

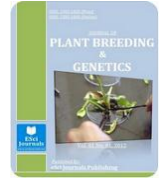


Available Online at ESci Journals

Journal of Plant Breeding and Genetics

ISSN: 2305-297X (Online), 2308-121X (Print)

http://www.escijournals.net/JPBG



COMBINE SELECTION FOR EARLINESS AND YIELD IN PEDIGREE DEVELOPED SORGHUM (*SORGHUM BICOLOR* L. MOENCH) PROGENIES IN ERITREA

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ABSTRACT

Thirteen progenies of sorghum (*Sorghum bicolor* L. Moench) crosses (Amal and ICSV 91078) that selected using pedigree breeding method, were evaluated along with their parental checks to obtain information on yield potential, earliness, genetic and morphological diversity. The genotypes were evaluated in randomized block design with three replications for three years (2007-2009) at Halhale research center. Significant mean squares were obtained for almost all characters in the individual analysis of variance as well as the combined analysis across seasons, suggesting that, these sorghum genotypes were highly variable for almost all the characters studied, therefore, would respond to selection. Mean values for the combined analysis of the progenies showed that Hal-1-1, Hal-4-9, Hal-13-33, Hal-11-30 and Hal-9-24 were promising cultivars in terms of grain yield and earliness. Combined analyses also showed most characters had relatively higher genotypic and phenotypic variance components and little difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) indicating their variation has a genetic origin that can be exploited for further breeding programs. The genotypes also exhibited varying degrees of heritability estimates. Characters such as plant height, days to 50 % flowering and grain yield responded positively to selection because of high broad sense heritability estimates. High heritability and genetic advance was noted for plant height and days to 50% flowering indicating that these parameters were under additive gene effect and responded well for genetic improvement. However, grain weight showed high heritability with low genetic advance indicating that the trait has non additive gene action and might respond well due to its heterosis.

Keywords: GCV, PCV, pedigree breeding, heritability, Eritrea.

INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] is Africa's second most important cereal crop after maize (FAOSTAT, 2012). Over 100 million people of sub-Saharan Africa depend on sorghum as their main staple food (Smith and Frederiksen, 2000). It is primarily a crop of resource-poor small-scale farmers and is grown predominantly in low- rainfall, arid to semi-arid environments. The crop is well adapted to withstand harsh conditions, which are the characteristic feature of tropical regions (Ramu *et al.*, 2013). It is well adapted to a wide range of precipitation, temperature levels and

altitudes of as high as up to 2000 meters above sea level (Fetene *et al.*, 2011). Due to its adaptation to a wide range of stresses, this crop is a choice of east African farmers where they experience frequent droughts. In Eritrea sorghum is widely grown in the lowland and mid-highland regions where rainfall is too low for the cultivation of most other cereals (Tesfamichael *et al.*, 2014). Its adaptation to wide environments, fast growth, high yield potential and good quality fodder makes it a choice of crop for poor farmers of the country. Besides, it is a major staple food prepared as 'enjera' (leavened bread) or as thick porridge.

Genetic variability for agronomic characters is a key component of breeding programs for broadening the gene pool of crops (Ahmad *et al.*, 2011). Heritability is a

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measure of the phenotypic variance attributable to genetic causes and has predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Knowledge of heritability influences the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the character, to predict gain from selection and to determine the relative importance of genetic effects (Waqar *et al.*, 2008; Laghari *et al.*, 2010). The most important function of heritability in genetic studies of quantitative characters is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value (Falconer and Mackay 1996). Characters with high heritability can easily be fixed with simple selection resulting in quick progress. However, it has been emphasized that heritability alone has no practical importance without genetic advance (Najeeb *et al.*, 2009). Genetic advance shows the degree of gain obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. Rafiq *et al.* (2010) and Akbar *et al.* (2008) have reported high heritability and high genetic advance for different yield controlling traits in maize.

Early maturity is an important agronomic trait for the adaptation of annual crops to any agro-ecological zone (Ayo-Vaughan *et al.*, 2011). Earliness of crop maturity is an essential trait in many regions especially in sub-Saharan Africa where drought is persistent. Earliness plays a key role in genotype adaptation to current and new environments and has a powerful effect on yield (Kumar and Abbo, 2001). It may also protect the crop from various biotic and abiotic stresses such as diseases and drought (Monpara and Dhameliya, 2013). As a result, early maturity continues to be one of sorghum breeding objectives. Early maturity is an important agronomic trait for sorghum breeding, however, drought stress can complicate recording of flowering/maturity date due to forced maturation caused by stress. Early maturation of the crop is a trait that is greatly appreciated by resource poor farmers. It enables them to harvest food and receive income sooner, and to escape many droughts, which is a persistent phenomenon in sub-Saharan Africa. Furthermore, model-based climate change projections for the eastern Africa region indicates that the change in climate will cause a further

increased temperatures and decreased periods of rainfall in the main growing season (Hulme *et al.*, 2001). There is a need therefore, to cop up with the climate change to sustain crop production in the region. One possible option is to improve the locally adapted landrace crop variety for earliness. This study was therefore conducted to improve a landrace sorghum variety, Amal, for its earliness by crossing with an early maturing sorghum variety, ICSV 91078.

MATERIALS AND METHODS

Plant materials: The parental sorghum varieties that were used for crossing were Amal and ICSV 91078. Amal is a late maturing popular landrace sorghum variety in Eritrea which is characterized by compact erect panicle, good yield potential and high quality for making enjera. It is among the best sorghum varieties after Taff, *Eragrostis teff*, for making enjera. ICSV 91078 is an improved early maturing sorghum variety from ICRISAT.

Description of the study site: Crossing and field evaluation activities were conducted at Halhale research center (15°03'44.3"N latitude, 38°49'02.1" E longitude and 917 masl) which is located about 35km south of Asmara, the capital city. The average maximum and minimum air temperatures during the experimental periods were 22.3°C and 14.9 °C respectively. Rainfall distribution for the years 2007 - 2009 is shown in Figure 1.

Breeding method: The parental varieties, Amal and ICSV 91078 were planted under field conditions at Halhale research center and crossed to produce F₁s and subsequent generations. Pedigree based breeding procedure as adapted from Poehlman (1987) was used to generate the progenies as shown in Figure 2. From selected F₂ plants, progenies of 25 plants were grown in plant rows in F₃. Superior plants from the best rows were selected and planted in families of plant rows in F₄-F₆; selection was made of best plants, in best rows, of best families. Preliminary trial was carried out at F₇ and advanced trials continued through F₁₀.

Field evaluation: Thirteen progenies selected from the pedigree breeding method along with their parental checks, Amal and ICSV 91078 were laid out in a randomized complete block design with three replications for three consecutive years/seasons. During sowing, the seeds were manually drilled into 4-row plots of 4 m length, spaced 0.75 m apart. At three weeks after sowing the seedlings were thinned to 0.2 m between plants, with one plant per hill. Phosphorus and nitrogen

fertilizers were applied at the recommended rates of 46 kg P₂O₅ ha⁻¹ and 54 kg nitrogen ha⁻¹ in the form of diammonium phosphate and urea, respectively. The plots

were manually weeded as frequently as needed, while pests and disease were controlled whenever they appear in the subsequent seasons.

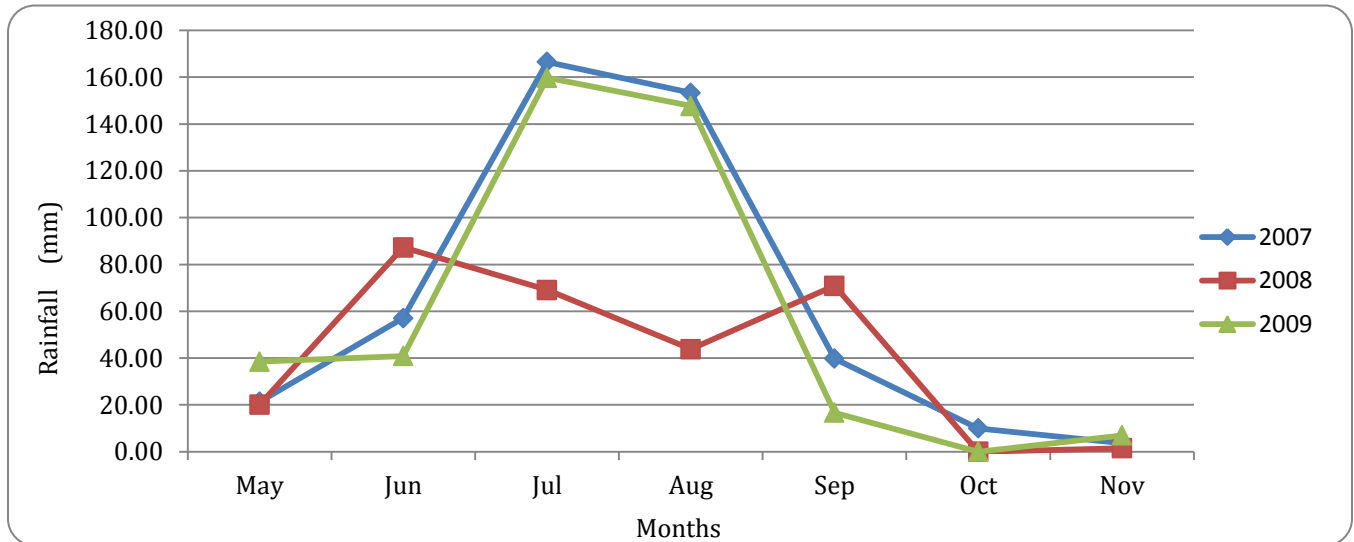


Figure 1. Effective monthly rainfall distribution pattern during the growing period for Halhale research center in the period 2007-2009.

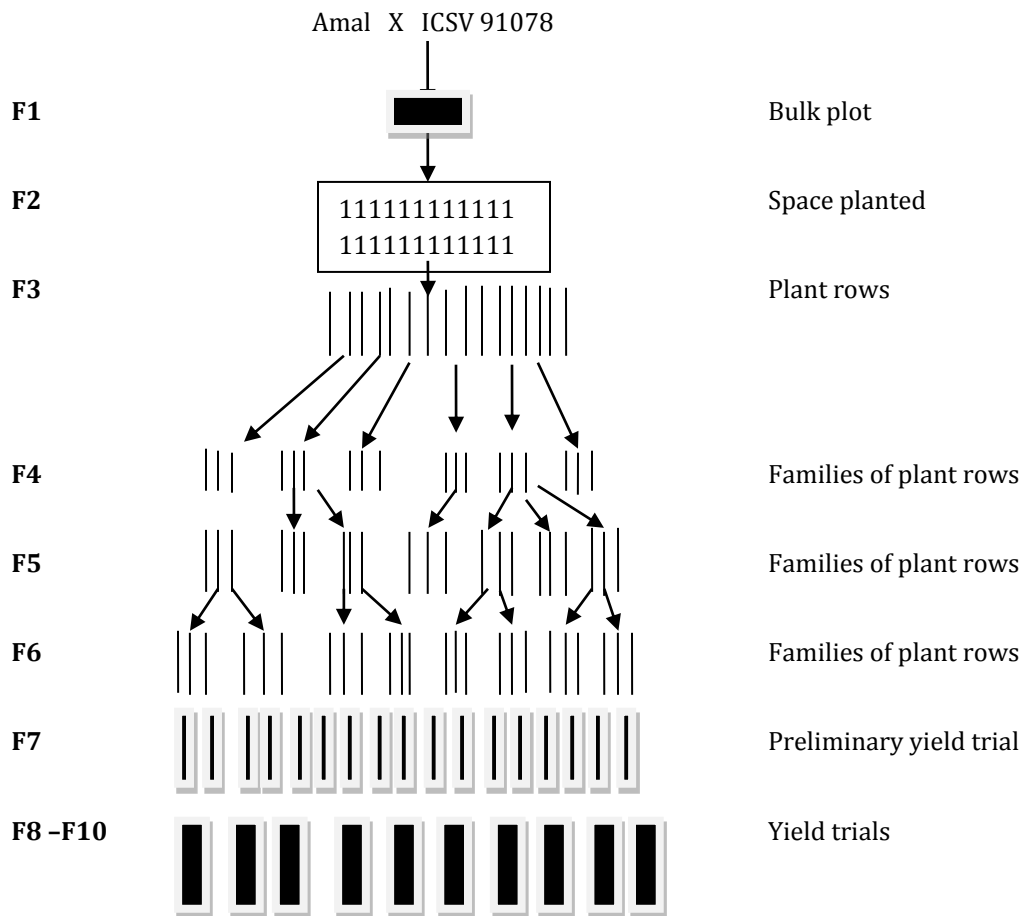


Figure 2. Scheme of pedigree method of breeding adapted from Poehlman (1987) used to select the progenies.

Data collection: Data were collected from the two middle rows with a net plot area of 6m² for the major agronomic traits such as days to 50% flowering, plant height, agronomic score (scored on a 1–5 scale, where, 1 = agronomic better and 5 = agronomic poor), grain yield (t ha⁻¹) and 100 seed weight (gm).

Data analysis: Data from the replicated trials were subjected to standard analysis of variance to determine variation among the entries for the traits studied using Genstat version 14 (Payne *et al.*, 2011). Correlations between the evaluated traits were performed using Pearson's correlation. Genetic parameters to identify genetic variability among the lines and determine genetic and environmental effects on various characters as described by Assefa *et al.* (1999). Accordingly, to identify the major traits contributing to the overall phenotypic variation among the entries and to estimate heritability for the various morpho-physiological traits the following formulae were used:

- i. Genotypic variance, $GV = (MSg - MSe)/r$, where MSg = mean square of genotypes, MSe = mean square of error, and r = number of replications.
- ii. Phenotypic variance, $PV = GV + MSe$, where GV = genotypic variance and MSe = mean square of error
- iii. Phenotypic coefficient of variation, $PCV = \frac{\sqrt{PV}}{\bar{x}} \times 100$, where PV = phenotypic variance and \bar{x} = mean of the character
- iv. Genotypic coefficient of variation, $GCV = \frac{\sqrt{GV}}{\bar{x}} \times 100$, where GV = genotypic variance and \bar{x} = mean of the character
- v. Heritability (Broad sense heritability), $H = GV/PV$, where GV and PV are genotypic and phenotypic variances respectively
- vi. Genetic advance (GA) expected and GA as percent of the mean assuming selection of the superior 5% of the genotypes estimated as:

$GA = K (Sph) (H)$, where Sph is the phenotypic standard deviation, \sqrt{Vph} ; is the heritability ratio; and \bar{x} is the respective trait grand mean and

GA (as % of the mean) = $(GA/\bar{x}) * 100$, where K is a constant (which varies depending upon the selection intensity).

RESULTS AND DISCUSSION

The mean performance of days to 50% flowering, plant height, agronomic score, hundred grain weight and grain yield of the evaluated progenies are shown in Table 1.

Days to 50% flowering for the progenies ranged from 75 to 96 days. The early and late flowering parents differed from each other by 27 days to flower, indicating involvement of divergent parents for flowering time. In the present study, genotypes Hal-4-9, Hal-1-1, Hal-11-30, Hal-9-24 and Hal-13-33 were found to be significantly early with days to flowering of 74.5, 77, 82.7, 83 and 83 respectively compared to the late flowering parental check, Amal (97 days). These genotypes flowered on average 17 days earlier than the late flowering parent; however none of these five lines have flowered as early as the early check. Similarly, agronomic score and hundred seed weight were better in the selected promising genotypes. The progenies showed wide range of variation for plant height. Plant height ranged from 109.61 to 141.78 cm where the genotype Hal-8-20 scored the highest height followed by Amal and Hal-2-5 (Table 1). Pooled analysis of variance for the three seasons showed the highest mean yield of 2.79 t ha⁻¹ was recorded by genotype Hal-9-24 which had yield advantage of 0.42 t ha⁻¹ and 0.21 t ha⁻¹ over the late and early maturing parental checks respectively (Table 1). This superior performance of the genotype, Hal-9-24 against its parents suggested that favorable additive alleles were brought by both parents, and/or that complementary interactions occur between alleles of different origins (Tefera *et al.*, 2003). The lowest grain yield was recorded by Hal-4-9 (1.74 t ha⁻¹) and the overall grand mean was 2.23 t ha⁻¹. Besides, the progeny Hal-9-24 flowered 14 days earlier than the late maturing parent. Seetharama *et al.*, (1982) has reported breeding for earliness is an important breeding objective in sorghum and earliness has been successful for increasing the yield of rainy-season sorghums in India.

Mean squares for various traits are given in Table 2. Mean squares of genotypes for the characters such as days to flowering and grain yield were highly significant. This implies that parents involved in crossing were divergent in nature especially in earliness which resulted in distinct variation among the progenies. Such distinct variations for various traits could be due to heterotic effects. Quinby (1963) reported heterosis in sorghum in the form of increased grain yields, hastened flowering and increased height. The observed variations revealed also the genetic potentials of these progenies that can be used for selection of desired characters. Mean square analysis also showed highly significant difference for the seasons and genotype by seasons (Table 2).

Table 1. Combined mean values of the major traits from three consecutive season field evaluation of 13 progenies and their parental checks at Halhale research center.

Sr.	Genotypes	Days to 50% flowering (days)	Plant height (cm)	Agronomic score (1-5)	Hundred seed weight (gm)	Grain weight (t ha ⁻¹)
1	Hal-1-1	77.33	131.44	2.72	1.97	2.07
2	Hal-2-5	91.56	139.44	2.83	1.57	2.43
3	Hal-3-6	92.78	131.67	2.88	1.64	1.74
4	Hal-4-9	74.56	109.61	2.33	2.02	2.05
5	Hal-5-11	96.33	136.72	2.67	1.39	1.96
6	Hal-6-14	81.11	125.00	3.00	1.74	2.14
7	Hal-7-17	86.67	131.72	2.83	1.79	2.23
8	Hal-8-20	90.22	141.78	2.56	1.76	2.44
9	Hal-9-24	83.00	124.44	1.39	1.90	2.79
10	Hal-10-26	90.56	117.89	2.89	1.50	1.86
11	Hal-11-30	82.67	114.00	2.22	2.02	2.30
12	Hal-12-31	90.11	113.72	2.89	1.76	2.20
13	Hal-13-33	83.67	131.56	2.33	1.72	2.29
14	ICSV 91078	70.00	125.50	3.39	2.21	2.58
15	Amal	97.22	139.61	3.06	1.8	2.37
G. mean		85.85	127.61	2.67	1.79	2.23
CV%		3.70	5.30	14.2	15.30	4.70
LSD (0.05)		2.95	6.37	0.39	0.25	0.10
Fprob.		***	***	***	***	***

Key: ***highly significant at $P < 0.05$, G.mean = Grand mean, CV = coefficient of variation, LSD = least significant difference at 5%, F.prob = F probability.

Table 2. Mean square values of 5 traits in the progenies and their parents from a combined analysis of three consecutive seasons at Halhale Research Center.

Source of variation	DF	Days to flowering	Plant height	Agronomic score	100 seed weight	Grain yield
Season	2	80.76***	614.18***	43.33***	8.06***	20.99***
Rep. x Season	6	8.90	221.31***	0.42*	0.04	0.01
Genotypes	14	563.87***	931.71***	0.85***	0.42***	0.69***
Genotypes x Season	28	78.39***	236.37***	1.41***	0.41***	0.89***
Residual	84	9.92	46.25	0.17	0.07	0.01

F = probability differences at * $P \leq 0.05$ and *** $P \leq 0.001$; Rep = Replication.

The performance of the genotypes varied in the different seasons indicating the diversity of the genotypes and their differences in environmental responses across the three seasons/years for all the traits studied. This could be due to the variability in the amount and distribution of rainfall received in the growing season as shown in Figure 1. Similar findings were reported by Bello *et al.* (2012) on their study in maize. Genetic variability for the various traits was assessed to determine patterns of genetic variation for these characters among the progenies (Table 3). Hundred seed weight, grain yield and agronomic score

showed the highest values of phenotypic and genotypic coefficients of variations followed by days to flowering and plant height. This showed that not only selection can be effective for these traits but also indicated the existence of substantial variability, ensured ample scope for their improvement through selection. A very little difference between PCV and GCV (Table 3) for most of the characters showed their variation has a genetic origin. Similar results were reported by Sami *et al.* (2013) on their studies in sweet sorghum. Days to flowering, grain yield and plant height displayed high broad-sense heritability values while hundred seed

weight and agronomic score had relatively lower heritability. The high heritability estimates for days to flowering, grain yield and plant height suggest that these traits are likely to respond to direct selection. High heritability obtained for most of the traits is in agreement with the findings of Tomar *et al.* (2012). Genetic advance was the highest for days to 50%

flowering and plant height; however, hundred seed weight, agronomic score and grain weight scored lower genetic advances. Plant height revealed the highest heritability and genetic advance followed by days to flowering. Estimates of genetic advance were lowest for hundred seed weight and agronomic score coupled with relatively low heritability in broad sense.

Table 3. Genotypic variance, phenotypic variance, phenotypic coefficient of variation, genotypic coefficient of variation and heritability for 5 traits of 15 genotypes studied from a combined analysis of three seasons.

Trait	GM	GV	PV	PCV (%)	GCV (%)	H% (BS)	GA	GA (% mean)
Days to flowering	85.85	184.55	194.47	16.24	15.82	94.90	27.3	31.8
Hundred grain weight	1.79	0.12	0.19	24.36	19.00	60.85	0.5	0.6
Grain yield	2.23	0.23	0.24	21.78	21.27	95.34	1.0	1.1
Agronomic score	2.93	0.23	0.40	21.55	16.21	56.61	0.7	0.9
Plant height	127.61	295.15	341.40	14.48	13.46	86.45	33.0	38.4

Where, GM = grand mean, GV = genotypic variance, PV = phenotypic variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, $H_{(BS)}$ = Heritability in broad sense, GA = Genetic advance and GA (% of mean) = Genetic advance percentage of the mean.

The value of correlation coefficient (Table 4) indicated grain yield had no significant association with days to flowering, agronomic score, 100-seed weight and plant height. Similarly days to 50% flowering were negatively correlated with 100-seed weight but not with grain yield and plant height. Agronomic score had significant negative

correlation with plant height and positively correlated with 100-seed weight. Earliness could result in smaller seeds and it is important to select for earliness in combination with seed size and overall grain yield to combine earliness with good agronomic characteristics as reported by Vales *et al.* (2012).

Table 4. Correlation coefficients among the traits from a combined data of three seasons.

	Agronomic score	Days to flowering	Grain Yield	100 grain weight	Plant height
Days to flowering	-0.459	-			
Grain yield	0.325	-0.2651	-		
100 grain weight	0.611*	-0.8111***	0.4738	-	
Plant height	-0.548*	0.4862	0.1581	-0.385	-

Where, * and *** Significant at $P < 0.05$, and $P < 0.001$ respectively.

A study by Tesfamichael *et al.* (2013) reported that post flowering drought is the key yield reducing factor on farmers' field in Eritrea. Besides, the authors noted that the use of early maturing landraces and good adaptation to marginal areas coupled with some agronomic practices are the main options used by the farmers to mitigate drought. Hence the improvement of the late maturing popular landrace in terms of earliness with comparable yield could help the farmers to enhance their productivity.

CONCLUSION

The success of breeding programs depends upon the genetic variation in the genotypes at hand. The greater the genetic variability, the higher would be the heritability, hence the better the chances of success to be

achieved through selection. The present study indicated the availability of genetic variance for some useful traits such as grain yield and earliness in the progenies for exploitation through selection. The identified superior lines which recorded better mean performance for different traits may be used as potential for release and for further breeding work.

ACKNOWLEDGEMENT

The authors are grateful to National Agricultural Research Institute (NARI) of Eritrea for technical and material support; ICRISAT and Purdue University (through INTSORMIL, the International Sorghum and Millet Collaborative Research Support Program) for technical backstopping.

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