

Studies on Breeding for Improving Sweet Sorghum Yield

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ABSTRACT

Sorghum bicolor L. Moench, also known as sweet sorghum, is a sugar-based biofuel crop that grows in tropical climates. Although the majority of sweet sorghum cultivars are open-pollinated, hybrids may provide yield and seed production benefits. The study was to look at the performance of F1 sweet sorghum hybrids and their parents, as well as their agronomic traits, heterosis, heritability, inbreeding depression, and genetic advancement. GR Coba, AG SC2, AG SC3, and Brandes were used in this study as parents of sweet sorghum crosses. The mean Performance of all morphological traits including (stalk weight and stripped stalk weight) and the technological traits (Juice extraction, sucrose, purity and reducing sugar percentage) in addition to, yield traits (juice and ethanol yields/fed.). All crosses showed a significant difference among the evaluated different populations. For four traits in the three crosses (i.e stalk weight, stripped stalk weight, sucrose and reducing sugar) were used to determined heterosis, inbreeding depression, broad sense heritability and genetic advance, the dominant genetic variance in stalk weight, stripped stalk weight and sucrose percentage were high in the additive genetic variance except reducing sugar percentage trait was high in the dominance genetic variance. To summarize, the results of this study show that the third cross performbest cross in ethanol production.

Keywords: Sweet Sorghum, Breeding, Genetic diversity, Heterosis, Yield.

INTRODUCTION

Sorghum (*Sorghum bicolor* L. Moench) is one of the most valuable grains in the world, ranking sixth in output (63.9 million MT) and fifth in harvested area (58 million hectares) (FAO, 2019). As it can tolerate semi-arid climate variables, sorghum is considered one of the commercial sources of syrup and/or sugar production in addition to sugarcane and sugar beet (Da José et al., 2019). Sorghum is the second most valuable crop in Africa, and it grows well in tropical and sub-tropical climates. It performs in the flour, fuel, and fiber industries, as well as the fermentation and beer industries, and also the extraction of chemical compounds such as dextrin, windbreakers, and the construction of fences and fresh fodder crops, particularly in the summer (Assem et al 2014).

After wheat, maize, and rice, sorghum ranks fourth in Egypt in terms of consumption and production. It is primarily grown in the governorates of Assiut and Sohag, where the climatic temperature is high (Al-Naggar et al., 2007). In 2017, Egypt's grain sorghum cultivation area was reported to be around 148,460 hectares, with yearly production of 804,000 tons (FAOSTAT, 2017) and an average yield of 5.42 t/ha (Khaled et al., 2019).

Based on the Sweet sorghum variety and growing conditions, plant high ranged between 120 cm to 400 cm. On a moist basis, it contains roughly 19% leaf matter, 37% juice, 8% seed head, and 36% bagasse; however, this observation owing to the difference between the cultivated varieties. According to cultivar, climate, location, and production practices, sweet sorghum yields range from 32 to 112 Mg ha⁻¹ (fresh biomass) and 15 to 25 Mg ha⁻¹ (dry biomass)(Bellmer et al., 2010).

Any crop breeding program's success is dependent on knowing about and having access to genetic heterogeneity for efficient selection. Assessments of genetic similarity (or genetic distance) between genotypes aid in the selection of parental combinations for segregating populations in order to maintain genetic diversity in a breeding program (Becelaere et al., 2005) and the classification of germplasm into heterotic groups for hybrid crop breeding(Meena et al., 2017). Using morphological, biochemical, and molecular markers, researchers may quantify the genetic diversity of crop species (Shargie et al., 2005; Mehmood et al., 2008). Although assessing genetic diversity is easier with morphological characters, these traits are significantly influenced by the environment (Afolayan et al., 2019).

Generally, the heterotic effect is less effective in autogamous species than in allogamous species (Lombardi et al., 2018). Heterosis has been discovered in sweet sorghum for features that are directly or indirectly connected to ethanol production, such as total soluble solids, green mass production, and juice yield (Pfeiffer et al., 2010; Bunphan et al., 2015). As a result, heterosis-based breeding of sweet sorghum has been demonstrated to be a viable option. Genes with additive and non-additive gene action have been found in the expression of traits related to ethanol production in sweet sorghum, according to Bunphan et al., (2015), emphasizing the justification of breeding to obtain hybrid cultivars.

The phenotypic expression of numerous variables, particularly those related to ethanol production, such as mega-grams of Brix per hectare, total soluble solids, plant height, green mass production, and juice extraction, should be taken into account when evaluating the potential of a hybrid (Lombardi et al., 2015). However, as the crop develops, these features change in phenotypic expression (increase or decrease), affecting line and hybrid recommendations as well as plant agro-industrial planning (Borèm et al., 2014).

The purpose of this study is to assess the performance of F1 sweet sorghum hybrids and their parental lines, as well as their heterosis, heritability, inbreeding depression, and genetic advance.

MATERIALS AND METHODS

Experimental site

In the summers of 2016, 2017, 2018, and 2019, this experimental study was carried out at the Giza Research Station of Sugar Crops Research Institute (SCRI), Agricultural Research Center (ARC) Giza, Egypt.

Genetic materials:

Sugar Crops Research Institute (SCRI), Agricultural Research Center (ARC) Giza, Egypt, provided this experimental research with four variety of sweet sorghum [*Sorghum bicolor* (L.), Moench] as parents: GR Coba, AG SC2, AG SC3, and Brandes from Mississippi.

Experimental study design:

GR Coba x AG SC2 (Cross I), GR Coba x AG SC3 (Cross II), and Brandes x AG SC3 (Cross III) were crossed in the first growing season (2016) to yield F1 hybrid grains. Each cross's F1 hybrid grains and their parents were

seeded in the second growing season (2017). The F1 plants were selfed to generate F2 grains for each cross. Each cross's F1 and F2 hybrid grains, as well as their parents', were sowed in the third growing season of 2018. The F3 grains were produced by selfing the F2 plants from each cross. In 2019 season, the grains of the five populations i.e., P1, P2, F1, F2, and F3 of the three crosses were evaluated for all studied traits. Each experiment was conducted in a Randomized Complete Block Design with three replications. Each replicate comprised one row for each parent and F1 cross, six rows for each F2 and F3 populations for each cross. The experimental plot included one row of four meters long and 60 cm wide. Planting was done in hills spaced at 20 cm apart and hills were thinned at two plants / hill.

Data collection

Data were recorded on 30 plants for each of P1, P2 and F1, 90 plants for each of F2 and F3 populations from the three replications for each cross. The following agronomic traits were measured on a (random sample) of ten guarded plants in the middle row of each plot:

The morphological characters

including Stalk weight (gm) and Stripped stalk weight (gm).

Laboratory analysis

The juice quality analysis was performed at Giza Research Station of Sugar Crops Research Institute (SCRI), Agricultural Research Center (ARC) Giza, Egypt.

Juice quality trait including Total Soluble Solids (TSS or Brix), Sucrose % (Pol), reducing sugars and purity percentages were determined according to the methods of Meade and Chen (1977).

Sucrose percentage was calculated as follows:

Sucrose percentage = Direct reading of Saccharimeter $\times$ 1.04

Where, 1.04 is a factor depending on the length of Saccharimeter's tube (A.O.A.C. 2005).

Juice Purity (Purity): was calculated using the following equation:

Juice Purity = (sucrose percentage / Brix reading) $\times$ 100.

The total soluble sugars (TSS) were calculated as juice brix from pooled juice collected from sample plants using an automatic digital refractometer.

The raw juice was filtered and weight to calculate juice extraction percentage (JEP) and juice yield/fed. from the following equation:

$$\text{JEP} = (\text{Juice weight} / \text{stripped stalks weight}) \times 100$$

$$\text{Juice yield (ton/fed.)} = (\text{stripped stalk yield} \times \text{JEP}) / 100$$

Theoretical ethanol yield (EtOH) was calculated according to Smith and Buxton (1993)

Statistical analysis:

According to Gomez, (1984), data from the previous growing season were subjected to a regular analysis of variance using a randomized full blocks design. A standard analysis of variance of Randomized Complete Blocks Design was calculated for each examined character in each cross, and F test according to Cochran and Cox (1957) was done to see if significant differences existed among the different populations in each cross. LSD was also calculated at p 0.05 and 0.01 to examine the significance of the five parameter means.

In each cross, the mean and the variance were calculated for *i.e.* P_1 , P_2 , F_1 , F_2 and F_3 generation. The population means and variance were used to estimate the type of genetic action.

Genetic analysis:

Heterosis was calculated as the percentage of deviation from med parent according to following formulas:

$$H = F_1 - M.P / M.P \times 100$$

Genotypic and phenotypic coefficients of variation (GCV, PCV) were calculated as outlined by Singh and Chaudhary, (1977):

$$\text{Broad sense heritability } h^2 = 100 \times \sigma^2_g / \sigma^2_p$$

Genetic advance (GA) = $k \times h^2 \times \sigma_p$

With k : standard selection differential at 5 % selection intensity ($k = 2.063$)

Inbreeding depression (I.D.): was calculated as follows:

$$I.D. = F_1 - F_2 / F_1 \times 100$$

Where: F_1 = First generation mean; F_2 = Second generation mean

Genotypic variance (σ^2_g) = $(MS_g - MSe) / r$;
Environmental variance (σ^2_e) = $\sigma^2_{\text{error}} / r$;
Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

Where: MS_g and MSe are mean sum of squares for genotypes and error in the analysis of variance and r the number of replicates

Generation mean analysis: The mean of the five populations (P_1 , P_2 , F_1 , F_2 and F_3) in each cross and the parents were used to estimate five parameters of gene effects using five parameter models according to Jinks and Jones (1958). The parameters m , d , h , i and l refer to mean effects, additive, dominance, additive $\times$ additive and dominance $\times$ dominance, respectively.

RESULTS AND DISCUSSION

The present investigation was carried out on sweet sorghum on generation mean analysis using five populations of three crosses developed by involving the parents, F_1 , F_2 and F_3 .

Mean performance

Morphological traits

The mean Performance of all morphological traits including stalk weight and stripped stalk weight in cross I, II and III summarized in (Figures 1, 2 and 3), which showed a significant difference among the evaluated different populations.

In the cross GR Coba $\times$ AGSC2, the parent P_2 (AGSC2) (994.67 g) had a higher stalk weight than P_1 GR Gaba (780.33 g). In comparison to the mid-parent, the F_1 population (894.0) had a higher average stalk weight, but it was lower than the better parent. The weight of the stalks varied from 473 g for F_2 to 994.67 g for P_2 (AGSC2). In cross I, the mean of F_1 was 421 g higher than the mean of F_2 , indicating the importance of the dominance component of genetic variance in this cross. The findings of this study are consistent with those of Zou et al (2011). Both parents had considerably differing stripped stalk weights, with P_2 (AGSC2) recording a larger value (855.3 gm) than P_1 (627.3). In comparison to the mid-parent, the population F_1 (679.67gm) had a greater average plant weight and was higher than the lower parent. When comparing cross I to other hybrids, the mean of F_1 was 285.67 gm greater than the mean of F_2 (394 gm). This finding demonstrates the importance of the dominant component of genetic variance for this cross. Our findings are consistent with those of a prior study conducted by Pfeiffer et al (2010).

Whereas in cross II, F_1 had the maximum stalk weight (892.66 gm.), showing that the higher parent had the upper hand. However,

as compared to F2 (605.6 gm) and F3 (605.6 gm), both off parents P1 and P2 were higher (778 gm). The stalk weight of F1 was the highest (851 gm.). On the other hand, both parents P1 and P2 had larger weights than F2 (450 gm.) and F3 (450 gm.). (636 gm.).

While in cross III, The weight of the stalks varied from 743.66 gm for F2 to 1225.34 gm for P1 (Brandes). In the cross Brandes x AGSC3, there was a considerable variation in mean stalk weight between the parents, with the female parent P1 (1225.34 gm) recording a greater value than the male parent P2 (861.34 gm). While the hybrid F1 (1021.67 gm) had a higher average stalk weight than P2, it was still less than the better parent (Brands). The weight of the stalks varied from 528.66 gm for F2 to 1062 gm for P1 (Brandes). In the Brandes x AGSC3 cross, both parents differed considerably and the parent P1 (1062 gm) had a higher Stripped stalk weight than P2 (717.67). When compared to P2, the hybrid F1 (824 gm) had a higher average Stripped stalk weight (AGSC3).

Technological traits

The data in (Table 1) demonstrated that the technological traits in cross I differed significantly among the studied populations. In the cross GR Cobra x AGSC2, F3 had the highest percentage of Juice Extraction (51.72 %). The percentage of juice extracted ranged from 21.03 for P1 (GR Cobra) to 51.72 for F3. In the cross GR Cobra x AGSC2, the parent P1 GR Cobra (11.33 percent) had a higher sucrose percent than P2 AGSC2 (9.33). The mean of F1 (7.33%) was 1.08 percent greater than the mean of F2 (6.25%), demonstrating the significance of the non-additive component of genetic variance for this trait. For P1, the purity percent ranged from 40.56 percent to 58.64 percent. P1 (GR Cobra) and P2 (AGSC2) differed significantly from one another, with P1 (58.64%) recording higher purity than P2 (51.17%) in the GR Cobra x AGSC2 cross. In comparison to P2, the F3 population (53.86 percent) had a higher average purity, but it was lower than the better parent (P1). The F1 average (4.3%) had a higher lowering sucrose percentage than both parents. When comparing several populations of cross I, F1 had the highest value of lowering sugar percent (GR Cobra x AGSC2). The mean of F2 was 0.58 percent lower than the mean of F1, indicating the significance of the non-additive component of genetic variance for this trait. Previous research by Almodares and Hadi (2009) and Erdurmus et al., (2018) have found similar outcomes.

The technological traits in cross II, as shown in (Table 2), differed significantly across the evaluated populations. The highest percentage of Juice Extraction was found in F2 (37.9 percent). The Juice extraction percent of the hybrid F1 was much higher than that of both mid parents. These findings were consistent with Kumar et al., (2011), who showed that the F1's average performance in all crossings suggested a dominant gene effect. F1 (recorded the highest sucrose percent value) (12.4 percent). F1 had a much greater sucrose percent than both the mid parent and the better parent. Also, observed a dominant gene effect in F1 and obtained similar results. Purity percentages ranged from 47.8% for P2 to 63.15 percent for F1. F1 had a much greater purity percent than both the mid parent and the better parent. Reducing sugar percentages ranged from 2.47 in F2 to 4.67 in F3.

Data in (Table 5) showed the technological traits in cross III (Brandes x AGSC3), which varied significantly among evaluated different populations. F1 had the highest percentage of Juice Extraction (38.67 percent). When compared to P1, all populations (F1, F2, and F3) had the highest significant value of Juice Extraction percent (38.67, 26.6, and 38.47 percent, respectively) (Brandes, 17.87 percent). Almodares and Hadi, (2009) and Erdurmus et al., (2018) found significant differences in Juice Extraction percentage among evaluated sweet sorghum populations. Sucrose percentages ranged from 10.37 percent for P1 and 10.13 percent for F1 to 5.53 percent for F2. In comparison to P2, F1 had a significantly higher sucrose percent value (AGSC3, 7.5 percent). In the cross Brandes x AGSC3, the mean of F1 was 4.6 percent higher than the mean of F2, indicating the importance of the dominance component of genetic variance for this cross. These findings were consistent with Kumar et al., (2011), Purity levels ranged from 43.33 percent for F2 to 60.65 percent for P1. In comparison to P2 (AGSC3, 47.8%) and F2, F1 had a significantly higher sucrose percent value. These findings are in consistent with those of Almodares and Hadi, (2009) and Erdurmus et al., (2018), both found significant differences in purity percentage among sweet sorghum samples. Reducing sugar percentages ranged from 2.37 percent for F3 to 4.52 percent for P2 (AGSC3). The mean of F2 was 0.66 percent lower than the mean of F1, indicating the significance of the non-additive component of genetic variance in this cross (Brandes x AGSC3).

Yield traits:

Figure 4 depicted the juice yield (ton/fed) and ethanol yield, which differed significantly among the cross I populations studied. The largest Juice yields were reported by P2 and F1 (13.18 and 10.38 ton/fed, respectively). The findings ranged from 13.18 (AGSC2) to 7.02 (F3) for p2 (AGSC2). In addition, P2 (937.63) had a greater Ethanol output L/fed than F1 (642.84). When comparing different populations of cross I, P2 had the highest Ethanol output L/fed (GR Cobra x AGSC2). F2 had a mean of 270.17 L/fed, which was substantially lower than F1.

As shown in Figure 5, the yield of juice and ethanol varied significantly among the evaluated different populations of GR Cobra x AGSC3 Cross. F1 (GR Gaba) had the highest Juice yield (16.84 ton/fed), while P1 (GR Gaba) had the lowest Juice yield (7.98 ton/fed), indicating that the higher parent had the upper hand. Kumar et al., (2011) for example, achieved similar results. The mean Ethanol yield of F1 (1428.37 L/fed) was higher than that of both parents. When comparing different populations of cross II, F1 had the highest Ethanol output L/fed (GR Cobra x AGSC3). The mean of F₂ was significantly lower than the mean of F₁.

The data shown in Figure 6 revealed that the juice yield (ton/fed) varied significantly among the cross III populations studied (Brandes x AGSC3). The Juice yield of the hybrid F1 generation was the highest (20.28 ton/fed). Juice yield was significantly higher in the F1 generation than in the other four populations. These findings are consistent with those of a previous study by Kumar et al., (2011). The mean Ethanol yield L/fed of F1 (1500.72) was higher than that of both parents. When comparing different populations of cross III, F1 had the highest Ethanol yield L/fed (Brandes x AGSC3). The mean of F₂ was significantly lower than the mean of F₁ by 1010.62 L/fed, these results indicate the importance of non-additive component of genetic variance for this trait.

Phenotypic and Genotypic Coefficient of variation:

The phenotypic and genotypic coefficients of variation (PCV and GCV) for some traits in the three crosses are presented in the table below (Table 4-6). For some studied traits in the crosses, PCV was greater than GCV. These findings suggested that the environment played a significant role in the expression of these traits. The diverse genotypes can provide

materials for a sound breeding program, and there is enough scope for selection based on these characters. These findings are consistent with those obtained by (Elangovan et al., 2012).

In Cross III, the GCV was close to the PCV for characters like Stalk weight, and Stripped Stalk weight. The highest PCV values were found in Cross II for Stripped Stalk Weight. High GCV and PCV were also found in some traits, indicating that they have a broad genetic background and the ability to react effectively to selection in breeding programs. Bello et al., (2007) for example, found similar results. The presence of a large quantity of GCV and PCV showed that there was more room for selecting superior genotypes for these features. In Cross I, moderate levels of GCV and PCV were seen for Reducing sugars percent and sucrose percent; in Cross II, moderate values of GCV and PCV were observed for Reducing sugars percent and Stalk weight; and in Cross III, moderate values of GCV and PCV were observed for sucrose percent and Reducing sugars percent. The lesser degree or equal GCV and PCV for Stalk weight and Stripped Stalk weight suggested that such features could only be improved to a limited amount. Warkad et al., (2008) likewise came to similar conclusions. In sorghum, GCV and PCV were shown to be equal for stalk height (Reddy et al 2008). In general, the GCV is less powerful than the PCV. The efficiency of selection for any character is determined not only by genetic variability, but also by the transferability of traits from one generation to the next.

Heritability and genetic advance:

Individual assessment of the factors is less reliable and important than heritability estimates with genetic advance (Nwangburuka and Denton, 2012). The high estimates of broad sense heritability and high genetic advance expressed as a percent of mean were discovered in sucrose in cross I and cross III, showing a prevalence of additive gene action in the genetic control of this trait (Table 7-9).

The broad sense heritability and genetic advance estimates were also higher indicating usefulness of this trait in selection of desirable segregates due to its genetic control by additive gene action. This is in accordance with studies obtained by lemu et al., (2017) and Owusu et al., (2020). For Sucrose percentage in cross II its results showed that high heritability coupled with moderate and high genetic advance expressed as percent of mean, respectively indicating role of additive

gene action in their genetic control. Results of the present study are in corroborative with Akhtar et al., (2007), Ayodeji and Comfort, (2019), Roy and Shil, (2020). The findings of Reducing sugar percent in cross III, revolted medium heritability was discovered together with moderate and high genetic advance represented as a percent of mean, implying that this trait is under the control of epistatic interactions. In several variables, there was a high heritability combined with a low genetic progress represented as a percentage of the mean. High heritability estimates were coupled by modest genetic progress, implying non-additive gene action and the effectiveness of breeding approaches that utilize non-additive gene action, such as heterosis breeding. The effectiveness of selection for any character depends not only on the extent of genetic variability but also on the extent to which such traits can be transferable from one generation to the next.

Heterosis and inbreeding Depression

Heterosis and inbreeding depression is both the product of dominant gene activity, however heterosis is absent when features are only driven by additive gene action. True heterosis has the feature that the gain in vigor is limited to the F1 generation, with significant depression from F1 to F2 and later generations. The presence of substantial epistatic gene effects or partial dominant gene effects can explain low and negative heterosis. The findings were consistent with previous research by Radoev et al., (2008) and Jamieson et al., (2007) and Poyato-Bonilla et al., (2020) on the other hand, showed high, moderate, and low inbreeding depression scores in various research. The presence of transgressive segregates in the F2 population may account for negative estimations of inbreeding depression. In cross I, there was a lot of inbreeding depression combined with a lot of heterosis in terms of stalk weight, and stripped stalk weight, as well as stalk weight, stripped stalk weight. In cross II, there was a lot of inbreeding depression combined with a lot of heterosis in terms of stalk weight, and stripped stalk weight.

Generation means analysis:

As mentioned previously, results of the analysis of variance Table (4-6) indicated that there were significant differences among the Five generations, i.e. p_1 , p_2 , f_1 , f_2 and f_3 for all studied traits in the three crosses under study (Table 10); therefore estimates of genetic parameters is needed. Meantime, significant

differences between means of the two parents of each cross and significance of genetic variance among f_2 plants are also prerequisite for the validity of the Five generations means analysis for estimating of types of gene effect.

The link depicted by Jinks and Jones., (1958) was used to calculate the genetic analysis of generation means. The estimated f_2 mean effect parameter (m), which indicates the overall mean contributions. Except for reducing sugar percent in cross I and cross III, the gene impact was higher than additive dominance gene effect for stalk weight, stripped stalk weight and sucrose percent in all three crosses. The epistatic type; dominance $\times$ dominance gene interaction (l) was higher than The epistatic type; additive $\times$ additive gene interaction (i). For stalk weight, stripped stalk weight and sucrose% in the three crosses and reducing sugar% in cross I and cross III. The findings further demonstrate the importance of dominant $\times$ dominant type epistatic in the inheritance of stalk weight, stripped stalk weight and sucrose percent in the three crosses.

CONCLUSION

Heterosis was observed in sweet sorghum for several morphological, technical traits, and yields were often higher than inbred lines. For all the traits studied in the crosses, PCV was higher than GCV. Future hybrid breeding studies should include these lines. According to this research, F1 hybrids have an advantage over the parents in the important traits.

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Table 1: Mean Performance of technical traits in cross I (GR Coba x AG SC2).

	Juice extraction percentage	Sucrose%	Purity%	Reducing sugar%
P1GR Coba	21.03	11.33	58.64	3.5
P2AGSC2	28.45	9.33	51.17	4.03
F1	24.0	7.33	44.6	4.3
F2	29.03	6.25	40.56	3.72
F3	51.72	7.4	53.86	2.63
LSD	0.56	0.72	2.98	0.99

Table 2: Mean Performance of technological traits in cross II (GRCoba x AGSC3).

	Juice extraction percentage	Sucrose%	Purity %	Reducing sugar%
P1GR.Coba	21.03	11.33	58.54	3.8
P2AGSC3	36.06	7.5	47.8	4.52
F1	31.2	12.4	63.15	3.53
F2	37.9	9.03	55.8	2.47
F3	36.5	11.43	55.51	4.67
LSD	1.22	0.80	3.77	0.64

Table 3: Mean Performance of the technological traits in cross III (Brandes x AGSC3)

	Juice extraction percentage	Sucrose%	Purity%	Reducing sugar%
P1Brandes	17.87	10.37	60.65	2.87
P2AGSC3	36.07	7.50	47.80	4.52
F1	38.67	10.13	56.59	3.33
F2	26.60	5.53	43.33	2.67
F3	34.47	6.30	54.14	2.37
LSD	0.27	0.82	3.74	0.79

Table 4: Variance components, genotypic coefficient of variation and phenotypic coefficient of variation for some studied characters in cross I (GRCoba x AGSC2).

	Stalk weight	Stripped stalk weight	Sucrose%	Reducing sugar%
σ^2_p	988.01	709.197	0.949	0.341
σ^2_g	940.677	674.864	0.801	0.063
σ^2_e	47.333	34.333	0.148	0.278
PCV	4.23	4.42	11.7	16.4
GCV	4.13	4.31	10.75	6.9

σ^2_g : Genotypic variance; σ^2_e : Environmental variance; σ^2_p : Phenotypic variance

PCV: phenotypic coefficient of variation; GCV: genotypic coefficient of variation

Table 5: Variance components, genotypic coefficient of variation and phenotypic coefficient of variation for some studied characters in cross II (GR Coba x AGSC3).

	Stalk weight	Stripped stalk weight	Sucrose%	Reducing sugar%
σ^2_p	18443.61	17784.72	0.981	0.27
σ^2_g	1347.973	1044.203	0.798	0.151
σ^2_e	17095.63	16740.52	0.183	0.119
PCV	17.26	21.29	9.58	13.64
GCV	4.67	5.16	8.64	10.21

Table 6: Variance components, genotypic coefficient of variation and phenotypic coefficient of variation for some studied characters in cross III (Brandes x AGSC3).

	Stalk weight	Stripped stalk weight	Sucrose%	Reducing sugar%
σ^2_p	849.444	852.136	1.148	0.315
σ^2_g	762.277	793.303	0.956	0.137
σ^2_e	87.167	58.833	0.192	0.178
PCV	3.1	3.84	13.44	17.95
GCV	2.93	3.7	12.27	11.69

Table 7: Genetic parameters for some studied characters in cross I (GRCoba x AGSC2).

	Stalk weight	Stripped stalk weight	Sucrose%	Reducing sugar%
h^2_{bs}	95.21	95.16	84.41	18.49
GA	6173.89	5227.96	169.68	22.28
GAM	8.31	8.68	20.37	6.12
H %	0.73	-8.31	-29.04	14.36
ID %	47.1	42.03	14.73	13.83

h^2_{bs} : Broad sense heritability, GA: Genetic advance, (GA), GAM: Genetic advance of mean

H: Heterosis, ID: Inbreeding depression

Table 8: Genetic parameters for some studied characters in cross II (GR Coba x AGSC3).

	Stalk weight	Stripped stalk weight	Sucrose%	Reducing sugar%
h^2_{bs}	73.1	58.7	81.34	56.06
GA	2047.66	1615.33	166.18	60.12
GAM	2.6	2.58	16.07	15.77
H %	7.65	24.99	31.77	15.14
ID %	32.15	47.12	27.17	30.02

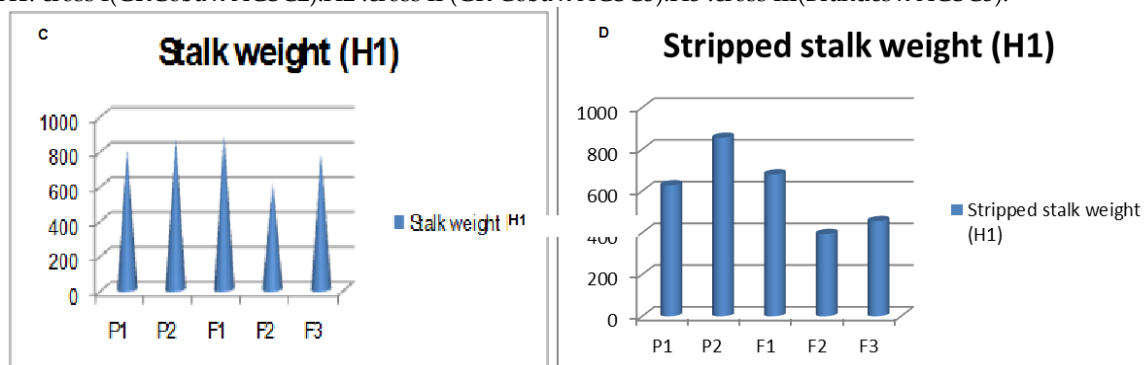
Table 9: Genetic parameters for some studied characters in cross III (Brandes x AGSC3).

	Stalk weight	Stripped stalk weight	Sucrose%	Reducing sugar%
h^2_{bs}	89.74	93.1	83.25	43.37
GA	5395.66	5606.4	184.02	50.2
GAM	5.73	7.37	23.09	15.89
H %	-2.07	-7.43	13.43	-9.7
ID %	27.21	35.88	45.4	19.81

Table 10: showing the estimated five parameters including means (m), additive (d), dominance (h), additive*additive (i), and dominance*dominance (l).

	H	Stalk weight	Stripped stalk weight	Sucrose%	Reducing sugar%
M	H1	473.0	394.0	6.3	3.7
	H2	605.6	450.0	9.0	2.5
	H3	743.7	528.3	5.5	2.7
D	H1	107.2	114.0	1.0	0.3
	H2	32.2	45.2	1.9	0.4
	H3	182.0	277.5	1.4	0.8
H	H1	9.5	25.1	-2.3	3.3
	H2	-268.4	-228.7	-4.2	-5.2
	H3	-102.7	-178.0	1.0	1.2
L	H1	1664.9	1092.5	9.0	-4.3
	H2	1685.0	2061.3	21.8	14.6
	H3	1317.4	1538.7	16.4	0.2
I	H1	217.4	314.7	2.7	3.3
	H2	-267.5	-316.8	-3.3	-3.8
	H3	283.0	-6.8	2.7	3.3

H1: cross I(GRCoba x AGSC2).H2 :cross II (GR Coba x AGSC3).H3 :cross III(Brandes x AGSC3).

**Figure 1:** Comparison of mean performance of different populations (P1, P2, F1, F2 and F3) of cross I of sweet sorghum A. Stalk weight and B. Stripped stalk weight during season 2019.

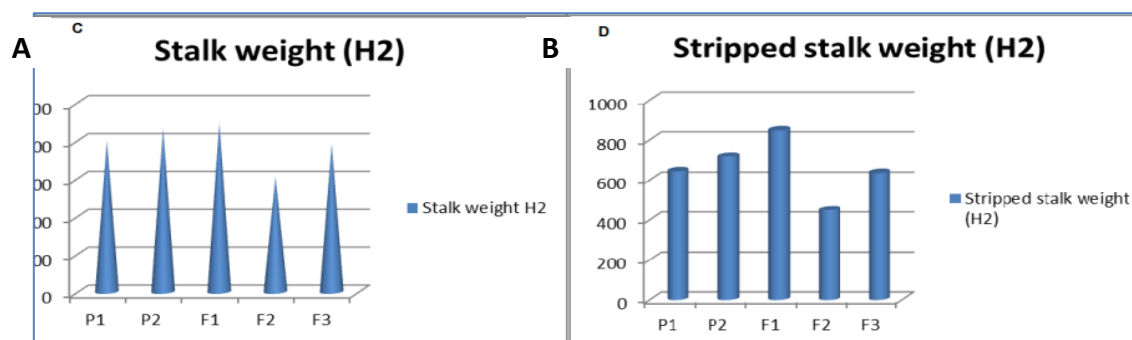


Figure 2: Comparison of mean performance of different populations (P1, P2, F1, F2 and F3) of cross II of sweet sorghum A. Stalk weight and B. Stripped stalk weight during season 2019.

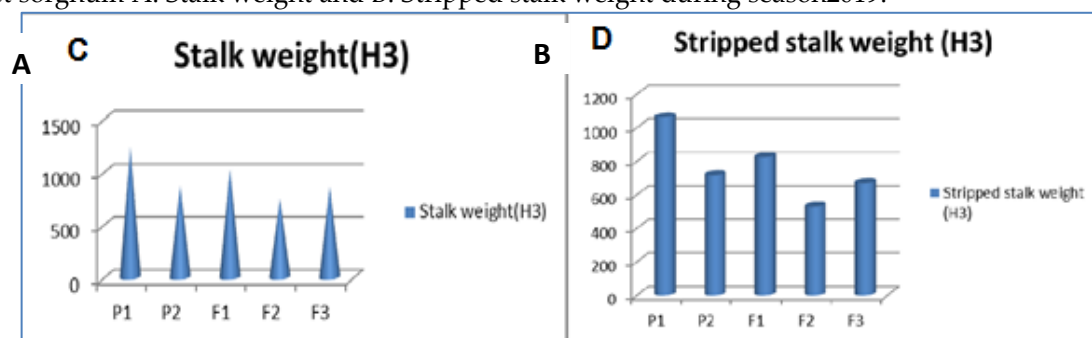


Figure 3: Comparison of mean performance of different populations (P1, P2, F1, F2 and F3) of cross III of sweet sorghum A. Stalk weight and B. Stripped stalk weight during season 2019.

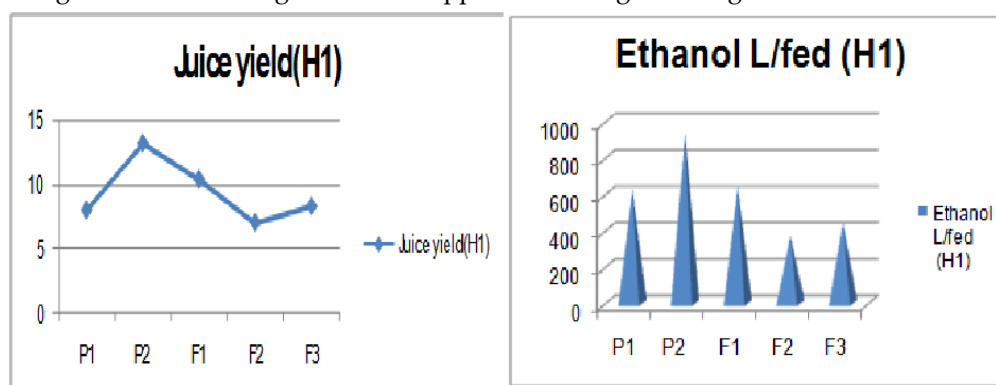


Figure 4: Comparison of mean performance of five populations (P1, P2, F1, F2 and F3) of cross I of sorghum for Juice and ethanol yield during four seasons.

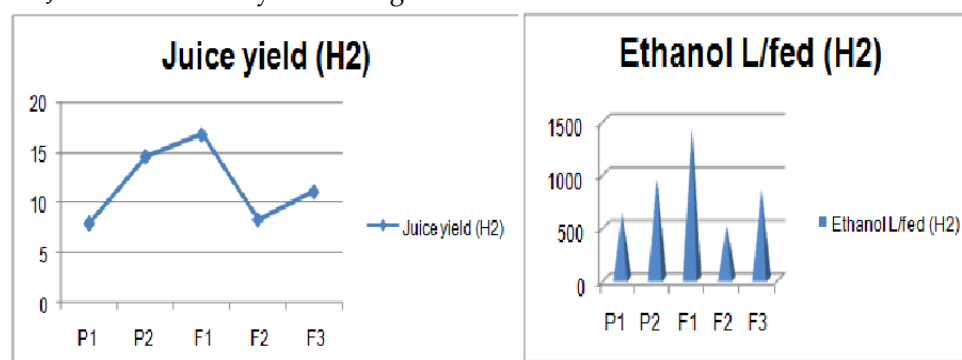


Figure 5: Comparison of mean performance of five populations (P1, P2, F1, F2 and F3) of cross II of sorghum for Juice and ethanol yield during four seasons.

