

Combining Ability and Heterosis of Locally Developed Sorghum (Sorghum Bicolor L. (Moench) Hybrids for Grain Yield and Forage

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Abstract

This study was conducted to estimate the magnitude of heterosis and combining abilities (general and specific) for forage and grain yield performance of sorghum hybrids. However, information on heterotic performance and combing ability of Ethiopian elite sorghum lines is for biomass and yield performance is inadequate. ANOVA revealed, mean squares had signifying substantial amount of variability amongst genotypes for most traits. Parents and Hybrids are significantly different for all traits except thousand grain weight, number of green leaves and panicle width. This revealed that hybrids can have better yield than OPVs. Hybrids, 106x94, 106x90, 106x102, 107x99 and 107x105 were found maximum heterotic hybrids for yield as compare to check. The estimations of parental GCA effects showed that female 106 and males 79, 96, 94 and 81 were good general combiners for yield and related traits. Based on perse performance, heterotic response and combining ability, female parent 106 and male parents 94, 102 and 90 were found most performed. Those parental lines could be used for further hybrid and germplasm development.

Keywords: Combining ability, GCA, Heterosis, Biomass, Hybrid, SCA, Sorghum
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Introduction

Sorghum is a diploid C_4 cereal crop which was domesticized in Africa particularly Ethiopia and Sudan. It has 2n = 20 chromosome and genome size of 750 Mb (Paterson *et al.,* 2009). Sorghum mainly reproduces through selfing with outcross reaching to 15-30% depending on the nature of head compactness and shape (Pfeiffer *et al.*, 2010). It is the fifth major cereal crop in the world and third in Ethiopia which is the most important dry land crop grown for food, feed, fuel, fodder and other traditional uses (Bahadure *et al.*, 2016). Its production over the years 1.49 tones ha^{-1}, 1.74 tones ha^{-1} and 2.71 tones ha^{-1} in the World, Africa and Ethiopia respectively (USDA, 2020).

In the initial stages, knowledge on combining ability and heterosis of parental materials is essential for a productive breeding program dedicated in development of high yielding and dual purpose sorghum hybrids, especially in the areas where drought is one of the major factor for forage and grain production (Amelework *et al.*, 2016). Though there has been a high level of genetic diversity, the potential of new locally developed inbred liens for hybrid cultivar development has no longer yet been exhaustively assessed. To satisfy the farmers' need for, its miles is vital to maximize the production and productivity through developing hybrids with excessive grain and fodder yield through established, formal and continuous breeding programs. Currently many thousands of inbred lines are found in Ethiopia which are developed in Ethiopian sorghum research program via a non-stop crossing program. Those elite lines aren't assessed exhaustively for hybrid production since they're progenies of elite traces which are having exact tendencies such as higher yield. In general, information on heterotic performance and combing ability on Ethiopian elite sorghum lines is limited.

In this study hybrids and elite lines were evaluated to assess their performance, heterotic pattern and heterobeltiosis for yield, forage and yield components by identifying best heterotic parents and good combiner parents for sorghum hybrid breeding program under moisture stress areas in Ethiopia.

The specific objectives include:

1) To identify hybrids under moisture stress environments for grain yield and forage
2) To estimate and determine heritability, heterosis and combining ability (GCA and SCA) of the hybrids for important agronomic traits.

Materials and Methods

Description of the Study Area

The study was conducted at the dry lowland sorghum growing area at Miesso which is situated at 1394 m.a.s.l. and a coordination of 9°14′N, 40°45′E. Miesso has a dry lowland climatic condition with an average maximum and minimum temperatures of 34 ^{0}c and 10 ^{0}c respectively and the average annual rainfall of the area is 790mm with dominant Vertisol soil.

Genetic Materials

The experiment was conducted for a total of 70 F1 hybrids which was derived using 2 standard female A-lines *viz* ETX623 and ICSA21 crossed with 35 inbred lines (pollinators). In this experiment both the hybrids and parents (male and female) including two hybrids (ESH-1 and ESH-4) and one recently released better biomass producing sorghum OPV variety (Argiti) were used as a standard check. In total the experiment consisted 110 genotypes. List of genetic material can be found on http://dx.doi.org/.

Experimental design and trial management

The experiment was laid down in alpha lattice design with two replications. During planting, the seeds was manually drilled into 5 meters long 2 row plots with a spacing of 0.75 m between rows in total each plot has of 7.5 m^2 area. Three weeks later of sowing, the seedlings were thinned to 0.20 m distance between plants. Nitrogen and Phosphorus fertilizers were applied at the recommended rates of 46 kg/ha P_2O^5 and 54 kg/ha. Phosphorus was applied in the form of DAP during planting and urea when the seedling reached at 5cm height.

Data Collection

Data was record on growth and phenological parameters (DTE (Days to emergence), DTF (Days to flowering), DTM (Days to physiological maturity), PHT (Plant height), NGL (Number of Green leaves), NSL (Number of Senescence leave), CHL (Chlorophyll content)) and yield and yield components (PL (Panicle length), TGW (Thousand grain weight), GY (Grain yield), Biomass, HI (Harvest index)) using electronic data collection tools (tablets, barcode readers, and computer program to weigh grain yield automatically) to avoid error and for data precision.

Statistical analysis

Analysis of Variances

Analysis of variance for single location was done using the following model:

$$Y_{ijl} = \mu + \tau_i + \gamma_j + \rho_{l(j)} + \varepsilon_{ijl}$$

Where;

- μ is the overall (grand) mean, is the overall (grand) mean,
- τi is the effect due to the i^{th} treatment, (i=1,2, 3…, t)
- γ_j is the effect due to the j^{th} replication, and, (j=1, 2…, r)
- $\rho_{l(j)}$ is block within replicate effect
- εijl is the error term where the error terms, are independent observations from an approximately Normal distribution with mean = 0 and constant variance σ $\varepsilon 2$.

The analysis was performed using R: R core team (2018). Genotypes were considered as fixed effects, replications and blocks within replications as random effects.

Combining ability analysis and Estimation of heterosis

Analysis of variance for combining ability was carried out using mean values across environments (Kempthorne, 1957), to test the significance of differences among the genotypes including crosses and parents (Snedecor and Cocharan, 1967). The sum of squares for hybrids was further partitioned into variation due to males, female and males * females interactions. The mean squares due to males and females were tested against the mean squares due to males * females, and the latter were tested against the pooled error. The mean squares due to environment * males and environment * females were tested against the mean squares due to environment * females * males, and the latter was tested against the pooled error. Estimate of GCA variances (σ^2GCA)andSCAvariances (σ^2SCA) were obtained (Singh and Chaudhary, 1977). Mid-parent, better parent and Better check heterosis were estimated and tested by working out the standard errors and tested by t test at 5 and 1% (Hays et al. 1955).

Proportional contribution of Females, Males and their interaction were found:

$$Contribution\ of\ Lines = \frac{SS_L}{SS_H} * 100 \quad , \quad Contribution\ of\ Testers = \frac{SS_T}{SS_H} * 100 \quad \text{and}$$

$$Contribution\ of\ LinesxTesters = \frac{SS_{LxT}}{SS_H} * 100$$

Correlation among variables was computed using R software (R Core Team, 2018).

Estimation of Genetic Components and Heritability

The phenotypic and genotypic variance components and coefficient of phenotypic (PCV %) and genotypic coefficients of variation (GCV %) was estimated based on the method suggested by (Burton and Devane, 1953). Heritability in broad sense for all characters was computed using the formula given by (Falconer, 1989).

Result and Discussion

Variability of genotypes for grain yield and Biomass component traits

An understanding of grain and biomass yield with good quality for sorghum grain and yield is essential to breeding and cultivation of sorghum to produce sorghum grain and forage for livestock. Sorghum has recently been viewed as the ideal candidate feedstock crops for generation of both forage and fuel in the form of bioethanol in addition to its grain production. This crop has low input requirements and particularly well-adapted to marginal growth conditions such as water deficits, salinity, alkalinity, and other constraints which are came up of strange for other crops. The analysis of variance for yield and yield component traits revealed that the parents and their hybrids involved in this study differed significantly for all the characters. The mean square values of grain yield and yield component traits of parent (females and males) and their hybrids are presented in Table 1.

All genotypes comprising parents, checks and hybrids are significantly different from each other for most traits except number of green leaves, total fresh weight and harvest index. Hybrids are significantly different for only for yield, head length, panicle width and number of productive tillers. Parents are significantly different for grain yield, plant height, head length, number of productive tiller and total dry biomass. Similarly, male lines are significantly different for grain yield, plant height, head length and number of productive tillers. The interaction of males and females is significantly different for grain yield, thousand seed weight ($p<0.05$), panicle width and number of productive tiller ($p<0.01$). Parents and Hybrids are significantly different for all traits except thousand grain weight, number of green leaves and panicle width. This revealed that hybrids can have better yield than OPVs.

Table 1:: Mean Squares for yield and Biomass component traits

SV	DF	GY	TSW	DTF	PHT	NGL	HL	PW	NPT	NH	TFW	TDBM	HI
Replications	1	0.0	48.2	139.2*	90.4	12.3**	144.7**	6.5**	0.6	26.3	34612.9	1860.7	32.7
Blocks (Rep)	8	0.0	14.5	66.8*	873.1*	0.6	16.7**	5.8**	0.5	29.2	154892.7	37305.7	31.1
Genotypes(G)	109	1.9**	22.8*	43.1**	1486.6**	1.2	23.6**	0.6*	6.0**	176.7*	98402.9	32402.5**	48.7
Hybrids(H)	69	2.0**	20.9	35.0	1051.1	1.4	11.8**	0.7*	3.2**	144.0	93819.7	27901.7	36.5
Checks (C)	2	3.1*	35.5	144.8*	2988.8*	0.9	0.9	2.0	36.8**	32.2	157667.0	41249.0	43.9
Parents(P)	36	1.2**	21.6	41.1	1539.2**	0.8	14.2**	0.4	6.4**	219.6	61655.8	22513.7*	57.9
Females (FM)	1	13.6**	76116.5	282.9**	336.4	2.1	89.6**	2.4	3.2	773.2**	76116.5	7.6	238.9
Males(M)	34	1.3**	23.5	27.2	1317.6**	0.9	9.1*	0.4	6.6**	226.9	58157.8	20020.0	64.6
FM*M	34	1.6**	25.8*	37.5	405.7	9.5	5.8	1.6**	3.4**	85.4	114206.2	26301.7	31.3
FM vs M	1	0.9	2.3	370.9**	10873.0**	1.3	164.4**	0.0	1.5	229.5	266240.1*	127589.8**	5.3
H vs P	1	4.9*	12.2	220.0*	21892.2**	3.2	923.9**	1.0	54.9**	1318.1**	907729.3**	619938.2**	233.6*
H vs C	1	6.9**	60.4	0.0	6482.8**	0.8	1.0	2.4*	45.0**	0.8	313303.9	97600.0	56.5
P vs C	1	1.5	46.3	65.7	1582.0	0.2	139.9**	1.4	11.6	134.7	115383.5	1613.2	2.5
Error	101	0.05	16.3	28.3	362.0	1.0	4.4	0.5	0.6	115.6	82710.0	19779.0	39.0
Total	219												

Magnitude of heterosis and hybrid performance for biomass and yield related traits

Magnitude of heterosis showed as for yield and biomass component traits was varied from traits to traits as well as from genotype to genotype. For the case of MPH for grain yield, it was ranged from 162.1 to -57.3 (%). The highest heterosis (162.1%) was recorded for hybrid 106 x 94 and the lowest MPH (-57.6 %) was recorded by 107 x 75. Among all hybrids 24 hybrids showed significant negative heterosis for grain yield and 14 hybrids were showed significantly positive heterosis. For better parent heterosis which was ranged from 111.1 to -66.1 (%) for hybrids 107 x 75 and 106 x 94 respectively, 20 hybrids showed that significant positive heterosis and 45 of hybrid exhibited negatively significant heterosis. 29 hybrids have negative significant heterosis from the standard check one (ESH-1) and 29 hybrids exhibited significant positive heterosis from the same standard check. regarding to standard heterosis from check two (ESH-4) 68 of hybrids showed positive significant heterosis and the rest 2 hybrids were showed none significant positive heterosis. In the case of standard heterosis in consider of standard check three (2005MI5064) only 2 hybrids showed none significant negative heterosis and 65 of them exhibited significant positive heterosis. In this case, since standard check 3 is an OPV we can look the yield advantage of hybrids over an OPVs is much better Table 2.

In the case of total fresh weight of biomass, the magnitude of mid parent heterosis was ranged from 233.2 for 107 x 93 to -37.2 % for hybrid combinations of 107 x 82. Similarly, better parent heterosis was ranged from 206.8 % to -57.9 % for hybrid combination of 107 x 93 and 107 x 82 respectively. The hybrid combination 107 × 84 (134.7%) showed the higher magnitude of significant and positive heterobeltiosis (Better parent heterosis) for total dry biomass weight. Hybrid of 107 x 105 showed highest significant positive standard heterosis over checks 109.3 (ESH-1), 181.1 (ESH-4) and 106.5 (2005MI5064).

Table 2: Magnitude of heterosis

Line	Tester	GY			PHT			DTF			NPT			TFW			TDBM		
		MPH	BPH	BCH	MPH	BPH	BCH	MPH	BPH	BCH	MPH	BPH	BCH	MPH	BPH	BCH	MPH	BPH	BCH
106	71	-36.4**	-48.1**	-45.1**	35.7**	17.1ns	7ns	6.3ns	0.6ns	-3ns	-100**	-100**	-100**	24.1**	-3.6**	13.5ns	60.8**	42**	19.5ns
106	72	43.6**	41.1**	54.9**	35.4**	10.9ns	15.3ns	2.4ns	1.4ns	-10.8*	100ns	0ns	-80**	40.9**	6.4**	35.9ns	10.1**	-12.5**	-4.3ns
106	73	-39.7**	-52.2**	-13.7ns	20.8ns	-2ns	4.6ns	1.4ns	0ns	-11.4*	11.1ns	0ns	-75**	34.7**	-5**	50.8ns	17.9**	-15.6**	25.8ns
106	74	35.9**	-1.9ns	3.9ns	61.6**	39.5**	27.5*	-3.3ns	-7.6ns	-12.7*	-11.1ns	-20ns	-80**	20.2**	-0.5**	-1.1ns	5.6**	-12.2**	-14.7ns
106	75	-24.1**	-38.9**	-35.3**	21.5ns	10.1ns	-10.1ns	3ns	-2.5ns	-6ns	-20ns	-45.5**	-70**	106.1**	85.6**	51ns	134.7**	109.8**	71.8*
106	76	23.1**	18.5**	25.5**	15.6ns	-15.5ns	21.4ns	3.7ns	0.7ns	-7.8ns	81.8**	42.9ns	-50**	48.2**	1.2**	80.5ns	48.1**	5.5**	60.1ns
106	77	-18.6**	-35.2**	-31.4**	34.7*	20.3ns	1.5ns	2ns	-3.1ns	-7.2ns	-11.1ns	-42.9**	-60**	87.5**	68**	38.3ns	84**	77.7**	23.1ns
106	78	81.4**	63**	72.5**	38.2**	11.2ns	21.1ns	3.2ns	0ns	-13.9*	-25ns	-25ns	-85**	112.1**	70.3**	83.2ns	54.6**	19.7**	40.5ns
106	79	2ns	-5.6ns	0ns	13.8ns	-9.9ns	2.4ns	5.6ns	0ns	-3.6ns	-50*	-62.5**	-85**	8**	-23.4**	19.4ns	22.5**	-4.6**	10.4ns
106	80	43.7**	-5.6ns	0ns	35.3*	30.3ns	-6.7ns	-11.7ns	-15.4*	-20.5**	-28.6ns	-50**	-75**	36.3**	31.6**	-7.9ns	26.1**	23.6**	-17ns
106	81	10.7**	-13.5**	62.7**	16.9ns	-13.9ns	20.8ns	-1.7ns	-4ns	-13.3*	-100**	-100**	-100**	39.7**	5.8**	33.9ns	47.4**	11.7**	39.5ns
106	82	1.6ns	-10*	23.5*	44.4**	13ns	32.7**	-2.9ns	-4.9ns	-18.1**	-9.1ns	-28.6ns	-75**	17.8**	-18.7**	39.6ns	18.8**	-14.2**	24.4ns
106	83	-5.2ns	-14.8*	-9.8ns	35.2**	12.6ns	12.2ns	-7ns	-10.9ns	-16.3**	-33.3ns	-40ns	-85**	43.2**	9.8**	34.1ns	45.4**	15.6**	26.4ns
106	84	-1.1ns	-16.7**	-11.8ns	34.3**	2.7ns	28.7**	-1ns	-7.3ns	-8.4ns	-33.3ns	-54.5**	-75**	66.5**	56.4**	16ns	97.7**	87.3**	35ns
106	85	4.3ns	-3.2ns	19.6*	34.1**	7.2ns	19ns	-2.5ns	-2.8ns	-16.3**	-11.1ns	-20ns	-80**	76.8**	42.2**	52.4ns	25.4**	-11.6**	39ns
106	86	58.6**	27.8**	35.3**	39.3**	22.3ns	7.3ns	-10.6ns	-14.7ns	-26.5**	125**	125**	-55**	157.2**	105.8**	123.6*	107.8**	71.5**	70*
106	87	109.1**	70.4**	80.4**	45.6**	26.5*	13.8ns	-5.8ns	-12.6ns	-12*	27.3ns	0ns	-65**	229.1**	206.8**	131.4*	158.2**	130.3**	89.4**
106	88	6.7ns	-3ns	25.5**	34.2**	14.7ns	7.3ns	5.8ns	3.3ns	-6.6ns	-40ns	-50ns	-85**	-1.1**	-29.1**	6.4ns	23.3**	0.1ns	3.4ns
106	89	34.7**	25.9**	33.3**	60.3**	35**	30.9**	-4.2ns	-4.8ns	-16.9**	50ns	50ns	-70**	85.6**	42.4**	73.6ns	93.9**	58.3**	61.3ns
106	90	80.5**	37**	45.1**	45.9**	21.5ns	21.1ns	-12*	-18.1**	-18.1**	-77.8*	-80*	-95**	85**	46.6**	63.4ns	109.9**	105**	38.7ns
106	91	27**	-13*	-7.8ns	44.2**	19.3ns	20.8ns	-10.2ns	-15.4*	-17.5**	40ns	16.7ns	-65**	60.3**	29.6**	37ns	93**	77.7**	36.2ns
106	92	30.5**	20.3**	51**	30.8**	4.4ns	16.2ns	-7.6ns	-8.8ns	-19.3**	-45.5ns	-57.1*	-85**	-7.1**	-40.5**	38ns	5**	-27.3**	21.8ns
106	93	50.5**	29.6**	37.3**	33.5*	21.6ns	-1.8ns	-1.3ns	-7.4ns	-9ns	-26.3ns	-53.3**	-65**	86.7**	63.6**	41.8ns	93.6**	68.1**	47.2ns
106	94	162.1**	111.1**	123.5**	55.8**	32.1**	26*	-12.2*	-16.9*	-19.9**	-41.2*	-61.5**	-75**	129.9**	117.1**	59.3ns	116.2**	99.4**	52.2ns
106	95	48.3**	38.7**	68.6**	47.2**	18.1ns	29.7**	-3.8ns	-5.4ns	-15.7**	25ns	25ns	-75**	22**	-8.2**	18.4ns	31.7**	-2.1**	29.8ns
106	96	-9.9*	-23.4**	15.7ns	19.9ns	0ns	-0.6ns	-2.4ns	-4.7ns	-13.9*	-23.8ns	-52.9**	-60**	40.1**	6.7**	32.9ns	34.3**	2**	26.5ns
106	97	45.5**	42.9**	56.9**	34.2**	16.7ns	4.9ns	-4.1ns	-5.4ns	-16.3**	0ns	-16.7ns	-75**	40.2**	12.1**	21.9ns	33.6**	10.1**	9.6ns
106	98	34.9**	3.7ns	9.8ns	35.5**	10.1ns	16.8ns	-9.8ns	-12.5ns	-19.9**	-11.1ns	-20ns	-80**	56.5**	38.1**	17.7ns	39.1**	21.3**	5.1ns
106	99	-34.5**	-35.7**	-29.4**	36.8**	9ns	21.7*	5ns	3.5ns	-10.8*	-100*	-100*	-100**	-2.9**	-31**	6.6ns	-0.7**	-26.8**	-0.6ns
106	100	-22.9**	-31.5**	-27.5**	31.4**	2.9ns	20.8ns	-0.3ns	-3.3ns	-11.4*	-14.3ns	-25ns	-85**	34.3**	2**	28.3ns	62.4**	39.3**	25.5ns
106	101	5.3ns	-7.4ns	-2ns	29**	-1.5ns	23.9*	-7.9ns	-12.6ns	-16.3**	-25ns	-25ns	-85**	59.4**	22.2**	49.4ns	70.5**	38.2**	43.4ns
106	102	34.5**	32.1**	45.1**	45.8**	33.1*	7ns	-9.1ns	-12.3ns	-18.7**	-9.1ns	-28.6ns	-75**	129.2**	104.6**	69.8ns	94.8**	67.9**	49.5ns
106	103	15.3*	-9.3ns	-3.9ns	54.5**	47.1**	8ns	-1.3ns	-7.9ns	-8.4ns	-47.4**	-66.7**	-75**	26.6**	-4.7**	23.1ns	42.6**	21.2**	11.6ns
106	104	-39.5**	-44.6**	-29.4**	34**	8.2ns	16.8ns	1ns	-2.6ns	-9.6ns	50ns	50ns	-70**	-27.5**	-48.9**	-18.9ns	7.8**	-15.8**	-3.6ns
106	105	22.9**	-20.4**	-15.7ns	55.1**	29.8*	27.8*	-5.8ns	-12.6ns	-12*	125**	125**	-55**	0.6**	-22.9**	-5.7ns	38.3**	14.6**	12.5ns
107	71	-8.9ns	-26.8**	-19.6*	59.8**	33.1*	21.7*	-0.7ns	-13.1ns	-16.3**	100**	80*	-55**	22.2**	-8.5**	7.7ns	41.9**	17.1**	-1.4ns
107	72	-26.8**	-26.8**	-19.6*	41.4**	12.1ns	16.5ns	0ns	-8.9ns	-19.9**	50ns	-25ns	-85**	33.6**	-2.6**	24.4ns	1.5**	-23.8**	-16.7ns
107	73	-51.4**	-60.9**	-29.4**	-2.9ns	-23.8*	-18.7ns	11.6ns	1.4ns	-10.2ns	-55.6ns	-60ns	-90**	79.4**	22.8**	94.9ns	67.3**	14.3**	70.4*
107	74	-42.5**	-58.9**	-54.9**	58.6**	32.1*	20.8ns	4.7ns	-7.6ns	-12.7*	11.1ns	0ns	-75**	75.8**	39.7**	38.9ns	20.3**	-6**	-8.6ns
107	75	-57.3**	-66.1**	-62.7**	14.6ns	0ns	-18.3ns	7.9ns	-5.6ns	-9ns	-100**	-100**	-100**	51.9**	30.7**	6.3ns	49.8**	24.9**	2.3ns
107	76	-52.8**	-55.4**	-51**	-1.6ns	-30**	0.6ns	18.4**	5.9ns	-3ns	-9.1ns	-28.6ns	-75**	-2.5**	-35.2**	15.5ns	2.7**	-30.2**	6.1ns
107	77	-29.5**	-44.6**	-39.2**	55.8**	34.1*	13.1ns	5.4ns	-7.5ns	-11.4*	-77.8**	-85.7**	-90**	73.3**	48.4**	22.1ns	114.5**	92**	32.9ns
107	78	-49.5**	-55.4**	-51**	17.1ns	-8.7ns	-0.6ns	24.4**	17.9*	-4.8ns	0ns	0ns	-80**	22.6**	-5.3**	1.9ns	30.5**	-4.3**	12.3ns
107	79	11.8*	1.8ns	11.8ns	30.6**	0.3ns	14.1ns	10ns	-3.8ns	-7.2ns	-50*	-62.5**	-85**	39.2**	-4.3**	49.2ns	78**	31.1**	51.8ns
107	80	-4.1ns	-37.5**	-31.4**	38.6*	28.2ns	-8.3ns	-0.7ns	-12.2ns	-17.5**	-57.1**	-70**	-85**	42.1**	30.5**	-8.7ns	35.5**	23**	-17.4ns
107	81	1.3ns	-19.8**	51**	22.2*	-12.4ns	22.9*	11.1ns	0ns	-9.6ns	0ns	-16.7ns	-75**	83.8**	34.5**	70.1ns	61.3**	16**	44.9ns
107	82	-42.9**	-48.6**	-29.4**	43.1**	8.6ns	27.5*	8.9ns	2.2ns	-15.7**	-45.5ns	-57.1*	-85**	-37.2**	-57.9**	-27.7ns	-31.1**	-52.6**	-31.2ns
107	83	-53.5**	-58.9**	-54.9**	30.3*	4.9ns	4.6ns	16.7*	3.2ns	-3ns	55.6ns	40ns	-65**	-5.9**	-30.4**	-15ns	-0.5**	-25.3**	-18.3ns
107	84	-11.8ns	-26.8**	-19.6*	47.8**	9.8ns	37.6**	6.3ns	-7.9ns	-9ns	-33.3ns	-54.5**	-75**	117.9**	94.9**	44.6ns	166.8**	134.7**	69.1*
107	85	-52.9**	-55.6**	-45.1**	34.5**	4.1ns	15.6ns	22.9**	13.4ns	-3ns	-55.6ns	-60ns	-90**	56.3**	20.9**	29.5ns	2.3**	-31.1**	8.4ns
107	86	-16.9**	-33.9**	-27.5**	23.5ns	4.5ns	-8.3ns	24.8**	20*	-6ns	75*	75ns	-65**	82.5**	40.4**	52.6ns	80.6**	40.1**	38.9ns
107	87	71.1**	37.5**	51**	55.8**	30.6*	17.4ns	2.4ns	-12ns	-11.4*	-100**	-100**	-100**	188.3**	156.1**	93.2ns	129.7**	91.2**	57.3ns
107	88	-47.5**	-51.5**	-37.3**	52.1**	25.5*	17.4ns	6.7ns	-4ns	-13.3*	-40ns	-50ns	-85**	18.2**	-17.8**	23.3ns	16.4**	-10.9**	-8ns
107	89	-6.8ns	-14.3*	-5.9ns	54.3**	25.6*	21.7*	10.9ns	1.4ns	-11.4*	-100**	-100*	-100**	75.9**	30.2**	58.7ns	77.6**	36.5**	39ns
107	90	23.8**	-7.1ns	2ns	62.3**	30.7**	30.3**	4.2ns	-10.2ns	-10.2ns	11.1ns	0ns	-75**	43**	9.1**	21.6ns	133.4**	111.1**	42.8ns
107	91	0ns	-32.1**	-25.5**	32.1*	5.7ns	7ns	9.2ns	-4.9ns	-7.2ns	-60*	-66.7*	-90**	32.4**	2.9**	8.8ns	86.2**	59.6**	22.3ns
107	92	48.3**	39.1**	74.5**	60.2**	23.9*	37.9**	1.1ns	-8.2ns	-18.7**	-9.1ns	-28.6ns	-75**	75**	9.6**	154.1**	43.9**	-4.6**	59.8ns
107	93	38.9**	17.9**	29.4**	42.5**	25ns	0.9ns	-1.1ns	-14.1*	-15.7**	-57.9**	-73.3**	-80**	233.2**	179.2**	142**	156**	108**	82.1**
107	94	46.1**	16.1**	27.5**	60.5**	31.4*	25.4*	10ns	-3.8ns	-7.2ns	-17.6ns	-46.2**	-65**	195.9**	166**	95.2ns	153.8**	117.9**	66.3*
107	95	-42.4**	-45.2**	-33.3**	43.7**	11.7ns	22.6*	17.9*	6.8ns	-4.8ns	-25ns	-25ns	-85**	38.6**	0.8**	30ns	37.6**	-2.8**	28.9ns
107	96	21.8**	5.2ns	58.8**	7.6ns	-13.2ns	-13.8ns	8.1ns	-2.7ns	-12*	-14.3ns	-47.1**	-55**	138.9**	75.7**	118.7*	79.7**	29.5**	60.6ns
107	97	3.6ns	3.6ns	13.7ns	33.1*	11.6ns	0.3ns	14.6*	4.1ns	-7.8ns	-20ns	-33.3ns	-80**	83.4**	41.1**	53.4ns	62.5**	25.9**	25.4ns
107	98	-15.3*	-35.7**	-29.4**	52**	19.6ns	26.9*	13.2ns	1.3ns	-7.2ns	-11.1ns	-20ns	-80**	36.4**	15.1**	-1.9ns	68.7**	37.6**	19.2ns
107	99	42.9**	42.9**	56.9**	47.2**	13.7ns	26.9*	10.4ns	2.9ns	-13.9*	-100*	-100*	-100**	39.3**	-3.9**	48.3ns	35.5**	-5**	29ns
107	100	-22.4**	-32.1**	-25.5**	22.8*	-6.8ns	9.5ns	16.9*	4.6ns	-4.2ns	-100*	-100*	-100**	75.7**	28.7**	62ns	86.3**	49.8**	34.9ns
107	101	-5.2ns	-17.9**	-9.8ns	24.6*	-7.5ns	16.2ns	10.4ns	-3.1ns	-7.2ns	100**	100*	-60**	40.9**	4.3**	27.4ns	53.1**	16.9**	21.4ns
107	102	-28.6**	-28.6**	-21.6*	20.3ns	5.7ns	-15ns	11.7ns	-0.6ns	-7.8ns	-27.3ns	-42.9ns	-80**	97.7**	68.6**	39.9ns	78.2**	43.9**	28.1ns
107	103	21.8**	-5.4ns	3.9ns	53.1**	40*	2.8ns	8.1ns	-6.7ns	-7.2ns	-36.8*	-60**	-70**	-1**	-28**	-7ns	25**	-0.4*	-8.2ns
107	104	35.5**	26.2**	60.8**	39.9**	9.3ns	18ns	10.2ns	-1.9ns	-9ns	175**	175**	-45**	80.5**	23.5**	96ns	83.1**	35.3**	54.8ns
107	105	116.7**	39.3**	52.9**	95.8**	58.4**	56**	0.3ns	-13.8*	-13.3*	25ns	25ns	-75**	201.2**	122.7**	172.4**	170**	110.2**	106.5**

Combining ability analysis for grain yield and Biomass related traits

From the Table 3 analysis of variances for combining ability analysis showed that except days to flowering and total fresh biomass weight are significantly different for all traits of genotypes.

Table 3:ANOVA for combining ability of the studied traits

SV	Df	DTF	PHT	NGL	HL	PW	NPT	TSW	GY	TDBM	TFW	HI
Replications	1	139.2*	90.4	12.3**	144.7**	6.5**	0.6	48.2	0.0	1860.7	34612.9	376.0
Genotypes	106	46.6	1621.2**	1.3*	23.9**	1.2*	5.7**	25.8**	2.1**	41522.2**	116903.9	60864.7**
Parents (P)	36	56.9**	1842.7**	0.8	21.2**	0.9	8.0**	31.9**	1.9**	33749.1*	89896.7	70142.4**
P vs H	1	325.5**	29384.8**	5.6**	895.9**	4.5*	83.2**	33.2	8.3**	789155.7**	1359223.6**	29619.8
Hybrids(H)	69	37.1	1100.0**	1.6**	12.7*	1.3*	3.4**	22.4*	2.2**	34855.1**	113381.4	56342.5**
Females (FM)	1	282.9**	336.4	2.1	89.6**	2.4	3.2	3.2	13.6**	7.6	76116.5	470600.5**
Males(M)	34	29.4	1816.8**	1.9	17.4**	0.9	3.5	19.6	2.4	44433.4	113652.7	60037.8
FM X M	34	37.5	405.7	1.2	5.8	1.6**	3.4**	25.8*	1.6**	26301.7	114206.2	40463.2**
Error	111	34.4	419.8	1.0	8.2	0.9	1.3	16.1	0.1	20857.0	86913.1	18637.1
Total	219											

Mean squares due to Females were significant different for only DTF, HL, GY, NH and HI. Mean square due to Male lines are also significantly different for traits only PHT, HL and NH. Whereas Hybrids (interaction of Males x Females) PW, NPT, GY and HI were also significant ($P<0.01$ or $P<0.05$). Similarly, Parents and Hybrids are significantly different from each other for all measured traits except HI.

Table 4: Proportional contribution of Females, Males and their interactions to total variance

SV	DTF	PHT	HE	NGL	CHL	HL	PW	NPT	TSW	GY	TDBM	TFW	HI
Females	11.1	0.4	0.8	1.9	0.2	10.2	2.8	1.3	0.2	9.2	0.0	0.4	12.1
Males	39.1	81.4	57.4	61.2	55.7	67.3	35.6	49.8	43.0	54.2	62.8	50.0	52.5
FM x M	49.8	18.2	41.7	36.9	44.1	22.6	61.7	48.9	56.8	36.6	37.2	49.7	35.4

The total variance is a contribution of genotype as in their interaction. In this case, Females and Males including their interaction have its own contribution for the total variance in combining ability analysis. So, the highest contribution is due to males for GY and the contribution of Females for the total variance due to TDBM is null and 0.4 for TFW. Means that Male lines are responsible for the increment of variations for all traits and female lines were less in their biomass. Similarly, the second higher contribution is due to the interaction of males and female lines for TFW. The variance for TFW is almost equally contributed by both Male lines and the interaction of Males and Females (Table 4). We can conclude that Male parents are more likely important to increase grain yield and total dry biomass simultaneously.

General and Specific combining ability effects of yield and Biomass component traits

Both female lines showed that highly significant general combining ability (GCA) effect for traits of grain yield, head length and total fresh biomass weight at probability level of ($p<0.01$). Since, female lines are two the magnitude of GCA effects are equal and the only difference is direction of magnitude. That is one female line will be positive and the other female line will be negative (Table 5 and Table 6). Both female lines exhibited significant GCA effect at $p<0.05$ probability level and female line 106 was negative and female 107 showed positive GCA effects. This means, female line 106 was flowered earlier than female 107.

All male lines exhibited highly significant GCA effects except male line 79 for Grain yield. Among these male lines 18 of them showed highly significant negative GCA effects and 16 of them showed positive significant GCA effects for GY. Male line 81, 87, 92 and 94 exhibited positive highly significant magnitude GCA effects of 1.31, 1.53, 1.46 and 1.78 respectively. Male lines 71, 74, 75, 77 and 83 exhibited negative significant GCA effects with magnitude of -0.97, -0.8, -1.4, -1.05 and -0.97 respectively. Based on this situation male lines 81, 87, 92 and 94 can be selected for good positive combiner for varietal development. Generally, 16 male parents are highly significant ($p<0.01$) positive combiner and the rest 18 males are highly significant negative combiner for Grain yield. In this case positive GCA effects are selectable to increase grain yield and those which exhibited highly significant positive GCA effect can be go further for varietal development based on the magnitude of their GCA effects.

For Plant height male lines 73 (-33.7), 75(-48.6), 80(-33.4), 86(-24.5), 93(-25.9), 96(-33.1) and 102(-27.6) showed that highly significant negative GCA effect. Contrarily, 12 male lines exhibited highly significant positive GCA effects. These are male line 74 (15), 81(15.9), 82(23.4), 84(27.4), 89(17.2), 90(16.5), 92(21.7), 94(16.9), 95(21.0), 98(15.8), 99(16.8) and 105(47.6). Male line 94 exhibited positive highly significant GCA effect for Plant height and also it has highly significant positive GCA effect for GY. So, male line 94 can be selected for both high plant height and GY as a good combiner male parent. In general, 17 male lines are good combiner based on their GCA magnitude for increasing plant height (Table 5).

In the case of total fresh biomass weight, among all male lines 8 male lines exhibited positive significant GCA effect and 7 male lines showed significant negative GCA effects. The rest 20 males have explored none significant GCA effects. Male line 94 exhibited highest significant positive GCA effect valued 380.1 ($p<0.01$) followed by male lines 99 (306.2), 93 (270.4), 73 (267.5), 79 (220.2), 100(183.5), 81(178.30 and 102 (170.8).

For the trait total dry biomass weight (TDBM), 8 males exhibited positive significant GCA effect and 9 male lines showed negative significant GCA effect. Male line 94 exhibited highest GCA effect (192.9) followed by male lines 73 (159.3), 100(134.2), 79(126.9) and 93(116.2).

Male line 94 exhibited positive highly significant GCA effect for PHT, GY, total dry biomass weight (TDBM) and total fresh biomass weight (TFW). This implies male line 94 can be select to improve Biomass contest and GY as the same time and also male line 94 can be select to develop dual purpose varieties. All male and female parents showed none significant general combining ability (GCA) effects.

Table 5: GCA effects of GY and Biomass components for Male and Female lines

Parent (FM/M)	GY	TSW	DTF	PHT	NGL	HL	PW	NPT	NH	TFW	TDBM	HI
Female												
106	0.31**	0.15ns	-1.38*	1.5ns	0.12ns	-0.89**	-0.16*	0.15ns	2.35ns	-23.2**	0.5ns	1.3ns
107	-0.31**	-0.15ns	1.48*	-2.24ns	-0.12ns	0.86**	0.07ns	-0.15ns	-2.35ns	22.5**	-1.7ns	-1.3ns
SE	0.02	0.48	0.64	2.27	0.12	0.25	0.08	0.1	1.28	4.2	2.1	1.9
Male												
71	-0.97**	-1.11*	0.99ns	5.37*	-0.51**	2.19**	-0.29**	0.03ns	-5.36**	-179.9*	-85.7*	-1.3ns
72	0.31**	1.64**	-3.06**	1.34ns	-0.76**	-0.17ns	-0.49**	-0.47**	7.64**	-202.1**	-146.8**	2.5ns
73	-0.7**	0.52ns	0.46ns	-33.65**	0.49**	-0.54*	0.16ns	-0.47**	-10.36**	267.5**	159.3**	5.9ns
74	-0.8**	2.14**	-0.94ns	14.97**	-1.76**	1.32**	-0.26**	0.03ns	5.39**	24ns	9.1ns	0.5ns
75	-1.4**	-1.48**	4.97**	-48.63**	0.24*	4.2**	-0.1ns	-0.72**	-13.11**	-21.8ns	19ns	-2ns
76	-0.47**	-0.11ns	4.68**	-4ns	0.49**	-0.38ns	0.51**	1.53**	-2.86*	60.1ns	34ns	1ns
77	-1.05**	-2.36**	1.56*	-8.89**	-0.51**	2.15**	-0.36**	0.28**	-7.36**	-191.4*	-120.8**	-1.7ns
78	0.13**	-1.11*	2.72**	-10.58**	-0.26*	0.44ns	-0.77**	-0.47**	0.39ns	-11.6ns	-14.7ns	1ns
79	0ns	-2.11**	4.98**	-8.1**	0.74**	0.11ns	-0.14ns	-0.72**	0.89ns	220.2**	126.9**	0.1ns
80	-0.55**	0.39ns	-6.3**	-33.35**	-1.01**	2.33**	-0.71**	-0.22*	6.39**	-64.9ns	-175.1**	-5ns
81	1.31**	2.27**	-0.26ns	15.86**	0.74**	-1.93**	0.54**	-0.97**	16.14**	178.3*	94.3*	1.1ns
82	-0.22**	2.64**	-4.36**	23.36**	-1.01**	0.32ns	-0.76**	-0.22*	-0.11ns	-124.3ns	-183.6**	-3.5ns
83	-0.97**	-2.48**	1.42*	-10.57**	-0.51**	-0.48ns	-0.09ns	0.28**	-2.61*	-107ns	20.2ns	2.6ns
84	-0.54**	-2.48**	3.19**	27.42**	-0.01ns	-0.4ns	0.4**	0.28**	1.14ns	34.3ns	28ns	0ns
85	-0.47**	0.89ns	2.07**	6.37**	-0.01ns	-1.23**	-0.45**	-0.72**	0.89ns	-68.8ns	-4ns	1.3ns
86	-0.05*	3.39**	-3.91**	-24.46**	-0.01ns	-2.09**	0.39**	1.78**	-6.36**	-16.9ns	-13.5ns	-5.2ns
87	1.53**	1.52**	0.29ns	4.12ns	0.49**	-3.11**	0.87**	-0.47**	3.89**	-39.4ns	18.7ns	-3.2ns
88	-0.3**	-1.86**	1.2ns	-1.77ns	-1.01**	2.44**	-0.56**	-0.72**	-6.86**	-285.9**	-210.2**	0.2ns
89	0.2**	3.89**	-1.15ns	17.15**	0.74**	-1.49**	-1.09**	-0.72**	-0.86ns	74ns	63.9ns	2.8ns
90	0.46**	0.02ns	-2.08**	16.53**	0.24*	0.17ns	0.09ns	-0.72**	0.89ns	-181.3*	-113.8**	-4.5ns
91	-0.57**	-2.86**	-1.1ns	0.19ns	-0.26*	-1.03**	0.1ns	0.03ns	-2.86*	-89.5ns	98.7**	0.7ns

Parent (FM/M)	GY	TSW	DTF	PHT	NGL	HL	PW	NPT	NH	TFW	TDBM	HI
Female												
92	1.46**	3.02**	-6.6**	21.69**	0.74**	-0.21ns	0.25**	-0.22*	4.39**	-26.1ns	-29.9ns	4ns
93	0.71**	2.27**	0.17ns	-25.89**	1.74**	4.9**	0.83**	0.53**	-4.11**	270.4**	116.2**	0.2ns
94	1.78**	4.02**	-0.83ns	16.86**	-0.51**	-2.03**	-0.35**	0.78**	15.89**	380.1**	192.9**	3.1ns
95	0.3**	-0.61ns	1.65*	20.98**	0.24*	-2.52**	0.28**	-0.22*	-0.36ns	-150.9*	-144.5**	-7.5ns
96	0.81**	-2.23**	-0.71ns	-33.13**	0.74**	1.54**	0.05ns	2.03**	-3.86**	125.9ns	100.9**	5.2ns
97	0.76**	0.14ns	-0.67ns	-19.01**	0.49**	0.73**	0.48**	0.03ns	-1.61ns	7.8ns	66ns	-0.7ns
98	-0.4**	-1.36**	-2.13**	15.8**	-0.76**	-0.46ns	-0.07ns	-0.22*	0.14ns	-112.9ns	7.1ns	-1.1ns
99	0.21**	0.52ns	0.01ns	16.8**	0.24*	-3.48**	-0.13ns	-2.22**	1.89ns	306.2**	60.4ns	2.2ns
100	-0.82**	-0.86ns	2.54**	6.31**	0.24*	-2.08**	-0.04ns	-1.47**	-8.36**	183.5*	134.2**	5.4ns
101	-0.29**	-1.61**	-0.26ns	7.98**	0.74**	-1.61**	-0.19*	0.53**	-2.86*	-115.7ns	2.5ns	1.2ns
102	0.16**	3.27**	-0.89ns	-27.64**	-0.51**	2.72**	0.15ns	0.03ns	-0.61ns	170.8*	55.5ns	-2.3ns
103	-0.15**	-3.98**	2.97**	-17.75**	0.24*	-2.6**	-0.17*	0.53**	-3.36*	-22.1ns	-38.5ns	-2.1ns
104	0.26**	-3.11**	1.63*	7.85**	-0.26*	1.91**	0.09ns	2.03**	5.39**	-196**	-69ns	0.6ns
105	0.33**	-0.86ns	-0.53ns	47.57**	-0.01ns	-0.05ns	0.18*	1.28**	12.39**	-106.2ns	-78.6*	-1.8ns
SE	0.05	0.47	0.5	1.98	0.12	0.36	0.19	0.19	1.3	73.7	36.1	34.1

Estimates of specific combining ability (SCA) effects for GY and other agronomic traits for all hybrids computed are presented in Table 23. SCA is used to designate deviations of certain crosses from expectations on the basis of the average performance (GCA effects) of the parents involved. In the current study, among seventy single cross hybrids that demonstrated significant and positive SCA effects for GY, cross combination of female line and male line of 106 x 78 (1.3), 107 x 99 (1.4), 107 x 104(1.5), 107 x 105(1.2) and 106 x 94 (1.0) had the highest SCA effect. Among all Crosses Female line 106 x Male line 94, which exhibited the highest GY mean, was among the top five crosses with highly significant and positive SCA effect of 1.0. These crosses contain parents (female line 106 and male line 94) with high GCA effects for GY, indicating the increased concentration of favorable alleles. On the other hand, Vasal et al. (1992) argued that positive SCA effects indicate that lines are in opposite heterotic groups while negative SCA effects indicate that lines are in the same heterotic group. For TSW, DTF, PHT, NGL, HL, HI and PW almost all except few crosses showed none significant SCA effects, indicating the ability of the crosses to produce single cross hybrids having increased performance of these traits is failed (Table 6).

A cross of female line 107 and male line 105 exhibited highest significant positive SCA effect valued as 458.8 for total fresh biomass weight (TFW). a cross of these parents showed higher GY mean performance, these parents can be selected for dual purpose hybrid production. That means, female line 107 and male line 105 exhibited reasonable GY mean and Highest positive significant SCA effect for TFW and this implies by crossing these two parents we can get reasonable GY and high Biomass product for feed and forage use. Across of these two parents also exhibited highly significant positive SCA effect for total dry biomass (TDBM) weight (Table 6).

Similarly, for trait of Number of productive tiller (NPT) which can contribute to improve both GY and Biomass contents, across of 107 x 71(2.4) exhibited high positive significant SCA effect followed by 106 x 87 (1.6). productive tillers have positive contribution for increasing grain yield as well as biomass content as the same time (Table 6).

Table 6: SCA effects of GY and biomass related traits

FM	Male	GY	TSW	DTF	PHT	HL	PW	NPT	NH	TFW	TDBM	HI
106	71	-0.64**	-4.9ns	7.06ns	-14.21ns	1.42ns	0.07ns	-2.4**	-6.6ns	45.7ns	56.4ns	-6.8ns
106	72	0.64**	-3.65ns	5.31ns	-3.21ns	1.17ns	-0.18ns	0.1ns	-8.1ns	62.1ns	36.6ns	-3.3ns
106	73	-0.11**	0.47ns	1.37ns	12.55ns	-2.06ns	0.37ns	0.6ns	-1.1ns	-107.8ns	-108.2ns	-1.1ns
106	74	0.44**	-1.65ns	1.48ns	5.05ns	-0.52ns	-0.15ns	-0.4ns	0.65ns	-84ns	-19ns	-0.5ns
106	75	0.04ns	1.47ns	2.52ns	6.19ns	0.14ns	0.96ns	1.35*	-7.35ns	154.4ns	151.6*	2.5ns
106	76	0.66**	0.6ns	-0.61ns	12.33ns	0.59ns	0.91ns	1.1ns	3.9ns	203.3ns	118.4ns	-0.3ns
106	77	-0.21**	-1.9ns	2.92ns	-7.95ns	-0.51ns	-0.06ns	1.35*	0.9ns	71.2ns	-21.3ns	-3.4ns
106	78	1.26**	3.85ns	-1.51ns	17.24ns	0.7ns	0.19ns	-0.4ns	-4.35ns	242.4ns	57.1ns	3.5ns
106	79	-0.46**	-0.4ns	2.57ns	-8.24ns	0.19ns	0.22ns	-0.15ns	1.15ns	-61.2ns	-90.2ns	-2.2ns
106	80	0.09**	-3.4ns	0.48ns	-3.52ns	0.31ns	0.19ns	0.35ns	-0.35ns	27ns	0.8ns	-2.6ns
106	81	-0.16**	-1.53ns	0.3ns	-6.83ns	0.58ns	0.54ns	-1.4*	-0.6ns	-81.8ns	-16.6ns	-2.9ns
106	82	0.36**	4.35ns	0.36ns	0.32ns	-0.86ns	0.63ns	0.35ns	0.15ns	205.2ns	131.1ns	6.2ns
106	83	0.26**	1.72ns	-4.02ns	5.12ns	-0.28ns	0.26ns	-1.15*	3.65ns	156.1ns	99.7ns	3.7ns
106	84	-0.21**	-1.03ns	0.66ns	-7.51ns	-0.05ns	-0.88ns	-0.15ns	3.4ns	-35.4ns	-63.4ns	-2.4ns
106	85	0.51**	1.1ns	-3.21ns	-1.79ns	-0.21ns	0.25ns	0.35ns	-2.85ns	62.8ns	49.7ns	3.2ns
106	86	0.49**	5.35ns	-7.19ns	11.01ns	-1.82ns	-0.36ns	0.35ns	10.9ns	217.5ns	70.7ns	2.6ns
106	87	0.06**	2.22ns	0.19ns	-0.96ns	-0.75ns	0.05ns	1.6**	4.65ns	155.9ns	87.8ns	2.5ns
106	88	0.49**	-3.4ns	3.63ns	-4.67ns	1.82ns	0.24ns	-0.15ns	-4.1ns	-17.6ns	24.5ns	-1.9ns
106	89	0.19**	1.85ns	-0.14ns	5.51ns	0.78ns	-0.1ns	1.35*	-1.1ns	44.5ns	38.6ns	1.6ns
106	90	0.24**	3.72ns	-2ns	-10.11ns	-0.4ns	-0.26ns	-1.15*	0.15ns	144.2ns	-1.6ns	0.7ns
106	91	-0.09**	1.85ns	-2.9ns	12.36ns	2.23ns	0.67ns	1.1ns	-2.1ns	106.6ns	34.2ns	4.4ns
106	92	-0.61**	-2.03ns	0.67ns	-13.49ns	-0.25ns	-0.13ns	-0.65ns	2.65ns	-306.6*	-88.3ns	-0.6ns
106	93	-0.21**	-2.03ns	5.04ns	-4.94ns	0.73ns	-0.57ns	0.6ns	-2.85ns	-279.3ns	-84.8ns	1.1ns
106	94	0.91**	0.47ns	-2.96ns	-2.19ns	0.66ns	0.46ns	-0.65ns	7.65ns	-95.1ns	-36.8ns	0.3ns
106	95	0.99**	0.35ns	-4.3ns	8.81ns	0.77ns	0.49ns	0.35ns	14.4ns	9.8ns	11.4ns	-1.8ns
106	96	-0.86**	0.97ns	-0.31ns	12.79ns	-0.4ns	-0.27ns	-0.4ns	-2.1ns	-199.5ns	-64.7ns	2.5ns
106	97	0.24**	-2.15ns	-1.91ns	-1.07ns	-3.35*	-0.61ns	0.1ns	-0.85ns	-63.7ns	-31.1ns	-1.4ns
106	98	0.19**	3.1ns	-3.87ns	-9.75ns	-1.19ns	0.34ns	-0.15ns	1.9ns	79.3ns	-33ns	0.5ns
106	99	-1.41**	-3.78ns	1.47ns	-0.64ns	0.42ns	-0.6ns	-0.15ns	-4.35ns	-73.2ns	-55.8ns	-1.8ns
106	100	-0.34**	-0.4ns	-1.41ns	5.62ns	-1.57ns	-0.24ns	0.6ns	-4.1ns	-85.4ns	-25.5ns	1.3ns

FM	Male	GY	TSW	DTF	PHT	HL	PW	NPT	NH	TFW	TDBM	HI
106	101	-0.21**	1.35ns	-2.06ns	5.15ns	-0.05ns	0.22ns	-1.4*	-0.6ns	90.9ns	50.3ns	-1.9ns
106	102	0.54**	1.47ns	-2.11ns	13.2ns	1.56ns	0.56ns	0.1ns	-0.85ns	94.9ns	34.9ns	4ns
106	103	-0.41**	0.47ns	1.03ns	0.93ns	0.26ns	-0.11ns	-0.4ns	-0.1ns	100.2ns	46.2ns	-1.5ns
106	104	-1.46**	-1.4ns	0.85ns	0.31ns	-0.12ns	-0.81ns	-1.4*	-0.35ns	-313.4*	-133.6ns	-2.4ns
106	105	-1.19**	-3.15ns	0.87ns	-20.52ns	0.5ns	-0.65ns	0.85ns	-1.35ns	-458.1**	-204.9**	-2ns
107	71	0.64**	4.9ns	-7.16ns	14.95ns	-1.39ns	0.02ns	2.4**	6.6ns	-45ns	-55.2ns	6.8ns
107	72	-0.64**	3.65ns	-5.41ns	3.95ns	-1.14ns	0.27ns	-0.1ns	8.1ns	-61.4ns	-35.4ns	3.3ns
107	73	0.11**	-0.48ns	-1.47ns	-11.81ns	2.09ns	-0.27ns	-0.6ns	1.1ns	108.5ns	109.4ns	1.1ns
107	74	-0.44**	1.65ns	-1.58ns	-4.32ns	0.54ns	0.25ns	0.4ns	-0.65ns	84.7ns	20.2ns	0.5ns
107	75	-0.04ns	-1.48ns	-2.62ns	-5.46ns	-0.11ns	-0.87ns	-1.35*	7.35ns	-153.7ns	-150.4*	-2.5ns
107	76	-0.66**	-0.6ns	0.51ns	-11.6ns	-0.56ns	-0.81ns	-1.1ns	-3.9ns	-202.6ns	-117.2ns	0.3ns
107	77	0.21**	1.9ns	-3.02ns	8.68ns	0.54ns	0.15ns	-1.35*	-0.9ns	-70.6ns	22.4ns	3.4ns
107	78	-1.26**	-3.85ns	1.41ns	-16.51ns	-0.67ns	-0.09ns	0.4ns	4.35ns	-241.7ns	-55.9ns	-3.5ns
107	79	0.46**	0.4ns	-2.66ns	8.98ns	-0.17ns	-0.13ns	0.15ns	-1.15ns	61.9ns	91.4ns	2.2ns
107	80	-0.09**	3.4ns	-0.58ns	4.25ns	-0.29ns	-0.1ns	-0.35ns	0.35ns	-26.3ns	0.4ns	2.6ns
107	81	0.16**	1.53ns	-0.4ns	7.57ns	-0.56ns	-0.45ns	1.4*	0.6ns	82.4ns	17.8ns	2.9ns
107	82	-0.36**	-4.35ns	-0.46ns	0.42ns	0.88ns	-0.54ns	-0.35ns	-0.15ns	-204.5ns	-129.9ns	-6.2ns
107	83	-0.26**	-1.73ns	3.92ns	-4.38ns	0.3ns	-0.17ns	1.15*	-3.65ns	-155.4ns	-98.5ns	-3.7ns
107	84	0.21**	1.03ns	-0.76ns	8.25ns	0.07ns	0.97*	0.15ns	-3.4ns	36.1ns	64.6ns	2.4ns
107	85	-0.51**	-1.1ns	3.11ns	2.53ns	0.23ns	-0.16ns	-0.35ns	2.85ns	-62.1ns	-48.5ns	-3.2ns
107	86	-0.49**	-5.35ns	7.09ns	-10.27ns	1.85ns	0.46ns	-0.35ns	-10.9ns	-216.8ns	-69.5ns	-2.6ns
107	87	-0.06**	-2.23ns	-0.29ns	1.7ns	0.78ns	0.04ns	-1.6**	-4.65ns	-155.2ns	-86.6ns	-2.5ns
107	88	-0.49**	3.4ns	-3.73ns	5.41ns	-1.79ns	-0.15ns	0.15ns	4.1ns	18.3ns	-23.3ns	1.9ns
107	89	-0.19**	-1.85ns	0.04ns	-4.78ns	-0.75ns	0.19ns	-1.35*	1.1ns	-43.8ns	-37.4ns	-1.6ns
107	90	-0.24**	-3.73ns	1.9ns	10.85ns	0.42ns	0.35ns	1.15*	-0.15ns	-143.6ns	2.8ns	-0.7ns
107	91	0.09**	-1.85ns	2.8ns	-11.62ns	-2.21ns	-0.57ns	-1.1ns	2.1ns	-105.9ns	-33ns	-4.4ns
107	92	0.61**	2.03ns	-0.77ns	14.23ns	0.27ns	0.23ns	0.65ns	-2.65ns	307.2*	89.5ns	0.6ns
107	93	0.21**	2.03ns	-5.14ns	5.68ns	-0.71ns	0.66ns	-0.6ns	2.85ns	279.9ns	86ns	-1.1ns
107	94	-0.91**	-0.48ns	2.86ns	2.93ns	-0.63ns	-0.36ns	0.65ns	-7.65ns	95.8ns	38ns	-0.3ns
107	95	-0.99**	-0.35ns	4.2ns	-8.07ns	-0.74ns	-0.4ns	-0.35ns	-14.4ns	-9.1ns	-10.2ns	1.8ns
107	96	0.86**	-0.98ns	0.21ns	-12.05ns	0.43ns	0.37ns	0.4ns	2.1ns	200.2ns	65.9ns	-2.5ns
107	97	-0.24**	2.15ns	1.81ns	1.81ns	3.38*	0.7ns	-0.1ns	0.85ns	64.4ns	32.3ns	1.4ns
107	98	-0.19**	-3.1ns	3.77ns	10.49ns	1.21ns	-0.25ns	0.15ns	-1.9ns	-78.6ns	34.2ns	-0.5ns
107	99	1.41**	3.78ns	-1.57ns	1.37ns	-0.4ns	0.69ns	0.15ns	4.35ns	73.8ns	57ns	1.8ns
107	100	0.34**	0.4ns	1.31ns	-4.88ns	1.6ns	0.33ns	-0.6ns	4.1ns	86.1ns	26.7ns	-1.3ns
107	101	0.21**	-1.35ns	1.96ns	-4.41ns	0.07ns	-0.12ns	1.4*	0.6ns	-90.2ns	-49.1ns	1.9ns
107	102	-0.54**	-1.48ns	2.01ns	-12.46ns	-1.53ns	-0.46ns	-0.1ns	0.85ns	-94.2ns	-33.7ns	-4ns
107	103	0.41**	-0.48ns	-1.13ns	-0.19ns	-0.23ns	0.21ns	0.4ns	0.1ns	-99.5ns	-45ns	1.5ns
107	104	1.46**	1.4ns	-0.95ns	0.42ns	0.14ns	0.91ns	1.4*	0.35ns	314.1*	134.8ns	2.4ns
107	105	1.19**	3.15ns	-0.97ns	21.25ns	-0.48ns	0.74ns	-0.85ns	1.35ns	458.8**	206.1**	2ns
SE		0.02	2.85	3.76	13.45	1.49	0.49	0.56	7.6	147.4	72.2	68.3

Genetic and Phenotypic correlation for GY and Biomass traits

Genetic correlation for many traits of GY and Biomass indicates that as there was a significant genetic correlation between traits and improving one trait can help to improve the other correlated traits as the same time. The correlation matrix showed that, GY was perfectly correlated with TFW and this may be disproved the fact that many works define as biomass was not positively correlate with GY. in similar way GY showed negatively strong correlation with DTF that indicates the earlier flowered Genotypes could exhibit higher GY. HI also strongly correlated with GY and this indicates that to improve HI of the given genotype can improve GY as the same time. GY was correlated strongly with NH, TSW, NGL, PW and PHT. Some findings indicate that GY was not positively correlate with PHT and other biomass componential traits. But the present study finds that GY was strongly correlated with PHT and Biomass component traits (Table 7).

TFW and TDBM strongly correlated with PW and improving genotypes for higher PW can improve genotypes for Biomass contents (TFW and TDBM) simultaneously.

Table 7: Genetic correlations for GY and Biomass component traits

Traits	GY	DTF	PHT	HL	PW	TSW	NH	NGL	TFW	TDBM
DTF	-0.76**									
PHT	0.41**	0.01**								
HL	-0.09ns	-0.5ns	-0.13**							
PW	0.59**	0.3**	0.54ns	-0.04**						
NPT	-0.07ns	0.57**	-0.32**	-0.25**	-0.42**					
TSW	0.81**	-0.35**	0.6ns	-0.13ns	0.13**					
NH	0.82**	0.2ns	0.13**	-0.42ns	-0.05ns	0.19**				
NGL	0.65**	0.86**	-0.51**	-0.22**	0.5ns	-1*	-0.27**			
TFW	1**	0.83**	0.73**	0.12**	1**	-0.15**	-1**	-0.59ns		
TDBM	0.75**	0.46**	0.62ns	0.2**	1**	-0.02**	-0.68ns	-0.13**	0.82**	
HI	0.79**	-0.49**	0.28**	0.08**	0.27**	0.22**	0.02**	-0.54ns	-0.11**	0.47**

Phenotypic correlation indicates that GY was Significant negatively correlated with DTF and this implies that genotypes that can flower earlier could have good yield as compared to genotypes that flower lately. In the other way GY was correlated positively with biomass component traits (PHT, TFW, TDBM and HI) and where strongly positively correlated with TFW and TDBM. PHT also showed positive significant correlation with TFW and TDBM. TFW shows positive strong correlation with TDBM. Panicle width also exhibited positive strong correlation with total fresh biomass weight and total dry biomass weight as well (Table 8).

Table 8:Phenotypic correlations of GY and Biomass component traits

Traits	GY	DTF	PHT	HL	PW	TSW	NH	NGL	TFW	TDBM
DTF	-0.44**									
PHT	0.38**	-0.16ns								
HL	-0.04ns	-0.24*	-0.1ns							
PW	0.39**	-0.05ns	0.27**	0.05ns						
NPT	-0.09ns	0.31**	-0.24*	-0.22*	-0.16ns					
TSW	0.49**	-0.5**	0.4**	-0.1ns	0.28**					
NH	0.53**	-0.33**	0.23*	-0.3**	0ns	0.34**				
NGL	0.33**	0.13ns	-0.15ns	-0.14ns	0.34**	0.05ns	0.05ns			
TFW	0.55**	-0.19ns	0.4**	0.05ns	0.57**	0.55**	0.01ns	0.32**		
TDBM	0.55**	-0.17ns	0.46**	0.09ns	0.57**	0.47**	0ns	0.31**	0.85**	
HI	0.42**	-0.46**	0.27**	0.02ns	0.3**	0.6**	0.29**	0.14ns	0.38**	0.53**

Summary and Conclusion

Analysis of variance for all genotypes showed that highly significant difference for all measured traits except number of green leaves, Total fresh biomass and harvest index and this revealed that as there was variability between genotypes. The F1 hybrids are significantly different only for yield, head length, panicle width and number of productive tillers whereas hybrid parents are significantly different for grain yield, plant height, head length, number of productive tiller and total dry biomass. There was a difference in magnitude of heterosis which showed for yield and biomass component traits that varied from traits to traits as well as from genotype to genotype. Similarly, there was yield advantage over the OPV check in yield and biomass production.

For total dry biomass weight, male line 94 exhibited highest GCA effect (192.9) followed by male lines 73 (159.3), 100(134.2), 79(126.9) and 93(116.2). Male line 94 exhibited highest significant positive GCA effect valued 380.1 (p<0.01) followed by male lines 99 (306.2), 93 (270.4), 73 (267.5), 79 (220.2), 100(183.5), 81(178.30 and 102 (170.8) for total fresh biomass weight. Male line 94 exhibited highly significant positive GCA effect for PHT, GY, total dry biomass weight (TDBM) and total fresh biomass weight (TFW). This implies male line 94 can be select to improve forage and grain yield as the same time and it could be select to develop dual purpose varieties.

Information stating the degree of association between traits could serve for the simultaneous improvement of those traits. In specific in the improvement of quantitative traits such as drought tolerance, it is suggested to use secondary traits that have higher heritability. The correlation between and among the various yield and other agronomic traits and the biomass components was strong and significant while some others have weak association. Among the studied traits, grain yield and biomass component traits were significantly and positively correlated each other. That means GY, PHT, DTF, PW and HL were found significantly and positively correlated with biomass yield related traits (TFW, TDBM and HI).

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