.102	0.279*	0.484**	0.478**	0.441**	0.465**
No. of leaves	**G**		**1**	0.837 **	0.433**	0.587**	0.504**	0.646**	0.319**	-0.199-	0.525**	-0.159-	0.997 **	0.792 **	0.944**	0.708 **	0.836**
	P			-0.126	0.322**	0.326**	0.302**	0.367**	0.289*	0.127	0.280*	0.222	-0.012	0.290 *	0.321**	0.391 **	0.408 **
No. of branches	**G**			**1**	0.238 *	0.392**	0.507 **	0.581 **	0.581**	0.348 **	0.863**	0.264 *	0.148	0.147	0.756**	0.822 **	0.944**
	P				0.271 *	0.312 **	0.332 **	0.620 **	0.348**	-0.179	0.367 **	0.202*	-0.120	0.365**	0.374 **	0.270 *	0.319**
Collar diameter	**G**				**1**	0.456**	0.530 **	0.687**	0.813 **	0.331 **	0.896 **	0.224**	0.157	0.357 **	0.145	0.568 **	0.752 **
	P					0.483**	0.472**	0.520 **	-0.138	-0.318	0.228 *	-0.363	0.296*	0.248 *	0.358 **	0.103	0.102
Survival percent	**G**					**1**	0.124	0.143 *	0.289 **	0.810 **	0.399 **	0.638**	0.329 **	0.362**	0.458 **	0.383**	0.420**
	P						0.717**	0.964 **	0.203 *	0.371 **	0.276 *	0.347**	-0.081	-0.425**	0.407**	0.303 **	0.412**
Seedling height	**G**						**1**	0.164 **	0.260 *	-0.102-	0.309 **	0.800**	0.441 **	0.487**	0.509**	0.417**	0.468**
	P							0.915**	0.184	0.265	0.211*	0.239 *	-0.159	0.263*	0.281*	-0.118	-0.091
Root length	**G**							**1**	0.355 **	0.112	0.407 **	0.872**	0.469 **	0.602**	0.610 **	0.381**	0.433**
	P								0.254*	0.395 **	0.273*	0.386 **	0.344 **	0.377 **	0.402**	0.666**	0.715**
Root fresh weight	**G**								**1**	0.230 **	0.765**	-0.175	-0.042	0.199	0.625**	0.966**	0.120-
	P									-0.055	0.589 **	-0.079	0.513**	0.779 **	0.423**	-0.071	-0.042
Root Fresh weight	**G**									**1**	0.288**	0.602 **	0.304**	0.393 **	0.427 **	0.320**	0.357**
	P										-0.037	0.753 **	0.429**	0.390**	0.416**	-0.074	0.197
Shoot dry weight	**G**										**1**	0.210*	-0.308	0.621**	0.698 **	0.114-	0.136
	P											-0.094	0.606**	0.368**	0.598 **	0.035	0.016
Root dry weight	**G**											**1**	0.244*	0.389 **	0.445 **	0.282*	0.308**
	P												0.433 **	0.303**	0.399 **	-0.010	-0.137
Root shoot ratio	**G**												**1**	0.802 **	-0.105	0.708**	0.109-
	P													0.243*	-0.222	0.448**	0.075
Total fresh Biomass	**G**													**1**	0.676 **	0.967**	0.198
	P														0.590**	0.890**	0.117
Total Dry Biomass	**G**														**1**	0.483 **	0.209*
	P															0.331**	-0.060
Sturdiness	**G**															**1**	0.716 **
	P																0.638**
Dicksons Quality index	**G**																**1**
	P																

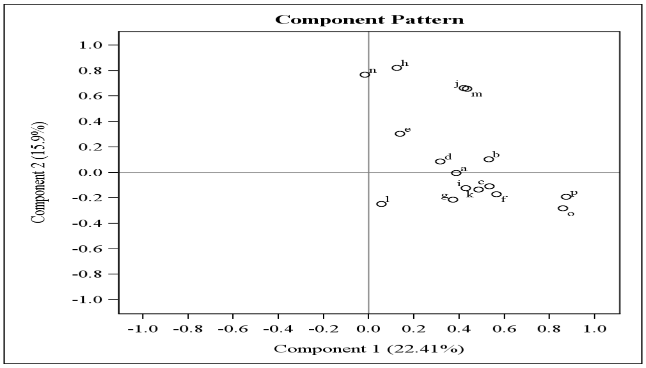

Fig. 1 : Component pattern plot of growth and biomass parameters of *Robinia pseudoacacia* Linn.

(0.944) and significantly positive phenotypic (0.321) correlation with total dry biomass. Highly significant and positive genotypic (0.944) and significant phenotypic (0.319) correlation was exhibited by number of branches with Dicksons quality index. This suggests that selection for any one of these traits would be a reliable measure of the other trait also.

Highly significant and positive genotypic correlation existed between collar diameter and shoot dry weight (0.896), number of branches and shoot dry weight (0.863), number of leaves and Dicksons quality index (0.836), number of branches and sturdiness (0.822), collar diameter and shoot fresh weight (0.813), survival percent and root fresh weight (0.810), root shoot ratio and total fresh biomass (0.802) and seedling height and root dry weight (0.800).

Highly significant and positive phenotypic correlation existed between survival percent and root length (0.964) whereas significant and positive correlation existed between shoot fresh weight and total fresh biomass (0.77), root fresh weight and root dry weight (0.753), survival percent and seedling height (0.717) and root length and Dicksons quality index (0.715). Therefore, these characters must be given proper emphasis during selection programme. Strong correlation at genotypic level suggests either the existence of linkage or pleiotropy or both between the correlated characters. This can be exploited for indirect selection as a mechanism for the genetic improvement of the species.

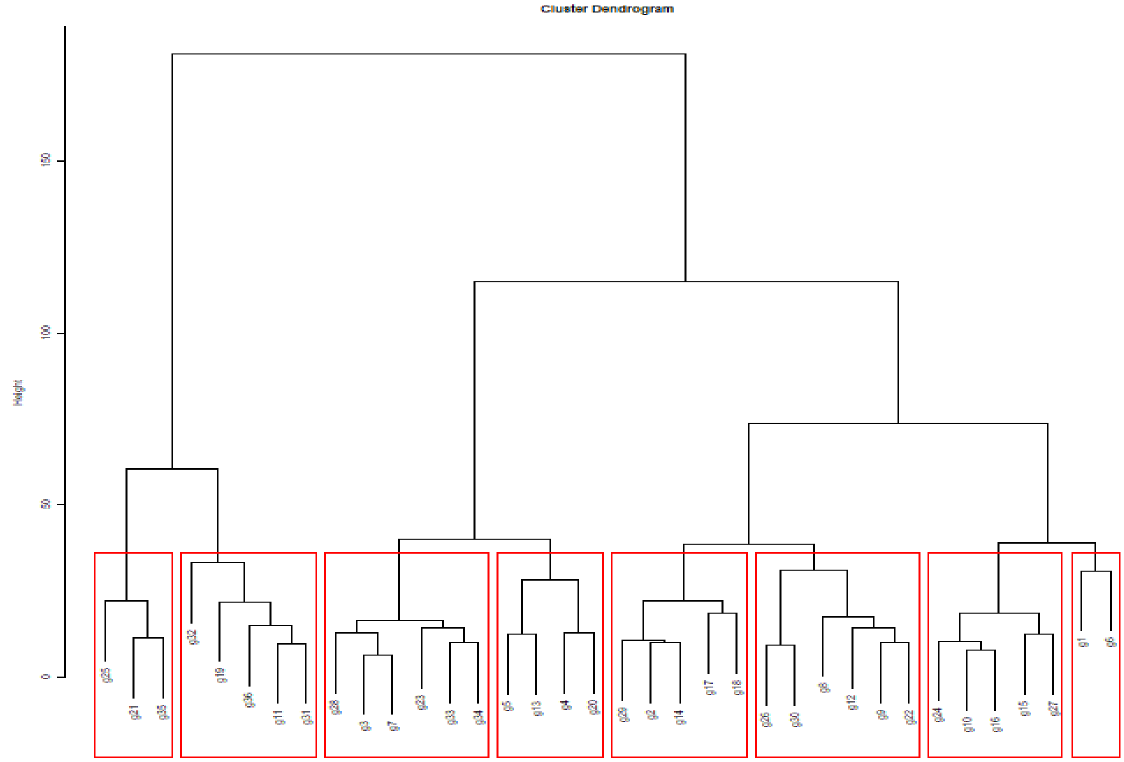

Fig. 2 : Dendrogram based cluster analysis of growth and biomass parameters of *Robinia pseudoacacia* Linn.

The above results find the support of the findings of Srivastava (1995) in different seed sources of *Bauhinia variegata*, Mohapatra (1996) in *Acacia catechu*, Manga and Sen (1998) in *Prosopis cineraria*, Chauhan and Verma (1993) in *Acacia catechu*, Thakur *et al.* (2000) in *Alnus nitida* and Anand (2003) in *Bauhinia variegata*.

Principal component analysis of growth and biomass parameters

Table 4 indicated that six out of sixteen components had eigen value greater that unity. These four components were retained for further analysis as they contribute (78.76%) of total variation. The first component explains

Table 4 : Principal component analysis of growth and biomass parameters of *Robinia pseudoacacia* Linn.

Characters	Code	Principal components					
		1	2	3	4	5	6
Seed germination	a	0.204	-0.002	-0.194	0.405	0.002	0.246
Number of leaves	b	0.279	0.064	-0.033	-0.523	0.163	0.080
Number of branches	c	0.281	-0.069	-0.254	-0.177	0.490	-0.182
Collar diameter	d	0.166	0.054	-0.387	-0.438	-0.114	-0.216
Survival percent	e	0.073	0.191	-0.154	0.370	0.150	-0.049
Seedling height	f	0.298	-0.106	-0.265	0.226	-0.119	-0.380
Root length	g	0.196	-0.134	-0.054	-0.075	0.114	0.798
Shoot fresh weight	h	0.064	0.514	0.035	0.077	0.291	0.063
Root Fresh weight	i	0.227	-0.077	0.459	0.021	0.386	-0.108
Shoot dry weight	j	0.222	0.416	0.022	-0.073	-0.433	0.144
Root dry weight	k	0.256	-0.083	0.484	-0.029	0.124	-0.092
Root shoot ratio	l	0.030	-0.155	0.408	-0.055	-0.305	-0.108
Total fresh Biomass	m	0.229	0.412	0.173	-0.170	-0.252	-0.009
Total Dry Biomass	n	-0.009	0.482	0.083	0.190	0.176	-0.114
Sturdiness	o	0.453	-0.176	0.009	0.147	-0.180	-0.028
Dickson’s Quality index	p	0.461	-0.120	-0.011	0.208	-0.117	0.009
Eigenvalue		3.586	2.544	2.371	1.815	1.271	1.019
Proportion		22.41	15.90	14.82	11.34	7.94	6.37
Cumulative		22.41	38.31	53.13	64.47	72.41	78.78

(22.41%) of total variation. The highest value (0.461) was exhibited in Dicksons Quality index followed by (0.453) for sturdiness, (0.298) for seedling height and (0.281) for number of branches. The second component accounted for (15.90%) of total variation, defined by shoot fresh weight (0.514) which was followed by total dry biomass (0.482), shoot dry weight (0.416) and total fresh biomass (0.412).

The third component accounted for (14.82%) of total variation. The highest value (0.484) was exhibited in root dry weight followed by root fresh weight (0.459) and root shoot ratio (0.408). The fourth component accounted for (11.34%) of total variation, defined by seed germination (0.405) followed by survival percent (0.370) and seedling height (0.226).

The fifth component accounted for(7.94%). The highest value was exhibited by number of branches (0.490) followed by root fresh weight (0.386), corresponding to 6.37% of the sixth component to the total variation which was defined by root length (0.798).

The pattern component plot (Fig. 1) represents the positive and negative correlation trend between the components and variables. The positive correlation between two principal components was defined by number of leaves (b), collar diameter (d), survival percent (e), shoot fresh weight (h), shoot dry weight (j) and total fresh biomass (m).

Dendrogram based cluster analysis of growth and biomass parameters of *Robinia pseudoacacia* Linn.

In order to discern genetic differentiation for growth and biomass traits of various genotypes dendrogram was constructed to visualize their clustering pattern (Fig. 2). The dendrogram showed that the distribution of various genotypes into clusters and within cluster was somewhat random.

Eight clear clusters were displayed by dendrogram. According to dendrogram the genotypes 21, 25 & 35 and genotypes 11, 19, 31, 32 & 36 were separated from the rest of the genotypes giving information about their most diverse nature, which are categorized as cluster 1& cluster 2. The remaining genotypes exhibited in seven clear clusters. Overall cluster 1& 2 was found to be 52 per cent similar with cluster 5 and 8.

Cluster 3 comprises of six genotypes *viz*., 3, 7, 23, 28, 33 and 34 having 35 per cent similarity with cluster 1 & 4. Cluster 4 was categorized by four genotypes *viz*., 4, 5, 13 & 20 which exhibited 35 per cent similarity with cluster 1 and 3. Cluster 5 comprises of five genotypes *viz*., 2, 14, 17, 18 & 29. The cluster 6 having six genotypes *viz*., 8, 9, 12, 22, 26 & 30 having 55 per cent similarity with cluster 1 and 6. The genotypes 10, 15, 16, 24 & 27 are categorized by cluster seventh having 52 per cent similarity with cluster 5 & 6. The cluster eight comprises of two genotypes viz., 1 & 6, having 45 percent (%) similarity with cluster 1 and 2. The results are in line with the findings of Weiguo and Yile (2004) in *Morus* species, Ozrenk *et al*. (2010) in *Mulberry*, Kumar *et al.* (2011) in *Dalbergia sissoo*, Sherry *et al*. (2011) in *Prosopis* species, Hossain *et al*. (2002) and Qi *et al*. (2003) in jute species, Vaishali *et al*. (2008) in , Wang *et al*. (2011) in *Dalbergia sissoo*, and Goswami and Ranade (1999) in *Prosopis* species.

Conclusion

Growth and biomass characters exhibited a highly significant and positive genotypic and phenotypic correlation for seed germination and root shoot ratio, total fresh biomass with sturdiness, seed germination and total dry biomass, Number of leaves and total dry biomass, number of branches and Dicksons quality index. Thus, suggests that selection for any of these traits would be a reliable measure for other traits. Genotypes presented in cluster 1 & cluster 2 were separated from the rest of the genotypes giving information about their most diverse nature. These genotypes are highly varied and should be used for hybridization and improvement programmes.

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