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Full Length Research Paper

Variability for yield, yield related traits and association among traits of sorghum (*Sorghum Bicolor* (L.) Moench) varieties in Wollo, Ethiopia

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Sixteen sorghum varieties were tested in a randomized complete block design with three replications at Sirinka Agricultural Research Center and Kobo sub-center in 2010 with the objectives of estimating the genetic variability, associations among the traits and determining the direct and indirect effect of the traits on grain yield of varieties across the two locations. Analysis of variance revealed that there were statistically significant differences among the varieties for most of the traits across the two locations. From this combined analysis of variance, significant (P=0.01) effect due to location, varieties and GxE was observed for most of the traits. In terms of mean value performance, the varieties showed wider variability in grain yield which ranged from 762.6-2533.3 kg/ha over locations. A relatively high phenotypic coefficient of variation (PCV) values (>20%) were obtained for leaf area index, plant height, panicle weight, panicle yield, grain yield and harvest index across locations. Similarly, high genotypic coefficient of variation (GCV) values (> 20%) were also obtained for leaf area index, plant height, panicle yield, grain yield and harvest index. High heritability estimates (> 80%) were obtained for days to heading, days to flowering, leaf area index, days to maturity, plant height, panicle length and 1000 seed weight. But a relatively high genetic advance was obtained for only leaf area index, plant height, panicle yield, grain yield and harvest index. Grain yield showed significant (P=0.01) positive phenotypic correlations with plant height, panicle weight, panicle yield and harvest index and genotypic correlations with panicle yield. Similarly, significant (P=0.01) positive phenotypic and genotypic correlations between the independent traits was observed. From the path analysis, plant height, panicle weight and harvest index showed high positive phenotypic direct effect on grain yield whereas panicle yield showed negligible positive phenotypic direct effect with considerable indirect effect via panicle weight. At genotypic level, panicle yield showed the highest positive direct effect followed by harvest index and plant height whereas panicle weight showed negative direct effect with high positive indirect effect via panicle yield.

Key words: Genotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, correlation, direct and indirect effect.

INTRODUCTION

Grain sorgum (*Sorghum bicolor* L. Moench) ranks fourth in important as a cereal crop after wheat, rice and maize with a total cultivated area of 150 thousand hectare (Ezzat et al., 2010). In Ethiopia, sorghum is one of the most important cereal crops planted as food insurance, especially in the lowlands of eastern and in the north and north-eastern parts of the country where the climate is characterized by unpredictable drought and erratic rainfall (Degu et al., 2009). Improvement in sorghum yield depends on the nature and extent of genetic variability, heritability and genetic advance in the base population. Besides, the information on the nature of association between yield and its components helps in simultaneous selection for many characters associated with yield improvements (Mahajan et al., 2011). Being an indigenous crop, tremendous amount of variability exists in Ethiopia. In addition, a number of varieties are released by Melkasa agricultural research center and Sirinka agricultural research center (MoARD, 2008).

However, the existence of variation alone in the population is not sufficient for improving desirable characters and little study has been conducted on the genetic variability of the released early maturing sorghum varieties. Hence, estimation of the extent and pattern of genetic variability existing in the available germplasm is essential to breeders. Breeders are also interested in the relationship that may exist between or among characters. When more characters are involved in correlation study, it becomes difficult to ascertain the characters that really contribute to yield because of the existence of some amount of interdependence. Under such complex situations, path coefficient analysis provides more effective means of separating direct and indirect factors; permitting a critical examination of the specific forces acting to produce a given correlation and measuring the relative importance of the causal factors. The path coefficient analysis under such situations helps to determine the direct contribution of these characters and their indirect contributions via other characters (Tesfaye et al., 2014).

Therefore, this study was conducted: to determine the degree of genetic variability among early to medium maturing released sorghum varieties; to investigate associations among yield and yield related traits and to determine the major yield related traits causing direct and indirect effect on grain yield.

MATERIALS AND METHODS

The study was conducted during the 2010 main season at Sirinka Agricultural Research Center (Altitude 1850 m above sea level, average annual rainfall 1023 mm and average maximum and minimum temperature is 26 and 13°C) and Kobo sub center (Altitude 1468 m above sea level, average annual rainfall 310.5 mm and average maximum and minimum temperature is 14.86 and 29.30°C). The data for rainfall and temperature of the locations are obtained from their respective meteorological stations. Sixteen early to medium maturing sorghum varieties were grown in a randomized complete block design (RCBD) with three replications. The experimental unit was a four-row plot of 3 m long, spaced at 0.75 m apart and plant-to-plant distance of 0.15 m. Data were taken from the two central rows of the plot. Urea (50 kg/ha) and phosphorus (100 kg/ha) were applied to the entire plot.

Data collected from the two locations were subjected to combined ANOVA and Duncan's Multiple Range Test was used for mean comparison. The phenotypic and genotypic variance were estimated according to the methods suggested by Burton and de Vane (1953) and these components of variance (σ^2p, σ^2e, σ^2g) were used for the estimation of coefficients of variation (PCV, GCV) as described by Singh and Chaudhary (1977) as follows:

PCV= $\frac{\sqrt{\delta^2 P}}{x}x\,100$ and GCV= $\frac{\sqrt{\delta^2 g}}{x}$ X100

Heritability and expected genetic advance (K=2.06 at 5% selection intensity) were computed for each character based on the formula developed by Allard (1960). Phenotypic and genotypic correlation coefficients were estimated using the method described by Miller et al. (1958) from corresponding variance and covariance. The direct and indirect effects were determined through path coefficient analysis using the phenotypic as well as genotypic correlation coefficients following the method suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

From the analysis of variance for the combined ANOVA, significant differences among the varieties were observed for all the traits under investigation due to variety indicating the existence of genotypic differences among the varieties. Except plant height and 1000 seed weight, significant variations were obtained due to location for all the rest traits. This indicates that the conditions in the two locations were not similar in many aspects and the phenotypic performance of those traits of the varieties was different across the two locations.

Significant effect due to variety × location (interaction) was also obtained for all the traits, except days to emergence and leaf area index. This significant interaction effect of the traits suggested that the environmental conditions in the two locations influenced the performance of the varieties which resulted in the inconsistency in performance of these sorghum varieties across the two locations. This indicates the importance of testing the varieties across locations and over years to check their stability for use as reliable genetic materials for crop improvement in a specific location. The reader expects comparisons between this study and related work in discussion. Similar results for significant effect due to variety × location (interaction effect) is reported by Ezzat et al. (2010), for days to 50% flowering, plant height, 1000 grain weight and grain yield. Significant influence of genotype by location interaction on plant height and leaf area index is also obtained from late

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Table 1. Mean, Range, estimates of components of variance and coefficient of variation of the varieties across locations.

Trait	Range	Mean	σ^2p	σ^2g	σ^2e	PCV (%)	GCV (%)	ECV (%)
DE	7.00-9.67	7.93	1.72	1.31	0.41	16.62	14.41	8.07
DH	53.17-77.00	68.70	68.36	67.44	0.92	12.04	11.95	1.40
DF	56.67-81.67	73.10	74.35	73.34	1.01	11.80	11.72	1.37
LAI	1.15-2.91	2.25	0.49	0.40	0.09	31.11	28.11	13.33
DM	98.50-126.83	116.94	87.10	85.62	1.48	7.98	7.91	1.04
PH	108.1-172.87	137.60	1136.41	1099.73	36.68	24.50	24.10	4.40
PL	18.58-25.52	21.08	9.44	8.62	0.82	14.57	13.93	4.30
PW	44.47-71.33	61.90	178.92	113.82	65.10	21.61	17.24	13.03
PY	17.28-45.43	35.24	157.16	117.26	39.90	35.57	30.73	17.92
Sw	26.28-35.92	32.31	18.97	16.07	2.90	13.44	12.37	5.25
GY	762.6-2533.3	1937	561906.91	404744.29	157162.6	38.69	32.84	20.46
HI	10.34-26.32	20.00	37.70	29.26	8.44	30.70	27.05	14.53

σ^2p=phenotypic variances, σ^2g=genotypic variances, σ^2e=environmental variance, PCV and GCV=phenotypic and genotypic coefficient of variation, ECV=environmental coefficient of variation DE=days to 75 % emergence, DH=days to 75% heading, DF=days to 75% flowering, LAI= leaf area index, DM=days to 75% physiological maturity, PH=plant height (cm), PL=panicle length (cm). PW=panicle weight (g), PY=Panicle yield (g), Sw=1000 seed weight (g), GY=grain yield (kg/ha), HI=harvest index (%), σ^2p=phenotypic variance, σ^2g=genotypic variance, σ^2e=environmental variance.

research by Abubakar and Bubuche (2013).

Range, mean, estimates of variance components and coefficients of variation

From the combined analysis, most of the traits showed wide range of variability for days to heading; days to flowering; panicle length; 1000 seed weight and panicle weight per plant and days to maturity (Table 1). Panicle yield per plant showed very wide variability ranging from 17.28-45.43 g/plant with a mean of 35.24 g. The highest mean value of panicle yield per plant across locations was obtained from Misikr followed by Grana-1, Teshale, Macia and Hormat (Table 2). Harvest index ranged from 10.34-26.32%. In the present study, Red Swazi followed by 76T1#23 and Yeju showed high value of harvest index indicating the efficiency of the varieties in converting biological yield into economic yield.

Grain yield, which is the primary interest in most breeding programs, showed a wide range of variation (762.6-2533.30 kg/ha) among the varieties across locations with a mean value of 1937 kg/ha. The highest grain yield per hectare was obtained from Grana-1 (2533.30 kg/ha) followed by Misikr (2428.70 kg/ha), Hormat (2411.20 kg/ha) and Teshale (2333.30 kg/ha) (Table 3). Therefore, the presence of such range of variations of the traits indicated that the presence of large amount of genetic variation among the released varieties which is the source of variable genetic material.

As compared to its corresponding environmental variance, combined analysis of variance showed that all the traits exhibited larger genotypic variance than environmental variance (Table 2). Higher genotypic variance estimates than the environmental variance estimates indicated that the variation in phenotypic expression of the varieties across locations is more of due to genetic constituent and the contribution of environment is fairly small. High values of phenotypic and genotypic variance of the present study for plant height and 1000 seed weight is in agreement with the findings of Can and Yoshida (1999).

Tariq et al. (2007) also reported higher phenotypic and genotypic variance for grain yield among the varieties which supported the present study. Similarly, Bello et al. (2007) reported higher genotypic variance than environmental variance for panicle length, plant height, grain weight per panicle, days to flowering, days to maturity and grain yield per hectare, which is supported by the present study, and also for number of leaves per plant and number of grain per panicle. In general, the variance components across locations showed that all of the traits had higher genotypic variance estimates than the environmental variance estimates suggesting that expressions of the traits were more of due to genetic which can be exploited by breeding.

Phenotypic coefficient of variation (PCV) ranged from 7.98-38.69% and genotypic coefficient of variation (GCV) ranged from 6.71-32.84%. With these ranges, high value for PCV was obtained by grain yield/ha (38.69%) followed by panicle yield per plant (35.57%), leaf area index (31.11%), harvest index (30.70%), plant height (24.50%) and panicle weight per plant (21.61%) (Table 2).

Similarly, the maximum value of GCV also obtained from grain yield per hectare followed by panicle yield per plant, leaf area index, harvest index and plant height with a value of 32.84, 30.73, 28.11, 27.05 and 24.10%, respectively. These high values of PCV and GCV revealed that the varieties have a broad base genetic background so that they can respond positively to

Table 2. Mean performance of the varieties across the two locations.

Varieties	Mean Value											
	DE	DH	DF	LAI	DM	PH	PL	PW	PY	Sw	GY	HI
Teshale	7.17^{cd}	66.50^{hi}	70.83^{g}	2.34^{cd}	115.67^{f}	172.87^{a}	19.92^{fg}	62.83^{abc}	43.23^{ab}	34.39^{abc}	2333.3^{abcd}	23.34^{ab}
Yeju	7.50^{bcd}	61.50^{j}	65.33^{h}	1.81^{f}	113.50^{g}	152.33^{c}	21.47^{de}	63.00^{abc}	38.29^{abc}	35.19^{abc}	2195.4^{abcde}	24.28^{a}
Abuare	7.50^{bcd}	67.50^{fgh}	72.83^{f}	2.06^{def}	116.50^{ef}	133.23^{d}	22.53^{cd}	66.67^{abc}	38.47^{abc}	30.93^{def}	2164.6^{abcde}	20.52^{bc}
Hormat	7.50^{bcd}	66.50^{hi}	70.50^{g}	2.35^{cd}	114.17^{g}	163.52^{b}	22.42^{cd}	69.50^{ab}	40.22^{abc}	35.44^{a}	2411.2^{abc}	20.34^{bc}
Grana-1	7.00^{d}	68.00^{fg}	72.67^{f}	2.50^{bc}	120.83^{c}	171.30^{a}	19.93^{fg}	70.00^{ab}	43.42^{ab}	35.91^{a}	2533.3^{a}	20.16^{bc}
Misikr	7.83^{bcd}	70.67^{e}	74.67^{e}	2.31^{cd}	116.67^{ef}	154.32^{c}	20.80^{ef}	67.33^{abc}	45.43^{a}	33.74^{abc}	2428.7^{ab}	19.25^{cd}
Raya	7.83^{bcd}	77.00^{a}	81.67^{a}	2.89^{a}	126.83^{a}	165.70^{ab}	18.80^{gh}	68.42^{ab}	33.15^{cd}	26.28^{h}	1887.9^{cdef}	15.89^{d}
Gedo	9.17^{a}	73.17^{bc}	78.00^{c}	2.29^{cd}	121.50^{c}	115.73^{efg}	22.08^{cd}	44.47^{e}	17.28^{f}	33.11^{bcd}	762.6^{h}	10.34^{e}
Birhan	8.17^{b}	72.17^{cd}	76.17^{d}	2.28^{cde}	121.67^{bc}	111.48^{fgh}	24.47^{b}	59.80^{bc}	32.49^{cd}	35.05^{abc}	1670.8^{ef}	23.58^{ab}
Gobiye	9.67^{a}	67.00g^{hi}	71.33^{g}	1.99^{def}	118.67^{d}	108.10^{h}	22.87^{c}	48.40^{de}	24.24^{ef}	31.38^{de}	1177.0^{gh}	16.14^{d}
Abshir	9.67^{a}	68.33^{f}	72.83^{f}	1.91^{ef}	116.17^{ef}	118.32^{ef}	25.52^{a}	57.00^{cd}	26.64^{de}	33.06^{cd}	1480.0^{fg}	19.40^{cd}
76TI#23	7.67^{bcd}	66.17^{i}	70.83^{g}	1.78^{f}	108.67^{h}	122.37^{e}	19.17^{gh}	63.50^{abc}	38.23^{abc}	31.52^{de}	2077.2^{abcde}	24.92^{a}
Meko	7.50^{bcd}	71.67^{de}	76.67^{d}	2.80^{ab}	117.33^{de}	149.25^{c}	18.93^{gh}	67.83^{abc}	39.45^{abc}	35.32^{ab}	2165.8^{abcde}	17.77^{cd}
Redswazi	7.00^{d}	53.17^{k}	56.67^{i}	1.15^{g}	98.50^{i}	118.33^{ef}	18.58^{h}	49.50^{de}	25.33^{de}	28.16^{gh}	1947.9^{bcdef}	26.32^{a}
Macia	7.67^{bcd}	76.17^{a}	80.33^{b}	2.62^{abc}	123.0^{b}	108.62^{gh}	20.98^{ef}	71.33^{a}	41.95^{ab}	29.86^{efg}	1964.2^{bcdef}	18.67^{cd}
Tegemeo	8.00^{bc}	73.67^{b}	78.33^{c}	2.91^{a}	121.33^{c}	136.17^{d}	18.88^{gh}	60.83^{abc}	36.03^{bc}	29.19^{fg}	1799.6^{def}	19.05^{cd}
Mean	7.93	68.7	73.1	2.25	116.94	137.60	21.08	61.90	35.24	32.41	1937.48	20.00
CV (%)	8.03	1.4	1.37	13.24	1.04	4.40	4.29	13.03	17.93	5.25	20.46	14.52
Critical range	0.74-0.89	1.11-1.34	1.16-1.41	0.34-0.42	1.41-1.71	6.99-8.48	1.04-1.27	9.31-11.3	7.29-8.85	1.96-2.38	457.5-555.2	3.35-4.07

CV=coefficient of variation; DE=days to 75% emergence, DH=days to 75% heading, DF=days to 75% flowering, LAI=leaf area index, DM=days to 75% physiological maturity, PH=plant height (cm), PL=panicle length (cm). PW=panicle weight (g), PY=Panicle yield (g), Sw=1000 seed weight (g), GY=grain yield (kg/ha), HI=harvest index (%).

selection. The high values of PCV and GCV across locations for certain traits like plant height, panicle yield per plant and grain yield per hectare were obtained by Bello et al. (2007) which are supported by the present study. Bello et al. (2007) also reported high value of PCV and GCV for panicle length per plant, 1000 seed weight, days to flowering and days to maturity in contrary to the present study. In another case, low GCV was observed for days to maturity (7.91%) which indicated that improvement of this traits through selection is less effective due to lack of genetic variability among the varieties which is the basic prerequisite in which positive response due to selection depends on. In general, GCV value was generally smaller than their corresponding PCV values for all the traits considered indicating the contribution of environmental variance for the expression of phenotypic variance of the traits.

Heritability and expected genetic advance

Heritability estimates for traits under study for combined over locations is depicted in Table 3. The estimated values of broad sense heritability ranged from 23.76-98.65% over locations. According to Singh (2001), high heritability of a trait (≥ 80%) provides selection for such traits could be fairly easy due to a close correspondence between the variety and the phenotype due to the relative small contribution of the environment to the phenotype. In other words, if environmental variability is small in relation to genotypic differences, selection will be efficient because the selected character will be transmitted to its progeny. But selection may be considerably difficult or virtually impractical for traits with low heritability (≤ 40%) due to the masking effect of the environment so that the greater the proportion of the total variability is due to environment.

Based on this benchmark, high broad sense heritability was estimated for days to heading (98.65%), days to flowering (98.64%), leaf area index (81.63%), days to maturity (98.3%), plant height (96.77%), panicle length (91.31%) and 1000 seed weight (84.71%) across locations.

Table 3. Broad sense heritability (h^2), genetic advance (GA) and genetic advance as percent of the mean (GA %) of the varieties across locations.

Parameter	DE	DH	DF	LAI	DM	PH	PL	PW	PY	Sw	GY	HI
h^2 (%)	76.12	98.65	98.64	81.63	98.30	96.77	91.31	63.62	74.61	84.71	72.03	77.61
GA	1.65	17.23	17.43	1.16	16.50	48.30	4.35	15.48	17.12	6.23	949.92	11.30
GAM (%)	20.76	25.09	23.85	51.57	14.11	35.10	20.61	25.00	48.59	19.22	49.03	56.52

$h^{2=}$ heritability in broad sense (%), GA=genetic advance, GAM=genetic advance as percent of mean, DE=days to 75% emergence, DH=days to 75% heading, DF=days to 75% flowering, LAI=leaf area index, DM=days to 75% physiological maturity, PH=plant height (cm), PL=panicle length (cm). PW=panicle weight (g), PY=Panicle yield (g), Sw=1000 seed weight (g), GY=grain yield (kg/ha), HI=harvest index (%).

Mahajan et al. (2011) also reported similar results of high heritability for days to flowering, panicle length per plant and plant height at a location. High estimated heritability values of the present study for panicle length per plant, plant height, days to maturity and days to flowering agreed with the findings of Bello et al. (2007). In general, high broad sense heritability of the traits indicated their potential to respond positively to selection at different locations.

Grain yield also showed moderate heritability value (72.03%) across locations. On the other hand, high heritability value of grain yield was reported by Mahajan et al. (2011) and Tariq et al. (2007) (95.18%). Bello et al. (2007) also found low heritability of grain yield (10%). This highly variable result of heritability of grain yield indicated that it is a typical example of quantitative trait in which its phenotypic expression is highly influenced by environmental variations. Harvest index showed moderate estimated value of heritability. But Tariq et al. (2007) and Mahajan et al. (2011) found high heritability value which is not in agreement with the present study.

High heritability with low genotypic coefficient of variation may hinder easy to selection and improvement of these traits through selection. Genetic progress expected from selection increases with an increase in genotypic variance. In line with this statement, leaf area index and plant height showed high heritability coupled with high genotypic coefficient of variation across locations which indicated that these traits may respond effectively to phenotypic selection. Bello et al. (2007) found high heritability coupled with high genotypic coefficient of variation for traits such as panicle length per plant, plant height, days to flowering and days to maturity across locations. From these traits only plant height is in agreement with the present study. Mahajan et al. (2011) also reported high heritability coupled with high genotypic coefficient of variation for panicle yield per plant and harvest index which is not in agreement with the findings of the present study due to the fact that these traits have medium heritability but high genotypic coefficient of variation.

The estimated value of expected genetic advance expressed as percentage of mean ranged from 9.32-56.52% across locations. Leaf area index, plant height, grain yield per hectare, harvest index and panicle yield per plant, which have better genotypic coefficient of variation, showed a relatively high expected genetic advance. Mahajan et al. (2011) also reported high value of expected genetic advance expressed as percent of mean for harvest index, plant height and panicle yield per plant. Selection based on those traits with a relatively high genetic advance as percent of mean will result in the improvement of the performance of the varieties for the traits. Therefore, from this study, traits such as leaf area index, plant height, panicle yield per plant, grain yield per hectare and harvest index have the potential to respond positively to selection across different environments because of their better broad sense heritability coupled with relatively high genetic advance across locations.

Correlation studies

Traits of crop plants are generally correlated and correlations between characters are frequent features in plant breeding which can be either negative or positive. The phenotypic and genotypic correlation coefficients worked out among yield and yield related traits across locations are presented in Table 4.

Phenotypic correlations

From the combined analysis, grain yield showed significant (p=0.01) high positive phenotypic correlations with plant height (r=0.624) and panicle weight per plant (r=0.745) (Table 5). This is in conformity with Ezeaku and Mohammed (2006) who found high positive phenotypic correlation coefficients of grain yield with head

Table 4. Phenotypic (above diagonal) and genotypic (below diagonal) correlations of the varieties across locations (2010).

Parameter	DE	DH	DF	LAI	DM	PH	PL	PW	PY	Sw	GY	HI
DE		0.257	0.248	-0.004	0.252	-0.505*	0.524*	-0.420	-0.608*	-0.060	-0.691**	-0.488
DH	0.380		0.983**	0.738**	0.939**	-0.015	0.042	0.236	0.091	-0.088	-0.214	-0.572*
DF	0.387	0.998**		0.689**	0.906**	-0.034	-0.005	0.227	0.072	-0.072	-0.217	-0.543*
LAI	-0.059	0.901*	0.889*		0.727**	0.323	-0.158	0.498*	0.356	-0.022	0.069	-0.421
DM	0.365	0.962**	0.942**	0.902*		0.117	0.176	0.227	0.123	0.006	-0.210	-0.594*
PH	-0.642	-0.013	-0.032	0.380	0.122		-0.411	0.486	0.528*	0.236	0.624**	0.112
PL	0.690	0.059	0.018	-0.240	0.179	-0.485		-0.063	-0.249	0.303	-0.357	-0.086
PW	-0.980**	0.474	0.490	0.591	0.402	0.703	-0.267		0.819**	0.104	0.745**	0.274
PY	-1.078*	0.152	0.155	0.371	0.154	0.732	-0.492	1.152		0.076	0.729**	0.358
Sw	-0.231	-0.117	-0.124	-0.043	0.016	0.310	0.387	0.155	0.138		0.102	0.114
GY	-1.198	-0.273	-0.271	0.073	-0.268	0.802	-0.597	1.069*	0.933*	0.097		0.599*
HI	-0.812	-0.738	-0.728	-0.653	-0.771	0.127	-0.156	0.158	0.311	0.072	0.549	

*;** significant at 5% and 1% probability levels. DE=days to 75% emergence, DH=days to 75% heading, DF=days to 75% flowering, LAI=leaf area index, DM=days to 75% physiological maturity, PH=plant height (cm), PL=panicle length (cm). PW=panicle weight (g), PY=Panicle yield (g), Sw=1000 seed weight (g), GY=grain yield (kg/ha), HI=harvest index (%).

weight and plant height across two locations. Grain yield also showed significant (p=0.01) high positive phenotypic correlations with panicle yield per plant (r=0.729) and harvest index (r=0.599). The correlation of grain yield with harvest index is in agreement with the findings of Tariq et al. (2007). Generally, grain yield showed positive phenotypic associations with leaf area index, plant height, panicle weight per plant, panicle yield per plant, 1000 seed weight and harvest index and negative association with all the rest traits across locations. Therefore, the positive association of grain yield with these traits suggested that the possibility of simultaneous improvement of grain yield through indirect selection of these positively correlated traits.

Days to heading showed significant (p=0.01) strong positive phenotypic correlations with days to flowering (r=0.983), leaf area index (r=0.738) and days to maturity (r=0.939). Days to flowering also showed significant (p=0.01) high positive phenotypic correlations with leaf area index (r=0.689) and days to maturity (r=0.906). Significant (p=0.01) strong positive phenotypic correlation was also obtained between leaf area index and days to maturity (r=0.727) and panicle weight per plant and panicle yield per plant (r=0.819). Significant (p=0.05) negative phenotypic correlation was obtained from plant height (r=-0.505) and panicle yield per plant (=-0.608) with days to emergence. Similarly, harvest index also showed significant (p=0.05) negative phenotypic correlations with days to heading (r=-0.572), days to flowering (r=-0.543) and days to maturity (r=-0.594). Generally, positive correlation of any pairs of traits of the present sorghum population indicated the possibility of correlated response to selection. In contrary to this, the negative correlation prevents the simultaneous improvement of those traits along with each other.

Genotypic correlations

The results obtained from the combined analysis showed significant (p=0.05) strong positive genotypic correlations of grain yield with panicle weight per plant (r=1.069) (Table 5). This is in accordance with the result obtained by Ezeaku and Mohammed (2006). Grain yield also showed significant (p=0.05) and high positive genotypic correlation with panicle yield per plant (r=0.933). Ezeaku and Mohammed (2006) also found significant high positive genotypic correlations of grain yield with plant height and 1000 seed weight across locations which were positive but non-significant in the present study. Significant (p=0.01) strong positive genotypic correlations were also obtained for days to heading with days to flowering (r=0.998) and days to maturity (r=0.962). Significant (p=0.01) positive genotypic correlation was also obtained between days to

Table 5. Environmental correlations of the varieties across locations (2010).

Parameter	DE	DH	DF	LAI	DM	PH	PL	PW	PY	Sw	GY	HI
DE		-0.326	-0.291	0.097	-0.242	-0.120	0.111	0.106	0.004	0.242	-0.025	0.004
DH			0.716**	0.041	0.268	-0.040	-0.166	-0.375*	-0.144	0.055	-0.161	-0.113
DF				-0.166	0.212	-0.061	-0.210	-0.333	-0.217	0.183	-0.156	-0.002
LAI					-0.053	0.132	0.110	0.444	0.345	0.021	0.065	-0.013
DM						0.022	0.193	-0.108	0.107	-0.066	-0.146	-0.092
PH							0.210	0.347	0.084	-0.061	0.354	0.109
PL								0.283	0.287	0.057	0.154	0.095
PW									0.562**	0.058	0.493**	0.395*
PY										-0.012	0.504**	0.421*
Sw											0.112	0.187
GY												0.667**
HI												

*,**: Significant at 5% and 1% probability level. DE=days to 75% emergence, DH=days to 75% heading, DF=days to 75% flowering, LAI=leaf area index, DM=days to 75% physiological maturity, PH=plant height (cm), PL=panicle length per plant (cm), PW=panicle weight per plant (g), PY=Panicle yield per plant (g), Sw=1000 seed weight (g), GY=grain yield (kg/ha), HI=harvest index (%).

flowering and days to maturity (r=0.942). Leaf area index showed significant (p=0.05) positive genotypic correlation with days to heading, days to flowering and days to maturity with a correlation coefficient of 0.901, 0.889 and 0.902, respectively. On the other hand, significant (p=0.01) but negative correlation existed between days to emergence and panicle weight per plant (r=-0.980).

Generally, the values of genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients for most of the traits suggesting that there was inherent relationship between these traits. This is in accordance with the findings of Mahajan et al. (2011) and Ezeaku and Mohammed (2006). The positive association between all possible pair of traits suggested that the possibility of correlated response to selection so that with the improvement of one trait, there will be an improvement in the other positively correlated trait. The positive genotypic association allows simultaneous genetic improvement for grain yield. This is because a positive genetic correlation between two desirable traits makes the job of plant breeder easy for improving both traits simultaneously. Unlike positive correlation, negative correlation between two desirable traits may impede or makes it impossible to achieve the simultaneous improvement of those traits along with each other.

Generally, the existence of strong positive correlation between grain yield and other traits helps in identifying traits that could be used for indirect selection for the improvement of grain yield. Therefore, to facilitate selection in breeding for high yield and other desirable traits, it is logical to examine various components and give more attention to those having the greatest influence on grain yield.

Environmental correlations

From the combined analysis, grain yield per hectare showed significant (P=0.01) and positive environmental correlations with panicle weight per plant (r=0.493) (Table 5). This is in agreement with the finding of Ezeaku and Mohammed (2006). It also showed significant (P=0.01) and positive environmental correlations with panicle yield per plant (r=0.504) and harvest index (r=0.667). Significantly (P=0.01) high positive environmental correlations were obtained between days to heading and days to flowering (r=0.716) and panicle weight per plant and panicle yield per plant (r=0.562). Harvest index showed significant (p=0.05) positive correlations with panicle weight per plant (r=0.395) and panicle yield per plant (r=0.421).

In general, the positive environmental correlation between pairs of traits justified that any

Table 6. Estimates of direct (bold diagonal) and indirect (off diagonal) phenotypic effects of the traits on grain yield of the varieties across locations.

Variable	PH	PW	PY	HI	Rp
PH	0.346	0.202	0.026	0.047	0.624
PW	0.168	0.417	0.041	0.116	0.745
PY	0.182	0.341	0.051	0.152	0.729
HI	0.038	0.114	0.018	0.427	0.599

R=0.4248, PH=plant height, PW=panicle weight, PY=panicle yield, HI=harvest index (%), Rp=phenotypic correlation coefficient, R=residual factor.

Table 7. Estimates of direct (bold diagonal) and indirect (off diagonal) genotypic effects of the traits on grain yield of the varieties across locations.

Variable	PH	PW	PY	HI	Rg
PH	0.239	-0.172	0.701	0.033	0.802
PW	0.168	-0.244	1.102	0.041	1.069
PY	0.175	-0.281	0.958	0.081	0.933
HI	0.030	-0.039	0.298	0.259	0.549

R=0.1821, PH=plant height, PW=panicle weight, PY=panicle yield, HI=harvest index (%), rg=genotypic correlation coefficient, R= residual factor.

environment that favors/disfavors the expression of one trait will also favors/disfavors the expression of other positively correlated trait. However, the negative correlation indicated that some environmental variables that are favorable for the increment of the value of one trait might have caused a value decrement of negatively correlated trait.

Path coefficient analysis

By using grain yield as a dependent variable, the phenotypic and genotypic correlations were partitioned into direct and indirect effects for only four traits that are believed to have a direct relationship with grain yield from the data obtained from across locations.

Phenotypic path analysis

Partitioning of phenotypic correlations into direct and indirect effects on grain yield revealed that all the traits included in the path analysis showed positive direct effects (Table 6). The positive phenotypic direct effect of plant height and harvest index on grain yield is in agreement with Mahajan et al. (2011). Ezeaku and Mohammed (2006) also found positive direct effect of panicle weight on grain yield which is supported by the present study. Harvest index showed the highest direct effect on grain yield (0.427) followed by panicle weight (0.417) and plant height (0.346) while panicle yield showed negligible positive phenotypic direct effect (0.051) and contributed indirectly to grain yield via panicle weight (0.341). The synchronization of significant high positive correlation and considerable direct effects of plant height, panicle weight and harvest index on grain yield justified that the need to identify the nature of relationships between yield and yield related traits by using path analysis. Significant high positive correlation of panicle yield and its negligible direct effect revealed that indirect effect of panicle yield was cause of correlation. Therefore, such considerable indirect effects should be considered simultaneously for selection. The phenotypic residual value (0.4248) indicated that the traits which are included in the phenotypic path analysis explained 57.52% of the variation in grain yield.

Genotypic path analysis

Genotypic path analysis showed that plant height, panicle yield and harvest index showed positive direct effect (Table 7). The positive genotypic direct effect of plant height is in conformity with the results obtained by Mahajan et al. (2011) in their study on variability, correlation and path coefficient analysis in sorghum. The same authors also found negative direct effect of harvest index which is positive in the present study. Panicle yield which had significant high positive correlation with grain yield exerted considerable high positive direct effect (0.958). The correlation coefficient (0.933) of this trait is equivalent to its direct effect. This indicated that the correlation of this trait with grain yield was found to be mainly due to its direct effect. Therefore, there existed a true relationship and a direct selection, though this trait will be effective.

Panicle weight had negative direct effect (-0.244) and considerable indirect effect (1.102) via panicle yield. But its correlation was significantly high and positive. Matching of significantly high positive correlation and negative direct effect of this trait indicated that the indirect effect of this trait seem to be the cause of correlation. Therefore, the indirect causal factor should be considered simultaneously.

Plant height was another trait which had positive direct effect which is small as compared to its correlation coefficient. But it also contributed high positive indirect effect to grain yield via panicle yield. Therefore, high positive correlation of plant height with grain yield was due to both its positive direct effect and indirect effect via panicle yield. Harvest index which have positive genotypic correlation with grain yield showed considerable positive direct effect. Beside its direct effect, it also showed relatively large positive indirect effect via panicle yield. This indicated that the correlation was the result of both direct and indirect effects. Therefore, such considerable indirect effects should be considered for selection. The genotypic residual value (R=0.1821) indicated that the traits which are included in the genotypic path analysis explained 81.79% of the variation in grain yield.

Conclusions

Twelve characters were involved in the combined analysis of variance across the two locations. The study revealed the existence of significant genetic variability among the tested varieties for different traits. The presence of significant genetic variability among the varieties suggested the possibility of improving the traits through direct and indirect selection. Traits with high heritability and genetic advance are important traits which should be given attention in order to bring an effective response of grain improvement of the concerned varieties. The study of relationships is also important for assessing the feasibility of joint selection of two or more traits and hence for evaluating the effect of selection for secondary traits on genetic gain for the primary trait under consideration.

The path coefficient analysis revealed that all the traits included in the path analysis showed positive phenotypic direct effect. As a result of this, traits that exerted positive direct effect and positive and significant correlation with grain yield needs much attention in selection program. Traits that also showed considerable positive indirect effects via other traits should be considered simultaneously as indirect selection criteria for grain yield improvement. Therefore, in order to bring an effective improvement of grain yield, more attention should be given for traits such as plant height, panicle weight, panicle yield and harvest index which showed high positive phenotypic and genotypic correlation coefficients with a considerable direct and indirect effect on grain yield.

Conflict of Interest

The authors have not declared any conflict of interests.

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Genetic effects on panicle traits of crossbred rainfed rice cultivars using generation mean analysis

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The nature and magnitude of gene effects involved in expression of panicle traits in rainfed rice cultivars were estimated among a wide range of crosses using generation mean analysis. The parental lines comprised of two low-land and six upland rain-fed rice. The lowland parents were used as pollen parents and the upland genotypes were maintained as the seed parents. Crosses were made between them to obtain the F_1 hybrids. Backcrosses were produced by crossing the F_1 hybrids to their pollen parent to obtain $BC_{1.1}$ and seed parents to produce $BC_{1.2.}$ The result revealed significant differences ($P \leq 0.05$) among the genotypes for all the characters studied. Except for Max x CT7127-49 where P_2 and F_2 plants of WITA 4 x NERICA 1 that produced long panicles (29.28 and 26.13 cm) that differed significantly ($P \leq 0.05$) from other generations, F_1 plants produced the longest panicles in the other crosses followed by the F_2 plants. For most traits, F_1 generation means were higher than the mid-parent values. Significant differences observed between the F_1 and F_2 generation means in majority of the cases for percentage fertile spikelet and spikelet number per panicle is thought to be due to the diversity in these traits among the parental lines. The means of BC_1 and BC_2 tended to be located close to those of their respective recurrent parents. Digenic epistatic model was adequate to explain variation in generation means for all the panicle traits for the pooled analysis. Most of the crosses manifested non-allelic interactions for number of spikelet per panicles and fertile spikelet per panicle and is an indication that epistasis is determined to some extent by the genotypes used for the study.

Key words: Generation mean, dominance, additive, epistasis, F_1, F_2, parental line and backcross.

INTRODUCTION

In Africa, there are two rice cultivation ecosystems: The upland system on well drained soils with rain-fed crops and the lowland systems on swampy ecosystems under flooded conditions. Rain-fed upland is the major rice growing ecology in West Africa, accounting for nearly 60% of the total regional rice production area. For Nigeria upland rice accounts for 55 to 60% of the total cultivated rice land area with a productivity of 30 to 35% of total national rice production while lowland rain-fed rice production area estimates to 25% constituting some of the high yields ranging from 2 to 8 tonnes/ha, which contributes to 43 to 45% of total national rice production (Singh and Mowa, 1997). Optimizing grain yield has remained a major focus of rice production in almost all

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rice producing countries of the world. Panicle characters represent the most important part of rice plant with respect to yield improvement. Yield increase in modem rice was possible through improvement of panicle characters through long panicles, increased number of filled grains, more primary and secondary rachis (Seetharaman et al., 1973).

Genetic effect implies the capacity of a parent to produce superior progenies when crossed with another parent (Won et al., 2002). The choice of the most efficient breeding procedures predicates on the knowledge of the genetic systems controlling the characters under selection. Generation mean analysis belongs to the quantitative biometric methods based on measurements of phenotypic performances of certain quantitative traits on basic experimental breeding generations (parental, filial, backcross and segregation generations). Kearsey and Pooni (1996) reported that generation mean analysis is a useful technique in plant breeding for estimating main gene effects (additive and dominance) and their digenic (additive x additive, additive x dominance, and dominance x dominance) interactions responsible for inheritance of quantitative traits. This helps us in understanding the performance of the parents used in crosses and productivity potential of crosses for use in heterosis exploitation or in pedigree selection (Sharma and Sain, 2003). However, it is possible to ignore non-allelic (epistasis) interactions when these additive-dominance models are utilized. The presence or absence of epistasis can be detected by the analysis of generation mean using scaling test which measures epistasis accurately whether it is complementary (additive x additive) or duplicate (additive x dominance) and (dominance x dominance) at the digenic level (Farshadfar et al., 2008). The mode of inheritance and nature of genetic components of panicle characters in rice have been reported (Kim, 1987; Chang et al., 1998 Mahmood et al., 2004; Iftekharuddaula et al, 2008).

In this investigation six generations (parental, F_1, F_2, $BC_{1.1}$ and $BC_{1\cdot2}$) was undertaken to study gene action on panicle traits in two lowland and six upland rice genotypes using their generation means.

MATERIALS AND METHODS

The experimental materials consisted of six generations [P_1, P_2, F_1, F_2, $BC_{1.1}$ (P_1 x F_1)] and $BC_{1.2}$ (P_2 x F_1). The parental lines consisted of two lowland and six upland rice genotypes chosen for their differing panicle characters: WITA 4, Max, WAB 96-1-1, IR57689-73, EMPASC 105, Fofifa 16, CT7127- 49 and NERICA 1. Crosses between these genotypes with different rain-fed ecologies were performed to obtain hybrids. The lowland genotypes were used as pollen parents while the upland ones were used as the seed parents and crosses were made between them to obtain the F_1 hybrids. Backcrosses were produced by crossing the F_1 plants back to both their seed and pollen parents. All entries were grown in randomised complete block design with three replications at the Teaching and Research Farm of the Federal University of Technology, Owerri, Nigeria during the season of 2009. Each generation was planted in 1 m × 1 m plot with a spacing of 20 cm × 20 cm within and between plots. Panicle lengths and primary branches of panicle were measured in centimetre from five randomly selected plants and the mean data were used for statistical analysis. Similarly, number of spikelet per panicle and number of seeds per primary branch of panicle were determined. All measurements were taken according to SES of rice (1988).

The statistical analysis and genetic effects were performed using the GLM procedure of the SAS program (SAS institute, 1999) according to the randomized complete block design considering experiments and genotypes as fixed effects. Analyses of variances and F-tests following Steel and Torrie (1980) and Obi (2002) were carried out on six populations (P_1, P_2, F_1, F_2, $BC_{1.1}$ and $BC_{1.2}$) within each cross to determine the significance of genotypic differences for the traits studied. The least significant difference (LSD) was used to separate the treatment means.

The estimate of gene effects of the panicle traits was determined using the mean data from the parental lines (P_1 and P_2), F_1, F_2, $BC_{1.1}$ and $BC_{1.2}$ populations as described by Gamble (1962) and modified by Yang et al. (1997) as follows:

$M = F_2;$
$a = BC_{1.1} - BC_{1.2};$
$d = -\frac{1}{2} P_1 - \frac{1}{2} P_2 + F_1 - 4 F_2 + 2BC_{1.1} + 2BC_{1.2};$
$aa = - 4F_2 + 2BC_{1.1} + 2 BC_{1.2}$
$ad = - P_1 + P_2 + 2BC_{1.1} - 2BC_{1.2}$
$dd = P_1 + P_2 + 2F_1 + 4F_2 - 4BC_{1.1} - 4BC_{1.2}$

Where: a = additive effect; d = dominance effect; aa = additive × additive type of epistasis; ad = additive × dominance type of epistasis; dd = dominance × dominance type of epistasis; $BC_{1.1}$ =Back Cross one (1), and BC1.2 = Back Cross two (2).

RESULTS

Generation mean analysis of the lowland x upland rice genotypes

The result of the mean performance of the crosses between eight genotypes of rice studied is presented in Table 1. Significant differences ($P \leq 0.05$) were observed among the genotypes for all the characters studied. For panicle length, significant differences ($P \leq 0.05$) were observed for all crosses. Except for Max x CT7127-49 where P_2 produced the longest panicle (29.28 cm) followed by F_1 plants (29.18 cm) and WITA 4 x NERICA 1 where F_2 produced the longest panicles (26.13 cm), F_1 plants produced the longest panicles in all the other crosses followed by the F_2 plants. The F_1 and F_2 plants produced more secondary branches per panicle in WITA 4 x IR57689-73, WITA 4 x WAB 96-1-1 and WITA 4 x NERICA1. The F_2 plants produced more fertile spikelets in WITA 4 x IR57689-73 (93.77%), WITA 4 x CT7127- 49 (94.53%), WITA 4 x Fofifa 16 (90.57%), WITA 4 x NERICA 1 (95.15%), Max x CT 7127- 49(95.52%) Max x EMPASC 105 (92.23 %) and Max x WAB 96-1-1 (93.22%) than the other generations. Similarly, P_2 plants were more fertile in WITA 4 x EMPASC 105 (93.4%), Max x Fofifa 16 (96.43%) and Max x NERICA 1 (93.17%) crosses. Significant differences ($P\leq 0.05$) were recorded for number of spikelets per panicle in all the crosses. The

Table 1. Generation means and least significant differences (LSD) for panicle traits in eight rain-fed rice crosses.

Crosses/generation	Panicle length (cm)	Primary branch /panicle	Fertile spikelet (%)	No of spikelet/panicle	Seed/primary branch of panicle
WITA 4 × IR 57689-73					
P1	24.40	9.00	87.82	85.33	9.67
P2	22.03	9.33	92.81	84.38	9.16
F1	25.57	10.33	78.57	74.50	8.67
F2	24.53	9.83	93.77	91.83	11.17
BC1	24.35	9.33	80.73	79.67	9.83
BC2	24.22	8.67	61.37	66.33	9.67
LSD(0.05)	1.262	1.146	6.42	15.282	1.461
WITA 4 × CT 7127 – 49					
P1	26.22	11.17	80.98	98.50	11.17
P2	26.20	11.50	91.02	139.40	13.19
F1	29.22	10.67	83.6	86.17	8.12
F2	27.05	9.17	94.53	115.67	13.83
BC1	24.15	11.17	77.02	90.17	9.50
BC2	25.75	8.33	58.77	65.33	10.33
LSD(0.05)	2.513	2.113	8.894	24.964	2.759
WITA 4 x EMPASC 105					
P1	21.90	10.50	88.27	94.50	10.67
P2	22.47	10.83	93.40	114.8	12.17
F1	23.90	9.83	78.32	81.17	8.67
F2	22.32	10.00	87.93	115.17	12.00
BC1	22.23	10.67	70.27	77.83	9.00
BC2	21.72	8.67	58.32	64.17	10.33
LSD(0.05)	2.075	1.853	12.754	23.843	1.231
WITA 4 x Fofifa 16					
P1	22.98	10.33	84.77	96.17	10.17
P2	22.98	9.33	89.57	91.00	10.90
F1	25.25	10.17	75.27	71.67	7.33
F2	24.42	10.67	90.57	99.00	10.83
BC1	22.57	10.50	78.42	81.33	10.17
BC2	22.54	7.50	71.20	76.67	9.17
LSD(0.05)	2.027	2.659	8.40	13.758	2.340
WITA 4 x WAB96-1-1					
P1	25.02	9.83	81.52	94.83	9.97
P2	24.29	10.17	90.88	95.50	10.83
F1	27.05	10.50	65.63	71.83	9.17
F2	25.15	9.93	91.82	108.67	9.04
BC1	24.28	10.34	78.50	81.00	9.50
BC2	23.22	8.83	73.83	79.67	9.47
LSD(0.05)	1.995	1.435	7.454	17.055	1.856
WITA 4 x NERICA 1					
P1	23.27	9.83	81.15	113.29	11.16
P2	22.56	10.15	94.50	96.83	10.82
F1	24.50	10.5	86.42	84.34	8.92
F2	26.13	10.66	95.15	102.36	10.71
BC1	22.82	10.16	79.23	99.53	9.53
BC2	21.75	8.91	78.98	81.64	9.17
LSD(0.05)	1.378	1.435	8.423	20.641	1.856

Table 1. Contd.

Max x IR 57689-73					
P1	21.65	9.83	89.63	83.50	10.83
P2	22.12	10.00	87.33	112.60	12.38
F1	23.72	10.83	63.35	76.50	9.32
F2	22.78	10.00	91.23	97.17	10.84
BC1	23.03	9.17	83.83	89.83	10.47
BC2	24.4	7.67	71.67	94.16	12.96
LSD(0.05)	1.32	2.074	7.679	10.009	1.761
Max x CT 7127-49					
P1	25.83	12.14	83.91	119.53	11.33
P2	29.28	12.17	94.85	122.83	13.32
F1	29.18	12.67	87.00	96.17	12.64
F2	25.72	11.50	95.52	123.17	12.67
BC1	24.22	11.00	79.63	101.67	10.83
BC2	25.12	10.00	54.92	77.67	11.00
LSD(0.05)	1.79	1.62	8.411	26.758	2.648
Max x EMPASC 105					
P1	21.48	11.00	81.08	96.83	12.83
P2	22.48	12.15	91.80	110.17	12.19
F1	23.93	10.33	81.93	86.92	10.02
F2	21.83	11.50	92.2	116.67	11.17
BC1	21.57	11.17	73.02	8217	10.17
BC2	22.37	9.333	61.05	78.00	11.50
LSD(0.05)	2.002	1.686	9.481	33.119	2.894
Max x Fofifa 16					
P1	22.60	10.83	85.58	95.33	11.33
P2	22.46	10.57	95.43	92.67	10.33
F1	25.37	9.67	84.30	81.67	8.67
F2	23.05	9.62	90.15	93.17	11.50
BC1	22.02	9.17	81.72	81.72	9.83
BC2	22.10	8.83	68.48	61.33	10.33
LSD(0.05)	2.574	1.424	7.478	19.05	2.383
Max x WAB 96-1-1					
P1	24.48	10.83	86.83	92.17	11.33
P2	24.03	11.17	91.33	97.33	10.67
F1	27.32	10.67	83.78	94.50	9.83
F2	26.15	10.83	93.22	113.22	11.17
BC1	24.20	9.67	84.20	86.00	10.00
BC2	22.23	8.67	66.72	63.50	9.93
LSD(0.05)	2.40	1.24	7.175	25.171	2.451
Max x NERICA 1					
P1	22.72	12.83	81.87	110.18	11.83
P2	22.58	11.83	93.17	96.37	15.51
F1	23.77	12.33	86.33	69.81	9.50
F2	23.33	11.17	90.37	130.13	14.17
BC1	21.65	10.83	74.61	94.17	11.67
BC2	22.15	9.67	70.38	81.56	11.83
LSD(0.05)	1.859	1.869	6.47	20.189	2.194

Table 2. Estimates of genetic effects on panicle traits of the rice genotypes studied in 2009.

Characters	M	A	D	AA	AD	DD	Type of epistasis
Panicle length (cm)	24.49	0.58*	-0.512	-2.76	0.673	7.644**	-
Primary branch/panicle	10.46	0.94*	-2.92*	-2.76*	2.16**	6.72*	Duplicate
Spikelet /panicle	106.13	7.72*	-102.17**	-91.4**	18.58**	140.063**	Duplicate
Fertile spikelet (%)	95.59	9.66**	-89.15**	-83.083**	23.062**	129.334**	Duplicate
Seed/primary branch/panicle	11.95	-0.05	-6.575*	-5.622*	0.313	8.952*	Duplicate

P_2 and F_2 plants produced more spikelets which differed from others in WITA 4 x CT7127- 49, WITA 4 x EMPASC 105, Max x CT7127- 49, Max x EMPASC 105, Max x WAB 96-1-1 while P_1 and F_2 in WITA 4 x IR57689-73, WITA 4 x Fofifa 16, WITA 4 x NERICA 1, Max x Fofifa 16 and Max x NERICA 1 produced more spikelet than others. P_2 and F_2 produced more seeds per secondary branch of panicle in WITA 4 x CT7127- 49, WITA 4 x EMPASC 105, WITA 4 x Fofifa 16, WITA 4 x WAB 96-1-1, Max x CT7127- 49 and Max x NERICA 1. On the other hand, P_1 and F_2 produced more seeds than plants from other generations in Max x Fofifa16 and Max x WAB 96-1-1.

Estimates of gene effects of panicle traits on lowland x upland rice genotypes

There were variations in gene effects on the panicle traits in the chosen parents and in the crosses. The results of generation mean analysis provide estimates of the main and first order interaction gene effects (Table 2). The additive and dominance gene effects were involved in the expression of the characters studied. In spite of the fact that most values of dominant effect (d) were negative, the mean of the F_2 (m) and additive effect (a), recorded values that were significantly different from zero (Table 3) indicating that the generation means were not only controlled by the additive and dominance effects of the genes and thus suggests that a non allelic interaction (epistasis) was influencing the expression of the characters. The result of the pooled estimate of genetic effect showed predominant positive additive (a) components which had lower values for most negative dominance (d) components and higher values for all traits except for number of seeds per primary branch of panicle. Among the crosses, additive gene effect influenced the inheritance of primary branch per panicle only in WITA 4 x CT 7127-49, WITA 4 x EMPASC 105, WITA 4 x Fofifa 16 and Max x EMPASC 105 as well as percentage fertile spikelet in all the hybrids except WITA 4 x CT 7127-49, WITA 4 x EMPASC 105, WITA 4 x Fofifa 16. On the other hand, dominance gene affected the inheritance of seeds/primary branch of panicle in WITA 4 x WAB 96-1-1 and fertile spikelet/ panicle and seeds/primary branch of panicle in WITA 4 x NERICA 1. Dominance gene effects recorded very high and significant values for spikelet/ panicle, fertile spikelet/ panicle and number of seeds/ primary branch of panicle indicating that alleles responsible for the less yield-related characters were dominant over the alleles controlling the high ones. The three types of gene interaction namely: Additive, dominance and epistasis were observed to be significant though negative in dominance effect in the pooled result (Table 2) in primary. Duplicate epistasis was involved in all the parameters measured in the cross of Max x WAB 96-1-1 branch/panicle, fertile spikelet/panicle and spikelet/panicle. Similar results were recorded for fertile spikelet/panicle in WITA 4 x IR 57689-73, WITA 4 x CT7127-49, Max x IR 57689-73, Max x CT 7127- 49, Max x Fofifa 16 and Max x WAB 96-1-1. Among the digenic epistasis, dominance x dominance had higher and more significant values than additive x additive effect which were mostly negative.

Gene interaction did not influence the inheritance of panicle length and primary branch per panicle in WITA 4 x IR 57689-73, WITA 4 x EMPASC 105, WITA 4 x WAB 96-1-1, WITA 4 x NERICA 1 as well as seed per primary branch of panicle in Max x EMPASC 105, Max x Fofifa 16 and Max x NERICA 1.

DISCUSSION

Considerable amount of variability was observed in the characters evaluated for generation mean analysis. High mean value was the main selection criterion for a long time. Gilbert (1958) suggested that the parents with good mean performance would result in better genotypes since it is the actual realized value in the experiment. The result showed that the means of BC_1 that is P_1F_1 and BC_2 that is P_2 F_1 tended to be located close to those of their respective recurrent parents. For most traits, F_1 generation means were higher than the mid-parent values. Significant differences were observed between the F_1 and F_2 generation means in majority of the cases for percentage fertile spikelets and spikelet number per panicle which is thought to be due to the diversity in these traits among the parental lines. Panicle length contributes to grain yield in rice (Zafar et al., 2004). Maximum panicle length was observed for CT 7127-49 (29.41 cm) among the parents while among the

Table 3. Estimates of the genetic effects of the panicle traits of the lowland x upland rice genotypes studied in 2009.

Characters	M	A	D	AA	AD	DD	Type of Epistasis
WITA 4 x IR 57689-73							
Panicle length (cm)	24.53	0.13	1.35	-1.00	-2.10	1.433	-
Primary branch/panicle	9.83	0.67	-2.17	-3.33	1.67	6.33	-
Spikelet /panicle	91.83	13.33	-86.17**	-75.33*	26.67	103.00*	Duplicate
Fertile spikelet (%)	93.77	19.37**	-101.11**	-90.87**	38.73**	141.43**	Duplicate
Seed/primary branch/panicle	11.17	-1.83	-8.67	-3.63	-9.67	19.33**	-
WITA 4 x CT7127-49							
Panicle length (cm)	27.05	-1.60	5.39	-8.40	-3.22	19.45**	-
Primary branch/panicle	9.17	2.83*	1.67	2.33	6.00**	-2.67	-
Spikelet /panicle	115.67	24.83	-184.00**	-151.67**	49.67*	290.00**	Duplicate
Fertile spikelet	94.53	18.25**	-113.96**	-106.57**	36.53**	184.24**	Duplicate
Seed/primary branch/panicle	13.83	-0.83	-18.83**	-15.67**	-1.67	22.33**	Duplicate
WITA 4 x EMPASC 105							
Panicle length (cm)	22.32	0.517	0.533	-1.367	1.03	5.27	-
Primary branch/panicle	10.00	2.00*	-2.17	-1.33	4.33*	- 3.67	-
Spikelet /panicle	115.17	13.67	-200.00**	-176.67**	27.33	264.00**	Duplicate
Fertile spikelet (%)	87.93	11.95	-104.08**	-94.57**	23.03	169.72**	Duplicate
Seed/ primary branch/panicle	12.00	-1.33	-15.08**	-13.33**	-3.17	20.83**	Duplicate
WITA x Fofifa 16							
Panicle length (cm)	24.42	0.00	-5.13	-7.41	0.00	13.60*	-
Primary branch/panicle	10.67	3.00*	-6.33	-6.667	5.01	10.67*	-
Spikelet /panicle	99.00	4.67	-98.91*	-80.02	14.50	100.50	-
Fertile spikelet (%)	90.57	7.22	-72.43**	-63.03**	14.23	83.67**	Duplicate
Seed/ primary branch/panicle	10.83	1.00	-5.25	-4.67	0.50	8.50	-
WITA 4 x WAB 96-1-1							
Panicle length (cm)	25.15	1.07	-3.52	-5.63	2.03	14.63*	-
Primary branch/panicle	9.93	1.15	0.03	-1.66	1.12	7.26	-
Spikelet/panicle	108.01	1.33	-136.67**	-113.33**	3.33	126.03*	Duplicate
Fertile spikelet (%)	91.82	4.67	-86.17**	-62.61**	8.71	67.60*	Duplicate
Seed/ primary branch/panicle	9.04	0.92	21.61**	3.12	0.82	-1.24	-
WITA 4 x NERICA1							
Panicle length (cm)	26.13	1.08	13.78**	-15.37**	1.47	21.03**	Duplicate
Primary branch/panicle	10.16	-0.56	0.38	-0.08	1.16	7.16	-
Spikelet /panicle	133.67	17.89	45.47	-47.1	19.32	63.56	-
Fertile spikelet (%)	95.15	0.25	-68.8*	-64.17*	0.5	3.18	-
Seed/ primary branch/panicle	9 .76	-0.69	20.11**	0.46	102.67**	7.94	Duplicate
Max x IR 57689-73							
Panicle length (cm)	22.78	-1.367	5.8	3.73	-2.733	-7.867	-
Primary branch/panicle	10	1.5	-5.417	-6.333	3.167	14.167*	-
Spikelet /panicle	97.17	4.333	-4.5	-38	8.667	7.333	-
Fertile spikelet (%)	91.23	12.163*	-79.052**	-53.921**	22.026*	46.58	-
Seed/secondary branch/panicle	10.83	-2.463	1.215	3.5	-3.432	-8.514*	-
MAXx CT7127-49							
Panicle length (cm)	25.72	-0.91	-0.85	-4.22	-1.84	15.57*	-
Primary branch/panicle	11.53	1.03	-3.42	-4.12	2.17	11.53*	-
Spikelet/panicle	123.17	24.02	-159.00*	-134.00*	51.333	209.99**	Duplicate
Fertile spikelet (%)	95.52	24.72**	-116.97**	-112.97**	49.43**	26.98**	Duplicate
Seed/ primary branch/panicle	12.67	-0.17	-7.67	-7.04	-0.33	15.33*	-

Table 3. Contd.

Max x EMPASC 105							
Panicle length (cm)	21.83	-0.8	2.483	0.533	-0.6	3.433	-
Primary branch/panicle	11.51	1.83*	-5.67*	-5.04	3.67*	6.67	-
Spikelet /panicle	116.67	4.17	-160.17**	-146.33*	21.667	212.33*	Duplicate
Fertile spikelet (%)	92.23	11.97*	-103.31**	-100.81**	20.65	177.42**	Duplicate
Seed/ primary branch/panicle	11.17	-1.33	-1.17	-1.33	-2.67	9.67	-
Max x Fofifa 16							
Panicle length (cm)	23.05	-0.08	-1.21	-3.97	-0.17	11.67*	-
Primary branch/panicle	9.62	0.33	-3.75	-2.67	0.5	7.5	-
Spikelet /panicle	93.17	15.02	-99.67*	-97.33**	47.33	193.33**	Duplicate
Fertile spikelet (%)	90.15	13.23**	-61.91**	-60.20**	27.93**	100.42**	Duplicate
Seed/ primary branch/panicle	11.50	-0.54	-3.83	-5.67	-2.01	12.33	-
Max x WAB 96-1-1							
Panicle length (cm)	26.15	1.97	-8.68	-11.73*	3.48	22.02**	Duplicate
Primary branch/panicle	10.83	1.05	-7.00*	-6.67*	2.33	13.33**	Duplicate
Spikelet /panicle	113.52	22.5	-160.25**	-155**	60.17*	244.53**	Duplicate
Fertile spikelet (%)	93.22	17.48**	-77.58**	-71.03**	34.97**	117.43**	Duplicate
Seed/ primary branch/panicle	12.17	0.667	-8.5*	-10.00*	1.33	19.67**	Duplicate
Max x NERICA 1							
Panicle length (cm)	23.33	-0.5	-4.62	-5.73	-1.13	10.97*	-
Primary branch/panicle	11.17	1.167	-3.67	-3.67	1.33	12.04*	-
Spikelet /panicle	130.33	12.67	-121.84*	-89.98	8.34	81.61	-
Fertile spikelet (%)	90.37	4.22	-77.03**	-71.55**	8.43	137.93**	Duplicate
Seed/ primary branch/panicle	14.17	1.83	-8.33	-5.67	4.33	10.06	-

m= mean of F_2; a = additive gene effect; d = dominance gene effect; aa = additive × additive gene effect; ad = additive × dominance gene effect; dd = dominance x.

progenies the F_1 of CT 7127-47 x Fofifa 16 (29.32 cm) had the longest panicle. The highest number of secondary branch per panicle (14) were observed for CT 7127-49 and NERICA 1 among the parental lines and in F_1 (14.13), BC_1 (13.96) and F_1 of CT7127-49 x EMPASC 105 (12.67). The number of spikelet per panicle which is assessed after heading, greatly influences grain yield in rice and measures yield related characters. The highest number of spikelet per panicle were observed in CT 7127-49(139.4) and EMPASC 105 (124.21) amongst parental lines while among the progenies F_1 and F_2 hybrids of CT 7127-49 x EMPASC 105 had 153.86 and 128.36 respectively. Likewise, F_2 hybrids of Max x CT 7127-49 had 123.17. Percentage fertile spikelet which is determined by feeling the ripened spikelet to ensure there is grain in it; recorded highest values for Fofifa 16 (96.43%) and NERICA 1(96%) among the parents while the F_2 of WAB 96-1-1 x NERICA1(97.9%) and Fofifa 16 x NERICA1(97.45%) had the highest among the progenies.

Although percentage fertile spikelet contributes positively to grain yield in rice (Anyanwu, 2009), yet, highest percentage filled grain is not the only factor responsible for grain yield. In the present study, Fofifa 16 and NERICA 1 which recorded highest percentage filled grains did not have corresponding values for spikelet number per panicle and other yield related traits recorded lower yields. Generation mean analysis is commonly utilised in evaluation of effect of the genes which are involved in quantitative traits in rice breeding programmes. The analysis of gene effects revealed that additive, dominance and epistatic effects were involved in the inheritance of most traits. The result of the pooled analysis of genetic effects of the traits agrees with the work of Kim (1987) who obtained non allelic gene interactions for all the panicle traits he studied. On the other hand, Chang et al. (1998) reported epistasis for number of primary branches per panicle and number of spikelet per panicle. However, they explained the inheritance of primary branch length using the additive-dominance genetic model. The performance of most of the crosses manifesting non-allelic interactions for number of spikelet per panicles and fertile spikelet per panicle is an indication that epistasis is determined to some extent by the genotypes used for the study.

Recurrent selection has been suggested for non-allelic inheritance traits in rice (Subraman and Rangasamy, 1989; Vijayakumar et al., 1996), wheat (Sharma et al., 1995) and mungbean (Khattak et al., 2001). The present study suggests the use of recurrent selection for panicle traits in most of the genotypes used especially in WITA 4 x CT 7127-49, WITA 4 x EMPASC 105, Max x CT 7127-49 and Max x WAB 96-1-1. Except for WITA 4 x IR 57689-73 and Max x EMPASC 105 where panicle length was not affected by gene interaction, epistasis influenced its expression in the other crosses. It could therefore be improved through recurrent selection in the other cross combinations. It might be possible to follow the recommendation of Khattak et al. (2001) to use a bi-parental approach *inter se* crossing and/or recurrent selection for developing high yielding rice lines in advanced generations if we want to exploit all types of gene effects.

Mather and Jinks (1982) reported that when opposite signs of additive x additive (aa) and dominance x dominance (dd) are involved in a cross, that it indicates prevalence of duplicate epistasis and complementary epistasis when both signs are the same. Duplicate epistasis was observed in most of the crosses for spikelet/panicle and fertile spikelet (%) as well as seeds/primary branch of panicle except for Max 4 x IR 57689-73. Similarly, positive dominance x dominance gene action was recorded for WITA 4 x Fofifa 16, WITA 4 x NERICA 1 and Max x NERICA 1 while duplicate epistasis was observed only for percentage fertile spikelet. This effect would tend to obscure the manifestation of any genetic progress made since in the early generations. Falconer and Mackay (1996) had earlier suggested that in self- pollinated plants, epistasis is more important than dominance which lasts for a short time with progressive selfing but non allelic interaction can generate segregates some of which may represent real genetic advance over their parents. It might be possible to follower the suggestion of Moreno-Gonzalez and Cubero(1993) that where epistasis is more important, recurrent selection and reciprocal recurrent selection can be efficient techniques for selecting desirable cultivars.

Conclusion

The analysis of gene effects revealed that additive, dominance and epistatic effects were involved in the inheritance of most traits. Most of the crosses manifested non-allelic interactions for number of spikelet per panicles and fertile spikelet per panicle indicating that epistasis is determined to some extent by the genotypes used for the study. The presence of significant duplicate epistasis restricted the scope of simple selection for the characters studied. Therefore delaying selections to later generations will enhance success in improving panicle characters in the genotypes studied. Recurrent selection could be used in improving panicle traits in WITA 4 x CT 7127-49, WITA 4 x EMPASC 105, Max x CT 7127-49 and Max x WAB 96-1-1.

Conflict of Interest

The authors have not declared any conflict of interests.

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Genetic diversity and trait association between growth, yield and seed component of *Jatropha curcas* (L.) source collection from Indian sub-continent

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Seventy-two *Jatropha curcas* clonal accessions, collected from different parts of India, were grown in randomized block design and evaluated for 13 characters. These showed significant differences in growth, yield and seed characteristics, except for number of primary branches per plant. The accessions AFRI-35, AFRI-52 and AFRI-56 showed above mean value for 12 growth, fruit and seed yield characters except for number of primary branches, seed width and seed thickness. Accessions AFRI-12, AFRI-20, AFRI-21 and AFRI-39 showed above mean value for 11 traits. All the growth traits except for number of primary branches were positively correlated with fruit and seed yield. The magnitude of genotypic correlation coefficient (r_g) was higher than their corresponding phenotypic coefficient of correlations (r_p) for almost all the growth and yield characters, indicating the strong genetic linkage among all the characters. Kernel oil percentage was positively correlated with 20-seed weight and seed/kernel ratio. Seed/kernel ratio and oil percentage were negatively and non-significantly correlated with seed length and width. Principal component analysis revealed that plant height, collar diameter, number of secondary branches, crown diameter, fruit yield, seed yield, 20-seed weight, seed length, seed width, seed thickness, S/K ratio and oil percentage could be used as characters to distinguish the germplasm entries. *K*-means clustering revealed that trees from different geographic regions were grouped together in a cluster as well as trees from the same geographical area were placed in different clusters, suggesting that geographical diversity did not go hand in hand with genetic diversity. In addition, clustering identified promising accessions with favourable traits for future establishment of elite Seedling Seed Orchard (SSO) and Clonal Seed Orchard (CSO) for varietal and hybridization programmes.

Key words: Biodiesel, clustering, genetic variation, growth performance, principal component analysis

INTRODUCTION

The increased prices of petroleum products coupled with depletion of fossil fuel reserves and compulsion to reduce greenhouse gas emission, have evoked worldwide interest in searching for alternative sources of raw material for fuels (Mohapatra and Pande, 2010). Biodiesel, bio-ethanol and biomass gasification are the three major bio-energy and fast developing options which have huge potential in India to develop as renewable energy sources, where investment made would be economical (Parikh and Walia, 2002; Mishra, 2009). Bio-energy generated from bio-fuels constitute a suitable renewable energy source that may help to cope up with rising energy prices and offer new livelihood opportunities to farmers and rural communities around the world (Hazell and Pachauri, 2006; Rao et al., 2009). In recent years *Jatropha curcas* L., a perennial plant belonging to the family Euphorbiaceae has received considerable attention from researchers as a non-edible tree-born oil-seed crop (Tiwari et al*.,* 2007; Das et al., 2010). It is a native of tropical Central America and is domesticated widely in Africa and Asia due to its ability to grow in varied climatic zones of tropical and subtropical regions particularly in marginal lands (Rao et al., 2008). *J. curcas* is a prominent species with a wide variety of uses: seeds, leaves and bark used in traditional medicine and for veterinary purpose (Heller, 1996) and oil as an insecticidal agent, in preparation of soap, candle, by-product glycerine and as germination promoter (Ginwal et al., 2005; Nabil and Yasser, 2012; Sharma et al., 2012). It is a highly promising species as bio-diesel crop of short gestation period, hardy nature, high quality oil contents and wide adaptability compared to most other non-edible oil yielding species. The seeds of *J. curcas* contain about 35 to 40% of non-edible oil (Keith, 2000). The magnitude of genetic variability present in base population of any crop species is pivotal to crop improvement; however, no species simultaneously performs best in respect to its all attribute (Vongadow and Bredenkamp, 1992; Raje and Rao, 2000; Idahosa et al., 2010). Considering the vast semi-wild distribution of *J. curcas* in different parts of India, there exists considerable genetic variability which can be exploited for potential economic yield (Pant et al., 2006; Rao. et al., 2008). Detection and exploitation of natural genetic variability in *J. curcas* is the need of the hour to deliver the best genotypes from the working germplasm collections to meet the immediate requirement of the growers. The first step in this process is selection criteria, which is, the retention of desired genotypes and elimination of undesirable ones. Once the selection criterias are clarified, the next is to choose a proper system of selection. Selection index maximizes genetic gain in a desired direction and is usefully applied to develop better cultivars with target traits (Ceron-Rojas et al., 2006). In a population under selection for quantitative characters, gene frequencies are altered and these are further modified by the mating systems that may be utilized to advance the selected individuals to the next generation (Chopra, 2000). Ginwal et al. (2005) reported variability of *J. curcas* from central India limited to seed source, morphology, germination and seedlings growth. Kaushik et al*.* (2007) reported divergence in seed oil traits of *J. curcas* in 24 locally collected accessions Srivastava et al. (2011) mentioned the paucity of date on growth performance and yield of *J. curcas*.

One important limitation for selection for improvement is the extent of diversity present in the germplasm. Quantitative characters such as yield and its determinants exhibit substantial degree of interaction with the environment thus it is imperative to analyse the variability present in the germplasm and partition it into genotypic, phenotypic nature. Release of high yielding cultivars is impossible without ascertaining the magnitude of variation present in the available germplasm, interdependence of growth pattern with yield, extent of environmental influence on these factors, heritability and genetic gain of the materials (Rao et al., 2008). The potentiality of plants for optimum yield (seed yield and oil percentage) is dependent both on environmental and genotypic factor. The knowledge of genetic variation/diversity would be useful for selection especially when the desired ideo type is yet to be defined due to its wide adaptability. Knowledge of genetic variation for attributes viz: branching pattern, female to male flower ratio, pest resistance, drought hardiness and yield attributes in germplasm of *Jatropha* is of great significance in tree improvement programmes and particularly for selection of genotypes having more seed yield and oil content (Burely et al*.,* 1984; Voncarlowitz, 1986, Wen et al., 2012; Ndir et al., 2013). Basha and Sujatha (2007) indicated modest levels of genetic variation in the Indian germplasm based on random amplified polymorphic DNA (RAPD) and inter simple sequence repeat (ISSR) markers. Reddy et al*.* (2007) reported 8 to 10% (AFLP; Amplified Fragment Length polymorphism; genetic fingerprinting technique) and 14 to 16% (RAPD) polymorphism in 23-selected provenances from 300 collections. Randae et al*.* (2008) reported a wide diversity in 12 germplasm of *J. curcas* through molecular markers. Sakaguchi and Somabi (1987) studied 40 genotypes of *J. curcas* from different places in Thailand. Mahajen et al*.* (2009) reported significant variation in oil content of *J. curcas* for Uttarakhand States of India.

In the present investigation the magnitude of genetic variability is quantified in terms of morphological traits present in the existing base population (72 *J. curcas* clonal accessions) collected from different regions of India (Map 1) and to identify important yield attributing characters to provide useful information for developing improved high yielding *J. curcas* genotypes for establishment of elite seedling seed orchard (SSO) and clonal seed orchard (CSO) with favorable traits for future

*Corresponding author. E-mail: atultripathi86@gmail.com plantation and breeding programmes.

MATERIALS AND METHODS

Experimental site

Experiment was conducted at the experimental site of Arid Forest Research Institute, Jodhpur (AFRI) (24° 40´ N and longitude 71° 15´ E), India. The experimental site was flat, had loamy sand soil. The soil pH was 7.8 (recorded by digital pH meter) and organic matter content in the soil was about 0.25% (analyzed at laboratory level). The average annual rainfall of the region during the study period from 2007 to 2010 ranged between 139.2 mm in 2010 to 321.2 mm in 2007. Average number of rainy days annually is 10 to 15 and maximum temperature goes as high as 49°C in summer and drops to 0°C in winter (source: metrological database of CAZRI (Central Arid Zone Research Institute, Jodhpur).

Collection of plantation material

In the present study a representative set of clonal material in the form of stem cuttings of 72 accessions of *J. curcas* from different geographical regions of India were evaluate for genetic variation and cluster analysis. The collection of the clonal material in the form of stem cutting ranged from latitude 10.0°46' to 32°02'N and longitude 72.0° 45' to 95.0° 1'E (Table 1). The selection were made on phenotypic assessment of characters of economic interest, that is, plant height, number of primary and secondary branch, branching pattern, crown spread, girth, fruit and seed yield. Clonal material in the form of stem cuttings was raised to saplings under nursery conditions and when plants were 4-months old were used for planting. Care was taken to avoid trees infested with pests and diseases.

Plantation at experimental site

The plants were planted in the pits of 45 cm^3 filled with mixture of FYM (farm yard manure): sand: soil in 1:1:1 ratio at 3 x 3 m spacing in randomized block design (RBD) having three replicates. Each replicate consisted of one plant propagated by stem cuttings of single mother plant. The plantation was done in July to August 2007. Plants were irrigated immediately after planting. Further, the irrigation was done at 15-days interval in summer and 30-days interval in winter. Mortality was replaced with new plants up to six month.

Data measurements

Measurements were taken in August 2010 for plant height (cm), collar diameter (cm), number of primary branches, number of secondary branch, crown diameter (cm). Fruit were collected and seed were harvested from five to eight picking of dried black fruits at 15 to 20 days interval from July to November in 2010; these were weighed and expressed as yield (g) per plant. Seed characteristics were analysed after separating seeds from the fruit, cleaned and stored in muslin cloth bags at ambient conditions (26°C and 55% RH). All seed lots were dried in hot air oven at 60°C till constant weight. The 20-seeds weight (g) were determined by using calibrated electronic balance to the nearest 0.01 g), seed/kernel ratio (S/K ratio) was calculated in order to determine the proportion of seed coat and length (mm), width (mm) and thickness (mm) of seed was recorded with digital calliper to the nearest 0.01 mm as per ISTA, (1976). For estimate oil content three replicates for each seed lot were used, 20 g of kernel were ground and powdered before placing in Soxhlet apparatus and were extracted with petroleum ether (60°C) for six hours without interruption by heating it at 60±5°C over water bath. Oil content was calculated on percentage basis. In the present investigation the data of 2010 have been analysed.

Statistical analysis

Data were subjected to analysis of variance by using SPSS (version 8.0; SPSS Inc.). Linear correlation coefficients were calculated at both genotypic (r_g) and phenotypic (r_p) levels among the studied traits, as described by Mode and Robinson (1959). The estimated studied traits mean were subjected to a principal component analysis (PCA) to investigate the dimensionality of studied data sets in test population and to identify new meaningful underlying variables under particular growth environment. Non-hierarchical (*K*-means) Euclidian cluster analysis was done for growth and yield traits and seed characters in planted *J. curcas* accessions separately.

RESULTS

Variability in growth and yield attributes

Significant variation at p<0.01 in the mean value was observed in plant height, collar diameter, number of secondary branches, crown diameter, fruit yield and seed yield. Number of primary branch showed non-significant variation among all the tested accessions of *J. curcas* (Table 2). Maximum mean plant height 272.50 cm was recorded in AFRI-39 followed by 267.50 cm in AFRI-35, while minimum was 90.00 cm in accession AFRI-16. The maximum collar diameter 11.49 cm was in AFRI-35 closely followed by 11.15 cm in AFRI-9. The high degree of variability with regard to the number of secondary branch was observed as AFRI-7 had 22.00 secondary branches followed by 21.00 in (AFRI-9, AFRI-12 and AFRI-43), which were almost five times compared to the lowest rank series 4.00 in (AFRI-16, AFRI-28 and AFRI-63). Crown diameter ranged from 62.50 cm in AFRI-23 to 260.00 cm in AFRI-35. The recorded data pertaining to fruit and seed yielding parameters showed significant variation among the accessions. Out of 72 tested accessions only 65 seeded after a period of 36 month. Among the seeded plants fruit and seed yield was minimum 30.00 and 22.00 g in accessions AFRI-50 and varied up-to 1586.00 and 812.50 g in AFRI-32, respectively. Out of 72 accessions only 21 and 23 accessions expressed significant higher fruit and seed yield per plant, respectively over general mean.

Variability in seed characters

Table 2 revealed that from 72 studied accessions only 65 were seeded so the seed characteristic study was restricted to these seed yielded accessions only. Analysis of components of total variability in the germplasm

Table 1. Source detail of *J. curcas* and their geographical locations.

Source code	Locality	Rainfall	Mean temperature	
			Minimum (℃)	Maximum (℃)
AFRI 1	Coimbatore, Tamil Nadu	765.6	18.7°	35.3°
AFRI 2	Coimbatore, Tamil Nadu	765.6	18.7°	35.3°
AFRI 3	Coimbatore, Tamil Nadu	765.6	18.7°	35.3°
AFRI 4	Coimbatore, Tamil Nadu	765.6	18.7°	35.3°
AFRI 5	Coimbatore, Tamil Nadu	765.6	18.7°	35.3°
AFRI 6	Coimbatore, Tamil Nadu	765.6	18.7°	35.3°
AFRI 7	Palakkad, Kerala	2658.7	19.0°	36.0°
AFRI 8	Palakkad, Kerala	2658.7	19.0°	36.0°
AFRI 9	Palakkad, Kerala	2658.7	19.0°	36.0°
AFRI 10	Palakkad, Kerala	2658.7	19.0°	36.0°
AFRI 11	Palakkad, Kerala	2658.7	19.0°	36.0°
AFRI 12	Palakkad, Kerala	2658.7	19.0°	36.0°
AFRI 13	Dhar, Madhya Pradesh	1083.4	19.5°	34.0°
AFRI 14	Indore, Madhya Pradesh	890.0	10.0°	40.0°
AFRI 15	Ujjain, Madhya Pradesh	1768.4	9.0°	48.0°
AFRI 16	Shahjahanpur, Madhya Pradesh	NA	NA	NA
AFRI 17	Sidhi, Madhya Pradesh	NA	8.1°	42°
AFRI 18	Satna, Madhya Pradesh	NA	8.8°	42.3°
AFRI 19	Sahadol, Madhya Pradesh	1065.2	8.4°	41.4°
AFRI 20	Rangareddy, Andhra Pradesh	776.8	14.2°	38.7°
AFRI 21	Rangareddy, Andhra Pradesh	776.8	14.2°	38.7°
AFRI 22	Vishakhpatnam, Andhra Pradesh	1279.8	21.0°	32.6°
AFRI 23	Rangareddy, Andhra Pradesh	776.8	14.2°	38.7°
AFRI 24	Mahaboobnagar, Andhra Pradesh	596.3	25°	40.9°
AFRI 25	Vishakhpatnam, Andhra Pradesh	1279.8	21.0°	32.6°
AFRI 26	Panchmahal, Gujarat	1418.2	14°	45°
AFRI 27	Bhavnagar, Gujarat	732.1	15°	44°
AFRI 28	Banaskantha, Gujarat	1375.1	5°	45°
AFRI 29	Panchmahal, Gujarat	1418.2	14°	45°
AFRI 30	Banaskantha, Gujarat	1375.1	5°	45°
AFRI 31	Banaskantha, Gujarat	1375.1	5°	45°
AFRI 32	Pulbhani, Orissa	943.0	NA	NA
AFRI 33	Gurdaspur, Punjab	1032.4	6.0°	41.0°
AFRI 34	Mandi, Himachal Pradesh	1265.2	3.0°	35.0°
AFRI 35	Shimla, Himachal Pradesh	1200.6	NA	NA
AFRI 36	Lucknow, Uttar Pradesh	914.4	11.0°	48.0°
AFRI 37	Lucknow, Uttar Pradesh	914.4	11.0°	48.0°
AFRI 38	Mahoba, Uttar Pradesh	NA	4.1°	48.2°
AFRI 39	Jhajjar, Haryana	444.0	7.0°	40.5°
AFRI 40	Gurdaspur, Punjab	1032.4	6.0°	41.0°
AFRI 41	Chittorgarh, Rajasthan	1121.8	11°	44°
AFRI 42	Rajsamand, Rajasthan	666.6	7.8°	38.6°
AFRI 43	Nainital, Uttrakhand	1022.9	3.0°	27.0°
AFRI 44	Pauri Gharwal, Uttarkhand	1857.1	NA	NA
AFRI 45	Bilaspur, Chhatisgarh	1091.7	NA	NA
AFRI 46	Pauri Gharwal, Uttarkhand	1857.1	NA	NA
AFRI 47	Dehradun, Uttrakhand	1735.0	13.3°	27.8°
AFRI 48	Ranchi, Jharkhand	1555.9	10.3°	37.2°
AFRI 49	Plamau, Jharkhand	1163.4	5.6°	46.7°
AFRI 50	Ranchi, Jharkhand	1555.9	10.3°	37.2°

Table 1. Contd.

AFRI 51	E. Singhbhum, Jharkhand	1500.0	6.0°	44.0°
AFRI 52	E. Singhbhum, Jharkhand	1500.0	6.0°	44.0°
AFRI 53	W. Champaran, Bihar	1422.0	5.0°	46.0°
AFRI 54	W. Champaran, Bihar	1422.0	5.0°	46.0°
AFRI 55	Raipur, Chhatisgarh	1206.7	13°	42°
AFRI 56	Begusarai, Bihar	1384.0	6.0°	34.0°
AFRI 57	Durg, Chhatisgarh	886.4	11.0°	42.2°
AFRI 58	Karbi Anglong, Assam	925.0	6.0°	32.0°
AFRI 59	Lakhimpur, Assam	NA	10.0°	31.0°
AFRI 60	Papumpare, Arunachal Pradesh	2148.1	5.5°	29.0°
AFRI 61	Imphal, Manipur	846.2	3.5°	36.0°
AFRI 62	Mon, Nagaland	2600.0	5.0°	32.0°
AFRI 63	Mokokchung, Nagaland	2500.0	8.0°	24.0°
AFRI 64	Palakkad, Kerala	2658.7	19.0°	36.0°
AFRI 65	Palakkad, Kerala	2658.7	19.0°	36.0°
AFRI 66	Coimbatore, Tamil Nadu	765.6	18.7°	35.3°
AFRI 67	Purulia, West Bengal	NA	NA	NA
AFRI 68	Sirohi, Rajasthan	1545.5	8.0°	47.0°
AFRI 69	Bilaspur, Himachal Pradesh	1348.0	5.0°	42.0°
AFRI 70	Udaipur, Rajasthan	1092.0	11.6°	38.3°
AFRI 71	West Tripura, Tripura	1954.8	10.0°	33.0°
AFRI 72	Guragaon, Haryana	340.5	5.1°	40.0°

indicated significant difference among the accessions for all the seed characteristic traits. Highest 20 seed weight was noticed 12.80 g in AFRI-3 nearly followed by 12.72 and 12.65 g in AFRI-31 and AFRI-30, respectively. Whereas lowest 20 seed weight was observed 5.87 g in AFRI-63 closely followed by 5.88 g in AFRI-64 accession. The highest seed/kernel ratio and oil % was shown by accession AFRI-30 which had 0.81 and 57.32%, respectively while the lowest was showed by AFRI-6 with the value of 0.31 and 27.43%, respectively. Thirty accessions expressed significantly higher values over general mean of oil percent. Maximum seed length was observed 17.63 mm in AFRI-32 closely followed by 17.53 mm in AFRI-51 and minimum was 13.11 mm in AFRI-48. Seed width ranged from 9.24 mm in AFRI-22 to 11.51 mm in AFRI-30 accession which was closely followed by 11.46 mm in AFRI-40. Maximum seed thickness was observed 8.74 mm in AFRI-3 and minimum 7.10 mm in AFRI-28 accessions.

Table 3 showed positive association of correlation coefficient among different growth and yield traits. For growth and yield traits phenotypic correlation and genotypic correlation ranged from 0.087 to 0.978 (r_p) and 0.100 to 1.00 (r_g). Plant height and collar diameter exhibited significant correlation with all growth and yield traits at both phenotypic level and genotypic level. Number of primary branch exhibit higher r value for genotypic correlation (r_g) than phenotypic correlation (r_p) with number of secondary branch, crown diameter, fruit yield and seed yield. At phenotypic level its exhibited positive significant correlation only with number of secondary branch and crown diameter (it was 0.335 and 0.268, respectively). Number of secondary branch exhibited positive significant correlation with crown diameter, fruit yield and seed yield at both level. Crown diameter showed positive significant correlation with fruit and seed yield at both level. The maximum correlation coefficient for both r_p and r_g was observed between fruit and seed yield at both level with 0.978(r_p) and 1.002(r_g). Data in Table 3 revealed that seed yield showed higher values of genotypic correlation for all parameters (that is, plant height, collar diameter, number of primary branch, number of secondary branch, crown diameter and fruit yield) compared to phenotypic correlation.

Table 4 showed the correlation coefficient between various seed characteristics here it ranged from -0.048 (seed length with oil % on kernel basis) to 0.682 (Seed width with seed length) of r_p and -0.039 (Seed length with seed/kernel ratio) to 0.715 (Seed kernel ratio with 20-seed weight) of r_g. 20 seed weight exhibited a significant positive correlation at $p<0.01$ with seed/kernel ratio, oil %, seed length and seed thickness at both phenotypic and genotypic level whereas there was no significant positive correlation between seed width and 20-seed weight. High r_g value of 20 seed weight with seed/kernel ratio and oil % observed than $r_{p.}$ Seed/kernel ratio showed positive significant correlation only with oil percent at phenotypic and genotypic level. Positive value of r was registered

Table 2. Mean values for growth characteristics of different *J. curcas* accessions.

Accession	Height (cm)	Collar diameter (cm)	Number of primary branch	Number of secondary branch	Crown diameter (cm)	Fruit yield (g)	Seed yield (g)	20-seed weight (g)	Seed/kernel ratio	Oil % on kernel basis	Length (mm)	Width (mm)	Thickness (mm)
AFRI 1	205.00	8.44	2.00	11.50	207.50	720.00	340.00	7.53	0.48	42.92	15.89	10.13	7.70
AFRI 2	232.50	8.27	2.50	13.00	172.50	135.00	87.50	8.61	0.45	40.90	16.53	10.61	8.28
AFRI 3	193.33	7.10	2.67	10.67	173.33	440.00	279.25	12.80	0.78	48.82	16.90	11.24	8.74
AFRI 4	240.00	9.57	1.50	17.00	170.00	392.50	231.95	9.24	0.62	42.91	16.35	11.13	8.40
AFRI 5	215.00	7.14	2.00	10.50	192.50	-	-	-	-	-	-	-	-
AFRI 6	182.50	7.09	2.00	10.00	137.50	62.50	27.50	5.98	0.31	27.43	15.29	10.11	7.71
AFRI 7	207.50	7.42	2.50	22.00	170.00	1122.50	647.50	9.17	0.62	45.81	15.75	10.30	8.05
AFRI 8	230.00	7.02	2.50	18.50	182.50	305.00	187.50	11.42	0.69	51.36	16.40	10.94	8.09
AFRI 9	247.50	11.15	3.00	21.00	241.25	777.50	450.00	7.43	0.60	46.56	15.34	10.28	7.62
AFRI 10	165.00	5.96	2.00	8.00	98.75	387.50	212.50	9.38	0.63	48.77	15.90	10.95	8.05
AFRI 11	232.50	10.86	2.50	19.00	232.50	1270.00	790.00	7.40	0.53	44.58	15.69	11.00	7.84
AFRI 12	220.00	9.89	3.00	21.00	167.50	60.00	32.50	9.91	0.71	51.22	16.15	10.75	8.44
AFRI 13	145.00	5.61	2.00	6.00	80.00	255.00	155.00	10.11	0.64	48.60	16.19	10.70	8.03
AFRI 14	172.50	6.59	3.00	15.00	140.00	-	-	-	-	-	-	-	-
AFRI 15	130.00	5.10	2.00	6.00	71.25	182.50	95.70	7.85	0.58	42.57	16.67	10.63	8.43
AFRI 16	90.00	4.30	2.00	4.00	92.50	-	-	-	-	-	-	-	-
AFRI 17	160.00	4.24	2.50	6.50	105.00	240.00	147.50	9.73	0.63	48.42	16.55	10.83	8.25
AFRI 18	125.00	3.79	2.00	5.00	88.75	-	-	-	-	-	-	-	-
AFRI 19	182.50	6.38	1.50	6.50	78.75	315.00	190.00	10.03	0.66	52.78	16.47	11.04	7.89
AFRI 20	215.00	8.44	2.50	12.50	190.00	210.00	137.50	10.60	0.65	48.31	16.69	10.84	8.41
AFRI 21	247.50	9.49	3.50	11.00	172.50	980.00	580.00	9.85	0.64	50.56	16.34	10.70	7.78
AFRI 22	255.00	6.07	1.50	14.00	117.50	125.00	35.00	6.96	0.56	40.90	15.13	9.24	7.15
AFRI 23	115.00	3.83	1.50	4.50	62.50	222.31	84.81	10.06	0.63	45.34	16.51	10.47	7.76
AFRI 24	165.00	5.96	2.00	10.00	113.75	182.50	107.50	9.18	0.53	39.60	15.87	10.30	7.47
AFRI 25	205.00	7.21	2.00	13.00	127.50	-	-	-	-	-	-	-	-
AFRI 26	212.50	7.30	2.00	19.00	178.75	52.50	26.00	8.48	0.52	38.62	15.42	10.10	7.77
AFRI 27	200.00	7.25	2.50	12.00	141.25	850.00	460.00	8.70	0.62	54.66	14.87	10.56	7.88
AFRI 28	105.00	3.75	2.00	4.00	90.00	50.00	25.00	5.35	0.46	32.48	14.50	9.78	7.10
AFRI 29	240.00	7.81	2.00	14.00	207.50	570.00	310.00	8.77	0.54	41.03	16.60	10.94	7.99
AFRI 30	210.00	6.98	3.00	11.00	185.00	277.00	225.00	12.65	0.81	57.32	17.00	11.51	8.35
AFRI 31	215.00	6.89	2.00	14.00	202.50	204.00	138.20	12.72	0.64	51.72	16.70	11.10	8.49
AFRI 32	250.00	9.16	1.50	16.50	245.00	1586.00	812.50	7.85	0.47	35.29	17.63	11.26	8.68
AFRI 33	207.50	7.48	3.00	20.00	205.00	322.50	157.50	9.14	0.54	36.25	16.99	11.25	8.40
AFRI 34	162.50	8.26	1.50	11.00	137.50	370.00	250.00	11.72	0.67	55.82	16.72	10.93	8.30
AFRI 35	267.50	11.49	2.00	17.00	260.00	1285.00	810.00	9.74	0.63	48.25	16.71	11.04	8.39
AFRI 36	247.50	6.81	2.00	13.50	207.50	200.00	117.50	10.27	0.69	47.11	16.43	10.72	7.78

Table 2. Contd.

AFRI 37	212.50	6.57	2.50	10.50	193.75	360.00	167.50	7.01	0.51	41.56	15.75	11.01	8.02
AFRI 38	145.00	5.33	2.00	5.50	90.00	92.50	46.00	7.62	0.57	41.22	15.88	10.79	8.06
AFRI 39	272.50	8.48	2.50	16.00	230.00	687.50	363.50	9.29	0.58	50.91	15.59	10.88	8.18
AFRI 40	155.00	4.39	1.00	7.00	92.50	487.50	257.50	10.90	0.55	54.20	17.33	11.46	8.24
AFRI 41	265.00	8.77	2.50	12.00	182.50	790.00	365.50	8.11	0.48	42.16	17.38	11.13	8.52
AFRI 42	235.00	7.67	2.50	19.50	211.25	407.50	199.50	9.31	0.61	47.39	16.31	10.59	7.73
AFRI 43	240.00	7.86	2.00	21.00	193.75	190.00	112.75	7.07	0.62	59.51	15.20	10.75	7.51
AFRI 44	160.00	6.91	3.00	6.00	92.50	-	-	-	-	-	-	-	-
AFRI 45	260.00	7.88	1.50	7.50	222.50	405.00	200.00	9.56	0.60	40.88	15.70	10.61	8.08
AFRI 46	227.50	8.08	2.50	4.50	160.00	55.00	29.00	9.57	0.66	47.28	16.01	10.31	7.84
AFRI 47	235.00	8.17	2.50	11.50	160.00	140.00	87.50	9.96	0.70	42.33	13.29	9.62	7.48
AFRI 48	210.00	7.49	2.00	7.00	100.00	268.50	148.50	6.08	0.69	43.39	13.11	9.63	7.22
AFRI 49	200.00	7.71	2.00	4.50	187.50	70.00	34.70	9.38	0.64	44.00	15.02	10.01	8.01
AFRI 50	192.50	6.82	3.00	13.50	96.25	30.00	22.00	9.07	0.62	41.83	15.19	10.35	8.14
AFRI 51	252.50	10.00	2.50	14.00	187.50	408.50	212.50	11.31	0.59	43.54	17.52	11.11	9.12
AFRI 52	265.00	9.74	2.50	15.00	177.50	1020.00	537.00	10.24	0.63	52.33	16.16	10.58	8.10
AFRI 53	230.00	9.01	2.50	17.50	217.50	401.50	195.50	9.94	0.64	51.23	16.32	11.03	8.25
AFRI 54	250.00	7.39	4.00	11.50	205.00	70.00	32.00	7.34	0.57	41.60	15.08	9.70	7.35
AFRI 55	205.00	8.25	2.50	11.50	157.50	325.00	181.00	9.32	0.64	51.22	15.41	10.57	8.26
AFRI 56	240.00	10.27	3.50	15.00	215.00	919.00	586.50	9.77	0.64	54.64	16.16	10.89	8.02
AFRI 57	202.50	7.74	2.50	17.00	193.75	306.50	161.00	7.44	0.52	42.11	16.03	10.66	7.86
AFRI 58	170.00	6.97	2.50	11.50	247.50	469.00	265.50	7.66	0.62	45.75	14.99	10.69	7.84
AFRI 59	230.00	8.72	3.50	17.50	178.75	-	-	-	-	-	-	-	-
AFRI 60	185.00	8.62	2.00	7.50	96.25	226.00	126.50	10.00	0.66	44.91	16.41	11.00	8.70
AFRI 61	193.33	8.28	2.00	11.67	135.83	102.50	51.30	11.03	0.63	53.60	16.53	10.57	8.15
AFRI 62	197.50	6.86	1.50	14.00	108.75	197.50	126.00	7.60	0.67	39.80	14.96	10.80	7.97
AFRI 63	110.00	5.14	1.00	4.00	88.75	151.50	53.50	5.87	0.33	35.52	16.78	10.79	8.28
AFRI 64	265.00	9.13	2.00	17.50	245.00	840.00	475.00	5.88	0.49	42.43	15.39	10.63	7.61
AFRI 65	190.00	9.00	2.00	10.50	132.50	180.00	120.00	9.51	0.62	44.38	15.86	10.90	8.16
AFRI 66	215.00	5.66	2.50	14.50	157.50	1185.00	681.00	8.26	0.47	40.50	16.30	10.75	8.00
AFRI 67	180.00	6.92	2.50	14.50	203.75	50.00	30.00	7.59	0.49	47.29	14.84	10.19	7.44
AFRI 68	215.00	9.14	2.50	17.00	200.00	875.50	489.00	8.33	0.61	43.69	16.21	10.95	7.88
AFRI 69	205.00	9.05	2.00	16.50	190.00	623.50	323.50	7.28	0.52	37.99	15.73	10.80	8.32
AFRI 70	232.50	7.43	2.00	16.00	205.00	1214.50	685.75	9.06	0.55	44.32	16.49	11.07	8.04
AFRI 71	215.00	9.30	2.00	17.50	191.25	288.00	150.00	11.98	0.70	50.03	16.65	11.02	8.19
AFRI 72	225.00	7.73	2.00	14.50	190.00	813.50	463.50	9.31	0.57	39.93	17.08	11.05	8.31
Mean±SD	205.03±45.2	7.54±1.8	2.25±.84	12.50±5.3	163.23±57.3	443.11	248.17	9.02±1.7	0.592±.09	45.40±6.2	16.01±1.4	10.68±.02	8.03±.02
SEM	1.9760	.0870	.0740	.2630	3.1300	35.80	20.72	.1100	0.0050	.3860	.0390	0.0220	0.0200
CD 1%	41.92	1.61	NS	5.68	61.95	256.79	174.79	1.16	0.05	2.65	2.32	1.15	1.10

CD = critical difference, SE = standard error of mean.

Table 3. Genotypic (r_g) and phenotypic (r_p) correlation coefficients between plant growth traits for studied *J. curcas* accessions.

Trait		Collar diameter	Primary branches	Secondary branch	Crown diameter	Fruit yield	Seed yield
Height	r_p	0.750**	0.308**	0.619**	0.732**	0.451**	0.443*
	r_g	(0.742)	(0.389)	(0.613)	(0.793)	(0.100)	(0.480)
Collar diameter	r_p		0.290**	0.623**	0.708**	0.382**	0.395**
	r_g		(0.495)	(0.551)	(0.685)	(0.451)	(0.478)
Primary branch	r_p			0.335**	0.268**	0.087	0.098
	r_g			(0.592)	(0.672)	(0.329)	(0.373)
Secondary branch	r_p				0.661**	0.351**	0.358**
	r_g				(0.670)	(0.440)	(0.451)
Crown diameter	r_p					0.467**	0.473**
	r_g					(0.499)	(0.488)
Fruit yield	r_p						0.978**
	r_g						(1.002)

Table 4. Genotypic (r_g) and phenotypic (r_p) correlation coefficients between seed characteristics for studied *J. curcas* accessions.

Traits		Seed/Kernel ratio	Oil % on kernel basis	Seed length	Seed width	Seed thickness
20-seed weight	r_p	0.666**	0.582**	0.210**	0.1108	0.186**
	r_g	(0.715)	(0.635)	(0.147)	(0.070)	(0.136)
Seed/kernel ratio	r_p		0.656**	-0.0355	-0.0427	0.0281
	r_g		(0.705)	(-0.039)	(-0.032)	(0.022)
Oil% on kernal basis	r_p			-0.048	-0.0433	-0.0169
	r_g			(-0.007)	(-0.025)	(-0.002)
Seed length	r_p				0.682**	0.576**
	r_g				(0.080)	(0.070)
Seed width	r_p					0.548**
	r_g					(0.062)

between seed/kernel ratio and seed thickness without any significance at phenotypic and genotypic level. There was non-significant negative correlation between seed/kernel ratio and seed length and width. Non significant negative correlation was also observed between oil % and seed length, width and thickness at phenotypic and genotypic levels. Seed length exhibited highly significant positive correlation value of r_p with seed width and seed thickness but also exhibited low level of genotypic correlation between them. Seed width showed significant positively correlation with seed thickness at r_p level but poorly associated at r_g level.

Principal component analysis

Table 5 revealed that the first principal component explained 36.15% of the total variation and dominated by plant height (0.876), crown diameter (0.862), collar diameter (0.838) and number of secondary branches (0.831). The coefficient of the second PC revealed a positive relationship with seed size and weight and

Table 5. Results of principal component analysis (PCA) of growth, yield and seed traits of *Jatropha curcas* collection.

Variables	Component			
	PC I	PC II	PC III	PC IV
Initial eigenvalues	4.34	2.95	1.85	1.00
% of variance	36.15	24.62	15.43	8.36
Cumulative %	36.15	60.77	76.20	84.56
Eigenvector				
Pl ant height	0.876	-0.031	0.104	0.159
Collar diameter	0.838	0.098	0.122	0.188
Secondary branch	0.831	0.021	0.014	0.129
Crown diameter	0.862	0.074	-0.050	0.237
Fruit yield	0.328	0.154	-0.065	0.922
Seed yield	0.331	0.147	-0.003	0.925
20 seed weight	0.033	0.529	0.748	-0.120
Seed/kernel ratio	0.063	0.030	0.926	-0.104
Oil% on kernel basis	0.063	0.089	0.888	0.113
Seed length	-0.008	0.917	0.028	0.128
Seed width	0.057	0.859	0.196	0.239
Seed thickness	0.089	0.914	0.117	-0.005

received large contribution from seed length, seed thickness, seed width (0.917, 0.914 and 0.859, respectively). The PC II explained an additional 24.62% of total variation. The coefficient of third PC explained large contribution from S/K ratio, oil % on kernel basis and 20-seed weight (0.926, 0.888 and 0.748, respectively) and contributes 15.43% of total variation. The fourth PC (8.36% of total variation) largely contributed by fruit (0.925) and seed yield (0.922).

Genetic divergence in growth characteristics

Six clusters were delineated by *K*-mean clustering for the 72 accessions of *Jatropha* shown in Table 6. Cluster VI had highest 30 members in it and cluster IV had lowest 2 members in it. Cluster I and II had 13 and 10 members and cluster III and V had 9 and 8 members, respectively. Cluster I consisted of high mean value of height (267.50 cm), collar diameter (11.49 cm), number of secondary branches (17.00) and crown diameter (260.00 cm). Cluster IV consisted of highest mean of number of primary branches which had mean value of 2.50. The minimum inter-cluster distance seen between II and III (42.58) followed by I and VI (49.65). While maximum inter-cluster distance was seen between I and V with value of 192.69 depicted in Figure 1.

Genetic divergence in yield and seed characteristics

Sixty-five accessions of *Jatropha* were grouped in six clusters on the basis of *K*-mean clustering shown in Table 7. Minimum one accession was separated in cluster III and maximum 25 were placed in cluster V followed by 20 in cluster IV. Accession AFRI-32 which is placed in cluster III showed highest mean value for fruit and seed yield, seed length, seed width and seed thickness and this showed lowest mean value for 3 characters viz. (20 seed weight, seed/kernel ratio and oil % on the basis of kernel). Lowest mean value for fruit and seed yield, seed length, seed width and seed thickness was showed by cluster V which had 25 members in it. Highest mean of seed/kernel ratio and oil % was seen in cluster VI with the value of 0.63 and 50.30%, respectively. Inter-cluster distance between cluster III and IV was the maximum at 1634. Minimum inter-cluster distance was seen between cluster IV and V followed by cluster I and VI with the distance value of 257.91 and 258.05, respectively (Figure 2).

DISCUSSION

Study revealed that different accessions of *J. curcas* exhibited considerable amount of morphological variability. The sources were statistically at par with respect to the plant height, collar diameter, numbers of secondary branches, crown diameter, fruit yield, seed yield, 20-seed weight, seed/kernel ratio, oil percent, seed length, seed width and seed thickness but the number of primary branches did not differ significantly as this favours the finding of Pant et al. (2006) and Vijayanand et al. (2009). The variability in growth performance of

Table 6. Composition of Euclidean clusters and cluster mean values obtained by K-means Non-hierarchical clustering for growth traits in *Jatropha curcas* accessions.

Cluster	No. of accession	Accession name and number	Height	Collar diameter	Number of primary branch	Number of secondary branch	Crown diameter
I	13	AFRI-9, AFRI-11, AFRI-29, AFRI-32, AFRI-35, AFRI-36, AFRI-39, AFRI-42, AFRI-45, AFRI-53, AFRI-54, AFRI-56, AFRI-64	267.50	11.49	2.00	17.00	260.00
II	10	AFRI-6, AFRI-14, AFRI-22, AFRI-25, AFRI-27, AFRI-48, AFRI-55, AFRI-61, AFRI-62, AFRI-65	255.00	6.07	1.50	14.00	117.50
III	9	AFRI-10, AFRI-17, AFRI-19, AFRI-24, AFRI-34, AFRI-40, AFRI-44, AFRI-50, AFRI-60	182.50	6.38	1.50	6.50	78.75
IV	2	AFRI-58, AFRI-67	170.00	6.97	2.50	11.50	247.50
V	8	AFRI-13, AFRI-15, AFRI-16, AFRI-18, AFRI-23, AFRI-28, AFRI-38, AFRI-63	90.00	6.56	2.00	4.00	92.50
VI	30	AFRI-1, AFRI-2, AFRI-3, AFRI-4, AFRI-5, AFRI-7, AFRI-8, AFRI-12, AFRI-20, AFRI-21, AFRI-26, AFRI-30, AFRI-31, AFRI-33, AFRI-37, AFRI-41, AFRI-43, AFRI-46, AFRI-47, AFRI-49, AFRI-51, AFRI-52, AFRI-57, AFRI-59, AFRI-66, AFRI-68, AFRI-69, AFRI-70, AFRI-71, AFRI-72	225.00	7.73	2.00	14.50	190.00

Plant height, collar diameter and crown diameter in cm.

Table 7. Composition of Euclidean clusters and cluster mean values obtained by K-means Non-hierarchical clustering for yield and seed characteristics traits in *Jatropha curcas* accessions.

Cluster	No. of accession	Accession name and number	Fruit yield	Seed yield	20-seed weight	Seed/Kernel ratio	Oil %	Length	Width	Thickness
I	9	AFRI-1, AFRI-9, AFRI-27, AFRI-29, AFRI-39, AFRI-41, AFRI-64, AFRI-69, AFRI-72	741.33	394.56	8.03	0.54	44.29	15.98	10.71	8.01
II	5	AFRI-7, AFRI-11, AFRI-35, AFRI-66, AFRI-70	1215.40	722.85	8.72	0.56	44.69	16.19	10.83	8.06
III	1	AFRI-32	1586.00	812.50	7.85	0.47	35.29	17.63	11.26	8.68
IV	21	AFRI-3, AFRI-4, AFRI-8, AFRI-10, AFRI-13, AFRI-17, AFRI-19, AFRI-30, AFRI-33, AFRI-34, AFRI-37, AFRI-40, AFRI-42, AFRI-45, AFRI-48, AFRI-51, AFRI-53, AFRI-55, AFRI-57, AFRI-58, AFRI-71	353.88	198.80	9.84	0.63	47.73	16.22	10.90	8.16
V	25	AFRI-2, AFRI-6, AFRI-12, AFRI-15, AFRI-20, AFRI-22, AFRI-23, AFRI-24, AFRI-26, AFRI-28, AFRI-31, AFRI-36, AFRI-38, AFRI-43, AFRI-46, AFRI-47, AFRI-49, AFRI-50, AFRI-54, AFRI-60, AFRI-61, AFRI-62, AFRI-63, AFRI-65, AFRI-67	129.65	71.44	8.70	0.58	43.58	15.76	10.45	7.92
VI	4	AFRI-21, AFRI-52, AFRI-56, AFRI-68	948.63	548.13	9.54	0.63	50.30	16.22	10.78	7.94

Fruit and seed yield in (g) plant^{-1} , 20-seed weight in (g), oil content in % on kernel basis, seed length, seed width and seed thickness in mm.

accessed accession significantly differs and the finding agreed with Saikia et al. (2009) in which they got considerable amount of variation in plant height, stem girth and 100-seed weight in 34 accessed *J. curcas* accession collected from 17 States of India. The apparent variability in growth performance indicates that economic benefits may be obtained. The results of the present study will be valuable for the conservation of genetic variation, prospects of improvement and assessment of the potential of the locally adapted accession source. In present study fruit and seed yield significantly differ and agree with the finding of Francis et al. (2005) but in contrast with genetic variability, which is rather small in Indian germplasm (Basha and Sujatha, 2007). Seed oil content variation is more widely reported not only in annual crops but also in a wide variety of trees borne oil seed (Kaura et al., 1998). The variation found in oil content in the present study along with other seed morphological attributes presents us with a viable selection alternative at a very early stage (collection of germplasm) from base seed material. This could be of use in improvement programmes of *J. curcas*. The variation in *J. curcas* population has been recorded earlier by Wani et al. (2006) for oil content (27.8 to 39% on kernel basis) and 100-seed weight (44 to 77 g), in India accessions and by Kaushik et al. (2007) in 100 seed weight (49 to 69 g) and oil content (28 to 39%) in Haryana-India accessions. Similarly Rao et al. (2008) found wide variation in 100 seed weight (57 to 79 g) and oil content (30 to 37%) for Andhra Pradesh, India, accessions. Srivastava et al. (2011) reported 17 to 34% oil yield in ten restricted accessions screened on the basis of growth performance and biomass characterization. Large variation in average seed weight (0.46 to 0.83 g/seed) has been reported among 18 natural provenances of *J. curcas* in Mexico (Martinez-Herrera et al., 2010). Ouattara et al. (2013) reported high variability in *J. curcas* seed traits with 100 seed weight ranging from 63.68 to 77.83 g among the 19 accessions collected from Senegal. In the present investigation, the 20 seed weight ranged from 5.87 to 12.80 g whereas oil % on kernel basis ranged from 27.43 to 57.32% in 65 seeded accession out of 72 collected accessions. Variation in characters could be due the fact that the species had been collected over a wide range of rainfall, temperature and soil type. Wen et al. (2012) observed that seed weight and oil content of *J. curcas* were positively correlated with the mean annual sunshine duration, mean annual temperature, mean minimum daily temperature of the coldest month, mean maximum daily temperature of the warmest month and the mean annual evaporation, but negatively correlated with altitude and the mean annual precipitation. Ndir et al. (2013) observed that seed oil content and seed thickness were correlated to rainfall; however, seed length, breadth and 20 seed-weight were not correlated to rainfall. Moreover, genetic diversity was not correlated to geographic position in *J. curcas* (Ndir et al., 2013). However, one part of variability is under genetic control. Kaushik et al. (2007) envisaged that environment has comparatively low influence on the seed traits and oil content. High heritability and high genetic advance for 100 seed weight have been reported by Kaushik et al. (2007) in *J. curcas*. Hence these characters can be considered as best gain characteristics for *J. curcas* improvement program because of its strong genetic control and the wide variability. Plant height and number of branches are also important characters that can be-looked upon as major selection indices when the objective is to incorporate *J. curcas* in an agro-forestry system. Variation observed in yield characters can be useful in selecting plant types for block plantations with high yield and higher % of oil in seed as the primary objective. The fruit and seed yield as expected is positively associated (r_p and r_g) with plant height and number of secondary branches suggesting that phenotypic and genotypic relation is reliable and in turn offer good scope for selection of CPP (Candidate plus plant) at primary level. Knowledge of genetic diversity within natural population in and outside the centre of origin is required to know the potentially valuable genetic material. Here the growth and yield attributes in these *J. curcas* accessions can be of great potential in improvement programs.

Correlation analysis is an important tool to bring information about relationship between growth and yield attributes, however lack of relationship between traits and environment makes selection of CPP poorly predictable for improvement program. The degree of correlation depends upon the gene causing such variation and their developmental relation. Correlation matrix revealed interesting relationship in the growth traits, yield traits and seed characters studied. The magnitude of genotypic correlation coefficient (r_g) was higher than their corresponding phenotypic coefficient of correlations (r_p) for almost all the growth and yield characters indicating the strong genetic inherent association ship or gene linkage among all the characters and suggests that their phenotype are more regulated with gene and less influenced by environmental effect. Such positive and significant correlation was registered in *J. curcas* and these characters are an advantage to the breeder for bringing improvement of traits (Ginwal et al*.,* 2004; Das et al., 2010). It has been well known that seed related characteristics can also be used to examine variability with in plant species (Rawat and Bakshi, 2011). Ouattara et al. (2013) observed that seed length was significantly correlated to all seed traits excepted Seed/fruit ratio in *J. curcas*. In the present investigation positive significant correlation of 20-seed weight existed with seed/kernel ratio, oil %, seed length and seed thickness at both r_g and r_p level from these result it is evident that these traits are interrelated at their gene level or these are QTL (Quantitative Trait Loci) therefore, seed weight is important trait for early selection of seed sources. This is further in agreement with the finding of Rao et al. (2008) in *J. curcas* and Kaura et al. (1998) in *Azadirachta indica*. 20-seed weight exhibited positive relationship with seed width at both r_g and r_p level but it's not at significant level. Very high degree of direct relationship observed between fruit yield and seed yield per plant at both r_p (0.978) and r_g (1.002) level indicate that both are in same and strong genetic control. Here, seed/kernel ratio exhibited high r_p

and r_g value with oil % indicated that both characters are in strong genetic control and suggested the effectiveness of indirect selection for kernel oil content through 20-seed weight. The estimation of 20-seed weight being less expensive and laborious compared to kernel oil content, the former can be used as a tool during selection process. The existence of negative correlation at both phenotypic and genotypic level between oil % and seed length, seed width and seed thickness indicated that both characters are independent on each other at both level and these traits variation in response to changing environmental condition (Valencia-Diaz and Montana, 2005). Significant correlations between fruit and seed yield with plant height, collar diameter, number of secondary branches and crown diameter also indicates that plant with good height and branching tend to develop more crown and flower subsequently fruit and seed. It indicates that the selection in any one of these yield attributing traits will lead to increase in the other traits, thereby finally enhancing the yield. Selection from early plantations of *J. curcas* can be made on the basis of these characters because of the difficulty in selecting plants solely based on yield as the full potential of yield is reached only after several years of growth in *J. curcas*. Similar relations have been reported in *Pennisetum typhoedes* by Van Osteroma et al. (2006) as well and in *Chenopodiem quinoa* by Bhargava et al. (2007).

The results from principal component analysis indicate that among all the 12 studied variable, variation is contributed by plant height, collar diameter, number of secondary branch, crown diameter, fruit yield, seed yield, 20-seed weight, seed length, width, thickness, S/K ratio and oil %. The first four components in the collection with eigen values were able to explain 84.56% of the total variance for morphological traits. According to Mardia et al. (1979), the total variance accumulated by principal component close to 80% explains satisfactorily the variability manifested between individuals. It is concluded that the above variables could be used as characters to distinguish the germplasm entries and might also be taken into consideration for effective selection of parents during hybridization program of this use full plant.

Genetic diversity

Analysis of genetic diversity in collections facilitated reliable classification of accessions and identification of core subsets of the accessions for future utility in specific breeding purposes. K-means clusters clustering pattern in this study revealed that trees from different geographic regions were grouped together in a cluster and also trees from the same geographical area placed in different clusters, suggesting that geographical diversity did not go hand in hand with genetic diversity. K-means clustering is done to understand the trend of evolution and choose genetically diverse parents for obtaining desirable recombination (Tams et al., 2006). By clustering of growth attributes the maximum inter-cluster distance (192.69) was observed between I/V cluster while in yield and seed characters the distance was (1634.1) observed between III/V cluster indicating substantial segregation.

Existence of substantial variation and diversity can be utilized for further tree improvement programmers of the species. Selection of parent material from such cluster for hybridization programme will develop elite plant with desirable characters. The minimum inter-cluster distance observed in growth attributes (42.58) between II/III and in yield and seed attributes (257.91) between IV/V indicates that accessions in these groups are closely related. Therefore, the selection of parent plant from these clusters should be avoided. Finally the cluster that are having more inter-cluster distance and high mean will produce divergent candidate.

Conclusion

In the study, most of the accessions are growing well in arid climate region of, Rajasthan, India. However, accession AFRI-35, AFRI-52, AFRI-56, AFRI-12, AFRI-20, AFRI-21 and AFRI-39 performing better among studied 72 accessions. Significant positive association of kernel oil content (percent) with 20-seed weight suggested the effectiveness of indirect selection for kernel oil content through 20-seed weight. Principal component analysis stated that plant height, collar diameter, number of secondary branch, crown diameter, fruit yield, seed yield, 20-seed weight, seed length, width, thickness, S/K ratio and oil percent could be used as morphological marker to distinguish the germplasm. On the bases of observations recorded here on a divergent group of *J. curcas* accessions, it is concluded that hybridization between the accessions of variable clusters may help to produce wide spectrum of variation in the segregating progeny and thus may be helpful in hybridization program to cope up the fore coming limitations pertaining to improvement of bio-fuels species for biodiesel industry. It is also suggested that for creating variability and developing the best selection a large number of divergent lines, instead of few should be used in the hybridization.

Conflict of Interest

The authors have not declared any conflict of interests.

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Review

Some medicinal plant resources and traditional uses in Pakistan

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Present communication describes lesser known plant resources which have been used over the centuries by local communities and indigenous populations for their medicinal and nutritional properties. Many of these plants are now being discovered by modern science and medicine and their value recognized. The idea is to call attention of research institutions and policy makers to these "forgotten gems" which have the potential of bringing economic returns to the communities that depend on them and of pulling so many out of poverty as well as capitalizing on traditional knowledge.

Key words: Medicinal plant resources, research institutions, policy makers.

INTRODUCTION

Pakistan has rich natural resources, diverse ecological zones, rich flora of over 6000 plant species. In Pakistan medicinal plants are naturally grown in many ecological zones throughout the country and on small scale some species are also cultivated. Temperatures fluctuate from below zero in the mountainous range to 50℃ in the southern plains. About 6000 plant species are reported in Pakistan and more than 1000 species are identified as medicinal and aromatic plants species .The demand of medicinal plants is increasing both in the developed and developing countries.

The local communities of different regions of Pakistan have centuries old knowledge about traditional uses of the plants occurring in their areas. This indigenous knowledge of plants has been transferred from generation to generation. The herbal system of medicine generally considered low cost treatment for various common diseases and rich diversity of medicinal plants an important source of livelihood for majority of the rural and mountainous communities. The use of plants as medicine is an ancient practice. The uses of medicinal plants vary in different parts of the country due to indigenous knowledge and method of utilization. Different plant species have been used to cure a single disease or several diseases at a time. Approximately, 350 to 400 medicinal plants species are traded in different drug markets in Pakistan and also used by Unani and Homeopathic Doctors.

Most of the raw material of medicinal plants is harvested from forests and rangelands, only few medicinal plants are cultivated. Deforestation, over exploitation, over grazing, conversion of natural habitats to agricultural fields resulted scarcity of medicinal plants. According to a survey of different Pansar stores (herbal stores) in Pakistan indicate that total turnover of crude drug in country is worth about Rs.120 million.

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Few medicinal plants are also exported to different countries in small quantities. The prices of medicinal plants at village level are very low and villagers are generally not well informed about market prices. The market value of medicinal plants increases 3 to 5 times from village to local shops and the prices at national market may be doubled to triple of the same item.

IMPORTANT MEDICINAL PLANTS RESOURCE

Many medicinal plants are found in the mountainous and plains areas of Pakistan. Some species with high market value are over exploited like *Glycyrrhiza glabra, Commiphora wightii, Ephedra intermdia, Saussurea lappa, Ferula foetida, Valeriana wallachii, Colchicum luteum, Bergenia ciliate, Paeonia emodi, Morchella* species etc and their productivity is also declining. Ecological conditions play a major role in the cultivation of medicinal plants and their active ingredients. Pakistan has a good potential of biodiversity of medicinal plants due to its varied climatic conditions. Medicinal plants are found more abundantly in the mountainous areas than in plains due to naturally conducive habitat and suitable climatic conditions. Over exploitation of medicinal plants in Pakistan causes serious threat to the survival and regeneration of many plant species. Therefore, there is further need of research and development activities of medicinal plants in areas like ethnobotany, biodiversity conservation, productivity, propagation, cultivation, active ingredients, quality control, value addition, value chain and policy both at national and provincial levels. The medicinal plants resources of Pakistan covers large number of species and not possible to include all in this paper, only major and important medicinal plants species of various ecological zones of Pakistan are highlighted with traditional uses (Table 1).

The traditional uses of plants are mainly in the form of crude plant extracts. However, the traditional uses of plants have also provided many active ingredients of many medicines in developed and developing countries. Advanced microbial and chemical methods can synthesis many medicinal and aromatic compounds from plants. Many active compounds have been isolated from the plants used in traditional medicines like Aloin from *Alo vera*, santonin from *Artemisia* species, glycyrrhizin from *Glycyrrhiza*, ephedrine from *Ephedra*, berberine from *Berberis* species, silymarin from milk thistle. In the nutrition point of view, Amla is one of the richest sources of vitamin C. Garlic a widely used plant in Pakistan is best known for its cholesterol lowering, anti-diabetic, antifungal properties. The compound Ajoene in garlic is one of the most important constituents and extensively investigated for its potent antiplatelet activity. Chicory (*Cichorium intybus*) plant traditionally used for many diseases now proved have properties of demulcent, anti-inflammatory, diuretic and blood purifier. Ispaghula (*Plantago ovta*) now used all over the world due to its proven properties like stomach problems, constipation, and cholesterol lowering. Haldi has been proved as antioxidant, anti-diabetic, anti-inflammatory, anti-thrombotic, anti-cancer and neuroprotective role. Tibbe-e-Nabvi provides the base for the traditional Unani system of medicine in Pakistan. According to a Hadith said by Hazrat Muhammad (Peace be upon him) Kalonji is the treatment of all diseases except death. Some recent studies also revealed that Kalonji is antioxidant, anti-inflammatory, anti-diabetic and anti-hyperchloestrolemic. Further to this, Kalonji seeds contain over 100 valuable nutrients and regulate the immune system, treat allergy, improves digestion, lower blood sugar, dispel worms and parasites. In Europe sea buckthorn juice, jellies, liquors, candy, vitamin C tablets and ice creams are readily available. Clinical studies on the anti-tumor functions of sea buckthorn oils in China showed positive results. Sea buckthorn juice or oil has been successfully used to treat high blood pressure and cardiovascular diseases. The medicinal plants are the important source of primary health care in Pakistan. Still there are many unexploited medicinal plant species of Pakistan which may bring positive impact in the control of many emerging diseases after the discovery of active compounds and mode of action.

RECOMMENDATION

Further efforts and research on conservation, management, sustainable utilization, marketing, ethnobotany, chemistry, pharmacology and genomics are required to unlock the treasure and potential of medicinal plants resources of Pakistan. Based on traditional knowledge, current scientific techniques are continually exploring the active constituents in plants and new drug formulation are being made. Besides this, many medicinal plants have great potential in cosmetic industry, culinary herbs, herbal teas, and essential oils. The demand of alternative medicines and natural food products are increasing both in developed and developing countries. Therefore, international development community and research organizations need to devote attention and invest some resources for further research and development of apparently neglected medicinal plants/herbs for nutritional and medicinal uses. Such an investment would go a long way in pulling so many out of poverty in the developing world especially the rural and indigenous people, as a source of economic livelihood and make a major contribution to health and well-being based on natural remedies.

Conflict of Interest

The authors have not declared any conflict of interest.

Table 1. Medicinal plants and traditional uses.

Botanical name	Common name	Parts used	Traditional uses
Achillea millefolium Linn.	Yarrow, Biranjasif	Leaves and flowers	Toothache, treat earache, tuberculosis, stomach disorder and fever
Achillea wilhelmsii	Boh-e-Madran	Leaves and stem	Stomach pain, fever, motion, jaundice
Acacia nilotica Lam.	Babul, Kikar	Stem bark, gum, seeds	Gum as a tonic, bark in diarrhea
Allium sativum Linn.	Garlic, Lassan	Cloves	For high blood pressure, cardiac problems and blood purifier
Aloe barbadensis Linn.	Aloe vera	Leaves	Burners, skin problems and complexion improvement, laxative, tonic, minor wounds.
Althaea officinalis Linn.	Marshmallow, Khitmi	Roots, flowers and seeds	Inflammations of mouth and digestive tract, cold, cough
Anthum graveolens Linn.	Soya, Dill	Seeds	Stomach troubles, increase breast milk in nursing mothers
Artemisia Species	Wormwood	Whole plant	Fever, vomiting, cough
Azadirachta indica L.	Margosa tree, Neem tree	Leaves, bark	Blood purification, skin diseases, jaundice, asthma, malaria, tooth ache
Bauhina veriegata Linn.	Wild Ebony, Kachnar	Flowers, seeds, bark	Flowers are also used as vegetable
Berberis lycium Royle	Zarch	Roots	Joint pain, rheumatism, chest infection, wounds, fractured bones
Bergenia ciliate Sternd.	Zakham-e-Hayat	Roots	Ulcer, wound healing, Joints Pain
Caralluma tuberculata	Marmooth	Tubers	Jaundice, dysentery, stomach pain, constipation, diabetes, high blood pressure, also used as a vegetable
Carthamus tinctorius Linn.	Safflowers, Saffron Thistle	Flowers, seeds	Food flavoring
Crataegus oxycantha	Hawthorn, Ghunza	Berries	Heart problem, blood pressure
Cassia fistula Linn.	Amaltas	Seed, root and bark	Hepatitis, jaundice, constipation
Cassia senna Linn.	Sana, Sana-i-Makki	Pods, seeds	Blood purification and abdominal discomfort
Citrus aurantifolia Christm.	Lime, Limun	Fruit Juice	Vomiting, burning in chest, diarrhea, lemon juice is used during summer season, flavoring salads, also used in pickles
Cichorium intybus Linn.	Chicory, Kasni	Leaves, seeds, roots	Digestion, astehma, spleen problems
Coriandrum satvum Linn.	Coriander, Dhaniya	Leaves and seeds	Fresh flowers and dry seeds are used in many cooking dishes
Commiphora wightii	Gumgugul, Guggal	Gum	Resin to treat piles, plant fumigants used to keep snakes away from homes
Crocus sativus Linn.	Saffron, Zafran	Flowers (stigmas)	Food flavoring, tonic, heart problem
Cuminum cyminum L.	White Cumin	Seeds	Condiment or spice in curries, pickles and flavor in confectionery
Curcuma longa Linn.	Turmeric, Haldi	Tubers, rhizomes	Wound healing, major ingredient of many foods
Datura stramonium Linn.	Thorn apple, Datura	Leaves, seeds	Parkinson disease
Ephedra intermdia	Ephedra	Whole plant	Asthma, chest infection, typhoid
Eugenia jambolana Linn.	Black Plum, Jamun	Fruits	For diabetic control
Foeniculum vulgare L.	Fennel, Saunf	Seeds	Carminative, eyesight improvement, used as a culinary and pickles making.
Ferula foetida Regel.	Asafoetida, Hing	Stem, leaves, gum resin	Toothache, cough of infants, to kill intestinal worms
Grewia asiatica Linn.	Phalsa, Falsa	Fruit	Syrup used during summer months for internal cooling
Glycyrrhiza glabra Linn.	Liquorice, Mulethi	Roots	Cough and chest problem
Hippophae rhamonide L.	Sea-buckthron,	Berries	Tonic, blood pressure
Hyoscyamus niger Linn.	Henbane, Ajwain Khurasani	Seeds	Digestive problems, colic

Table 1. Contd.

Juniperus excels	Juniper,	Berries	Eye diseases, chest infection, body itching
Lallemantia royleana Benth.	Lallemantia, Tukamhm-e-Balangu	Seeds	Seeds are used in cold drinks as cooling and sedative
Linum usitatissimum Linn.	Linseed, Alsi, Flax	Seeds	Laxative, back pain, tonic
Mentha arvensis Linn.	Mint, Jangli Pudina	Leaves and stem	Cough, cramps, nausea, diarrhea, stomach upset
Moringa oleifera Lam.	Horse Radish, Sohajna	Bark, flowers, seeds, roots	For liver and spleen problems, rheumatism
Morus nigra Linn.	Mulberry, Shahtut	Fruit	Cough, throat problems
Morchella species	Black Mushrooms, Gucchi	Mushrooms	High priced item, mostly local communities collect and sold, high demand in international market
Nannorrhops ritchieana	Piesh	Seeds	Tonic, dysentery control
Nigella sativa Linn.	Black Seeds, Kalonji	Seeds	Seasoning dishes, flavoring ingredient in pickles
Peganum harmala Linn.	Rue, Harmal	Seeds	Stomach pain, plant smoke is used for measles patients
Pinus gerardiana Willd.	Chilgoza	Nut	Dry fruit, tonic
Plantago ovate Forssk.	Plantain, Ispaghul	Husk, seeds	Chronic diarrhea, dysentery, constipation, laxative used to regulate bowel movement.
Pistacia atlantica	Wild Pistacia, Gowan	Seeds	Dysentery, cough, seeds are also eaten like a nut
Portulaca oleracea Linn.	Purslane, Kulfa	Whole plant	Jaundice, typhoid, iron deficiency, skin allergy, also used a vegetable
Ricinus communis Linn.	Castor Seed, Arand	Seeds, seeds oil	Joint pain, bark for healing wounds, root for toothache, seed oil as a laxative
Rosa damascene Mill.	Red Rose, Gulab	Flowers	Skin problems, digestive problems
Sapindus mukorossi Gaertn.	Soap Nut, Ritha	Seeds	Hair improvement
Saussurea lappa (DC.) Sch. Bip.	Costus, Kuth	Roots	Skin allergies, pimples, stomach pain, typhoid fever
Sesamum indicum DC.	Sesame, Til	Seeds	Sweets making, urine problems
Terminalia arjuna Roxb.	Arjuna Myrobalan, Arjan	Bark	Heart problems
Thymus serphyllum Linn.	Wild Thyme	Whole plant	Fever, cough, digestion, also used as a herbal tea
Tribulus terrestris Linn.	Caltrops, Gokhru	Seeds	Stomach pain, back pain, removal of kidney stones
Trigonella foenum-graecum Linn.	Fenugreek, Methi	Leaves, seeds	Diabetic, food flavoring, vegetable
Truffles Species	Truffles, Morales, underground mushrooms	Truffles	As a vegetable
Viola ordorata Linn.	Sweet Violet, Banafsha	Flowers, leaves, root	Cough, sore throat
Vitex pseudo negundo Linn.	Five leaved Chaste tree, Nirgandi	Seeds, bark	Stomach pain, kidney stone, menstrual cycle problems
Zingiber officinale Roscoe.	Ginger, Adrak	Fresh and dry rhizome	Digestive problems, colic, restore appetite, culinary for many dishes
Zizphus jujube Mill.	Jujube berries, Unab	Seeds	Cough, throat problems

Sources: Ahmad et al. (2012)), Ahmad et al. (2008), Ahmad et al. (2011), Ahmad and Habib (2014), Alam et al. (2011), Arshad et al. (2011), Aslam and Aslam (2012), Awan and Murtaza (2013), Awan et al. (2013), Baloch et al. (2013), Begum and Yaseen (2013), Bokhari et al. (2013), FAO (1997), Gulshan et al. (2012), Hazrat et al. (2010), Hussain et al. (2013), Iftikhar et al. (2012), Ishtiaq et al. (2011), Jasn et al. (2011), Kakar et al. (2012), Khan et al. (2011), Khan et al. (2013), Khanzada et al. (2008, 2013), Khattak (2013), Mahmood et al. (2011), Panhwar and Abro (2007), Qaisar et al. (2013), Qamar et al. (2010), Qureshi (2012), Qureshi et al. (2007, 2010), Rizwana et al. (2011), Tareen et al. (2010), Wazir et al. (2004), and Zereen and Khan (2012).

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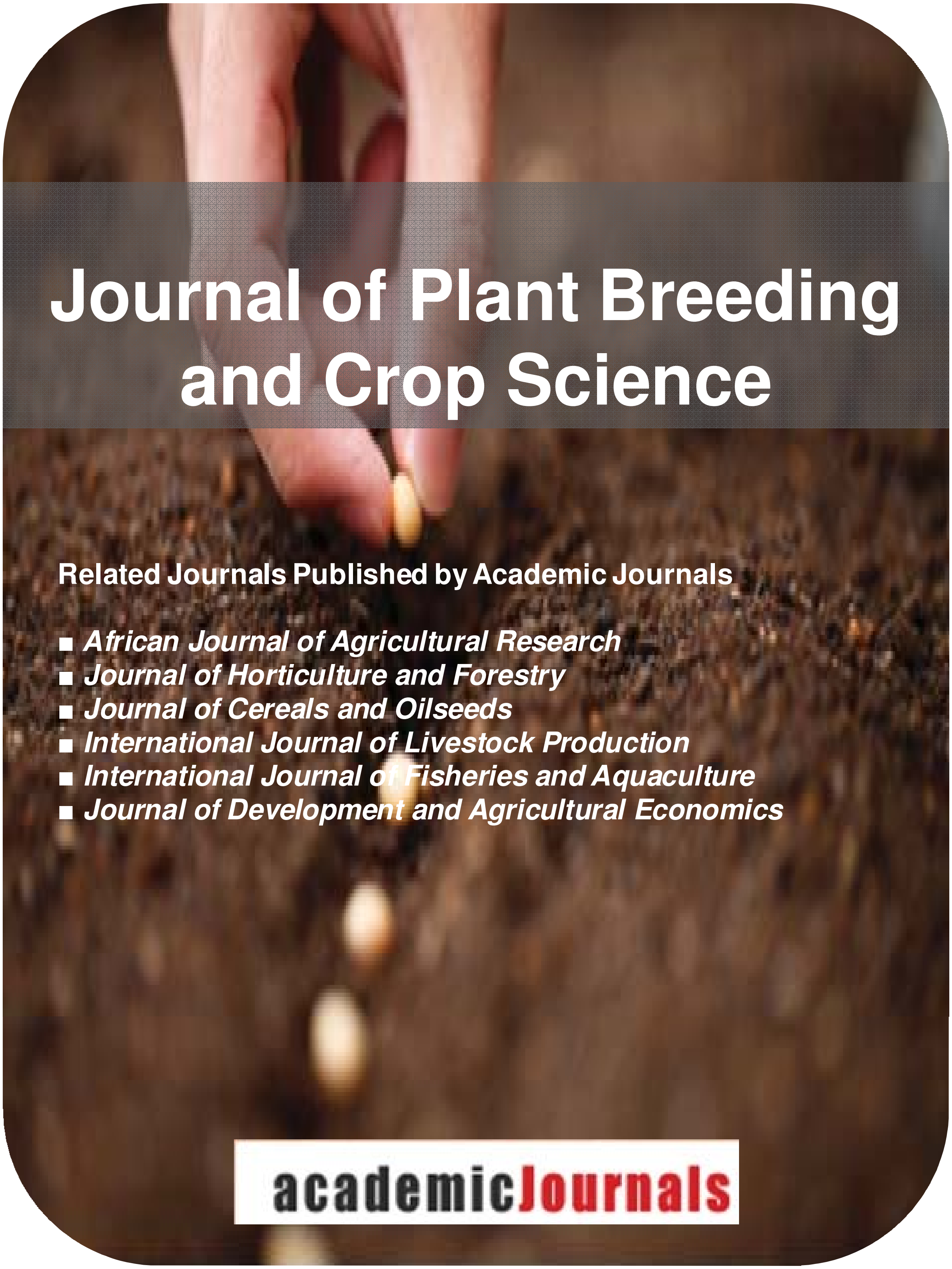

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