Original Article

Development and Evaluation of the Performance of Some Sugarcane Hybrids to Detect the Elite Ones

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Abstract:

The present study was conducted at the Breeding field of Sugar Crops Research Institute, Agriculture Research Center (ARC), Giza, Egypt, during 2018/2019 and 2019/2020 seasons to evaluate the potential of ten hybrids along with the check cultivar (GT54/9) and detect the elite ones. The experiment design was randomized complete block with three replications. The mean and range for stalk height, stalk diameter, number of stalk/stool, stalk weight, stool weight and Brix of each hybrid were recorded. In addition to, among and within hybrids variation i.e. genotypic and phenotypic variances; genotypic (GCV) and phenotypic coefficient of variation (PCV); heritability and genetic advance were estimated.

The results illustrated significant differences among hybrids as well as families within hybrids, revealing different genetic make-up for the obtained hybrids and their families.

Moreover, the results indicated that applying selection among evaluated hybrids would more effective than applying selection within hybrids and suggesting the selection among hybrids followed by selection within elite selected hybrids would increase selection efficiency.

According the high values and the high variation for studied traits, the results showed that, hybrids i.e. CP.63-35 X CP.46-115,CP.57-614 x Co. 617, Co.1129 x G.73-211, Co.744 X Bo.19, CP.67-412 x G.73-211 and H.86-37 X Co.617 were the best to improve stalk diameter. Moreover hybrids i.e. Co.744 X Bo.19, CP.67-412 X G.73-211 and H.86-37 X Co.617 proved to be elite hybrids for improving stalk weight. Hybrid i.e. CP.63-35 XCP.46-115 proved to be the best to improve stalk number and stool weight. The selection to improve Brix could be effective in hybrids i.e. Co.284 xCP.44-101, CP.63-35 X CP.46-115, CP.57-614 x Co. 617, Co.1129 x G.73-211, CP.63-35 X SP.81-1763, CP.57-614 X CP.44-101 and Co.284 X CP.57-614.

Results, also revealed that a great parts of the phenotypic variance due to genotypic variance for all studied traits, implying that improvement of these traits would be easy.

The high GCV and PCV obtained for stalk number/stool, stalk weight and stool weight indicating that the selection for these traits could be effective.

High broad sense heritability was observed for all studied traits. However, low genetic advance was recorded for stalk diameter and Brix, moderate for stalk height and high for stalk number/stool, stalk weight and stool weight.

Introduction

The ultimate goal of all sugarcane breeding programs is developing improved sugarcane cultivars producing high cane yield and sugar yield, in addition to resistance or tolerance to diseases, pests and adverse conditions prevailing in regions in which they will be grown. The development of sugarcane cultivars mainly depends upon evaluation and selection a large number of seedling derived from true seed obtained from intercrossing superior parents. Sugarcane breeders have traditionally used individual seedling selection to select superior clones at seedling stage and considerable gain have been achieved, in spite of the disadvantages of this method which are requiring high costs and intensive labor in addition of lack of replications and competition effects among seedling contribute to reduce selection efficiency (Skinner 1971; Hogarth *et al*., 1997 and Kimbeng and Cox, 2003). Recently, family selection has been widely used in sugarcane breeding programs and have been proved to be more effective than the individual selection in terms of gain from selection and efficiency of resource utilizing. Family selection is employed to identify families with a higher frequency of superior clones. Family selection proved to be useful for traits with low heritability because families can be replicated across years and sites and family data can be used to infer the breeding value of parents based on progeny performance (Kimbeng and Cox, 2003). It is widely recommended using combination of family and individual selection in the selection of original seedling (Olaoye, 2001; Mohamed, 2007; Bressiani *et al*., 2002; Doule and Balasundaram, 2003 and Shanthi *et al*., 2008).

Genetic variability, heritability and genetic advance are useful tools in increasing sugarcane breeding efficiency during the different stages of developing new sugarcane cultivars. The extent of genetic variability, high heritability and high genetic advance in genetic materials used to improve sugarcane crops are the fundamental parameters to the success of the breeding programs and these parameters have been estimated in all stages of sugar cane breeding programs (Tadesse *et al*. 2014; Sanghera *et al*., 2015 and Hiremath and Nagaraja, 2016).

The objective of this study was to evaluation the performance and genetic parameters of the important traits of ten sugarcane families and asses their potential to detect elite genotypes.

Materials and Methods

The present study was carried out at the Breeding field of Sugar Crops Research Institute, Agriculture Research Center (ARC), Giza, Egypt during 2018/2019 and 2019/2020 seasons. In 2018/2019, the studied hybrids were progressive through breeding program in nursery. In 2019/ 2020 season, the experiments were done to evaluate the potential of ten hybrids to detect elite ones comparing with the check cultivar (GT54/9). These hybrids were Co.284 xCP.44-101, CP.63-35 X CP.46-115, CP.57-614 x Co. 617, Co.1129 x G.73-211, CP.63-35 X SP.81-1763, Co.744 X Bo.19, Co.744 X Bo.19, Co.284 x CP.57-614, CP.67-412 x G.73-211and H.86-37 X Co.617(Table1)along with the check cultivar (GT54/9). The ten hybrids were represented in ranking by 45,11,28,13,12,15,8,13,10 and 24 seedlings, respectively. The experiment design was randomized complete block with three replications. Each plot included two rows. Each row was 3 m length, 100 cm apart with 50 cm plant to plant distances. The commercial GT54-9 cultivar was used as a check. The field was irrigated right after culture and all other agronomic practices were carried out as recommended. At harvest, after 12 months from planting, data on stalk length, stalk diameter, stalk weight, number of stalks per stool, stool yield and field brix were recorded for each genotype (stool) as follows:.

1- Stalk length (cm) was measured from soil surface to the visible dewlap.
2- Stalk diameter (cm) was measured at mid stalk with no reference to the bud groove.
3- Stalks number /stool.
4- Stalk weight (kg) was calculated by dividing stool yield by number of stalks per stool.
5- Stool yield (kg).
6- Brix (percent soluble solids) was determined with a hand refractometer. For all these traits mean and range were determined.

Table 1. Name and pedigree of the used sugarcane hybrids.

Hybrids number	Parents ♀	♂	Hybrids number	Parents ♀	♂
1	Co.284 X CP.44-101		6	Co.744 X Bo.19	
2	CP.63-35 X CP.46-115		7	CP.57-614 X CP.44-101	
3	CP.57-614 x Co. 617		8	Co.284 X CP.57-614	
4	Co.1129 X G.73-211		9	CP.67-412 X G.73-211	
5	CP.63-35 X SP.81-1763		10	H.86-37 X Co.617	

Statistical analysis

The collected data were analyzed statistically to assess the degree of among and within hybrids variations according to Snedecor and Cochran (1989). Revised LSD at 5% probability was used for means comparison of studied traits including hybrids and check.

The analysis of variance, phenotypic variance ($\sigma2p$) and genotypic variance ($\sigma2g$) were performed as Steel *et al.*(1997). The analysis of variance of infection percentage was done on Arcsine transformed data. Heritability in broad sense (H%) = ($\sigma2g$ / $\sigma2p$) ×100, and expected genetic gain=k σ p h2 based on 10% selection intensity was estimated as Falconer (1989) and GA % = GA / general mean.

Where; $\sigma2g$ is genotypic variance, $\sigma2p$ is phenotypic variance, $\sigma2ge$ is the $\sigma2e$ is pooled error variance, and r is the number of replications. Genotypic coefficient of variation (GCV%) and phenotypic coefficient of variation (PCV%) were calculated following Singh and Chaudhary (1979):

GCV%= ($\sigma2g$ / X) X100and PCV%%= ($\sigma2p$ / X) X100
Where; X is the grand mean of the trait.

Results and Discussion

1. Mean performance of the evaluated sugarcane families:

1.1. Analysis of variance for studied traits:

The analysis of variance of stalk height, stalk diameter, stalk number/stool, stalk weight, stool weight and Brix are shown in Table (2) indicated that among hybrids mean square for these traits was highly significant, indicating that the variation among hybrids was high than the variation within hybrids (families) for these studied traits. Consequently, this result implying that applying selection among hybrids would be more effective than applying selection within hybrids and suggesting the selection among hybrids will be more effective to determine the elite hybrids in sugarcane, indicating the different genetic make-up between the obtained hybrids.(Table 2). This result is in agreement with those obtained by Mohamed (2007) and Shanthi *et al*. (2008) who reported that selection of the best families based in their mean performance and further selection of individual clones within the best families in early stage of selection would improve the efficiency of selection.

Table 2. Mean squares of the ten hybrids for all studied treats

S.O.V.	Hybrids	Within hybrids (all families)
d.f	9	178
Stalk height,cm	28885.73**	6215.634
Stalk diameter,cm	0.48778397**	0.17196729
Stalk number/ stool	221.42644**	62.54144
Stalk weight,kg	3.00129106**	0.50906334
Stool weight,kg	318.764834**	118.82340
Brix%	73.1646433**	9.774169

1.2. Stalk height, stalk diameter and stalk number/stool

Mean value and range of the stalk height, stalk diameter and stalk number/stool presented in Table (3) showed that stalk height of the evaluated hybrids ranged from 233.39 cm (hybrid No. 1) to 290.46 (hybrid No. 2) with an average mean of 263.26 cm. It is obvious from the data that all evaluated hybrids had significantly tall stalk than those of check variety (G.T. 54/9). However, five

hybrids i.e. 2, 3, 6, 7 and 10 recorded higher values for stalk height compared to mean overall hybrids while 1, 4, 5, 8 and 9 hybrids had shorter stalk than those of mean overall hybrids. Range of stalk height varied within these evaluated hybrids. The range of the stalk height of hybrid (2) was the highest (33 to 380 cm) while the hybrid (1) had the narrowest range (135-390 cm). This result showing that the selection for stalk height in hybrids no. 2, 3, 6, 7 and 10 would be more effective than the selection for this trait in other hybrids. The differences in the stalk height among and within sugarcane hybrids were widely reported (Gouda *et al*., 2016, Tena *et al*., 2016 and Reddy *et al*., 2020).

Table 3. Min., max. and mean of stalk height, stalk diameter and stalk number/stool of ten hybrids and the check cultivar.

Hybrid no.	Stalk height (cm)			Stalk diameter (cm)			Stalk number/stool		
	Mean +SE	Min	Max	Mean +SE	Min	Max	Mean +SE	Min	Max
1	233.39±SE 4.30	135	390	2.18 ± SE 0.02	1.2	3.0	6.88 ± SE 0.41	1	28
2	290.46 ± SE 7.19	33	380	2.37± SE 0.04	2.0	2.8	15.18±SE 1.26	4	35
3	290.18 ± SE 4.88	84	355	2.34 ± SE 0.03	1.9	3.0	8.71 ± SE 0.45	1	20
4	252.82 ± S E 6.69	39	330	2.30 ± SE 0.04	1.9	3.0	7.46 ± SE 0.55	2	18
5	252.92 ± SE 6.29	36	310	2.13±SE 0.04	1.7	2.7	9.25 ± SE 0.87	2	23
6	278.89 ± SE 3.88	45	330	2.37 ± SE 0.03	2.0	3.0	8.13 ± SE 0.36	4	14
7	282.71 ± SE 5.64	24	330	2.14 ± SE 0.04	1.9	2.6	8.12 ± SE 0.59	4	14
8	255.00 ± SE 4.20	39	300	2.28 ± SE 0.03	1.7	2.6	8.23 ± SE 0.53	2	15
9	251.17± SE 5.69	30	310	2.41 ± SE 0.06	2.0	3.0	7.00 ± SE 0.07	1	13
10	279.51± SE 4.41	72	360	2.35±SE 0.03	1.9	3.0	7.62 ± SE 0.39	2	14
Check	180.00±SE 13.54			2.02± SE 0.11			12.08± SE 0.45		
Mean	263.26± SE 1.98			2.28± SE 1.98			8.24 ± SE 0.20		
R.LSD 0.05%	41.68			0.27			4.43		

Concerning stalk number/stool data in Table (3) indicated that stalk diameter mean ranged from 2.13 cm (Hybrid No. 5) to 2.41 cm (Hybrid No. 9) with mean over hybrids of 2.28 cm. It is evident that hybrids no. 2, 3, 4, 6, 9 and 10 hybrids recorded significantly thicker stalks than those of the check variety (GT 54/9) which were in bar with mean over hybrid's value. However, the other hybrids *i.e.*1, 5, 7 and 8 had stalk diameter values statistically equal to those of check variety and mean of overall hybrids. The lowest range of stalk diameter was recorded by hybrid no.7 and the highest by hybrids no. 3,4 and 10. It desirable according these obtained results that the selection for improving the stalk diameter should be practice in hybrids no. 2, 3, 4, 6, 9 and 10 hybrids to gain advantage in selection efficiency. Differences in stalk diameter values within and among sugarcane families were recorded by Mehareb *et al*. (2017).

Regarding stalk number/stool data in Table (3) showed that the mean of stalk number/stool ranged from 6.88 stalks/stool (Hybrid no. 1) to 15.18 stalks/stool (Hybrid no. 2) among the tested hybrids with mean over hybrids of 8.24 stalk/stool. Also, the data clear that one hybrid (no. 2) had insignificantly higher number of stalk number/stool than that of check variety, while five

hybrids *i.e*. 3, 5, 6, 7 and 8 had stalk number/stool insignificantly lower than that of check variety. However, four hybrids (no. 1, 4, 9 and 10) recorded stalk number/stool significantly lower than that of the check variety. It is interesting to note that one hybrid (no. 2) recorded significantly higher stalk number compared to that of the mean over all hybrids while most of the hybrids recorded stalk number/stool in bar with that of mean over all hybrids. The hybrids no. 6 and 7 recorded the narrowest range (10) for stalks number/stool while hybrid no. 2 recorded the widest range in this trait. Therefore, hybrid no. 2 proved to be the best hybrid to improve stalk number/stool since it has stalk number/stool insignificantly higher than that of check variety and significantly higher than that of mean over all hybrids. In addition, the widest range in stalk number/stool among clones within it. Mahmoud *et al*. (2012) evaluated fourteen sugar cane families and reported the variation in stalk number/stool among and within sugarcane families was observed.

1.3. Stalk weight, stool weight and Brix

Mean values and range of stalk weight, stool weight and Brix registered in Table (4) for the evaluated hybrids.

Table 4. Min., max. and mean of Stalk weight, stool weight and Brix for ten hybrids and check cultivar:

Hybrid no.	Stalk weight (kg)			Stool weight (kg)			Brix (%)		
	Mean +SE	Min	Max	Mean +SE	Min	Max	Mean +SE	Min	Max
1	0.972± SE 0.021	0.062	1.70	6.715 ± SE 0.420	0.186	29,40	26.74 ± SE 0.12	23	30.5
2	0.855 ± SE 0.049	0.350	1.50	14.493± SE 2.084	2.600	49.70	25.41± SE 0.32	21.5	28.0
3	1.271 ± SE 0.049	0.640	2.50	10.800±SE 0.606	1.070	23.10	25.27 ± SE 0.19	20.5	29.0
4	1.049 ± SE 0.062	0.490	1.97	8.220 ± SE 0.883	1.000	25.20	27.15 ± SE 0.29	22.0	30.0
5	1.181 ± SE 0.056	0.550	1.80	10.543 ± SE 0.966	2.180	24.65	27.42 ± SE 0.23	24.0	30.0
6	1.418 ± SE 0.054	0.550	2.13	11.691±SE 0.933	2.600	21.23	23.38 ± SE 0.26	19.5	27.0
7	1.330 ± SE 0.082	0.700	2.20	10.708 ± SE 0.933	4.000	18.60	25.19 ± SE 0.44	21.0	30.0
8	1.277 ± SE 0.035	0.950	1.66	10.202±SE 0.618	2.400	18.20	25.40 ± SE 0.23	22.0	29.0
9	1.496± SE 0.062	1.160	2.42	9.699± SE 0.898	1.320	16.90	25.80±SE 0.16	24.0	28.0
10	1.563± SE 0.050	0.850	2.78	12.396±SE 0.840	2.000	27.94	24.84 ±SE 0.20	28.5	28.5
Check	0.993± SE 0.124			12.190± SE 1.869			26.55 ± SE 0.51		
Mean over all genotypes	1.215±SE 0.018			9.975± SE 0.275			25.75 ± SE 0.08		
R.LSD at 0.05%	0.36			6.32			1.60		

These data showed that mean values of stalk weight for the evaluated hybrids ranged from 0.855 kg (hybrid no. 2) to 1.563 kg (hybrid No. 10) with mean over hybrids of 1.215 kg. Furthermore, hybrids No. 10, 9 and No. 6 recorded significantly higher values of stalk weight than that of check variety which they recorded stalk weight estimating by 1.563, 1.496 and 1.418 kg, respectively while the other hybrids recorded stalk weight statistically similar to that of check variety. Comparing the mean value of stalk weight for each hybrid with the mean over all hybrids indicated that all tested hybrids had stalk weight values statistically in bar with that of mean over all hybrids. The lowest variation in stalk weight was observed in hybrid no.8, but the highest variation was found in hybrid no. 10. It is interesting to note that hybrid no. 10 proved to be the best hybrid for improving stalk weight among tested hybrids and this due to the fact that this hybrid recorded stalk value significantly higher than that of check

variety and insignificantly higher than that of mean over all hybrids, in addition to, the highest variation among clones within it this results was in line with the results obtained by Mohamed, 2007 and Mahmoud *et al*., 2012.

Also, data in Table (4) indicated that stool weight mean values for the tested hybrids ranged from 6.715 kg. (hybrid no. 1) to 14.493 kg (hybrid no. 2) with over hybrids mean of 9.975 kg. The values of stool weight pointed out that all evaluated hybrids recorded stool weight statistically in bar with that of check variety and with that of over hybrid's mean. The lowest variation in stool weight was found among the clones of hybrid no. 7 while the highest variation in this trait was noticed among clones of hybrid no. 2.

Hybridno. 2 would be the most desirable hybrid among the evaluated hybrids to be used for improving stool weight depending upon their registering the highest mean value in stool weight and the largest variation in this trait among clones within it. The differences in stool weight values among and within sugarcane families were reported by Abu- Ellil *et al*, 2018.

Brix is used as indicator for quality traits in seedling stage selection. The higher Brix is obtained in seedling stage the higher quality traits will be achieved. The data in Table (4) indicated that mean values of Brix for the studied hybrids ranged from 23.38% (hybrid no. 6) to 27.42 (hybrid no. 5) with over hybrids mean equal to 25.75%. Two hybrids i.e. no. 6 and no. 10 recorded significantly lower Brix than that of check variety. Also, hybrid no. 6 recorded significantly lower Brix than that of over hybrids mean while hybrid no. 6 recorded Brix statistically lower than those of check variety and over hybrid's mean. The other evaluated hybrids recorded Brix value statistically similar to that of either check variety or over hybrid's mean. The data in Table (4) showed that Brix values among clones within hybrid no. 10 was equal and this means that the variation in Brix do not found in this hybrid and the selection for this traits cannot have applied in this hybrid. Furthermore, the lowest variation was found in hybrid no. 9 and the highest variation was found in hybrid no. 7. Selection for improving Brix could be effective in hybrids no. 1, 2, 3, 4, 5, 7 and 8 which Brix value similar to that of check variety and over hybrids mean and expectable variation. This results were in line with those obtained by Tena *et al*., 2016;Abu-Ellil *et al,* 2018 and Reddy *et al*., 2020.

2. Genetic parameter

2.1. Genotypic, environmental variance and phenotypic variance

Data presented in Table (5) indicated that genotypic variance represented 84.10%, 67.79%, 75.85%, 86.68%, 68.85% and 88.25% from the phenotypic variance for stalk height, stalk diameter, stalk number/stool, stalk weight, stool weight and Brix, respectively. While, the corresponded percentage for this traits for environmental variance were 15.90%, 32.21%, 24.15%, 13.32 %, 31.15% and 11.75% from that of phenotypic variance. It is obvious from these data that a great part of phenotypic variance due to genotypic variance while the participation of environmental variance was little indicating the effect of the

environmental factors on the expression of the studied traits phenotype was low and the improvement of these traits in seedling stage through selection should be freely easy. This due to the close correspondence between the genotypes and the phenotypes. These results were in agreement with those reported by Shanthi *et al*. (2008).

2.2. Variation, heritability and genetic advance

Data shown in Table (5) revealed that the phenotypic coefficient of variation (PCV) was high for stalk number/stool, stalk weight and stool weight, moderate for stalk weight and low for stalk diameter and Brix. The genotypic coefficient of variation (GCV) for all studied traits was higher than environmental coefficient of variation. The high GCV and PCV for stalk number/stool, stalk weight and stool weight indicated that selection could be effective based in these traits. Consequently, their phenotypic expression would be good indication of the genotypic potential. The high obtained values of G.C.V and P.C.V. were accordance with those illustrated by Abu- Ellil *et al.,* 2018, especially for stalk weight and its number.

Table 5. Variation, heritability and genetic advance of ten hybrids for all studied treats:

	Stalk height, cm	Stalk diameter, cm	Stalk number/ stool	Stalk weight, kg	Stool weight, kg	Brix%
Maximum	390	3.00	35.00	2.780	49.700	30.500
Min	135	1.2	1.000	0.062	0.1860	19.00
Grand Mean	262.34	2.27	8.2862	1.213	9.9995	25.7580
SE	23.46	0.1450	2.4611	0.2025	3.4505	0.9282
CD 5%	65.19	0.4029	6.8374	0.5625	9.5860	2.5786
CD 1%	85.78	0.5302	8.9978	0.7402	12.6148	3.3934
Env.V	1651.78	0.0631	18.1714	0.1230	35.7172	2.5845
Gen.V	8737.57	0.1328	57.0732	0.8002	78.9303	19.4105
Phen.V	10389.30	0.1959	75.2446	0.9232	114.6475	21.9950
E.C.V	15.49	11.0423	51.4438	28.9098	59.7667	6.2413
G.C.V	35.85	16.0200	91.1708	73.7445	88.8470	17.1043
P.C.V.	38.85	19.4572	104.6832	79.2097	107.0787	18.2074
H	84.10	67.79	75.85	86.68	68.85	88.25
GA1	176.5894	0.6181	13.5538	1.7156	15.1855	8.5259
GA2	67.3123	27.1720	163.5688	141.4316	151.8623	33.0999

CD : critical difference, H: the broad sense heritability, GA1: genetic advance in units, GA2: genetic advance as a percentage of the grand mean.

Tadesse *et al*. (2014) reported that selection might be effective based on the traits with high and low GCV and PCV values with consideration of heritability estimates.

High broad sense heritability estimates were found for stalk height, stalk diameter, stalk number, stalk weight, stool weight and Brix (Table 4). Implying the possibility of improvement of these traits through family selection. Mohamed (2007) reported high heritability for stalk diameter, stalk weight and Brix. The differences in heritability estimates among various studies, might be due to the different genetic materials used in each study.

Genetic advance under selection refers to the improvement of trait in genotypic value under one cycle of selection at given selection intensity and the improvement depend upon genetic variability, heritability and selection intensity. Estimates of genetic advance of the six studied traits at 5% selection intensity shown in Table (5) indicated that low genetic advance was recorded for stalk diameter and Brix, moderate genetic advance observed for stalk height and high genetic advance for stalk number/stool, stalk weight and stool weight. High heritability accompanied by high genetic advance for stalk number/stool, talk height and stool weight was observed. The linkage of high heritability with high genetic advance is due to additive gene action and these traits could be easy to improve through selection (Sanghera *et al*., 2015 and Hiremath and Nagaraja, 2016).

General conclusion

The present results revealed that the applying selection among sugarcane hybrids would more effective than the selection within hybrids(families belong the same hybrid), suggesting the selection among hybrids followed by selection within selected hybrids would increase selection efficiency and offer powerful way to improve the yield and quality of sugarcane.

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استنباط وتقييم أداء بعض هجن قصب السكر للكشف عن التراكيب المتفوقة

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الملخص

أجريت الدراسة الحالية في حقل التربية بمعهد بحوث المحاصيل السكرية، مركز البحوث الزراعية، الجيزة، مصر، خلال عامي ٢٠١٨/٢٠١٩ و ٢٠٢٠/٢٠١٩ لتقييم أداء عشر هجن مع الصنف التجاري (GT 54/9) للكشف عن التراكيب الوراثية المتفوقة. تم إستخدام تصميم القطاعات كاملة العشوائية بإستخدام ثلاث مكررات. تم تسجيل متوسط ومدى إرتفاع الساق، وقطر الساق، وعدد السيقان / للجورة، ووزن الساق، ووزن الجورة، والبركس لكل هجين. بالإضافة إلى التراكيب الوراثية داخل كل هجين. كما تم تقدير معامل التباين الوراثي (GCV) ومعامل التباين المظهري (PCV) وأيضا درجة التوريث والتقدم الوراثي.

أشارت النتائج إلى أن الانتخاب بين الهجن المُقيمة سيكون أكثر فاعلية من تطبيق الانتقاء داخل الهجن، كما أن الإنتخاب بين الهجن متبوعًا بإنتخاب التراكيب الوراثية داخل الهجن المنتخبة سيزيد من كفاءة الإنتخاب.

وفقا للقيم العالية والتباين العالي للصفات المدروسة ، أظهرت النتائج أن الهجن مثل CP.63-35 X CP.46-115، CP.57-614 x Co 617، Co.1129 x G.73-211، Co.744 X Bo.19، CP.67-412 x G.73-211 و H.86-37 X Co.617 كانت الأفضل لتحسين سمك الساق. علاوة على ذلك ، الهجن Co.744 X Bo.19، CP.67-412 X G.73-211 و H.86-37 X Co.617 أثبتت أنها أفضل الهجن لتحسين وزن الساق. الهجين CP.63-35 XCP.46-115 أظهر أنه الأفضل لتحسين عدد السيقان ووزن الجورة. وكان الإنتخاب لتحسين مستوى البركس فعالاً في الهجن مثل: Co.284 xCP.44-101، CP.63-35 X CP.46-115، CP.57-614 x Co. 617، Co.1129 x G. 73-211، CP.63-35 X SP.81-1763، CP.57-614 X CP.44-101 و Co.284 X CP.57-614.

أظهرت النتائج أيضًا أن جزءًا كبيرًا من التباين المظهري كان بسبب التباين الوراثي لجميع الصفات المدروسة، مما يعني أن تحسين هذه الصفات سيكون أمرًا سهلاً. وتم الحصول على أعلى قيم GCV وPCV لصفة عدد السيقان /الجورة ووزن الساق ووزن الجورة مما يشير إلى أن الانتخاب لهذه الصفات يمكن أن يكون فعالًا.

وأشارت النتائج الى ارتفاع درجة التوريث بمعناها العريض لجميع الصفات المدروسة. ومع ذلك فقد تم تسجيل تقدم وراثي منخفض لقطر الساق والبركس، ومتوسط لارتفاع الساق ومرتفع بالنسبة لعدد السيقان / للجورة ووزن الساق ووزن سيقان الجورة.