GENETIC VARIANCE, HERITABILITY AND GENETIC GAIN FROM SELECTION IN A YELLOW MAIZE POPULATION

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ABSTRACT: *The objective of this research was designed to assess the expected improvement of grain yield and other valuable agronomic traits in Gemmeiza yellow maize population (EV-2), through S1 progeny selection method. A total of 256 S1 random families were selected in 2000 season at Gemmeiza Research Station, and evaluated at Sakha and Gemmeiza Research Stations during the summer season of 2001. Data of each location and combined indicated that the average performance for grain yield was ranged from 3.17-32.91, 0.89-32.80 and 3.35-32.86 at Sakha, Gemmeiza and combined, respectively. However, all other studied traits were varied with the same pattern. However, the combined data indicated that the percentage of increase or decrease in the average performance of the selected families based on 10% selection intensity was 52, 48.9, -5.9, -16.3 –21.8 and 11.5% for grain yield per fad and per plant, number of days to 50% silking plant and ear height and resistance to late wilt, respectively. Estimates of phenotypic ($\sigma 2ph$) and genotypic ($\sigma 2g$) variances were significant for all studied traits at both locations and combined. The magnitude of $\sigma 2g$ was high for all studied traits in both locations and combined. It constitutes the major part of $\sigma 2ph$ for all studied traits. Heritability estimates were generally high for all studied traits at both locations and when data were combined over locations, except late wilt resistance (45.9 and 43.2 %) at Gemmeiza and in the combined data, respectively. Expected genetic gain from selection of the best 10% families was high and in the better direction for all studied traits indicating that this population could be considered as the best source for inbred lines isolation which could be utilized as a good material in hybrid breeding program.*

Key words: Maize, selection, genetic variance, Heritability, Genetic gain.

INTRODUCTION

Present attempts to increase maize (Zea mays L) production in Egypt seem to provide an excellent opportunity for populations improvement that are considered the backbone of breeding programs around the world. By inter- and intra-population improvement, the improved population(s) could be utilized per se as a new variety or used it as a source of new inbred lines for developing new high yielding hybrids.

S1 families' recurrent selection is widely used as an easy and simple procedure for intra-population improvement in maize. Evaluation of selected

lines (families) per se, however, allows measuring the breeding values of individuals of population without the masking effect of testers on the genotype being tested. In this respect, Genter (1971&1973), Dawoud (1984), Ismail et al (1984), Aboul-Saad et al (1989), Getschman and Hallauer (1991), El-Agamy et al (1992), Barakat (1998) and Mahmoud et al (1999) reported that selection based on S1 progeny performance is effective for selecting additive genetic effects and presents an opportunity for selection against major deleterious recessive genes that become homozygous with breeding.

Theoretically, selection based on S1 is expected to utilize additive genetic variance better than intra-population selection methods as reported by Hallauer and Mirenda (1981), Tanner and Smith (1987), Soliman (1991) and Mahmoud et al (1999). In this respect, Sulivan and Kannenberg (1987), Soliman (1991), and Aboul-Saad et al (1994) found a linear genetic gain for yield and other traits through two to eight cycles of S1 selection.

Heritability estimates from S1 families are higher than the other selection procedures because the component of genetic variance is mostly additive genetic effects. However, heritability estimates differed according to populations (genetic variance), characters, selection methods and environmental conditions as reported by, Adara and Kannenberg (1981), Abdalla et al (1984), Coors (1988), Aboul-Saad et al (1989), Soliman (1991), Walter et al (1991), El-Agamy et al (1992), Barakat (1998) Mahmoud et al (1999).and Vales et al (2001).

The genetic gain upon selection is considered among the most important contributions of quantitative genetic to maize breeders. Burten et al (1971), Mulumba et al (1983), Smith (1983), Sullivan and Kannenberg (1987), Soliman (1991), Aboul Saad et al (1994), Barakat (1998) and Mahmoud et al (1999) reported that change in genetic variance resulting from S1 selection for grain yield and some other yield components was related to the observed change with a significant average increase in population mean.

Heritability estimates were differed according to population, characters, selection methods and environmental factors. However, heritability estimated from S1 families was higher than that estimated from other selection methods (Hanson, 1963, Adara and Kannenberg, 1981, El-Kady et al 1983, Abdalla et al 1984, Walter et al 1991, El-Agamy et al 1992 and Barakat, 1998). This is due to that S1 selection utilizes additive genetic effects as reported by Genter (1971), Embig et al (1972) and Goulas and Lonnquist (1977).

The recent investigation was designed and carried out to provide information about genetic variance, heritability estimates and expected genetic gain used to improve Gemmeiza yellow maize population (C-2) for grain yield and some other agronomic traits.

MATERIALS AND METHODS

The present investigation was implemented in population Gemmeiza yellow maize population (C-2). This population was constructed (1987) at Gemmeiza Agriculture Research Station and this composed from two groups first one eight yellow maize genotypes, pool-33, pop-34, Giza-2, 4-T-2, pop-45-C_3, pop-31, Black see star (from turkey) and syn-73, second one B-ss- syn and yellow suptropical maize population (IITA) after two cycles improvement by recurrent selection methods, Half-sib and S_1 per se. Two cycles were completed at Gemmeiza Research Station to improve the maturity (to be earlier), plant height (to be shorter), average productivity and resistance to late wilt disease (Cephalosporium maydis).

In 2000 season, approximately 300 random plants were self pollinated at the breeding disease nursery of Gemmeiza. At harvest, a total of 256 selfed ears (S_1) with sufficient seed sitting were selected to plan the desired replicated yield trials and remnant seed were kept for the subsequent studies.

In 2001 summer season, the 256 S_1 progenies were evaluated In two (16 x 16) simple lattice yield trials with two replications at Sakha and Gemmeiza Research Stations, FCRI, ARC. Entries in both locations were grown in single-ridge plots, 6 m long and 80 cm width between ridges with plant spaced 25 cm between hills within the ridge. Hills were· thinned to one plant per hill before the first irrigation, providing 21000 plant per faddan (one faddan = 4200 m^2). Agronomic practices including adding fertilizer in recommended doses, weed and pest control were followed as recommended at the proper time to promote high productivity. Data were recorded for number of days to 50% silking, plant height (cm), ear height (cm), resistance to late wilt (%), grain yield per plant (g) and grain yield in ardabs/fad adjusted to 15.5 % grain moisture content (one ardab = 140 kg).

Its worth noting that the efficiency of the simple lattice design used in these trials was not much different from that of a randomized complete blocks design, therefore, the analysis of variance of the data for separate locations and combined were made assuming a RCBD according to Snedecor and Cochran (1967) (Table 1).

Table 1. Analysis of variance of 256 S_1 families for separate locations and combined.

S.O.V.	DF	MS	Expected mean squares
		Separate location	
Rep's (R)	1		
Genotypes (G)	255	MS_2	$\sigma^2_e + r\sigma^2_g$
Error	255	MS_1	σ^2_e
		Combined	
Locations (L)	1		
Genotypes (G)	255	MS_3	$\sigma^2_e + r\sigma^2_{gl} + rl\sigma^2_g$
G x L	255	MS_2	$\sigma^2_e + r\sigma^2_{gl}$
Pooled error	510	MS_1	σ^2_e

* σ^2_e , σ^2_g and σ^2_{gl} are experimental error, S_1 family and S_1 family x locations variances, respectively,

Bartelett test (Snedecor and Cochran 1967) for the homogeneity of error variance was calculated between the error mean squares of the two locations and found to be insignificant; therefore, combined analysis had been done for all studied traits. Based on the combined data, the components of variance were estimated by equating the mean squares to mean square expectations according to Hallauer and Miranda (1981) (Table 1).

According to the expected mean squares in Table (1), the following estimations were calculated:

$$\sigma^2_g = (Ms_3 - Ms_2)/rl \qquad \sigma^2_{gl} = (Ms_2 - Ms_1)/r \text{ (for combined)}$$

The phenotypic variance (σ^2_{ph}) of S_1 family means was estimated as:

$\sigma^2_{ph} = \sigma^2_g + \sigma^2_e/r$ (for one location)

$\sigma^2_{ph} = \sigma^2_g + \sigma^2_{gl} + \sigma^2_e/rl$ (for combined over locations)

Heritability in broad sense (h^2) was calculated as

$h^2 = (\sigma^2_g / \sigma^2_{ph}) \times 100$

Expected gain from selection (∆G) was calculated as:

$$\Delta G = \frac{k}{x} \cdot \frac{\sigma_g^2}{\sigma_{ph}^2} \times 100$$

where k is the standard selection differential (1.755) at 10% selection intensity and x is the general means of lines.

RESULTS AND DISCUSSION

Mean squares for analysis of variance at the two locations and its combined (Table-2) showed highly significant differences among the 256 S_1 families for all studied traits at Sakha, Gemmeiza and the combined data. The interaction effects of S_1 families with locations (environments) was also highly significant respecting all studied traits, except plant and ear height. Coefficient of variation (%) for all traits was relatively small or medium, indicating the homogeneity of soils at each location and greater minute in collecting data. However, comparing the magnitude of error mean squares for different traits at the two locations revealed that there was homogeneity between error mean squares in few traits, so the separate location as well as combined data were used herein.

Data in Table (3) show that grain yield fad ranged from 3.17-32.91, 0.89-32.80 and 3.35-32.86 ardab fad at Sakha, Gemmeiza and combined, respective-ely. The average grain yield was 15.31 ± 0.31, 10.68 ± 0.27 and 12.99 ± 0.27 ardab fad at the same locations and combined, respectively. However, average grain yield and its range were higher at Sakha than at Gemmeiza, indicating that Sakha location had more favorable environmental conditions than Gemmeiza. The same trend was observed In case of grain yield/plant. Respecting flowering date, It was noticed that the tested families were earlier at Sakha than at Gemmeiza with an average days to 50% silking by 60.7 ± 0.14, 62.1 ± 0.17 and 61.4 ± 0.14 days at both locations and combined, respectively. The average plant height at Sakha, Gemmeiza and combined was 209.5 ± 1.36, 189.5 ± 1.12 and 199.5 ± 1.16 cm, respectively. Also values of ear height at the same locations and combined were 113.3 ± 1.00, 102.0 ± 0.76 and 107.7 ± 0.82 cm, respectively. For resistance to late wilt disease, mean percentage of resistance at Sakha (92.4 ± 0.58%) was somewhat higher than at Gemmeiza (84.6 ± 0.91 %). The range at Gemmeiza (26.7 to 100.0) was wider than that at Sakha (50.5 to 100.0). These results indicated clearly that the selection for resistance to late wilt disease would be more effective when practiced on the basic data obtained at Gemmeiza location. Moreover, plants of the S_1 families tended to be earlier and taller with somewhat higher ear placement at Sakha than at Gemmeiza location.

Table 2. Mean squares for grain yield and other agronomic traits among 256 S_1 families evaluated at Sakha, Gemmeiza and their combined, in 2001 season.

S.O.V.	d.f.	Grain yield per faddan	Grain yield per plant	Days to 50% silking	Plant height	Ear height	Late wilt resistant
				Mean squares			
SAKHA							
Rep's	1	1.13	128.8	0.20	366.2	6.1	1.89
S1 families	255	50.49**	2101.9**	9.46**	940.2**	515.3**	174.48**
Error	255	0.89	179.6	3.05	163.7	109.8	33.39
C.V.(%)		6.17	11.9	2.88	6.10	9.24	6.25
GEMMEIZA							
Rep's	1	0.05	19.3	3.28	58.5	3195.0	6611.1
S1 families	255	38.20**	2127.4**	14.15**	646.6**	297.7**	419.1**
Error	255	0.81	40.2	3.83	192.7	107.1	206.0
C.V.(%)		8.43	7.4	3.15	7.3	10.2	16.9
COMBINED							
Locations (L)	1	5489.1**	176402.6**	568.5**	10312.3**	33180.9**	15749.5**
Rep (L)	2	0.6	74.1	1.7	212.3	1600.6	3306.5
S1 families	255	74.8**	3526.7**	19:2**	1384.3**	691.8**	420.6**
L x S1	255	13.9**	702.6**	4.4**	202.5	121.3	172.9**
Pooled error	510	0.9	109.9	3.4	178.2	108.4	119.7
C.V.(%)		7.0	10.6	3.0	6.7	9.67	12.4

** refer to highly significant differences, at 1% level of propability.

Table 3. Mean performance and range among 256 S_1 families, and mean of the selected families at the two locations and combined, in 2001 season.

Characters	Locations	256 S_1 families		C.V %	LSD 5%	% of families ≤ mean	Means of selected families
		Mean	Range				
Grain yield (ard/fed)	Sakha	15.31 ± 0.31	3.17 – 32.91	6.17	2.42	38.3	29.1
	Gemmeiza	10.68 ±0.27	0.89 – 32.80	8.43	2.30	37.5	17.9
	Combined	12.99 ± 0.27	3.35 – 32.86	7.23	2.54	40.6	19.8
Grain yield (g/plant)	Sakha	112.2 ± 2.03	33.2 –245.7	11.95	34.31	40.6	166.9
	Gemmeiza	85.9 ± 2.04	19.2 –204.0	7.37	16.23	40.6	136.5
	Combined	99.03 ± 1.86	34.4 –224.8	10.59	18.98	39.8	147.5
Days to 50% silking	Sakha	60.7 ± 0.14	55.5 – 67.0	2.88	2.29	57.0	57.1
	Gemmeiza	62.1 ± 0.17	57.0 – 72.0	3.15	2.63	50.0	57.9
	Combined	61.4 ± 0.14	56.0 – 68.5	3.02	1.75	52.3	57.8
Plant height (cm)	Sakha	209.5 ± 1.36	147.5-269.5	6.10	13.37	52.7	171.8
	Gemmeiza	189.5 ± 1.12	141.5-237.5	7.32	14.63	53.5	158.9
	Combined	199.5 ± 1.16	142.0-247.3	6.69	9.91	50.8	166.9
Ear height (cm)	Sakha	113.3 ± 1.00	63.0 – 159.0	9.24	3.37	52.3	86.0
	Gemmeiza	102.0 ± 0.76	68.5 – 137.5	10.15	3.72	48.4	81.0
	Combined	107.7 ± 0.82	67.5 – 144.5	9.67	2.51	48.4	84.2
Late wilt resistance (%)	Sakha	92.4 ± 0.58	50.5 – 100.0	6.25	12.11	66.4	100.0
	Gemmeiza	84.6 ± 0.91	26.7 – 100.0	16.97	14.65	60.2	100.0
	Combined	88.5 ± 0.64	57.2 – 100.0	12.36	9.50	60.9	100.0

The percentage of families which were equal to or better than the mean performance of S_1 progenies (Table-3) was approximately equal for all studied traits at both locations. However, number of S_1 families exhibited the lowest ear placement and the highest grain yield was higher at Sakha than that at Gemmeiza location. Based on the combined data, the percentage of S_1 families equal to or better than average of all families was high in all studied traits (40.6, 39.8, 52.3, 50.8, 48.4 and 60.9%, for grain yield per faddan and per plant, days to mid silk, plant height, ear height and late wilt resistance, respectively (Table 3). Using selection intensity of 10 %, grain yield and late wilt resistance could be used as selection criteria in the improvement of this population, since it possessed the highest frequency of the best families. In this respect, Soliman (1991), found similar results but Abdalla *et al* (1984)

reported that the distribution of selected families did not represent the 10 percent highest yielding families under their studies.

Estimates of phenotypic (σ^2ph) and genotypic (σ^2g) variances were significant for all studied traits at both locations and their combined over locations (Table 4).

Table 4. Components of variance, heritability estimates (h^2 %) and expected genetic gain (ΔG %) from selection for grain yield and other traits at Sakha, Gemmeiza and combined data, in 2001 season.

Characters	Locations	σ^2ph $\pm$ SE	σ^2g $\pm$ SE	σ^2gl $\pm$ SE	h^2 %	ΔG (%)
Grain yield (ard/fed)	Sakha	27.47 $\pm$ 2.23	24.80 $\pm$ 2.23	---	90.27	58.87
	Gemmeiza	20.79 $\pm$ 3.30	18.69 $\pm$ 1.68	---	89.94	58.30
	Combined	24.44 $\pm$ 1.65	15.24 $\pm$ 1.86	6.51 $\pm$ 0.61	62.28	9.78
Grain yield g/plant	Sakha	1144.3 $\pm$ 92.7	961.2 $\pm$ 93.4		84.0	47.82
	Gemmeiza	1157.6 $\pm$ 155.6	1043.6 $\pm$ 93.9		90.2	58.67
	Combined	1150.9 $\pm$ 77.8	706.0 $\pm$ 89.3	296.4 $\pm$ 31.7	61.4	7.97
Days to 50% silking	Sakha	5.19 $\pm$ 0.42	3.21 $\pm$ 0.46	---	61.6	8.79
	Gemmeiza	7.74 $\pm$ 0.85	5.16 $\pm$ 0.67	---	66.6	17.25
	Combined	5.86 $\pm$ 0.42	3.70 $\pm$ 0.51	0.50 $\pm$ 0.29	63.2	11.18
Plant height (cm)	Sakha	470.1 $\pm$ 61.1	388.3 $\pm$ 41.5	---	82.6	45.35
	Gemmeiza	354.3 $\pm$ 62.6	226.9 $\pm$ 96.4	---	64.1	12.76
	Combined	399.5 $\pm$ 30.5	295.5 $\pm$ 33.0	12.2 $\pm$ 14.3	73.9	30.18
Ear height (cm)	Sakha	281.4 $\pm$ 22.7	202.8 $\pm$ 23.7	---	72.1	26.83
	Gemmeiza	163.6 $\pm$ 30.5	95.3 $\pm$ 14.7	---	58.3	2.54
	Combined	201.8 $\pm$ 15.3	142.6 $\pm$ 17.0	6.5 $\pm$ 8.6	70.7	24.37
Late wilt resistance (%)	Sakha	95.2 $\pm$ 7.7	70.6 $\pm$ 7.9	---	74.1	30.40
	Gemmeiza	232.0 $\pm$ 18.6	106.5 $\pm$ 22.5	---	45.9	80.80
	Combined	143.4 $\pm$ 9.3	143.4 $\pm$ 9.30	26.6 $\pm$ 10.7	43.2	76.03

The magnitude of σ^2g was generally high for all studied traits in both locations and when data were combined over locations and constitute the major part of σ^2ph except for late wilt resistance at Gemmeiza. These results reflected the presence of wide genetic diversity among the S_1 families, and that can be attributed to the fact that this population is a composite of ten different sources of widely divergent origin. In addition, genotype x location interaction variance (σ^2gl) was also significant for all studied traits, indicating that the behavior of S_1 families differed under different environmental conditions. However, data showed that σ^2gl values were lower than σ^2g

values for all studied traits except late wilt resistance, which had the highest $\sigma^2 gl$ values. This indicates that late wilt resistance was more affected by environmental conditions than the other traits. Similar results were obtained by El-Rouby *el al* (1979), Adara and kannenberg (1981), El-Nagouly *et al* (1981), Ismail *et al* (1984), Shehata, *et al* (1987), Aboul- Saad *et al* (1989 and 1994), Dhillon and Khera (1989), Soliman (1991), Walter *et al* (1991) and El-Agamy *et al* (1992).

Broad sense heritability (h^2) estimates (Table 4) were relatively high for all studied traits at both locations and when data were combined over locations with few exceptions. Lower heritability values were obtained for silking date, ear height and percent of late wilt resistance at Sakha location. Silking date, plant and ear height as well as late wilt resistance exhibited moderately low values of broad sense heritability. The lowest estimates of broad sense heritability in case of the combined data for late wilt resistance (43.2%) than those obtained from Sakha (74.09%) and Gemmeiza (45.91%) was attributed to high values of $\sigma^2 gl$ (26.60). However, heritability estimates for days to mid silking, plant height and late wilt resistance were relatively close to each other at both locations. For grain yield and ear height, heritability estimates were somewhat high at Gemmeiza and Sakha, respectively. Embig *et al* (1972) suggested that the expected values of $\sigma^2 g$ would be equal to additive genetic variance (σ^2_A) if dominance and/or epistasis were lacking in the population or when gene frequency for the segregating loci is equal to 0.5. In this respect, heritability estimates obtained from the combined data over two locations will be more reliable than that obtained from data of single location. In addition, high heritability estimates for the studied traits indicate that selection based on the mean performance of S_1 families would be successful tool in improving this population. Similar results were reported by Dudlel and Moll (1969), Darrah *et al* (1972), El-Rouby *et al* (1979), El-Kady *et al* (1983), Abdalla *et al* (1984), Sadek *et al* (1988), Aboul-Saad *et al* (1989 and 1994), Soliman (1991) and Walter *et al* (1991).

Estimates of the expected genetic gain (%) from selection of the best 10% of the families for the two characters (grain yield and LWR %) which were used as selection criteria through S_1 progeny selection at each location and when the data were combined over locations are presented in Table 4. Expected genetic gain was 58.87, 58.30, and 9.78 % for grain yield and 30.40, 80.80 and 76.03 % for LWR at Sakha, Gemmeiza and combined data. These gains were of higher values than those of the other traits. This result attributed directly to the presence of more addition genetic variance. Genter (1971), and Horner *et al* (1973) suggested that gain achieved from S_1 progenies would directly result from the increase in frequency of genes with additive effects. Smith (1983), Shehata *et al* (1984), Sulivan and Kannenberg (1987), Walter *et al* (1991) and Aboul -Saad *et al* (1994) for grain yield, and Abdalla *et al* (1984), Shehata *et al* (1987), Sadek *et al* (1988) and Soliman (1991) for grain yield and late wilt resistance. They reported that genetic gain

when selecting the superior S_1 progenies was higher than that in the original population.

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التباين الوراثي ودرجة التوريث والتحسين الوراثي المتوقع من الانتخاب في عشيرة من الذرة الشامية صفراء الحبوب

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أجرى هذا البحث بهدف تقدير التحسين الوراثي المتوقع لمحصول الحبوب وبعض الصفات الزراعية الأخرى في " مجتمع الجميزة الأصفر" (EV-2) وذلك بطريقة الانتخاب بين عائلات الجيل الذاتي الأول (S₁ family selection). ففي موسم ٢٠٠٠ تم تكوين ٣٠٠ عائلة ذاتية التلقيح (S₁) بمحطة البحوث الزراعية بالجميزة، أنتخب منها أفضل ٢٥٦ عائلة ذاتية تحتوي كيزاتها على كمية كافية من الحبوب وتم تقييمها في الموسم التالي ٢٠٠١ في تجربتين حقليتين بمحطتي البحوث الزراعية بسخا والجميزة. أوضحت نتائج تحليل التباين المشترك للجهتين كلا على حـده أن متوسط محصـــــول الحبوب تراوح ما بين ٣٢,٩١-٣,١٧ ، ٣٢,٨٠-٠,٨٩ ، ٣٢,٨٦-٣,٣٥ إردب للفدان في محطتي سخا والجميزة والتحليل المشترك على الترتيب في العائلات المقيمة مما يدل على جدوى التحسين في هذا المجتمع. كما تباينت الصفات الأخرى موضع الدراسة بنفس المعدل تقريبا ، وقد دل تحليل التباين المشترك على أن متوسط الصفات موضع الدراسة قد تحرك بالزيادة في صفات محصول حبوب الفدان والنبات وكذا نسبة المقاومة للذبول المتأخر عند استخدام (١٠%) كثافة انتخابية بمقدار ٥٢% ، ٤٨,٩% ، ١١,٥% على الترتيب. كما أن صفات عدد الأيام حتى ظـهور ٥٠% من الحراير وارتفاع النبات والكوز عند نفس الكثافة الانتخابية قد نقصت أو انخفضت بمعدلات ٥,٩% ، ١٦,٣% ، ٢١,٨% على الترتيب وكان تقدير التباين المظهري والوراثي معنويا لجميع الصفات موضع الدراسة في كلا الجهتين وعلى مستوى التحليل المشترك، وقد وجد أيضا أن قيمة التباين الوراثي كانت عالية وأنها تمثل الجزء الأكبر من التباين المظهري وذلك لجميع الصفات موضع الدراسة. وكانت تقديرات النسبة المئوية للتوريث بصفة عامة عالية لحد ما بالنسبة لجميع الصفات في الجهتين والتحليل المشترك. وقد وجد أن النسبة

المئوية للتحسين المتوقع من انتخاب افضل ١٠% من العائلات للصفات موضع الدراسة كانت عالية في الاتجاه الأفضل (ارتفاع محصول كل من الحبوب والنبات، والتبكير في التزهير، وانخفاض ارتفاع كل من النبات والكوز وارتفاع درجة المقامة لمرض الذبول المتأخر)، مما يؤكد صلاحية هذه العشيرة للتحسين المستمر وأن تكون قاعدة وراثية يمكن زراعتها في الأراضي الجديدة كما تصلح أيضا لإمكانية عزل سلالات نقية متفوقة يمكن أن تدخل في برامج التحسين لإنتاج هجن جديدة عالية المحصول.