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An evaluation of genetic variability in early maturing pigeon pea genotypes and clustering of genotypes into different homogenous groups

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In Ethiopia, there has been no detail information on the extent and patterns of variability present in pigeon pea genotypes so far. As a result, hundred pigeon pea genotypes were tested in a 10 × 10 simple lattice design at Areka Research Center, Ethiopia during 2009 cropping season. The objectives of the study were to estimate the genetic variability, heritability and genetic divergence among 100 genotypes and cluster them in to genetically homogenous groups. The analysis of variance revealed highly significant difference ($p \leq 0.01$) for most traits. High phenotypic (PCV) and genotypic coefficient of variation (GCV) was recorded for harvest index and biomass yield per plant. High heritability coupled with high expected genetic advance as percent of mean was recorded for 100-seed weight, seed yield per plot, plant height, biomass yield per plant and harvest index. The genetic divergence was assessed using Mahalanobis D^2 statistics and the genotypes were grouped into six clusters. Distances between these clusters were significantly different for most of the cluster combinations. Therefore, the present study indicated that there is sufficient genetic diversity in pigeon pea germplasm that could be used as a base for improvement of the yield and other important attributes of this crop through direct selection and hybridization. Future work may also proceed in collecting and characterizing all the pigeon pea germplasms found in Ethiopia and developing short duration and high yielding varieties.

Key words: Variability, heritability, genetic advance and trait.

INTRODUCTION

Pigeon pea (*Cajanus cajan* (L.) is a deep rooted and drought-tolerant leguminous food crop used in several countries as a source of dietary protein (Troedson et al., 1990). Although it can grow in any warm climate, the pigeon pea is particularly popular throughout tropical and sub-tropical regions. Pigeon pea originated in India, where it has been grown for thousands of years

(Skerman et al., 1998). It reached Africa around 2000 BC, and a secondary centre of diversity developed in East Africa. With the conquest and slave trade, it reached the Americas probably via both the Atlantic and the Pacific oceans. Nowadays, it is grown all over the tropics, but it is most important in the Indian Subcontinent and East Africa (Yadav et al., 1997).

Pigeon pea endowed with rich dietary protein in its seed provides the much needed protein requirements of predominantly vegetarian population (Hari et al., 2006).

The seed contains 18-29% protein on dry weight basis

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which is about three times the value found in cereals and closer to soybean which is 34%. The protein is also of excellent quality, being high in lysine. The crop is, therefore; an important complements to cereal and root based diet (Van Der Maesen, 1990).

Variability in the population especially for the character for which improvement is sought is a prerequisite for successful selection (Tyagi and Khan, 2008). The assessment of the variation in the yield-determining quantitative traits of crop has become primary interest in the improvement of yield. Yield improvements have been achieved through directional selections for yield and contributing traits (Akbar and Kamran, 2006). It has been found that yield contributing traits have reliable and predictable effect on grain yields in grain legumes such as, mung bean, pea and pigeon pea (Tyagi and Khan, 2008).

At present majority of legume crops in Ethiopia are grown in the highlands as cool season crops and their production is poor. On the other hand, there are vast areas of land under arid and semi arid conditions and if we can find a legume suitable to these conditions, we may be able to reduce the gap between the demand and supply for protein in the diet. Therefore; pigeon pea a tropical legume is the one which holds such a promise (Cbadhokar, 2006).

Systematic breeding efforts on pigeon pea crop have so far been neglected in Ethiopia (Manju and Seelathakumary, 2002). Variability for most pulse crops in Ethiopia have been extensively studied except pigeon pea where there is no vigorous research yet done in any aspect (Cbadhokar, 2006). Therefore; by considering the importance of pigeon pea in the world economy and its potential for future Ethiopian economy, it is imperative to increase its productivity and other important traits through genetic manipulation. For genetic improvement of any crop plant, it is prerequisite to know the nature and magnitude of variability present in the available germplasm of the crop. Therefore; the present study was proposed to estimate the extent of variability, heritability and genetic advance in early maturing pigeon pea genotypes and thereby cluster the genotypes into different homogenous groups.

MATERIALS AND METHODS

Description of the study area

The field experiment was conducted at Areka Agricultural Research Center (AARC), Ethiopia during 2009 cropping season. It has an altitude of 1830 masl, 7° 09 latitude and 37° 47 E longitude (AARC, 2009). For this study, hundred early maturing pigeon pea genotypes introduced from India and maintained at Melkasa Agricultural Research Center (MARC) were used. A simple lattice design (10 × 10) was used. Each plot consisted of four

rows with spacing of 20 cm between plant and 75 cm between rows of 5.1 m long. For each genotype five randomly taken plants in each replication were used to record data on plant height (cm), pods per plant, primary branches per plant, number of seeds per plant, seeds per pod, seed yield per plant, biomass yield per plant and harvest index per plant. Days to flowering, days to maturity, 100-seed weight and seed yield per plot were recorded on plot basis.

Data analysis

Phenotypic and genotypic variance, phenotypic and genotypic coefficient of variation, range and mean of five randomly selected plants were used to estimate the variability in the population. Thus, phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and Devane (1953). Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance (σ^2_g) to the phenotypic variance (σ^2_p) and was estimated on genotype mean basis as described by Allard (1960). According to Johnson et al. (1955), genetic advance expected under selection and genetic advance in percent of the mean were calculated at 5% selection intensity ($K = 2.06$). Based on the squared distance (D^2) values, clustering of genotypes was done using Average Linkage Cluster Analysis method as described by Singh and Chaudhary, (1999).

RESULTS AND DISCUSSION

Estimate of range and mean

The 100 pigeon pea genotypes studied showed wide ranges of variability for most of the traits studied (Table 3). Wider ranges were recorded for seeds per plant, seed yield per plant, seed yield per plot, biomass yield per plant, seeds per pod and pods per plant whereas, the lowest ranges were recorded for days to flowering, days to maturity, plant height and reproductive phase. The highest mean seed yield was recorded from genotype ICP-9482 and the lowest was from genotype ICP-14803 (Table 1).

Sufficient variability for seed yield per plant, primary branches per plant, plant height and number of pods per plant was also reported by (Dahat et al., 2006). The present investigation revealed considerable amount of variations for most of the traits studied. Such wide variations indicated the scope for improving for these traits. Wide ranges of variability were also reported by Chattopadhyay and Dhiman, (2006) for primary branches per plant, days to maturity, plant height, days to flowering, seeds per pod and 100-seed weight in pigeon pea.

Table 1. Estimates of range, mean, genetic components of variance, heritability and genetic advance of pigeon pea genotypes.

Traits	Range	Mean	SE	σ^2_p	σ^2_g	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)
DF	85- 128	100.20	0.61	73.305	6.10	8.54	2.46	8.31	1.47	1.46
PF	44 -106	71.09	0.571	53.795	3.62	10.32	2.67	6.72	1.02	1.43
DM	149- 196	171.29	0.616	72.745	15.34	4.98	2.29	21.08	3.70	2.16
PH	54- 104	74.07	0.773	86.23	34.67	12.54	7.95	40.21	7.69	10.38
PBP	4.4- 24	10.71	0.246	13.75	0.86	34.62	8.66	6.25	0.48	4.46
BYP	18 -317	76.33	3.088	1332.72	269.10	47.83	21.49	20.19	15.18	19.89
PP	30.2-284.4	81.74	2.796	1185.46	172.07	42.12	16.05	14.52	10.30	12.59
SP	1.77- 6.14	2.92	0.049	0.525	0.02	24.81	4.19	2.86	0.04	1.46
SPLA	75.4-653	235.35	8.055	9833.16	236.84	42.13	6.54	2.41	4.92	2.09
SYPLA	7.54- 66.8	23.56	0.851	105.15	5.05	43.52	9.54	4.80	1.01	4.31
HI	0.1-0.74	0.33	0.008	0.015	0.01	37.11	21.43	33.33	0.08	25.48
HSW	6.0-14.0	10.00	0.106	2.11	0.69	14.53	8.31	32.70	0.98	9.79
ASP	289- 2430	822.54	20.03	81662	20734.00	34.74	17.51	25.39	149.47	18.17
SYH	377- 3174	1070.19	25.64	134020.5	37317.50	34.21	18.05	27.84	209.99	19.62

DF=Days to flowering, PF=Reproductive phase, DM=days to maturity, PH (cm) =Plant height, PBP= Number of primary branch per plant, BYP(g) =Biomass yield per plant, PP=Pod per plant, Sp=Seed per pod, SPLA=Seed per plant, SYPLA(g) =Seed yield per plant, HI(g) =Harvesting index, HSW(g) =Hundred seed weight, ASYP(g) =Adjusted seed yield per plot, and SYH(kg) =Seed yield per hectare, phenotypic(σ^2_p) and genotypic (σ^2_g) components of variances, phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad sense heritability (h^2), expected genetic advance (GA), SE= standard error and genetic advance as percent of the mean (GA%).

Estimates of phenotypic and genotypic variation

The overall range of phenotypic variation was high for most of the traits considered, but it was very high for seed yield per plant, seed yield per plot, pods per plant, biomass yield per plant, plant height, days to maturity, seeds per plant, days to flowering and pod filling duration while seeds per pod, harvest index, primary branches per plant and 100-seed weight showed a narrow range of variability. Similar result was reported by Manju and Sreelathakumar (2002) for seed yield per plant and seeds per plant.

The phenotypic variance (σ^2_p) and phenotypic coefficient of variation (PCV) was slightly higher than the genotypic variance (σ^2_g) and genotypic coefficient of variation (GCV) for all the traits but in most instances the two values differed only slightly suggesting the presence of environmental influence to some extent in the expression of these traits. According to Deshmukh et al. (1992), PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be medium. With this benchmark, high GCV value was recorded for biomass yield per plant and harvest index whereas medium GCV value was recorded for pods per plant and seed yield per plot. This offers a wide scope of opportunity to make selection for these traits. Similar result was also reported by Patil (2000) who observed high genotypic coefficient of variation for harvest index and number of pods per plant.

High PCV values recorded for seed yield per plant, seeds per plant, harvest index, pods per plant, seed yield

per plot, primary branches per plant, seeds per pod and biomass yield per plant indicated that the variation that exist will allow selection to improve this traits. Days to maturity and days to flowering showed lower estimate of PCV indicating lower opportunity for selection to improve these traits. High phenotypic and genotypic coefficient of variation was recorded for biomass yield and harvest index indicating that these traits are important for pigeon pea improvement. Contrary finding has been reported by Braham et al. (2010) for pods per plant and seed yield per plot in mung bean which had high genotypic and phenotypic coefficients of variation.

Estimate of broad sense heritability

The estimated heritability ranges from 2.41% for seeds per plant to 40.21% for plant height (Table 1). Dabholker, (1992) classified heritability estimates as low (5 to 10%), medium (10 to 30%) and high (30 to 60%). Considering this benchmark, heritability was high for plant height, 100-seed weight and harvest index thereby indicating a sufficient possibility of improvement for these traits through selection. High heritability value for harvest index in pigeon pea was also reported by Venkateswarlu (2006). However, high heritability values for seed yield per plant and number of primary branches per plant reported by Venkateswarlu, (2006) was not in agreement with the present study.

Likewise, low estimation of heritability value was observed for reproductive phase, seeds per pod, primary branches per plant, seeds per plant, days to flowering

Table 2. Distribution of 100 genotypes in to six clusters based on D² analysis for pigeon pea genotypes.

Clusters	Total no. of genotypes	Genotypes
I (14%)	14	ICP-14303,ICP-8785,ICP-8337,ICP-14880,ICP-8007,ICP-8786, ICP-3250 ICP-295,ICP-9806,ICP-14921,ICP-14955,ICP-14803,ICP-15027, ICP-7632
II (63%)	63	ICP-3537,ICP-9873,ICP-14945,ICP-233,ICP-8812,ICP-9704,ICP-8744, ICP-8755,ICP-14985,ICP-14453,ICP-3068,ICP-14885,ICP-7348, ICP-14970,ICP-11287,ICP-6945,ICP-14911,ICP-9684,ICP-3525 ICP-13209,ICP-7725,ICP-9644,ICP-15044,ICP-9623,ICP-10339 ICP-14949,ICP-7002,ICP-13690,ICP-14900,ICP-7643,ICP-12989 ICP-8750,ICP-3563,ICP-8870,ICP-10050,ICP-6951,ICP-3543 ICP-19645,ICP-8792,ICP-460,ICP-14452, ICP-14893,ICP-14410, ICP-9832, ICP-9825, ICP-14914,ICP-7848, ICP-8342,ICP-7850,ICP-8011 ICP-7148,ICP-7726,ICP-7655,ICP-8780,ICP-9356,ICP-9444,ICP-14886 ICP-8744,ICP-9451,ICP-13207,ICP-11294,ICP-10483,ICP-14913
III (17%)	17	ICP-14877, ICP-14883, ICP-6984, ICP-4048, ICP-3536, ICP-7828 ICP-7144, ICP-7898,ICP-9816, ICP-8525,ICP-7732 ICP-14738,ICP-4529, ICP-8872,ICP-8794,ICP-9444,ICP-13688
IV (4%)	4	ICP-3318, ICP-14836, ICP-9482, ICP-14619
V (1%)	1	ICP-10314
VI (1%)	1	ICP-9482

CL= clusters, ICP= International Center for pigeon pea.

and seed yield per plant whereas the remaining traits showed moderate heritability values which indicated that total variability was due to genetic causes as well as due to environment (Table 1). In this study low heritability values were observed from reproductive phase, seeds per pod, primary branches per plant, seeds per plant, days to flowering and seed yield per plant thereby indicating limited possibility of improvement for these traits through selection. Muhammad et al. (2002) also reported lower estimate of heritability for number of primary branches per plant and number of seeds per pod which is in agreement with the finding of the present study. Contrary to the result in this study, Patil et al. (2006) reported that seeds per plant and biomass yield per plant showed high heritability estimate.

Estimate of expected genetic advance

The genetic advance as percent of mean at 5% selection intensity for 14 traits are presented in Table 1. Estimate of GA for seed yield per hectare was 209.99 kg/ha indicating that whenever it is selected the best 5% high yielding genotypes as parents, mean yields of progenies could be improved by 209.99 kg/ha for the first cycle, that is mean genotypic value of the new population for seed

yield will be improved from 1070.19 to 1280.18 kg/ha and the same holds true for all traits considered under this study.

In the present study, estimates of genetic advance as percent of mean at 5% selection intensity ranged from 1.43% for pod filling duration to 25.48% for harvest index. Relatively high GAM values were observed for seed yield per plot, pods per plant, harvest index, plant height, biomass yield per plant and 100-seed weight. Patilet et al. (2007) also reported high genetic advance for seed yield per plot, harvest index and number of pods per plant in pigeon. However, studies completed by Patil et al. (2007) shown that data in days to flowering and days to maturity was not in accordance with the present study. However, similar high GAM value was reported by Vankateswarlu (2006) for plant height, pods per plant, seed yield per plot, harvest index and 100-seed weight in pigeon pea.

Number of primary branches per plant exhibited low heritability with moderate genetic advance which means that selection based on phenotypic observation will be of little importance in this trait, though a significant improvement may be possible through pedigree selection. The low expected genetic advance as percent of mean for days to flowering, pod filling duration and days to maturity is due to low variability for these traits

Table 3. Average intra (bold) and inter cluster (off diagonal) D^2 values among six clusters in pigeon pea genotypes.

Clusters	I	II	III	IV	V	VI
I	3.91					
II	16.76	7.4				
III	56.29**	16.47	3.94			
IV	183.38**	109.67**	55.01**	3.12		
V	650622**	650925**	650127**	651756**		
VI	369.78	269.90	188.51	70.95	649361	

**significance at 1 and 5% probability level respectively. $\sigma^2 = 23.68$, and 29.14 at 5 and 1% probability level respectively.

Table 4. Mean, minimum, maximum and standard deviation values of 14 quantitative traits of the 6 clusters for pigeon pea genotypes.

Traits	Clusters											
	I				II				III			
	Mean	Min	Max	STD	Mean	Min	Max	STD	Mean	Min	Max	STD
DF	84.26	75.90	92.40	6.44	88.70	75.40	100.40	6.00	92.51	84.90	104.40	5.68
PF	63.96	55.28	80.78	6.43	61.06	50.78	71.78	4.52	59.31	45.78	68.78	5.47
DM	149.89	134.36	161.36	7.58	151.44	133.36	164.36	6.85	153.50	145.36	163.36	5.17
PH	61.21	48.73	76.13	6.81	67.90	51.93	80.73	7.24	68.56	55.63	83.73	7.91
PBP	8.02	5.33	11.03	2.02	7.71	3.53	12.53	2.28	6.95	4.13	15.23	2.72
BYP	64.50	38.75	96.75	18.61	69.45	32.25	120.25	19.74	84.17	39.75	191.75	36.17
PP	73.92	48.85	100.05	14.91	77.58	35.95	149.35	23.74	78.97	49.95	115.15	18.43
SP	1.39	0.18	2.10	0.53	1.27	0.22	2.20	0.52	1.34	0.35	2.03	0.39
SPLA	216.88	156.73	320.53	49.58	231.06	95.63	413.63	67.87	235.23	153.53	350.83	63.53
SYPLA	21.20	13.92	35.87	6.80	21.19	9.00	39.00	7.10	21.22	13.30	33.30	6.25
HI	2.55	2.43	2.65	0.07	2.57	2.35	2.72	0.08	2.61	2.50	2.76	0.08
HSW	3.76	2.33	5.33	0.76	3.25	0.33	5.33	1.26	3.22	1.33	6.33	1.17
ASYP	540.31	360.51	627.48	71.67	768.50	640.90	922.06	74.67	1031.93	924.34	1191.83	83.78
SYH	707.12	472.10	821.09	93.68	1005.51	838.63	1206.16	97.61	1349.60	1209.13	1558.70	109.32

indicated by their respective low GCV and PCV values. Low and medium genetic advance coupled with low heritability was observed for reproductive phase, days to maturity, primary branches per plant, seeds per pod, seeds per plant and seed yield per plant thereby indicating these traits were greatly influenced by the environment. Result reported by Muhammad et al. (2002) was in accordance with the present study for number of primary branches per plant which had low heritability coupled with low genetic advance. Therefore, from heritability and genetic advance analysis it is concluded that traits like seed yield per plot, 100-seed weight, harvest index, pods per plant and plant height will provide a better opportunity for the improvement of this crop through selection and hybridization.

Cluster analysis

Mean values along with standard deviation of each cluster revealed that genotypes in cluster I had 14 genotypes (Table 4). This cluster could be characterized

by early flowering (84.26), early maturing (149.89), highest number of branches per plant (8.02), shorter in plant height (61.20), low seed yield per plot (540.31 g/plot) and seed yield per plant (21.20 g/plant) which was respectively (Table 4). This cluster was also characterized by low seed yield per hectare (707.12 kg/ha), low biomass yield per plant (64.50 g/plant), small number of pods per plant (73.92) and fewer number of seeds per plant (216.88) as compared to the other clusters.

The genotypes grouped in Cluster II were characterized by the following essential features: Early maturing (151.44), small number of days to flowering (88.70), short in height (67.90) and low biomass yield per plant (69.45) which was next to Cluster I. Cluster II had sixty three genotypes at which almost 63% of the total genotypes grouped under this cluster. Low seed yield per plant (21.22), small number of seeds per plant (231.06) and low yield per hectare (1005.51 kg/ha) which is again next to Cluster I was another important feature of Cluster II (Table 4).

The genotypes in cluster III were characterized by their

Table 5. Mean, minimum, maximum and standard deviation values of 14 quantitative traits of the 6 clusters for pigeon pea genotypes (continued).

Traits	Clusters											
	IV				V				VI			
	Mean	Min	Max	STD	Mean	Min	Max	STD	Mean	Min	Max	STD
DF	86.02	79.90	91.40	4.71	85.90	-	-	-	90.90	-	-	-
PF	66.90	61.30	80.30	9.01	58.80	-	-	-	57.80	-	-	-
DM	154.61	149.36	161.86	6.06	146.40	-	-	-	150.40	-	-	-
PH	66.08	58.63	77.63	8.55	80.70	-	-	-	79.80	-	-	-
PBP	7.15	5.93	9.83	1.80	10.70	-	-	-	6.20	-	-	-
BYP	108.50	54.25	157.25	45.80	116.80	-	-	-	185.80	-	-	-
PP	97.97	53.15	161.85	52.70	186.90	-	-	-	124.30	-	-	-
SP	1.39	0.80	02.01	0.61	1.80	-	-	-	1.90	-	-	-
SPLA	271.66	140.03	484.43	151.20	424.40	-	-	-	267.00	-	-	-
SYPLA	24.54	10.97	43.49	13.64	43.30	-	-	-	26.50	-	-	-
HI	2.59	2.48	2.70	0.11	2.53	-	-	-	2.72	-	-	-
HSW	3.08	2.33	5.33	1.50	4.30	-	-	-	3.30	-	-	-
ASYP	1450.10	1306.73	1553.51	103.61	1142.90	-	-	-	1710.80	-	-	-
SYH	1896.20	1708.04	2031.58	135.88	994.60	-	-	-	2235.70	-	-	-

DF=Days to flowering, PF=Reproductive phase, DM=days to maturity, PH (cm) =Plant height, PBP= Number of primary branch per plant, BYP(g) =Biomass yield per plant, PP=Pod per plant, Sp=Seed per pod, SPLA=Seed per plant, SYPLA(g) =Seed yield per plant, HI(g) =Harvest index, HSW(g) =Hundred seed weight, ASYP(g) =Adjusted seed yield per plot, and SYH(kg) =Seed yield per hectare, Min= Minimum value of each traits within cluster, Max= Maximum value of each trait within clusters, STD= Standard deviation of trait.

late flowering (92.51), medium duration of maturity (153.50), medium height (68.56) and medium number of primary branches per plant (6.95). Lower values was observed for seed yield per plant, seeds per plant, biomass yield per plant, harvest index and 100-seed weight as compared to Cluster III, IV and V but it was higher relative to Cluster I and II. The genotypes in the third cluster were also characterized by their higher value of seed yield per hectare next to Cluster IV and VI.

Cluster IV had 4 genotypes. This cluster could be characterized by medium days to flowering (86.02), late maturing(154.61), medium number of branches per plant (7.15) and shorter plant height (66.08).High seed yield per plot (1450.10 g/plot) and seed yield per hectare (1896.20 kg/ha) was another future with which the cluster is characterized (Table 5).

Cluster V and VI had one genotype each which was outstanding type by its performance in most of the traits or agronomic characters. The clusters were characterized by the following essential features: Early maturing (146.40, 150.40), late flowering (85.90, 90.90) and shorter pod filling duration (58.80, 57.80) respectively. Higher number of pods per plant (186.90, 124.30), number of seeds per pod (1.80, 1.90), seeds per plant (424.40, 267) and seed yield per plant (433 and 265) was also observed in Cluster V and VI respectively (Table 5). High seed yield per plot and per hectare was observed for Cluster VI and it was next to Cluster III and IV for Cluster V for seed yield per hectare. Cluster VI perform better than Cluster V in seed yield per plot, seed yield per

hectare and seeds per pod.

Harvest index in legumes is unpredictable and sensitive to environmental fluctuations and it is imperative to find genotypes with maximum harvest index as the result, Cluster VI consisted of genotypes with high harvest index whereas, Cluster V had the lowest harvest index value. Cluster V had better performance than VI in terms of early maturing, early flowering, high number of pods per plant, number of seeds per plant and seed yield per plant. Similar result was also reported by Malik et al. (1996) who found that some genotypes falling into a particular cluster showed outstanding in their performance in seed yield per plot and seed yield per hectare.

Generalized squared distance (D^2)

It is assumed that maximum heterosis is manifested in cross combinations involving the genotypes belonging to most divergent clusters. However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high-level of production. In the present research work, the maximum distance existed between Cluster VI vs. I, VI vs. II, VI vs. III and VI vs. V (Table 3). Considering the yield and growth duration, Cluster I and VI exhibit high heterosis for yield as well as earliness whereas Cluster V and VI exhibit maximum heterosis for yield as well as number of seeds per pod. From a serious of data analysis in pigeon pea genotypes, Dalsaniya et al. (2009) reported, genotypes showing greater divergence

would exhibit high heterosis for high yield.

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